

# David Angeles-Albores

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## 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 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

<sup>†</sup> 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*. 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 <sup>†</sup>**Angeles-Albores, D.**, <sup>†</sup>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 <sup>†</sup>**Angeles-Albores, D.**, <sup>†</sup>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

### 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*. doi:10.17912/W25Q2N

## Scientific Talks

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- 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     **21<sup>st</sup> 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

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- 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

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- 2015     Embryology, Marine Biological Laboratory at Woods Hole

## Teaching and Mentoring Experience

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### 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*

## Teaching and Mentoring Experience (continued)

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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

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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

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2014–Present      Genetics Society of America

2015–Present      Society for Developmental Biology

## References

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### **Toby Bloom**

VP of Information Technology, eGenesis,  
300 Technology Square  
Suite 301, Cambridge, MA 02139  
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### **Professor Eric J Alm**

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### **Professor Dianne K. Newman**

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### **Assistant Research Professor**

#### **Erich M. Schwarz**

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### **Ranjith Anand**

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### **Professor Paul W. Sternberg**

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### **Assistant Professor Matthew Thomson**

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