TARA D. ALPERT

Email: tara.alpert@yale.edu

Department of Molecular Biophysics and Biochemistry

333 Cedar St., New Haven, CT 06510

EDUCATION

2014-2020	Ph.D. in Molecular Biophysics and Biochemistry	Yale University
2009-2013	B.A. in Biochemistry	Washington University in St. Louis

RESEARCH EXPERIENCE

2014 – 2020 **Ph.D. Candidate** at Yale University. Thesis title: Coordination between pre-mRNA splicing and cleavage in budding yeast. Supervisor: Prof. Karla M. Neugebauer, Ph.D.

2011 – 2013 **Undergraduate researcher** at Washington University in St. Louis. Thesis title: Biochemical studies of phosphoethanolamine methyltransferase and serine decarboxylase from nematodes, plasmodium, and plants. Supervisor: Spencer T. Olin Prof. Joseph M. Jez, Ph.D.

2010 – 2011 **Undergraduate researcher** at Washington University in St. Louis. Effect of gene expression patterns on behavioral plasticity in the European honey bee *Apis mellifera*. Supervisor: Associate Prof. Yehuda Ben-Shahar, Ph.D.

2010 **Intern** at the Human BioMolecular Research Institute (San Diego, CA). Summer project on the cellular response to neurotoxin exposure.

2008 **Intern** at the Scripps Research Institute (San Diego, CA). Summer project aimed at drug discovery for Type II Diabetes. Implemented high-throughput screening of small molecules for insulin production in pancreatic cells.

PUBLICATIONS

1. **Alpert T**, Straube K, Carrillo Oesterreich F, Neugebauer KM (2020) Single molecule nascent RNA sequencing reveals a role for Nab2p in 3' end formation. *Cell Reports* (in preparation)
2. **Alpert T**, Reimer KA, Straube K, Neugebauer KM (2019) Long read sequencing of nascent RNA from budding and fission yeasts. *Methods in Molecular Biology* (accepted)
3. Herzel L, Ottoz DSM, **Alpert T**, Neugebauer KM (2017) Splicing and transcription touch base: co-transcriptional spliceosome assembly and function. *Nature Rev Mol Cell Biol* 18, 637-650. https://doi.org/10.1038/nrm.2017.63
4. **Alpert T**, Herzel L, Neugebauer KM (2016) Perfect timing: splicing and transcription rates in living cells. *Wiley Interdiscip Rev RNA*. https://doi.org/10.1002/wrna.1401

5. Lee SG, **Alpert TD**, Jez JM (2012) Crystal structure of phosphoethanolamine methyltransferase from *Plasmodium falciparum* in complex with amodiaquine. *Bioorg Med Chem Lett* 22, 4990-4993. https://doi.org/10.1016/j.bmcl.2012.06.032

6. Lee SG, Kim YC, **Alpert TD**, Nagata A, Jez JM (2012) Structure and reaction mechanism of phosphoethanolamine methyltransferase from the malaria parasite *Plasmodium falciparum* – an antiparasitic drug target. *J Biol Chem* 287, 1426-1434. https://doi.org/10.1074/jbc.M111.315267

ORAL PRESENTATIONS

2019 Cross Regulation Between Co-transcriptional RNA Splicing and Cleavage
Alpert T, Straube K, Neugebauer KM
University of Massachusetts Medical School – Invited talk

2019 Coupling Between Pre-mRNA Splicing and PolyA Cleavage
Alpert T, Straube K, Reimer K, Neugebauer KM
Cold Spring Harbor – Eukaryotic mRNA Processing – Oral presentation

2018 Gene-Specific Variation in the Kinetics of Co-transcriptional Splicing
Alpert T, Carrillo Oesterreich F, Herzel L, Straube K, Neugebauer KM
Oxford Nanopore Community Meeting – Recorded presentation

2017 Gene-Specific Variation in the Kinetics of Co-transcriptional Splicing
Alpert T, Carrillo Oesterreich F, Herzel L, Straube K, Neugebauer KM
Oxford Nanopore Community Meeting – Lightning Talk

INTRADEPARTMENTAL ORAL PRESENTATIONS

2019 C-Wing Hall Seminar

2018 C-Wing Hall Seminar

2018 Yale Center for RNA Science and Medicine's RNA Club

2018 Molecular Biophysics and Biochemistry Department Retreat

2017 Cellular and Molecular Biology Research in Progress Seminar

2017 C-Wing Hall Seminar

2016 C-Wing Hall Seminar

POSTERS

2019 Yale Center for RNA Science and Medicine Retreat

2019 Molecular Biophysics and Biochemistry Department Retreat

2018 Oxford Nanopore Community Meeting

2017 Molecular Biophysics and Biochemistry Department Retreat

2017 Oxford Nanopore Community Meeting

2017 EMBO - Regulation of RNA 3' end formation

2016 Yale Center for RNA Science and Medicine Retreat

2016	EMBO - Gene Transcription in Yeast: From Chromatin to RNA and Back
2013	ASPB - Plant Biology
2012	American Society for Biochemistry and Molecular Biology Annual Meeting

TEACHING AND CAREER ENRICHMENT

2020	Co-mentor for MB&B rotation student • Targeted sequencing of DoG RNAs during osmotic stress with Oxford Nanopore MinION in *M. musculus*
2019	Mentor for MB&B rotation student • Whole-genome nascent RNA sequence dataset with Oxford Nanopore MinION for Spt5 depletion in *S. cerevisiae*
2017 - 2019	Discussion coordinator for Bystander Intervention Training workshops in the MB&B Department at Yale University
2018	Bioinformatics and Oxford Nanopore training • Mentored by Smith and Mercer Labs at the Garvan Institute of Medical Research
2018	Mentor for Yale-NUS undergraduate student • Semester project using neural networks to model Oxford Nanopore datasets for optimization of analysis pipeline
2017	Hands-on Oxford Nanopore Sequencing workshop at Oxford Nanopore Community Meeting
2017	Completed the ASBMB Art of Science Communication Class
2017	Attendance at AAAS Annual Meeting: Serving Society through Science Policy
2016	Teaching fellow and discussion leader • MB&B 449a/749a Medical Impact of Basic Science • MB&B/MCDB 105a An Issues Approach to Biology
2016	Seminar on communicating science to the public by New York Times Science Writer Carl Zimmer
2015	Attended Practical Statistics for Experimentalists Workshop

HONORS, AWARDS, AND FELLOWSHIPS

2017	Sponsored by PEO chapter AL in Wilton, CT for PSA award
2013, 2014, 2015, 2016	National Science Foundation GFRP Honorable Mention
2012	American Society of Plant Biology Summer Undergraduate Research Fellowship
2011	American Society for Biochemistry and Molecular Biology Travel Award
2011	Howard Hughes Medical Institute Summer Undergraduate Research Fellowship

SOFTWARE SKILLS

Proficient in R and python

Expertise in data analysis for next-generation sequencing

Knowledgeable of biologically relevant tools and packages for data mining, sequence alignment, and genome analysis