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

01/2022 – *Present*	**Sr Computational Scientist**, Altos Labs
07/2020 – *Present*	**Visiting Scholar, Northwestern University** **Lab of Ilya Ruvinsky**
03/2021 – 01/2022	**Senior Scientist I**, Rheos Medicines Rheos was unable to secure Series B funding in 2021 and closed its doors in 2022.
11/2019 – 3/2021	**Computational Biologist II**, eGenesis I computationally designed compendium of pig promoters that stably express genes ubiquitously or with high tissue-specificy at desired levels with low burstiness, and developed technologies to identify safe harbors.
01/2019–11/2019	**Postdoctoral Associate, MIT**, **Lab of Eric J. Alm**

Research Publications

Journal Articles

1   Anand, R. P., Layer, J. V., Hirose, T., Lassiter, G., Heja, D., Akkad, A., **Angeles-Albores, D.**, Chao, J. C., Chhangawala, S., Colvin, R. B., Crabtree, J. N., Ernst, R. J., Esch, N., Firl, D. J., Getchell, K., Griffin, A. K., Guo, X., Hall, K. C., Hamilton, P., ... Qin, W. (n.d.). Rational design of a clinically compatible porcine donor for xenotransplantation. *in prep.*

2   **Angeles-Albores, D.**, Aprison, E. Z., Dzitoyeva, S., & Ruvinsky, I. (n.d.). A *C. elegans* male pheromone feminizes germline gene expression in hermaphrodites and imposes life-history costs. *in prep.*

3   Albright, A. R., **Angeles-Albores, D.**, & Marshall, W. (2023). Genome wide-analysis of anterior-posterior mrna localization in *Stentor coeruleus* reveals a role for the microtubule cytoskeleton. *bioRxiv.* `https://doi.org/https://doi.org/10.1101/2023.01.09.523364`

4   Aprison, E. Z., Dzitoyeva, S., **Angeles-Albores, D.**, & Ruvinsky, I. (2022). A male pheromone that improves the quality of the oogenic germline. *Proceedings of the National Academy of Sciences*, *119*(21), e2015576119. `https://doi.org/10.1073/pnas.2015576119`

5   Duncan, E. M., Nowotarski, S. H., Guerrero-Hernández, C., Ross, E. J., D'Orazio, J. A., McKinney, S., McHargue, M. C., Guo, L., McClain, M., & Alvarado, A. S. (2022). Molecular characterization of a flatworm *Girardia* isolate from guanajuato, mexico. *Developmental Biology*, *489*, 165–177. `https://doi.org/https://doi.org/10.1016/j.ydbio.2022.06.003`

6   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`

7   **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. `https://doi.org/10.1534/genetics.118.301133`

8   †**Angeles-Albores, D.**, †Puckett Robinson, C., 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`

9   †**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`

10   **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`

11   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`

12   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). Novel safe harbor sites for genomic engineering.

2 Layer, J., Qin, W., Kan, Y., Crabtree, J., Youd, M., Heja, D., **Angeles-Albores, D.**, Anand, R., Perrat, P., Ernst, R., & Paragas, V. (2021). Cells, tissues, organs, and/or animals having one or more modified genes for enhanced xenograft survival and/or tolerance, wo/2022/104155. `https: //patentscope.wipo.int/search/en/detail.jsf?docId=WO2022104155&_gid=202220`

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

Awards (continued)

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*

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