

# 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.  
Created an atlas of the pig kidney cortex  
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
- 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 performed research on microbiome analysis. I terminated my postdoctoral research prematurely as a result of a personal tragedy, 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I used this short period to finish some projects, and developed an unpublished algorithm for analysis of CRISPR screens in mammalian cells, using transcriptomes as phenotypes for genetic analysis.

## Research Publications

<sup>†</sup> denotes equal contributions.

### Journal Articles

- I    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*, 301(133), 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*
- 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*

## Scientific Talks (continued)

- 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 for attendance to the Embryology course at the Marine Biological Laboratory
- 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

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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 Paul W. Sternberg**

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### **Assistant Research Professor**

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

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