

David Angeles-Albores

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Education

- 2013–2018 **Ph.D.**, Biochemistry and Molecular Biophysics,
California Institute of Technology
- 2009–2013 **B.A., *cum laude***, Biology
Cornell University

Appointments

- 03/2021 – *Present* **Senior Scientist I**, Rheos
At Rheos, I help design experiments using single-cell RNA-seq, ATAC-seq and mass spectroscopy and perform the data analysis.
I leverage artificial intelligence and machine learning to extract novel insights from genomics datasets and identify or verify promising drug targets.
- 07/2020 – *Present* **Visiting Scholar**, Laboratory of Ilya Ruvinsky,
Northwestern University
I collaborate with the Ruvinsky lab on RNA-seq analyses of *C. elegans* biology.
- 11/2019 – 3/2021 **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.*
- 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 period immediately following my defense to finish projects with my Ph.D. advisor, Paul Sternberg, and a member of my committee, Matt Thomson, before moving on to my postdoctoral position at MIT in January, 2019. I developed active learning algorithms for analysis of CRISPR screens in mammalian cells, using transcriptomes as phenotypes.

Research Publications

[†] denotes equal contributions.

Journal Articles

- 1 Basta, D. W., **Angeles-Albores, D.**, Spero, M. A., Ciemniecki, 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*. <https://doi.org/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., McKinney, S., Guo, L., & Alvarado, A. S. (2020). A new species of planarian flatworm from Mexico: *Girardia guanajuatensis*. *bioRxiv*. <https://doi.org/10.1101/2020.07.01.183442>
- 3 **Angeles-Albores, D.**, & Sternberg, P. W. (2018). Using Transcriptomes as Mutant Phenotypes Reveals Functional Regions of a Mediator Subunit in *Caenorhabditis elegans*. *Genetics*, 301(1), 33.2018. <https://doi.org/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. <https://doi.org/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. <https://doi.org/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. <https://doi.org/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. <https://doi.org/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. <https://doi.org/10.1016/j.anndiagpath.2010.07.012>

Patents

- 1 eGenesis. (In prep). Cells, tissues, organs, and/or animals having one or more modified genes for enhanced xenograft survival and/or tolerance.

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*. <https://doi.org/10.17912/W25Q2N>

Scientific Talks

- 2021 **23rd International *C. elegans* Conference**, Aging and Stress
Transcriptomic analyses of hermaphrodite responses to the male pheromone
23rd International *C. elegans* Conference, Careers in Industry Panel
Moderator
- 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
- 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*
Summer 2015 **Tiffany Tsou**, UCSB undergraduate, experimental student, *California Institute of Technology*
2014–2015 **Isabelle Phinney**, Polytechnic School, computational student, *California Institute of Technology*

Outreach

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

Scientific Societies

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

References

Toby Bloom, Ph.D.

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