



# David Angeles-Albores, Ph.D.

✉ davidangelesalbores@gmail.com






in LinkedIn

🌐 <https://dangeles.github.io/>

## Education

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


## Appointments












- 01/2022 - Present  **Sr Computational Scientist**, Altos Labs  
I joined Altos Labs at launch. As one of its first bioinformaticians, I was a key contributor to its major lead rejuvenation candidate programs. I helped build out the genomics platforms for Altos Labs, and identified and initiated AI/ML research programs that are considered of top strategic importance. I developed end-to-end pipelines for analysis of Perturb-seq data, RNA-seq, ATAC-seq and pseudo-paired imaging/genomics data.
- 07/2020 - Present  **Visiting Scholar, Northwestern University**  
I research the effects of pheromone signaling on the lifespan, healthspan and sexual behaviors of *C. elegans* with Ilya Ruvinsky.
- 03/2021 - 01/2022  **Senior Scientist I**, Rheos Medicines  
I developed precision biology methods using multimodal genomics measurements to identify responder and non-responder populations to candidate drugs. 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 collaborated in the humanization of pig organs for transplantation into human patients by computationally designing a compendium of pig promoters that stably express genes ubiquitously or tissue-specificity in pig organs. I also developed methods to identify safe harbors resistant to epigenetic silencing. This work resulted in the transplantation of a pig kidney into a patient with end-stage renal disease who was able to leave the hospital without dialysis, and was featured in the **New York Times**.
- 01/2019–11/2019  **Postdoctoral Associate**, MIT,  
**Lab of Eric J. Alm**  
I developed computational methods to deconvolve individual transcriptomes from metatranscriptomes collected from communities with a known bacterial composition without the need for any molecular barcodes. This enabled novel kinds of experiments to be carried out easily and cheaply.


## Research Publications

† indicates equal contribution.

The Workshop for Developmental Biology, Clubes de Ciencias was taught and developed by me.





- 1 X. A. Yu, C. McLean, J.-H. Hehemann, **D. Angeles-Albores**, F. Wu, A. Muszyński, C. H. Corzett, P. Azadi, E. B. Kujawinski, E. J. Alm, and M. F. Polz, “Low-level resource partitioning supports coexistence among functionally redundant bacteria during successional dynamics,” *The ISME Journal*, vol. 18, no. 1, wrad013, Jan. 2024, ISSN: 1751-7362.  DOI: 10.1093/ismejo/wrad013. eprint: <https://academic.oup.com/ismej/article-pdf/18/1/wrad013/56820904/wrad013.pdf>.

