

David Angeles-Albores

+1 607 379 4030 davidaalbores@gmail.com
[@DavidAngeles13](https://twitter.com/DavidAngeles13) [dangeles.github.io](https://github.com/dangeles)
<https://github.com/dangeles>
47 Garden St, Apt 4, Boston, MA, 02114

Education

- 2013–2018 **Ph.D., Biochemistry and Molecular Biophysics,**
California Institute of Technology
Defense Date: 18 September, 2018
Degree Awarded: 31 October, 2018
- 2009–2013 **B.A., cum laude, Biology**
Cornell University

Appointments

- 11/2019 – **Computational Biologist II, eGenesis**
One of two founding members of the computational biology unit.
Introduced ATAC-seq, scRNA-seq and scATAC-seq to eGenesis.
I collaborated on the development of kidney dissociation protocols and used these protocols to create an atlas of the pig kidney cortex using scRNA-seq.
I used the above methods to generate a compendium of promoters that stably express genes ubiquitously or with high tissue-specificity at desired levels with low burstiness. *Patent pending.*
- 7/2020 – **Visiting Scholar, Laboratory of Ilya Ruvinsky,**
Northwestern University
I collaborate with the Ruvinsky lab on RNA-seq analysis of *C. elegans* biology.
- 01/2019–11/2019 **Postdoctoral Associate, Laboratory of Eric J. Alm,**
Massachusetts Institute of Technology
I developed methods for barcodeless, highly multiplexed RNA-seq of multiple bacterial species using a single library preparation protocol.
My main project centered around recreating the vaginal microbiome *in vitro* and dissecting the causal interactions between microbial species using a mixture of computational and experimental methods. I hoped to apply the algorithms I developed at Caltech (see below) to develop active learning models that combined iterative experimental minibatches with continuous computational analysis.
I terminated my postdoctoral research prematurely due to a major personal loss, unrelated to my work at MIT.
- 11/2018–01/2019 **Postdoctoral Fellow, Labs of Paul W. Sternberg and Matt Thomson,**
California Institute of Technology
I used this short period immediately following my Ph.D to finish some projects working with my Ph.D. advisor, Paul Sternberg, and a member of my committee, Matt Thomson, before moving on to my final postdoctoral position at MIT in January 2019. I studied algorithms for analysis of CRISPR screens in mammalian cells, using transcriptomes as phenotypes for genetic analysis.

Research Publications

[†] denotes equal contributions.

Journal Articles

- 1 Basta, D. W., **Angeles-Albores, D.**, Spero, M. A., Cierniecki, J. A., & Newman, D. K. (2020). Heat-shock proteases promote survival of *Pseudomonas aeruginosa* during growth arrest. *Proceedings of the National Academy of Sciences of the United States of America*. doi:10.1073/pnas.1912082117
- 2 Duncan, E. M., Nowotarski, S. H., Guerrero-Hernández, C., Ross, E. J., D'Orazio, J. A., Clubes de Ciencia México, W. f. D. B., ... Alvarado, A. S. (2020). A new species of planarian flatworm from Mexico: *Girardia guanajuatensis*. *bioRxiv*. doi:10.1101/2020.07.01.183442. eprint: <https://www.biorxiv.org/content/early/2020/07/02/2020.07.01.183442.full.pdf>
- 3 **Angeles-Albores, D.**, & Sternberg, P. W. (2018). Using Transcriptomes as Mutant Phenotypes Reveals Functional Regions of a Mediator Subunit in *Caenorhabditis elegans*. *Genetics*, genetics.301133.2018. doi:10.1534/genetics.118.301133
- 4 [†]**Angeles-Albores, D.**, [†]Puckett Robinson, Williams, B. A., Wold, B. J., & Sternberg, P. W. (2018). Reconstructing a metazoan genetic pathway with transcriptome-wide epistasis measurements. *Proceedings of the National Academy of Sciences*, 201712387. doi:10.1073/pnas.1712387115
- 5 [†]**Angeles-Albores, D.**, [†]Leighton, D. H. W., Tsou, T., Khaw, T. H., Antoshechkin, I., & Sternberg, P. W. (2017). The *Caenorhabditis elegans* Female-Like State: Decoupling the Transcriptomic Effects of Aging and Sperm Status. *G3 (Bethesda, Md.)* 7(9), 2969–2977. doi:10.1534/g3.117.300080
- 6 **Angeles-Albores, D.**, N. Lee, R. Y., Chan, J., & Sternberg, P. W. (2016). Tissue enrichment analysis for *C. elegans* genomics. *BMC Bioinformatics*, 17(1), 366. doi:10.1186/s12859-016-1229-9
- 7 Albores-Saavedra, J., Chable-Montero, F., **Angeles-Albores, D.**, Schwartz, A., Klimstra, D. S., & Henson, D. E. (2011). Early Gallbladder Carcinoma. *American Journal of Clinical Pathology*, 135(4), 637–642. doi:10.1309/AJCPFRKCFEDLV03Y
- 8 Albores-Saavedra, J., Schwartz, A. M., Henson, D. E., Kostun, L., Hart, A., **Angeles-Albores, D.**, & Chablé-Montero, F. (2011). Cutaneous angiosarcoma. Analysis of 434 cases from the surveillance, epidemiology, and end results program, 1973–2007. *Annals of Diagnostic Pathology*, 15(2), 93–97. doi:10.1016/j.anndiagpath.2010.07.012

