

# Stanford

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## Carlos Bustamante

Professor of Biomedical Data Science, of Genetics and, by courtesy, of Biology

 Curriculum Vitae available Online

### CONTACT INFORMATION

- **Alternate Contact**

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### Bio

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#### BIO

Dr. Carlos D. Bustamante is an internationally recognized leader in the application of data science and genomics technology to problems in medicine, agriculture, and biology. He received his Ph.D. in Biology and MS in Statistics from Harvard University (2001), was on the faculty at Cornell University (2002-9), and was named a MacArthur Fellow in 2010. He is currently Professor of Biomedical Data Science, Genetics, and (by courtesy) Biology at Stanford University. Dr. Bustamante has a passion for building new academic units, non-profits, and companies to solve pressing scientific challenges. He is Founding Director of the Stanford Center for Computational, Evolutionary, and Human Genomics (CEHG) and Inaugural Chair of the Department of Biomedical Data Science. He is the Owner and President of CDB Consulting, LTD. and also a Director at EdenRoc Sciences, LLC, founder of Arc Bio LLC (formerly IdentifyGenomics LLC and BigData Bio LLC), and an SAB member of Imprinted, Etalon DX, Columbia Care, and Digitalis Ventures.

#### ACADEMIC APPOINTMENTS

- Professor, Biomedical Data Science
- Professor, Genetics Operations
- Professor (By courtesy), Biology
- Member, Bio-X
- Member, Cardiovascular Institute
- Member, Maternal & Child Health Research Institute (MCHRI)
- Member, Stanford Cancer Institute

#### ADMINISTRATIVE APPOINTMENTS

- Founding Director, Stanford Center for Computational, Evolutionary, and Human Genetics (CEHG), (2012-2017)
- Inaugural Chair, Department of Biomedical Data Science, (2015-2019)

#### HONORS AND AWARDS

- Marshall Sherfield Fellow, Marshall Aid Commemoration Commission (2001-2)
- Sloan Research Fellow in Molecular Biology, Sloan Foundation (2007-9)
- Provost Award for Distinguished Research, Cornell University (2008)
- MacArthur Fellow, John D. and Catherine T. MacArthur Foundation (2010)

## **BOARDS, ADVISORY COMMITTEES, PROFESSIONAL ORGANIZATIONS**

- Editorial Boards, Genome Research (2008 - present)
- Advisory Board, Slim Initiative for Genomic Medicine in the Americas (2010 - present)
- Editorial Board, Human Biology (2010 - present)
- Advisory Board, External Evaluation Committee NIDDK T2D GENES project (2011 - present)
- Advisory Board, National Human Genome Research Institute Council (2011 - present)
- Advisory Board, Online Mendelian Inheritance in Man (OMIM) (2013 - present)
- Advisory Board, NIH Council of Councils (2013 - present)
- Advisory Board, National Geographic Genographic Project (2013 - present)
- Editorial Board, American Journal of Human Genetics (2013 - present)
- Senior Editor, Evolution, PLoS Genetics (2013 - present)

## **PROGRAM AFFILIATIONS**

- Institute for Computational and Mathematical Engineering (ICME)

## **PROFESSIONAL EDUCATION**

- B.A., Harvard University , Biology (1997)
- M.S., Harvard University , Statistics (2001)
- Ph.D., Harvard University , Biology (2001)
- Postdoc, University of Oxford , Mathematical Genetics (2002)

## **LINKS**

- Lab Website: <http://med.stanford.edu/bustamantelab>

## **Research & Scholarship**

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### **CURRENT RESEARCH AND SCHOLARLY INTERESTS**

My genetics research focuses on analyzing genome wide patterns of variation within and between species to address fundamental questions in biology, anthropology, and medicine. We focus on novel methods development for complex disease genetics and risk prediction in multi-ethnic settings. I am also interested in clinical data science and development of new diagnostics. I am also interested in disruptive innovation for healthcare including modeling long-term risk shifts and novel payment models.

