MattRalston
blend of bioinformatics and biochemistry

contact
Matt Ralston
1501 Parkside Ave, 7B
Ewing, NJ 08638

Phone: 302.547.2437
Email: mrals@udel.edu
matthewralston.us
LinkedIn:matthewralston

bioinformatics
Illumina RNASeq
Tuxedo Suite
BLAST, Samtools
Picard, Bedtools
DESeq, Circos
Bioconductor

programming
♥ Python, R, Node
Ruby, Haskell, Julia
Matlab, LaTeX, Elisp
MySQL, PostgreSQL
AWS, MongoDB
Javascript, CSS/HTML

laboratory
RNA-seq, qRT-PCR
Northern & Western
Spectrometry, HPLC
Immunofluorescence
Immunohistochemistry
Microscopy, HPLC
FACS, GC-MS
Mammalian cell culture
Anaerobic fermentation

open-source
Kmer.JS
NGS-CI

summary

Combines experiences in pharmaceutical discovery, biofuel engineering, and translational cancer research to diverse biochemical problems including Illumina sequencing, screening, and analysis. Offers interdisciplinary expertise for teams of scientists, engineers, and analysts.

education

2012-2015 **M.S.** Bioinformatics and Computational Biology **3.97**   University of Delaware
Thesis: *Assembling Improved Gene Annotations in Clostridium acetobutylicum with RNA Sequencing.*

2008–2012 **B.S.** Biochemistry   University of Delaware
Minor in Biochemical Engineering; Research Fellowship; Merit Scholarships

experience

2015–Now **BRISTOL MYERS SQUIBB**   Lawrenceville, NJ
Research Scientist II

- Developed a large dataset version-control system.
- Early-stage antibody-discovery sequencing informatics.

2012–2015 **DELAWARE BIOTECHNOLOGY INSTITUTE**   Newark, DE
Graduate Research Assistant

- Sequenced/assembled first transcriptome in *Clostridia*, D3JS genome browser.

2010-2012 **HELEN F. GRAHAM CANCER RESEARCH CENTER**   Newark, DE
Undergraduate Research Fellow

leadership

2014 **Bioinformatic Student Association**   Newark, DE
President

2013 **IGERT Business, Ethics, and Communication Project**   Newark, DE
Project Manager
Won a proposal for a revision to Fraunhoffer CMB's vaccine production process.

publications

- **"Complex and extensive post-transcriptional regulation revealed by integrative proteomic and transcriptomic analysis of metabolite stress response in *Clostridium acetobutylicum*",** contributing author. *Biotechnology for biofuels*. 8.1 (2015): 81.

- **"Overexpression of the *L. plantarum* peptidoglycan biosynthesis murA2 gene increases the tolerance of *E. coli* to alcohols and enhances ethanol production",** contributing author. *Applied Microbiology and Biotechnology* 98.19 (2014): 8399-8411.

- **"The *Clostridium* small RNome that responds to stress: the paradigm and importance of toxic metabolite stress in *C. acetobutylicum*",** contributing author. *BMC Genomics*. 14.1 (2013): 849.