

## The Graduate School: Application for Admission

Submitted Date	AY App # <b>5971765</b>	Entry Quarter <b>Fall 2015</b>
Intended Status <b>Full-time</b>	Applied to TGS before <b>N</b>	
Last Name <b>Shimko</b>	First <b>Tyler</b>	Middle <b>Carter</b>
Prior Last Name	Birthdate <b>01/26/1993</b>	Gender <b>Male</b>

Program **IBiS- Biological Sciences: PHD (B15PH)**

Specialization **Genome Biology**

Cluster

JD/PhD **N** DPT/PhD **N** VEF **N** CIC **N** US Vet/Active Forces **N**

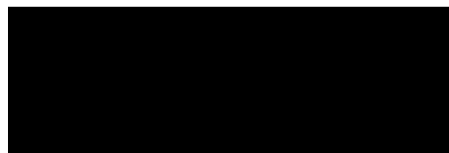
Ethnicity **White** Hispanic **N**

Citizenship **UNITED STATES** Visa

Citizenship Status **U.S. Citizen**

Country of Birth **UNITED STATES** Green Card #

Current Address



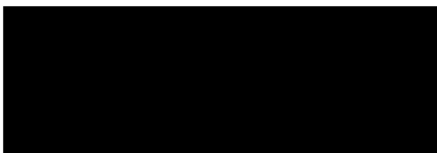
**UNITED STATES**

Primary Current Phone

Cell/Daytime Phone

Cur Phone Valid Until **05/01/2015**

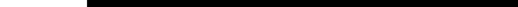
Permanent Address



**UNITED STATES**

Primary Perm Phone

Email



Email Valid Until **01/01/2099**

Previous Institution	From	To	Field of Study	Level	Degree	Date
Univ Utah	08/21/2011	05/05/2015	Biology	Undergraduate	US Bachelor of Science	

Cumulative UG GPA	<b>3.891</b>	Max UG GPA Scale	<b>4.000</b>
UG Junior/Senior Year GPA	<b>3.93</b>		
Cumulative Grad GPA		Max Grad GPA Scale	

---

Letters of Recommendation

1. **Erik** **Andersen**

2. **Leonid** **Kruglyak**

3. **Gillian** **Stanfield**

---

Are you interested in studying with specific faculty members? (List names below)

1. First Name **Erik** Last Name **Andersen**
2. First Name **Richard** Last Name **Morimoto**

---

Please indicate the highest level of education completed by your parent(s) or guardian(s) (the one or two people most responsible for raising you)

First individual's highest level of education completed: **Graduate or professional degree (ex: M.A. / Ph.D. / M.B.A. / M.**

If other, please explain:

Second individual's highest level of education completed: **Bachelor's degree or equivalent**

If other, please explain:

---

Language

Reading

Writing

Speaking

---

Self Reported Test Scores

GRE Gen	06/24/2014	Verbal	163	92	Quant	161	80	A.W.	5.0	93
GRE Sub								LSAT		
TOEFL								IELTS		
GMAT		Tot			Verb			Quant		
								A.W.		
								I.R.		
MCAT		Bioscience			Verbal			Physical Science		

---

Please list any honors you have been awarded

**Dean's List – All semesters**

**Myriad Academic Excellence Award – Spring 2014**

**Barry Goldwater Scholarship (Nationally competitive, research) – Spring 2013 Theodore Verender Hanks Scholarship – Spring 2013**

**University of Utah College of Science Dean's Scholarship – Spring 2013**

**Full Resident/Half Non-Resident Partial Tuition Waiver Scholarship (Merit-based) – Fall 2012-Spring 2014**

**Undergraduate Research Opportunities Program Assistantship – Spring 2012**

**Full Resident Partial Tuition Waiver Scholarship (Merit-based) – Fall 2011-Spring 2012**

---

Have you applied for or been awarded an external fellowship?

Yes ☒ No ☐ If yes, please specify;

**I have applied for the NSF-GRFP and the Hertz Fellowship. I have received a first round interview date for the Hertz, but have not been awarded either fellowship.**

---

Please describe your plans for the future.

**After completing my graduate study, I plan to pursue a career in research. As of yet, I am undecided whether this career will be in academic or industrial science. I hope to pursue a career where I can apply my mathematical and computational skills alongside my training and knowledge in the biological sciences. I am considering career paths specifically in the field of bioinformatics. I believe that bioinformatics will be critical for the future progression of the biological and health sciences and it is my goal to make major contributions to both of these fields.**

---

Other Universities Applied

1. School Drop Down **Stanford University**

5. School "other" **University of Washington**

2. School Drop Down **University of California- Los Angeles**

6. School "other" **UCSF**

3. School Drop Down **University of California-San Diego**

7. School "other"

4. School Drop Down

8. School "other"

---

Academic misconduct? Yes ☐ No ☒ Convicted of crime? Yes ☐ No ☒

If answered yes, applicant is asked to upload explanation. If uploaded, explanation will be attached to end of application PDF.