- 2 A. R. Albright, **D. Angeles-Albores**, and W. Marshall, "Genome wide-analysis of anterior-posterior mrna localization in *Stentor coeruleus* reveals a role for the microtubule cytoskeleton," *bioRxiv*, 2023.  DOI: <https://doi.org/10.1101/2023.01.09.523364>.
- 3 R. P. Anand, J. V. Layer, D. Heja, T. Hirose, G. Lassiter, D. J. Firl, V. B. Paragas, A. Akkad, S. Chhangawala, R. B. Colvin, R. J. Ernst, N. Esch, K. Getchell, A. K. Griffin, X. Guo, K. C. Hall, P. Hamilton, L. A. Kalekar, Y. Kan, A. Karadagi, F. Li, S. C. Low, R. Matheson, C. Nehring, R. Otsuka, M. Pandelakis, R. A. Policastro, R. Pols, L. Queiroz, I. A. Rosales, W. T. Serkin, K. Stiede, T. Tomosugi, Y. Xue, G. E. Zentner, **D. Angeles-Albores**, J. Chris Chao, J. N. Crabtree, S. Harken, N. Hinkle, T. Lemos, M. Li, L. Pantano, D. Stevens, O. D. Subedar, X. Tan, S. Yin, I. J. Anwar, D. Aufhauser, S. Capuano, D. B. Kaufman, S. J. Knechtle, J. Kwun, D. Shanmuganayagam, J. F. Markmann, G. M. Church, M. Curtis, T. Kawai, M. E. Youd, and W. Qin, "Design and testing of a humanized porcine donor for xenotransplantation," *Nature*, vol. 622, no. 7982, pp. 393–401, 2023.  DOI: [10.1038/s41586-023-06594-4](https://doi.org/10.1038/s41586-023-06594-4).
- 4 **D. Angeles-Albores**, E. Z. Aprison, S. Dzitoyeva, and I. Ruvinsky, "A *Caenorhabditis elegans* male pheromone feminizes germline gene expression in hermaphrodites and imposes life-history costs," *Molecular Biology and Evolution*, vol. 40, no. 6, msad119, May 2023.
- 5 E. Z. Aprison, S. Dzitoyeva, **D. Angeles-Albores**, and I. Ruvinsky, "A male pheromone that improves the quality of the oogenic germline," *Proceedings of the National Academy of Sciences*, vol. 119, no. 21, e2015576119, 2022.  DOI: [10.1073/pnas.2015576119](https://doi.org/10.1073/pnas.2015576119). eprint: <https://www.pnas.org/doi/pdf/10.1073/pnas.2015576119>.
- 6 E. M. Duncan, S. H. Nowotarski, C. Guerrero-Hernández, E. J. Ross, J. A. D'Orazio, W. f. D. B. Clubes de Ciencia México, S. McKinney, M. C. McHargue, L. Guo, M. McClain, and A. S. Alvarado, "Molecular characterization of a flatworm *Girardia* isolate from guanajuato, mexico," *Developmental Biology*, vol. 489, pp. 165–177, 2022, ISSN: 0012-1606.  DOI: <https://doi.org/10.1016/j.ydbio.2022.06.003>.
- 7 D. W. Basta, **D. Angeles-Albores**, M. A. Spero, J. A. Ciemniecki, and D. K. Newman, "Heat-shock proteases promote survival of *Pseudomonas aeruginosa* during growth arrest," *Proceedings of the National Academy of Sciences of the United States of America*, 2020, ISSN: 10916490.  DOI: [10.1073/pnas.1912082117](https://doi.org/10.1073/pnas.1912082117).
- 8 **D. Angeles-Albores**, R. Y. N. Lee, J. Chan, and P. W. Sternberg, "Two new functions in the WormBase Enrichment Suite," *microPublication Biology*, 2018.  DOI: [10.17912/W25Q2N](https://doi.org/10.17912/W25Q2N).
- 9 **D. Angeles-Albores** and P. W. Sternberg, "Using Transcriptomes as Mutant Phenotypes Reveals Functional Regions of a Mediator Subunit in *Caenorhabditis elegans*," *Genetics*, genetics.301133.2018, Jul. 2018, ISSN: 1943-2631.  DOI: [10.1534/genetics.118.301133](https://doi.org/10.1534/genetics.118.301133).
- 10 **D. Angeles-Albores**<sup>†</sup>, C. Puckett Robinson<sup>†</sup>, B. A. Williams, B. J. Wold, and P. W. Sternberg, "Reconstructing a metazoan genetic pathway with transcriptome-wide epistasis measurements," *Proceedings of the National Academy of Sciences*, p. 201712387, 2018, ISSN: 0027-8424.  DOI: [10.1073/pnas.1712387115](https://doi.org/10.1073/pnas.1712387115).
- 11 **D. Angeles-Albores**<sup>†</sup>, D. H. W. Leighton<sup>†</sup>, T. Tsou, T. H. Khaw, I. Antoshechkin, and P. W. Sternberg, "The *Caenorhabditis elegans* Female-Like State: Decoupling the Transcriptomic Effects of Aging and Sperm Status," *G3 (Bethesda, Md.)*, vol. 7, no. 9, pp. 2969–2977, 2017, ISSN: 2160-1836.  DOI: [10.1534/g3.117.300080](https://doi.org/10.1534/g3.117.300080).
- 12 **D. Angeles-Albores**, R. Y. N. Lee, J. Chan, and P. W. Sternberg, "Tissue enrichment analysis for *C. elegans* genomics," *BMC Bioinformatics*, vol. 17, no. 1, p. 366, 2016, ISSN: 1471-2105.  DOI: [10.1186/s12859-016-1229-9](https://doi.org/10.1186/s12859-016-1229-9).
- 13 J. Albores-Saavedra, F. Chable-Montero, **D. Angeles-Albores**, A. Schwartz, D. S. Klimstra, and D. E. Henson, "Early Gallbladder Carcinoma," *American Journal of Clinical Pathology*, vol. 135, no. 4, pp. 637–642, Apr. 2011, ISSN: 0002-9173.  DOI: [10.1309/AJCPFRKCFEDLV03Y](https://doi.org/10.1309/AJCPFRKCFEDLV03Y).

- 14 J. Albores-Saavedra, A. M. Schwartz, D. E. Henson, L. Kostun, A. Hart, **D. Angeles-Albores**, and F. Chablé-Montero, "Cutaneous angiosarcoma. Analysis of 434 cases from the surveillance, epidemiology, and end results program, 1973-2007," *Annals of Diagnostic Pathology*, vol. 15, no. 2, pp. 93-97, 2011, ISSN: 10929134.  DOI: 10.1016/j.anndiagpath.2010.07.012.

## 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                           |