### **CLINICAL TRIALS**

- Personal Genomics for Preventive Cardiology, Not Recruiting

## **Teaching**

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### **COURSES**

#### **2018-19**

- Biomedical Informatics Student Seminar: BIOMEDIN 201 (Aut)

#### **2016-17**

- Configuration of the US Healthcare System and the Application of Big Data/Analytics: BIODS 210 (Aut)

## STANFORD ADVISEES

### Postdoctoral Faculty Sponsor

Alexander Ioannidis, Alice Popejoy

### Postdoctoral Research Mentor

Jessica Chen, Aashish Jha, Alice Popejoy

## GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biology (School of Humanities and Sciences) (Phd Program)
- Biomedical Informatics (Masters Program)
- Biomedical Informatics (Phd Program)
- Genetics (Phd Program)

## Publications

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### PUBLICATIONS

- **Structural Variation Detection by Proximity Ligation from Formalin-Fixed, Paraffin-Embedded Tumor Tissue.** *The Journal of molecular diagnostics : JMD*  
Troll, C. J., Putnam, N. H., Hartley, P. D., Rice, B., Blanchette, M., Siddiqui, S., Ganbat, J., Powers, M. P., Ramakrishnan, R., Kunder, C. A., Bustamante, C. D., Zehnder, J. L., Green, et al  
2018
- **Polygenic risk scores: a biased prediction?** *Genome medicine*  
De La Vega, F. M., Bustamante, C. D.  
2018; 10 (1): 100
- **Rapid evolution of a skin-lightening allele in southern African KhoeSan.** *Proceedings of the National Academy of Sciences of the United States of America*  
Lin, M., Siford, R. L., Martin, A. R., Nakagome, S., Moller, M., Hoal, E. G., Bustamante, C. D., Gignoux, C. R., Henn, B. M.  
2018
- **Standardized biogeographic grouping system for annotating populations in pharmacogenetic research.** *Clinical pharmacology and therapeutics*  
Huddart, R., Fohner, A. E., Whirl-Carrillo, M., Wojcik, G. L., Gignoux, C. R., Popejoy, A. B., Bustamante, C. D., Altman, R. B., Klein, T. E.  
2018
- **The clinical imperative for inclusivity: Race, ethnicity, and ancestry (REA) in genomics.** *Human mutation*  
Popejoy, A. B., Ritter, D. I., Crooks, K., Currey, E., Fullerton, S. M., Hindorff, L. A., Koenig, B., Ramos, E. M., Sorokin, E. P., Wand, H., Wright, M. W., Zou, J., Gignoux, et al  
2018; 39 (11): 1713–20
- **DeepTag: inferring diagnoses from veterinary clinical notes** *NPJ DIGITAL MEDICINE*  
Nie, A., Zehnder, A., Page, R. L., Zhang, Y., Pineda, A., Rivas, M. A., Bustamante, C. D., Zou, J.  
2018; 1
- **Gene expression imputation identifies candidate genes and susceptibility loci associated with cutaneous squamous cell carcinoma.** *Nature communications*  
Ioannidis, N. M., Wang, W., Furlotte, N. A., Hinds, D. A., 23andMe Research Team, Bustamante, C. D., Jorgenson, E., Asgari, M. M., Whittemore, A. S., Agee, M., Alipanahi, B., Auton, A., Bell, R. K., et al  
2018; 9 (1): 4264
- **Data mining of digitized health records in a resource-constrained setting reveals that timely immunophenotyping is associated with improved breast cancer outcomes.** *BMC cancer*  
Lopez-Pineda, A., Rodriguez-Moran, M. F., Alvarez-Aguilar, C., Fuentes Valle, S. M., Acosta-Rosales, R., Bhatt, A. S., Sheth, S. N., Bustamante, C. D.  
2018; 18 (1): 933
- **Imputation-Aware Tag SNP Selection To Improve Power for Large-Scale, Multi-ethnic Association Studies.** *G3 (Bethesda, Md.)*  
Wojcik, G. L., Fuchsberger, C., Taliun, D., Welch, R., Martin, A. R., Shringarpure, S., Carlson, C. S., Abecasis, G., Kang, H. M., Boehnke, M., Bustamante, C. D., Gignoux, C. R., Kenny, et al