## Statement of Purpose (IBiS)

I first came to appreciate the power of biological research in my high school biology class. Through the instruction of my incredibly devoted teacher, I recognized that genomic research had the power to make predictions about and alter the traits of living creatures. Upon graduating from high school, I chose to attend the University of Utah, where, with the help of the school's Office of Undergraduate Research, I had an immediate opportunity to become deeply involved in research and pursue my interests to the fullest. Since beginning my undergraduate studies, I have been fortunate to take part in research at three universities across the United States and participate in projects ranging from molecular biology to neurobiology to quantitative genetics. Through these experiences my appetite for discovery has only grown. I now seek to undertake the next step in my scientific education, the pursuit of a PhD, to prepare myself for a career in research.

During my freshman year at the University of Utah, I joined the laboratory of Dr. Erik Jorgensen to assist in the construction of universal transgene insertion sites within the genome of *C. elegans*. My project eventually resulted in the creation of three distinct transgene landing sites. It was exhilarating to discover, create, and share knowledge with others. However, my exposure to the broader research community, through presentations at university-level events, alerted me that there were other opportunities to learn new skills and make significant contributions. To expand my research skill set, I sought summer internships in laboratories focused on computational methods in addition to molecular biology. I obtained an offer from Dr. Leonid Kruglyak, of Princeton University at that time.

In Dr. Kruglyak's lab I worked with Dr. Erik Andersen, a post-doctoral fellow. Dr. Andersen had previously completed a genomic mapping experiment wherein he had determined a region of the *C. elegans* genome that conferred resistance to the herbicide paraquat and enlisted my help to construct strains in an attempt to identify the causal genomic variations in that region. I explored different techniques, using both modern molecular biology and classical genetic crosses, to construct strains with which we could test the hypothesis that we had successfully identified causal genetic variants. Throughout the course of the summer, I supplemented my hands-on laboratory experience with instruction and practice with the computational methods that Dr. Andersen had employed in mapping experiments. This basic training in computer science and statistics eventually led me to take formal classes in these subjects at the University of Utah. These courses greatly expanded my research potential and prepared me to take on large projects with significant computational components. Dr. Andersen and I continued our collaboration in his new laboratory at Northwestern University in the following summers.

In the fall of 2012, I began a new project in the Jorgensen lab to identify suppressors of the phenotype associated with a mutant protein involved in synaptic vesicle endocytosis. I learned new techniques for the design and implementation of genetic screens and applied my new computational skills whenever possible. However, by the end of the academic year, it became apparent that the phenotype of interest was too weak for our suppressor screens to yield any useful information. While I was originally upset that our project and a year's worth of work were for naught, I quickly realized that failure is more of the rule than the exception in biological research. To continue toward a career in research, I would need to learn from failure and to fail gracefully. In fact, I learned that failure gives us many answers as well. In this respect, the year had not been wasted.

During my past two summers in Dr. Erik Andersen's lab, I have had the opportunity to explore how genetic variation dictates the way in which organisms respond to their environment. I sought to determine the ways in which the genetic variation present in the worldwide

## Statement of Purpose (IBiS)

population of the model nematode *C. elegans* affects responses to different chemicals including herbicides, pesticides, chemotherapeutic agents, and anthelmintics (compounds used to treat infections of parasitic nematodes). I helped to construct and optimize a high-throughput screening technique that allows us to measure the effects of the aforementioned compounds on nematodes in a multitude of ways. This pipeline has allowed us to conduct genome-wide association and linkage mapping studies. Over the past summer, I designed and built software to clean and process the data from our screening experiments and run statistical tests to map phenotypic differences to genetic variants. This software, *COPASutils*, has been published in the journal *PLoS ONE* and made freely available on the Comprehensive R Archive Network. My hope is that this software will gain widespread use in the model organism research community.

During my junior and senior years, I have worked in the lab of Dr. Gillian Stanfield at the University of Utah. My project has focused on identifying mutations that suppress premature sperm activation in male *C. elegans*. I carried out a series of crosses and positive phenotype selections as part of a genetic mapping scheme, and, at the end of my first year, several strains that displayed the suppressed phenotype were sent for sequencing in the hopes of being able to identify causal mutations. Now, in my second year in the lab, I am beginning to utilize raw genetic sequence and mapping data to identify variants implicated in suppression. Eventually this project may help to identify the causal mutation for each of the individual suppressed strains. This work will culminate in the publication of my honors thesis.

