John L. Pulice III

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EDUCATION

Harvard Medical School – Division of Medical Sciences — Boston, MA
Ph.D. Student – Biological and Biomedical Sciences — August 2017-Present
Meyerson Lab, Department of Medical Oncology, Dana-Farber Cancer Institute and Harvard Medical School — GPA: 3.868

Harvard College
A.B. with High Honors in Organismic and Evolutionary Biology, Secondary Field in English — Cambridge, MA, May 2015
Senior Thesis: "A Population Genomics Approach to Detecting Pairing Preference in Autotetraploid *A. arenosa*" — Overall GPA: 3.455
Advanced Coursework in Genetics, Molecular Biology, Biochemistry, Mathematics, Statistics, Physics — Concentration GPA: 3.689

University of Oxford – The Queen's College — Oxford, UK
Harvard Summer School Study Abroad – Darwin in Oxford — Summer 2013
Two-Course Program on History of Evolutionary Thought and Evolutionary Biology.
Recipient: David Rockefeller International Experience Grant

Thomas Jefferson HS for Science and Technology — Alexandria, VA
FCPS Advanced Studies Diploma. SAT: 750R 800M 670W — June 2011
Governor of Virginia Award for Academic Excellence — GPA: 4.301
National Merit Finalist, National Honor Society, AP Scholar with Distinction, QuestBridge finalist

LABORATORY WORK EXPERIENCE

Meyerson Lab, Department of Medical Oncology — Dana-Farber Cancer Institute and Harvard Medical School, Boston, MA
Graduate Student — August 2018 – Present

- Using cancer genomics approaches from cell lines and patient samples to interrogate the role of functional regulatory perturbations to oncogenic gene expression.

Kadoch Lab, Department of Pediatric Oncology — Dana-Farber Cancer Institute and Harvard Medical School, Boston, MA
Associate Computational Biologist I — June 2015 – August 2017

- Built from scratch a computational pipeline to align, analyze, and integrate genomic datasets (ChIP-seq, RNA-seq, ATAC-seq) in a variety of chromatin-related cancer projects to elucidate oncogenic mechanisms for therapeutic targeting.
- Developed frameworks for experimental design of genomic experiments, and worked with lab members to design and integrate biochemical and genomic conclusions in investigations.
- Worked on drug development as part of the Broad-Bayer collaboration to determine target genes for target validation of candidate compounds from high-throughput screens.
- Led the hiring and training process for a new computational biologist, reviewing resumes, interviewing candidates, and training hired candidate.

Bomblies Lab, Department of Organismic & Evolutionary Biology — Harvard University, Cambridge, MA
Undergraduate Honors Researcher — December 2013 – May 2015

- Tetraploid Inheritance Analysis of *Arabidopsis arenosa*: Created mathematical model for population genetics of pairing preference, using population structure and subgenome divergence. Developed statistical method for testing inheritance in tetraploid species on site-specific genomic data. Assembled methodology into an R package for future use on population data.
- Summer and Fall 2014 Harvard College Research Program fellow and Recipient of Harvard Herbaria Grant in Aid of Undergraduate Research
- Research co-advised by Prof. Daniel Hartl, with support from Dr. Levi Yant and Prof. John Wakeley.

JOURNAL ARTICLES

Sandoval, G.S.*, **Pulice, J.L.***, Pakula, H., Schenone, M.A., Takeda, D.Y., Pop, M., Boulay, G., Williamson, K., McBride, M.J., St. Pierre, R., Hartman, E., Garraway, L.A., Carr, S.A., Li, Z., Rivera, M.N., Ronco, L., Hahn, W.C., and Kadoch, C. Binding of TMPRSS2-ERG to BAF chromatin remodeling complexes mediates prostate oncogenesis (2018). Molecular Cell. *71*, 554-566 doi:10.1016/j.molcel.2018.06.040

McBride, M.J.*, **Pulice, J.L.***, Beird, H.C., Ingram, D.R., D'Avino, A.R., Shern, J.F., Charville, G.W., Hornick, J.L., Nakayama, R.T., Garcia-Rivera, E.M., Araujo, D.M., Wang, W., Tsai, J., Yeagley, M., Wagner, A.J., Futreal, P.A., Khan, J., Lazar, A.J., and Kadoch, C. The SS18-SSX Fusion Oncoprotein Hijacks BAF Complex Targeting and Function to Drive Synovial Sarcoma (2018). Cancer Cell. *33*, 1128-1141. doi:10.1016/j.ccell.2018.05.002

Nakayama, R.T.*, **Pulice, J.L.***, Valencia, A.M.*, McBride, M.J., McKenzie, Z.M., Gillespie, M., Ku, W.L., Teng, M., Cui, K., Williams, R.T., Cassel, S.H., He, Q., Widmer, C.J., Demetri, G.D., Irizaary, R.A., Zhao, K., Ranish, J., and Kadoch, C. SMARCB1 is required for widespread BAF complex–mediated activation of enhancers and bivalent promoters (2017). Nat. Genet. *49*, 1613–1623. doi:10.1038/ng.3958

Pulice, J.L. and Kadoch, C. (2017). Composition and Function of Mammalian SWI/SNF Chromatin Remodeling Complexes in Human Disease. Cold Spring Harb. Sym. doi:10.1101/sqb.2016.81.031021

Kadoch, C., Williams, R.T., Calarco, J.P., Miller, E.L., Weber, C.M., Braun, S.M.G., **Pulice, J.L.**, Chory, E.J. and Crabtree. G.R. (2017) Dynamics of BAF-Polycomb complex opposition on heterochromatin in normal and oncogenic states. Nat. Genet. *49*, 213-222. doi:10.1038/ng.3734

* - These authors contributed equally to this work.

POSTERS

Epigenomics 2016 – Pulice, J.L. and Kadoch, C. Defining the complete landscape of mSWI/SNF (BAF) complex perturbation in human cancer (February 2016).

FELLOWSHIPS AND GRANTS

HMS Molecular, Cellular and Developmental Dynamics (MCDD) T32 Training Grant (Fall 2018- Spring 2019) — 5T32GM007226-43
NDSEG Fellow — National Defense Science and Engineering Grant (NDSEG) Fellowship (Fall 2019-2023)
Honorable Mention — National Science Foundation (NSF) Graduate Research Fellowship Program (2018 competition)

SKILLS & INTERESTS

Extensive programming experience in R, Python, Bash Scripting, Cluster Computing (SLURM/LSF/UGER), LaTeX Additional experience in Java, C, HTML, CSS, PHP/MySQL, Mathematica

Microsoft Word, PowerPoint, Excel; Adobe InDesign, Illustrator, Photoshop; QuickBooks