

# Anna Lowegard

alowegard (at) utexas.edu | 214.208.2370

## EDUCATION

### DUKE UNIVERSITY

#### PH.D. IN COMPUTATIONAL BIOLOGY & BIOINFORMATICS

Expected May 2019 | Durham, NC  
Cum. GPA: 3.72 / 4.00

### THE UNIVERSITY OF TEXAS

#### B.S. IN MATHEMATICS

Completed May 2013 with Honors | Austin, TX

Specialization in Scientific Computation  
College of Natural Sciences  
Cum. GPA: 3.72 / 4.00

#### B.S. IN BIOLOGY

Completed May 2013 with Honors | Austin, TX

Conc. in Computational Biology  
College of Natural Sciences  
Cum. GPA: 3.72 / 4.00

## COURSEWORK

### GRADUATE

Physical Biochemistry  
Structural Biochemistry  
Computational Sequence Biology  
Structure of Biological Macromolecules  
NMR & X-Ray Crystallography  
Introductory Biochemistry I  
Genome Tools & Technologies  
Applied Algorithms

### UNDERGRADUATE

#### Mathematics:

Partial Differential Equations  
Applied Linear Algebra  
Introduction to Real Analysis  
Numerical Methods  
Ordinary Differential Equations  
Probability & Mathematical Statistics  
Sequences, Series, & Multivariable  
Calculus

#### Biology:

Computational Biology Lab  
Intro. to Computational Biology  
Neuroimaging Lab  
Evolution  
Neurobiology  
Human Microscopic & Gross Anatomy  
Cell Biology  
Molecular Biology  
Intro. Biology & Chemistry

## RESEARCH

### DONALD LAB | GRADUATE STUDENT/RESEARCHER

Aug 2014 – Present | Duke University | Durham, NC  
Working with **Bruce Donald** and his group to use structure-based protein design to design peptide inhibitors for three systems: LpxD, KRas, and CAL.

### TEXAS ADVANCED COMPUTING CENTER | UNDERGRADUATE RESEARCHER

September 2011 – May 2013 | Austin, TX  
Worked with **Matthew Vaughn** and **Karla Gendler** to develop a method using support vector machines to identify matrix attachment regions.

### CPRIT SUMMER UNDERGRADUATE EXPERIENCE | CANCER PREVENTION RESEARCH INSTITUTE OF TEXAS | UNDERGRADUATE RESEARCHER

June 2011 – August 2011 | Houston, TX  
Worked with **Eric Boerwinkle** adapting a weighted-sum statistical method to be applied to the X chromosome for use in disease association.

## FELLOWSHIPS, SCHOLARSHIPS, & HONORS

2017-18	Recipient	Duke University Department of Computer Science Outstanding Teaching Award
2018	Recipient	Duke University Graduate School Paul and Lauren Ghaffari Graduate Fellowship
2018	Recipient	PhRMA Foundation Pre Doctoral Fellowship in Informatics
2013	Recipient	Duke University Chancellor's Scholarship
2009-12	Recipient	University Honors, University of Texas at Austin
2009	Recipient	Roger Q. Mills Scholarship, University of Texas at Austin

## SOCIETIES & COMMITTEES

Nominated Member	2018 Hammes Teaching Award Selection Committee
Member	2018 GradX Organization Committee
Nominated Member	2015 Hammes Teaching Award Selection Committee
Member/Leader	Computational Biology Graduate Student Committee
Top 10%	Gamma Beta Phi, Honor Society
GPA > 3.5	Alpha Lambda Delta & Phi Eta Sigma, National Honor Society

## SKILLS

Java • Shell • Python • PyMol •  $\LaTeX$  • MATLAB  
Linux/Unix • Apple • Windows  
Microsoft Office

## TEACHING

2018	Teaching Assistant	Duke University	Discrete Math for Computer Science
2017	Teaching Assistant	Duke University	Discrete Math for Computer Science

## PRESENTATIONS

Lowegard, A., Frenkel, M., & Donald, B. (2018). **Predicting the Effect of Mutations in the KRas/c-Raf-RBD Protein-Protein Interface.** *Biophysical Journal*, 114(3), 576a.

Martin, J.W., Lowegard, A. U., Frenkel, M. S., Hallen, M.A., Ojewole, A., Jou, J.D., Wang, S., Holt, G.T., & Donald, B.R. (2018). OSPREY 3.0: Open-Source Protein Redesign for You, with Powerful New Features. *Poster Presentation*, Chicago, IL.

## PUBLICATIONS

Hallen, M. A., Martin, J. W., Ojewole, A., Jou, J. D., Lowegard, A. U., Frenkel, M. S., Gainza, P., Nisonoff, H.M., Mukund, A., Wang, S., Holt, G. T., Zhou, D., Dowd, E., & Donald B.R. (2018). **OSPREY 3.0: Open-Source Protein Redesign for You, with Powerful New Features.** bioRxiv, 306324.

Ojewole, A., Lowegard, A., Gainza, P., Reeve, S. M., Georgiev, I., Anderson, A. C., & Donald, B. R. (2017). **OSPREY predicts resistance mutations using positive and negative computational protein design.** In *Computational Protein Design* (pp. 291-306). Humana Press, New York, NY.