Most recently, I have become interested in the role of genomic sequence and regulation in cellular and organismal health. The genome encodes proteins and regulatory elements that work together to maintain the overall health and stability of an organism's cells, tissues, and organs. By understanding the forces acting upon the genome of an organism, we can better understand and predict the implications of new or dynamic environments. Many researchers at Northwestern are working to elucidate the molecular mechanisms encoded by or interacting with an organism's genome to influence its phenotype.

Primarily, I am interested in continuing my work with Dr. Erik Andersen to begin examining the role of gene-by-environment interactions on the determination of overall health and longevity using the model organism *C. elegans*. With Dr. Andersen's continued guidance, I am hopeful that I can make fundamental contributions to the understanding of these effects in metazoans. I am also interested in the work of Dr. Richard Morimoto, whose work has proved invaluable in the study of proteins in homeostatic maintenance. I believe that I could contribute my knowledge of genomics, computation, and statistics to further elucidate the regulatory pathways, starting with transcriptional control, that allow for the maintenance of homeostasis, especially in stressful environments. The work of Dr. Jason Brickner also interests me. Dr. Brickner's research group investigates the role of spatial positioning of cellular elements on the expression of specific genes. This work would give me the opportunity to investigate the effect of a non-genetic, non-environmental factor on the phenotypes of organisms and potentially draw predictive power from these findings. Additionally, I am interested in the work of Drs. Christian Petersen and Sadie Wignall, who have examined the regulatory pathways affecting regeneration and the molecular mechanisms responsible for faithful transfer of genetic information during cell division, respectively. I believe that the faculty at Northwestern will prepare me exceptionally well to begin a career in research and open my eyes to new and exciting scientific questions.



## Report Results

[Return](#)

University of Utah Unofficial Transcript

Name: SHIMKO, TYLER

Student ID: [REDACTED]

SSN: [REDACTED]

Birthdate: [REDACTED]

## HONORS AND AWARDS

Phi Eta Sigma Honor Society

## BEGINNING OF UNDERGRADUATE SEMESTER CAREER

TEST CREDIT	Earned Score
-------------	--------------

AP May 15, 2010 American History	6.000 4
AP May 15, 2011 Biology	6.000 5
AP May 15, 2011 Chemistry	8.000 5
AP May 15, 2011 Language/Comp	6.000 4

## Fall 2011

ANTH 2040 Anthropology of Humor	3.00 3.00 A
Diversity & Soc/Beh Sci Explor	
CHEM 2308 Online Prep Org Chem	1.00 1.00 A
CHEM 2310 Organic Chemistry I	4.00 4.00 A
CHEM 2315 Organic Chemistry Lab I	2.00 2.00 A
MATH 1050 Coll Alg	4.00 4.00 A

Quantitative Reasoning (Math)

Term GPA: 4.000	14.000 14.000
-----------------	---------------

Dean's List

## Spring 2012

BIOL 2010 Evol & Div of Life	3.00 3.00 A-
CHEM 2320 Organic Chemistry II	4.00 4.00 A
CHEM 2325 Organic Chem Lab II	2.00 2.00 A
MATH 1060 Trig	3.00 3.00 A-

Quantitative Reasoning (Math)

PRTS 1420 NR-Ski Alpine	2.00 2.00 CR
UGS 4800 Undergrad Research UROP	1.00 1.00 A

Term GPA: 3.862	15.000 15.000
-----------------	---------------

Dean's List

## Fall 2012

BIOL 2030 Genetics	3.00 3.00 A
BIOL 3510 Biological Chemistry I	3.00 3.00 B+
BIOL 5110 Molec Biol/Gen Eng	3.00 3.00 A-
HONOR 2102 Honors Core in Int Trad	3.00 3.00 A