μPublications

- 1 **Angeles-Albores, D.**, N. Lee, R. Y., Chan, J., & Sternberg, P. W. (2018). Two new functions in the WormBase Enrichment Suite. *microPublication Biology*. doi:10.17912/W25Q2N

Scientific Talks

- 2019 **Probabilistic Modeling in Genomics**
Genetics is an active learning algorithm for causal reconstruction of biological networks
Hanna H Gray Semifinalist Symposium
Phenotypes, epistasis, and probability theory
ASBMB Special Symposium: Evolution and Core Processes in Gene Expression
Transcriptomes as phenotypes
- 2018 **Bay Area Worm Meeting**
Allelic series analyses using transcriptomic phenotypes

Scientific Talks (continued)

- 2017 **21st C. elegans International Meeting**, WormBase: Tools, Content and Community Annotation, Workshop
Gene Set Analysis tool for Gene Ontology (GO), Phenotype, and Tissue Enrichment
Annual Departmental Retreat, California Institute of Technology
Genome-wide, unbiased experimental genetics
Biochemistry and Molecular Biophysics Seminar Series, California Institute of Technology
Transcriptomic Genetics: A new way to use RNA-sequencing data
Center for Environmental Microbial Interactions, California Institute of Technology
Genome-wide unbiased experimental genetics
- 2016 **Annual Biochemistry and Molecular Biophysics Program Retreat**, California Institute of Technology
Reconstruction of a genetic pathway using whole-organism expression profiles
Graduate Biology Seminar, California Institute of Technology
Transcriptome-wide epistasis in mRNA expression profiles

Awards

- 2020 eGenesis Leadership Award
- 2019 HHMI Hanna Gray Fellow Finalist
- 2015 Florence C. Rose and S. Meryl Rose Endowed Scholarship
- 2014 Amgen Graduate Student Fellowship
- 2012 EXROP Capstone Award
- 2011 EXROP HHMI Summer Fellowship

Scientific Courses

- 2015 **Embryology**, Marine Biological Laboratory at Woods Hole

Teaching and Mentoring Experience

Teaching

- 2017–2018 **Systems Genetics**, Teaching Assistant, *California Institute of Technology*
- 2016 **Introduction to Biology**, Teaching Assistant, *California Institute of Technology*
- 2015 **Order of Magnitude Biology**, Teaching Assistant, *California Institute of Technology*
- 2014 **Advanced Experimental Methods in Bioorganic Chemistry**, Teaching Assistant, *California Institute of Technology*

Mentoring

- 2016–2019 **Kyung Hoi Min**, Caltech undergraduate, experimental and computational student, *California Institute of Technology*
- Summer 2018 **Vladimir Molchanov**, Saint Petersburg Bioinformatics Institute undergraduate, experimental student, *California Institute of Technology*

Teaching and Mentoring Experience (continued)

Summer 2015	Tiffany Tsou , UCSB undergraduate, experimental student, <i>California Institute of Technology</i>
2014–2015	Isabelle Phinney , Polytechnic School, computational student, <i>California Institute of Technology</i>

Outreach

2020	Invited speaker , <i>Clubeando en casa, el Podcast</i> , Clubes de Ciencia México
2017	Speaker , <i>What is Clubes de Ciencias Mexico?</i> , SACNAS
2016	Co-instructor , <i>De Planarias y Derivas</i> , Clubes de Ciencia México, Guanajuato Co-instructor , <i>De Genes y Animales</i> , Clubes de Ciencia México, Ensenada
2015	Student selection committee , Clubes de Ciencia México
2014	Guest instructor , <i>Biología a través de los números</i> , Clubes de Ciencia México, Ensenada

Scientific Societies

2014–Present	Genetics Society of America
2015–Present	Society for Developmental Biology

References

Toby Bloom
VP of Information Technology, eGenesis,
300 Technology Square
Suite 301, Cambridge, MA 02139
✉ tbloom@alum.mit.edu

Professor Eric J Alm
Massachusetts Institute of Technology,
NE47-379, Cambridge, MA 02139
✉ burnss@mit.edu

Professor Paul W. Sternberg
California Institute of Technology,
MC 156-29, Pasadena, CA 91125
✉ pws@caltech.edu

Professor Dianne K. Newman
California Institute of Technology,
MC 147-75, Pasadena CA, 91125
✉ dkn@caltech.edu

Assistant Professor Matthew Thomson
California Institute of Technology,
216-76, Pasadena CA, 91125
✉ mthomson@caltech.edu

**Assistant Research Professor
Erich M. Schwarz**
Cornell University,
Biotechnology 351,
Cornell University, Ithaca,
NY 14853-2703
✉ ems394@cornell.edu