

# Philipp Ross

---

+1 631 561 8704 • 1141 W. Aaron Drive • Unit E • State College, PA • 16803  
philippross369@gmail.com • [pzross.com](http://pzross.com)

## Education

**Pennsylvania State University**, State College, PA USA (Anticipated, 2016)  
**Graduate Certificate, Applied Bioinformatics**  
Cumulative GPA to Date: 4.0/4.0

**Binghamton University**, Binghamton, NY USA (Spring 2013)  
**Bachelors of Science, Bioengineering**  
Major GPA: 3.71/4.0 Cumulative GPA: 3.53/4.0

**Earl L. Vandermeulen High School**, Port Jefferson, NY USA (Spring 2008)  
**Distinguished Regents Diploma with Honors**  
Cumulative GPA: 96/100

## Research Experience

**Computational Biologist**, Pennsylvania State University (Fall 2013 - Present)  
**Advisor: Manuel Llinás**

Contributed to several publications looking at various aspects of pre and post-transcriptional regulation in the deadliest human infecting species of the parasite that causes malaria, *Plasmodium falciparum*.

**Computational Simulation**, Binghamton University (Fall 2012 - Spring 2013)  
**Advisor: Hiroki Sayama**

Designed a computational simulation and graphical user interface looking at the socioeconomic consequences of the widespread adoption of 3D printers implemented in Mathematica and Python.

## Publications

Eshar S, Altenhofen L, Rabner A, **Ross P**, Fastman Y, Mandel-Gutfreund Y, Karni R, Llinás M, Dzikowski R. (2015) "*PfSR1 controls alternative splicing and steady state RNA levels in Plasmodium falciparum through preferential recognition of specific RNA motifs.*" Mol Microbiol. 2015 Mar 25. doi: 10.1111/mmi.13007

Amber Ferger, Wai Fai Lau, **Philipp Ross**, Wyman Zhao, Hiroki Sayama, and Steen Rasmussen, *Impact of personal fabrication technology on social structure and wealth distribution: An agent-based simulation study*, *Advances in Artificial Life: Proceedings of the Twelfth European Conference on the Synthesis and Simulation of Living Systems (ECAL 2013)*, Pietro Liò, Orazio Miglino, Giuseppe Nicosia, Stefano Nolfi and Mario Pavone, eds., MIT Press, pp.521-522.

<http://mitpress.mit.edu/sites/default/files/titles/content/ecal13/978-0-262-31709-2-ch075.pdf>

Chappell L, **Ross P**, Altenhofen L, Böehme U, Otto T, Rayner J, Newbold C, Matt Berriman, Llinás M  
"*Redefining the transcriptome of the human malaria parasite Plasmodium falciparum*" **In Preparation**

Santos JM, Campbell T, Joshi P, **Ross P**, Schieler A, Cristea I, Llinás M *"Red blood cell invasion by the malaria parasite is coordinated by an essential transcription factor PfAP2-I"* **In Preparation**

## Honors

**Graduate, Cum Laude**, Binghamton University

**Inducted to Tau Beta Pi Engineering Honor Society**, Binghamton University

**Deans List Recognition**, Binghamton University (Fall 2008 - 2011, 2012 & Spring 2009, 2010, 2013)

**SMART Grant Recipient**, Binghamton University (Fall 2009)

**Kathleen Mallory Memorial Scholarship**, Earl L. Vandermeulen High School (Summer 2008)

**Male Scholar Athlete**, Earl L. Vandermeulen High School (Summer 2008)

## Skills

### Biological Data Analysis

#### Transcriptomics

Processed and analyzed Illumina generated RNA-seq data. Experience includes read quality control, read mapping using a splice-aware aligner, reference guided transcript assembly, reference guided transcript annotation, gene-level quantification, and differential expression detection.

#### Protein-DNA Interactions

Processed and analyzed Illumina generated ChIP-seq and ChIP-exo data. Experience includes read quality control, read mapping, peak calling, and peak annotation.

#### Regulatory Element Analysis

Experience analyzing DNA and RNA sequence motifs including de novo discovery, search and enrichment analysis, cluster analysis, and transcript co-expression analysis to predict active DNA-binding protein interaction sites and functional roles for transcription factors.

#### Comparative Sequence Analysis

Experience comparing DNA and protein sequences to identify conservation and comparing whole genome sequencing data to identify single nucleotide polymorphisms.

### Statistical Modeling & Analysis

Experience modeling and analyzing biological data including multiple testing correction, linear regression, principle component analysis, k-means clustering, and non-metric multidimensional scaling using the R programming environment.

### Programming

Experience programming in multiple languages and environments suitable for scientific applications with a comfortable understanding of bash, awk, python, and R and basic understanding of perl, java, and mathematica.

### Web Development

Experience in utilization of common web development technologies including HTML5, CSS, Javascript, PHP, and SQL-based databases for application development and deployment on AWS.

## Involvement

**Contributor - The Biostars Handbook**, <https://leanpub.com/biostarhandbook>

**Current Member**, Center for Malaria Research at Penn State (CMaR)

**Current Member**, Center for Infectious Disease Dynamics (CIDD)

**Past Member**, Biomedical Engineering Society

**Past Member**, Undergraduate Chemical Society

## Leadership

**President & Founder**, Entrepreneurship Club, Binghamton University

**President**, Binghamton Bioengineering Club, Binghamton University

**Advisor**, Bioengineering Student Advisory Committee, Binghamton University

## Other

### Languages

**English**, Fluent

**German**, Native Speaker

**Spanish**, Basic Knowledge

### Certifications

**Certified Personal Trainer**, American Council of Exercise (ACE)

**Certified First Aid, CPR, and AED**, American Heart Association

**Certified Wilderness First Aid**, Stonehearth Open Learning Opportunities (SOLO)