Humanities Exploration

MATH 1170 Calc Biol I	4.00 4.00 A
-----------------------	-------------

Quant Reas (Math & Stat/Log)					
-----					
Term GPA: 3.813		16.000	16.000		
Dean's List					
Spring 2013					
BIOL 2021 Principles of Cell Sci	4.00	4.00	A		
Honors Course					
BIOL 3520 Biological Chemistry II	3.00	3.00	B		
BIOL 4955 Individual Research	3.00	3.00	A		
MATH 1180 Calc Biol II	4.00	4.00	A		
Quant Reas (Math & Stat/Log)					
MUSC 2100 Hist of Rock'n Roll	3.00	3.00	A		
Fine Arts Exploration					
-----					
Term GPA: 3.824		17.000	17.000		
Dean's List					
Fall 2013					
CS 1410 Object-Oriented Prog	4.00	4.00	A		
DES 2615 Intro Design Thinking	3.00	3.00	A		
Fine Arts Exploration					
Community Engaged Learning					
MATH 3070 Applied Statistics I	4.00	4.00	A		
QReas(Math&Stat/Log)&Intensive					
PHYS 2210 Physcs For Scien. & Eng. I	4.00	4.00	A-		
-----					
Term GPA: 3.920		15.000	15.000		
Dean's List					
Spring 2014					
BIOL 4995 Biology Honors Research	3.00	3.00	A		
Honors Course					
BIOL 5140 Genome Biology	3.00	3.00	A		
HONOR 3200 Research University	3.00	3.00	A		
Upper Division Comm/Wrtg					
Honors Course					
MATH 3080 Applied Statistics II	3.00	3.00	A-		
QReas(Math&Stat/Log)&Intensive					
PHYS 2220 Physcs For Scien. & Eng. II	4.00	4.00	A		
-----					
Term GPA: 3.944		16.000	16.000		
Dean's List					
Fall 2014					
BIOL 3215 Cell Lab	2.00	0.00	***		
BIOL 4995 Biology Honors Research	3.00	0.00	***		
Honors Course					
BIOL 5221 Human Evol Genetics	4.00	0.00	***		
Quantitative Intensive					
HONOR 3374 Special Topics	3.00	0.00	***		

Drones and Society  
Soc/Behav Science Exploration  
Honors Course  
HONOR 3900 Imagined Communities 3.00 0.00 \*\*\*  
Humanities Exploration  
Honors Course

-----  
Term GPA: 0.000 15.000 0.000

-----CAREER SUMMARY-----  
Cumulative GPA: 3.891  
Cumulative GPA Units: 91.000  
Units Enrolled: 108.000  
U of U Units Earned: 93.000  
Total Transfer Units: 0.000  
Total Test Credit: 26.000  
Total Other Credit: 0.000

-----  
Cumulative Units 119.000

END OF UNDERGRADUATE SEMESTER CAREER

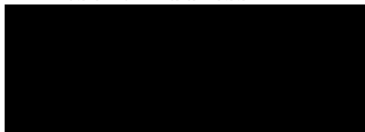
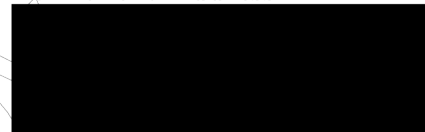
[Return](#)



Upcoming (Spring 2015) Courses:

1. BIOL 3370 - Microbial Biology
2. BIOL 3410 - Ecology and Evolution
3. NUTR 3620 - Cultural Aspects of Food
4. BIOL 4999 - Thesis Preparation

Applicant Copy

**Tyler C. Shimko**tyler.shimko@utah.edu  
tylershimko.com**Present Address****Permanent Address****Education**

H.B.S. in Biology, University of Utah, Salt Lake City, UT - Expected May 2015  
Minor in Chemistry  
Emphasis in Cellular and Molecular Biology  
3.891 GPA

**Research  
Experience**

**University of Utah**, Dr. Gillian Stanfield August 2014-May 2015  
Salt Lake City, Utah

- Designed pipeline to align, call variants, and filter paired end sequence data
- Continuation of Honors Thesis project, thesis in prep

**Northwestern University**, Dr. Erik Andersen May 2014-August 2014  
Evanston, Illinois

- Developed pipeline for the cleaning, mapping, and analysis of linkage mapping phenotype data in *C. elegans*
- Developed *COPASutils* R package
- Second publication in prep

**University of Utah**, Dr. Gillian Stanfield August 2013-May 2014  
Salt Lake City, Utah

- Mapped suppressors of Me-86 phenotype using CloudMap mapping protocol in *C. elegans*
- Honors Thesis project, thesis in prep

**Northwestern University**, Dr. Erik Andersen May 2013-August 2013  
Evanston, Illinois

- Refined high-throughput phenotyping assay using COPAS (Union Biometrica) BIOSORT large-particle flow cytometer
- Collected large *C. elegans* phenotype data sets for exposure to chemotherapeutics, pesticides, heavy metals, and anthelmintics

**University of Utah**, Dr. Erik Jorgensen August 2012-May 2013  
Salt Lake City, Utah

- Examined role of UNC-41 in synaptic vesicle recycling in *C. elegans*
- Attempted suppressor screen for Unc-41 phenotype

**Princeton University**, Dr. Leonid Kruglyak May 2012-August 2012  
Princeton, New Jersey

- Created near isogenic lines for confidence interval under identified quantitative trait loci for body length and fecundity
- Publication in prep

