

BIOGRAPHICAL SKETCH

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NAME: Hayes, Susan

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

POSITION TITLE: Postdoctoral Fellow

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 |
|---------------------------|---------------------------|-----------------------|-------------------------------|-------------------------------|
| Wake Forest University | BS | 08/2009 | 05/2013 | Engineering |
| Georgetown University | PHD | 08/2013 | 05/2019 | Molecular Biology |
| Michigan State University | Postdoctoral Fellow | 09/2019 | Present | Bioinformatics/ Immunology |

A. Personal Statement

My academic training and research experience have provided me with an excellent background in multiple biological disciplines including molecular biology, microbiology, biochemistry, and genetics. As an undergraduate, I conducted research with Dr. Xavier Factor on the mechanisms of action of a new class of antibiotics. As a predoctoral student with Dr. Tanti Auguri, my research focused on the regulation of transcription in yeast, and I gained expertise in the isolation and biochemical characterization of transcription complexes. I developed a novel protocol for the purification of components of large transcription complexes. I was first author of the initial description of the Most Novel Complex. A subsequent first author publication challenged a key paradigm of transcription elongation and was a featured article in a major journal. During my undergraduate and graduate careers, I received several academic and teaching awards. For my postdoctoral training, I will continue to build on my previous training in transcriptional controls by moving into a mammalian system that will allow me to address additional questions regarding the regulation of differentiation and development. My sponsor Dr. I.M. Creative is an internationally recognized leader in the transcription/chromatin field and has an extensive record of training postdoctoral fellows. The proposed research will provide me with new conceptual and technical training in developmental biology and whole genome analysis. In addition, the proposed training plan outlines a set of career development activities and workshops – e.g. grant writing, public speaking, lab management, and mentoring students – designed to enhance my ability to become an independent investigator. My choice of sponsor, research project, and training will give me a solid foundation to reach my goal of studying developmental diseases in humans. During my second postdoctoral year in Dr. Creative's lab, my father had a severe stroke that eventually ended his life. I was out of the lab for six months dealing with my father's incapacitating illness and end-of-life issues. This hiatus in training reduced my scientific productivity. I am confident this proposed research project and training plan will enhance my scientific portfolio and will help recuperate my scientific productivity. My long-term research goals involve becoming an independent researcher and developing a comprehensive understanding of key developmental pathways and how alterations in gene expression contribute to human disease.

1. **Hayes S**, Schneider K, Chen M, Auguri T. Rapid isolation and characterization of a novel transcription complex in *Saccharomyces cerevisiae* and its role in transcription elongation. *Journal of Cell Biology*. 2016; 128:770.

2. **Hayes S**, Auguri T. A tandem affinity purification tag approach allows for isolation of interacting proteins in *Saccharomyces cerevisiae*. *Proceedings of the National Academy of Sciences of the United States of America*. 2019; 98:151.
3. Yao M, Dionne CF, **Hayes S**, Murray GC. Up-regulation of *Drosophila* innate immunity genes in response to stress. *Science (New York, N.Y.)*. 2020; 304:1754.
4. **Hayes S**, Cescaloo Q, Murray GC. Structural analysis of *Drosophila* Rtc. *Nature*. Forthcoming 2021.

B. Positions, Scientific Appointments, and Honors

Positions and Scientific Appointments

| | |
|----------------|---|
| 2019 – Present | Postdoctoral Researcher, Michigan State University |
| 2015 – 2018 | Predocorial Fellowship for Minorities, Ford Foundation |
| 2013 – 2019 | Graduate Research Assistant, Georgetown University |
| 2012 – Present | Member, National Society for Bioinformatics and Biotechnology |
| 2010 – Present | Member, Association for Women in Science |
| 2010 – 2012 | Engineer, The IBeam Group Program |
| 2009 – Present | Member, Sigma Xi |

Honors

| | |
|-------------|--|
| 2013 | B.S. awarded with high honors, Wake Forest University |
| 2013 | Paula F. Laufenberg Award for best senior project in the Department of Engineering, Wake Forest University |
| 2013 | STAR award for public service in engineering, The IBeam Group |
| 2010 – 2011 | Scholarship, National Merit Scholarship Pr |
| 2009 – 2011 | Scholarship, Daughters of Hawaii Society |