**University of Utah**, Dr. Erik Jorgensen August 2012-May 2013  
Salt Lake City, Utah

- Constructed universal transgene landing sites in *C. elegans* genome

<b>Publications</b>	<p><b>*-Indicates peer-reviewed publication</b></p> <ul style="list-style-type: none"> <li>• <b>Tyler C. Shimko</b> and Erik C. Andersen. COPASutils: An R Package for Reading, Processing, and Visualizing Data from COPAS Large-Particle Flow Cytometers. <i>PLOS ONE</i>. (2014) *</li> <li>• <b>Tyler C. Shimko</b> and Erik M. Jorgensen. Universal Transgene Insertion in <i>C. elegans</i>. <i>University of Utah Undergraduate Research Abstracts Journal</i>, Volume 12. (2012)</li> </ul>
<b>Presentations</b>	<p><b>*-Indicates presenter</b> <b>§-Indicates poster</b></p> <ul style="list-style-type: none"> <li>• <b>Tyler C. Shimko*</b>. Linkage mapping with recombinant inbred lines. <i>Northwestern University Worm Club</i>. July 2014.</li> <li>• <b>Tyler C. Shimko</b>, Robyn E. Tanny, and Erik C. Andersen*. Using high-throughput fitness assays to decipher the genetic causes of <i>C. elegans</i> drug sensitivities. <i>Society for Molecular-Biology and Evolution Meeting</i>. July 2013. §</li> <li>• <b>Tyler C. Shimko</b> and Erik C. Andersen*. Using natural variation to decipher the complex genetic cause of <i>C. elegans</i> drug sensitivities. <i>19<sup>th</sup> International C. elegans Meeting</i>. June 2013.</li> <li>• <b>Tyler C. Shimko*</b>, Erik C. Andersen, and Leonid Kruglyak. Identifying the genes that control paraquat resistance in the roundworm <i>C. elegans</i>. <i>National Conference on Undergraduate Research</i>. April 2013. §</li> <li>• <b>Tyler C. Shimko*</b>, Erik C. Andersen, and Leonid Kruglyak. Identifying the genes that control paraquat resistance in the roundworm <i>C. elegans</i>. <i>Utah Conference on Undergraduate Research</i>. February 2013. §</li> <li>• <b>Tyler C. Shimko*</b>, Christian Frokjaer-Jensen, and Erik M. Jorgensen. Universal Transgene Insertion in <i>C. elegans</i>. <i>University of Utah Bioscience Symposium for Undergraduate Researchers</i>. April 2012. §</li> <li>• <b>Tyler C. Shimko*</b>, Christian Frokjaer-Jensen, and Erik M. Jorgensen. Universal Transgene Insertion in <i>C. elegans</i>. <i>University of Utah Undergraduate Research Symposium</i>. March 2012. §</li> </ul>
<b>Honors</b>	<p>Dean's List – All semesters          Myriad Academic Excellence Award – Spring 2014          Barry Goldwater Scholarship (<b>Nationally competitive, research</b>) – Spring 2013          Theodore Verender Hanks Scholarship – Spring 2013          University of Utah College of Science Dean's Scholarship – Spring 2013          Full Resident/Half Non-Resident Partial Tuition Waiver Scholarship (Merit-based) – Fall 2012-Spring 2014          Undergraduate Research Opportunities Program Assistantship – Spring 2012          Full Resident Partial Tuition Waiver Scholarship (Merit-based) – Fall 2011-Spring 2012</p>
<b>Related Activities</b>	<p>PLOS Student Blog Regular Contributor – Spring 2013-Present          Undergraduate Research Advisor – Spring 2013          Undergraduate Research Ambassador – Fall 2012-Fall 2014</p>
<b>Undergraduate Course Highlights</b>	<p>4 Semesters of Computer Labs in the R Language          2 Semesters of Probability and Statistics          1 Semester of Human Evolutionary Genetics (Population Genetics)          1 Semester of Genome Biology          1 Semester of Molecular Biology Theory</p>

1 Semester of Computer Labs in the Python Language  
1 Semester of Computer Labs in the Java Language

**Computer  
Languages**

**\*-Indicates self-assessed proficiency (1:Worst, 3:Best)**

R (\*\*\*)

Python (\*\*)

Bash (\*\*)

JavaScript (\*\*)

Java(\*)

Publications:

Shimko, Tyler C., and Erik C. Andersen. "COPASutils: An R Package for Reading, Processing, and Visualizing Data from COPAS Large-Particle Flow Cytometers." *PLoS One* 9.10 (2014)

Applicant Copy