C. Contributions to Science

1. **Early Career:** My early career contributions were focused on applying my knowledge of structural engineering to improving the design and integrity of tensile structures. More specifically, I worked with a team of engineers at the IBeam Group to develop concrete with a higher tensile strength that could be utilized in large structures such as suspension bridges. My particular role in the project was to identify candidate polymers, determine the ultimate tensile strength of these polymers, and make recommendations as to which polymer would afford concrete the most structural integrity under various stresses.
 - a. **Hayes S**, Janessa AJ. Redesigning the Golden Gate bridge. *National Undergraduate Symposium on Science and Engineering*; 2011; Baltimore, MD.
 - b. Lorentson C, **Hayes S**, Sauer N, Mehta S. Use of high-tensile concrete in cantilevered structures. *J Applied Engineering*. 2012; 63:413.
2. **Graduate Career:** My graduate research contributions focused on transcriptional gene regulation in *Saccharomyces cerevisiae*. Results from my research were highly relevant as they provided new details into the workings of complex biological systems and allowed for further extrapolations into the development of certain diseases and their progression. I originally developed a novel protocol for the purification of components of large protein complexes. A subsequent publication, in which I isolated and characterized a long sought-after transcription complex, challenged a key paradigm of transcription elongation and was a featured article in a major journal.
 - a. **Hayes S**, Schneider K, Chen M, Auguri T. Rapid isolation and characterization of the most novel transcription complex in *Saccharomyces cerevisiae* and its role in transcription elongation. *CSHL Meeting on Mechanisms of Eukaryotic Transcription*; 2015 August; Cold Spring Harbor, NY.
 - b. **Hayes S**, Schneider K, Chen M, Auguri T. Rapid isolation and characterization of a novel transcription complex in *Saccharomyces cerevisiae* and its role in transcription elongation. *Journal of Cell Biology*. 2016; 128:770.

- c. **Hayes S**, Auguri T. A tandem affinity purification tag approach allows for isolation of interacting proteins in *Saccharomyces cerevisiae*. Yeast Genetics and Molecular Biology Meeting; 2017 September; Seattle, WA.
 - d. **Hayes S**, Auguri T. A tandem affinity purification tag approach allows for isolation of interacting proteins in *Saccharomyces cerevisiae*. Proceedings of the National Academy of Sciences of the United States of America. 2019; 98:151.
3. **Postdoctoral Career:** As a postdoctoral fellow, my research has provided a compelling link between mutations arising in stress response proteins and the development of various autoimmune diseases in humans. Previous studies have shown dysregulation in the innate immune response lead to autoimmune diseases in humans. A few Rtc homologues have now been identified in humans and appear to play a role in the regulation of genes in the innate immune response. My research is focused on the transcriptional regulator Rtc from *Drosophila melanogaster*.
- a. **Hayes S**, Yager LN, Murray GC. Rtc is an essential component of the *Drosophila* innate immune response. Genetics. 2019; 145:884.
 - b. Yao M, Dionne CF, **Hayes S**, Murray GC. Up-regulation of *Drosophila* innate immunity genes in response to stress. Science. 2020; 304:1754.
 - c. **Hayes S**, Murray GC. Stress, flies, and videotape: the *Drosophila* stress response. Annual review of physiology. 2020; 346:223.
 - d. **Hayes S**, Cescaloo Q, Murray GC. Structural analysis of *Drosophila* Rtc. Nature. Forthcoming 2021.

Complete List of Published Work in My Bibliography:

<https://www.ncbi.nlm.nih.gov/myncbi/1VgYzYESn3Nke9/bibliography/public/>

D. Scholastic Performance

| YEAR | COURSE TITLE | GRADE |
|-----------------------|--|-------|
| GEORGETOWN UNIVERSITY | | |
| 2013 | Seminar in Molecular Biology | P |
| 2013 | Basic Biomedical & Biological Sciences | P |
| 2014 | Model Systems | P |
| 2014 | Statistics for the Life Sciences | P |
| 2014 | Current Topics in Molecular Genetics | P |
| 2015 | Ethics in Biological Research | CRE |
| 2015 | Biochemistry | P |
| 2015 | Physiology | P |
| 2016 | Seminar in Systems Biology | P |
| 2016 | Protein Chemistry | P |

Except for the scientific ethics course, Georgetown University graduate courses are graded P (pass) or F (fail). Passing is C plus or better. The scientific ethics course is graded CRE (credit) or NC (no credit). Students must attend at least seven of the eight presentation/discussion sessions for credit.