2018

- **In-solution Y-chromosome capture-enrichment on ancient DNA libraries** *BMC GENOMICS*  
Cruz-Davalos, D. I., Nieves-Colon, M. A., Sockell, A., Poznik, G., Schroeder, H., Stone, A. C., Bustamante, C. D., Malaspinas, A., Avila-Arcos, M. C.  
2018; 19: 608
- **Network enhancement as a general method to denoise weighted biological networks.** *Nature communications*  
Wang, B., Pourshafeie, A., Zitnik, M., Zhu, J., Bustamante, C. D., Batzoglou, S., Leskovec, J.  
2018; 9 (1): 3108
- **Ancient genomes from North Africa evidence prehistoric migrations to the Maghreb from both the Levant and Europe.** *Proceedings of the National Academy of Sciences of the United States of America*  
Fregel, R., Mendez, F. L., Bokbot, Y., Martin-Socas, D., Camalich-Massieu, M. D., Santana, J., Morales, J., Avila-Arcos, M. C., Underhill, P. A., Shapiro, B., Wojcik, G., Rasmussen, M., Soares, et al  
2018; 115 (26): 6774–79
- **Spectrum and prevalence of genetic predisposition in medulloblastoma: a retrospective genetic study and prospective validation in a clinical trial cohort** *LANCET ONCOLOGY*  
Waszak, S. M., Northcott, P. A., Buchhalter, I., Robinson, G. W., Sutter, C., Groebner, S., Grund, K. B., Brugieres, L., Jones, D. W., Pajtler, K. W., Morrissy, A., Kool, M., Sturm, et al  
2018; 19 (6): 785–98
- **Next-Generation Sequencing of the Complete Mitochondrial Genome of the Endangered Species Black Lion Tamarin *Leontopithecus chrysopygus* (Primates) and Mitogenomic Phylogeny Focusing on the Callitrichidae Family** *G3-GENES GENOMES GENETICS*  
de Freitas, P., Mendez, F., Chavez-Congrains, K., Galetti, P., Coutinho, L., Pissinatti, A., Bustamante, C.  
2018; 8 (6): 1985–91
- **Population structure in Argentina** *PLOS ONE*  
Muzzlo, M., Motti, J. B., Sepulveda, P., Yee, M., Cooke, T., Santos, M. R., Ramallo, V., Alfaro, E. L., Dipierri, J. E., Baillet, G., Bravi, C. M., Bustamante, C. D., Kenny, et al  
2018; 13 (5): e0196325
- **Medical relevance of protein-truncating variants across 337,205 individuals in the UK Biobank study** *NATURE COMMUNICATIONS*  
DeBoever, C., Tanigawa, Y., Lindholm, M. E., McInnes, G., Lavertu, A., Ingelsson, E., Chang, C., Ashley, E. A., Bustamante, C. D., Daly, M. J., Rivas, M. A.  
2018; 9: 1612
- **Genomic insights into the origin and diversification of late maritime hunter-gatherers from the Chilean Patagonia** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
de la Fuente, C., Avila-Arcos, M. C., Galimany, J., Carpenter, M. L., Homburger, J. R., Blanco, A., Contreras, P., Davalos, D., Reyes, O., Roman, M., Moreno-Estrada, A., Campos, P. F., Eng, et al  
2018; 115 (17): E4006–E4012
- **Whole-genome sequencing of Atacama skeleton shows novel mutations linked with dysplasia** *GENOME RESEARCH*  
Bhattacharya, S., Li, J., Sockell, A., Kan, M. J., Bava, F. A., Chen, S., Avila-Arcos, M. C., Ji, X., Smith, E., Asadi, N. B., Lachman, R. S., Lam, H. K., Bustamante, et al  
2018; 28 (4): 423–31
- **Whole-genome sequencing reveals the extent of heterozygosity in a preferentially self-fertilizing hermaphroditic vertebrate** *GENOME*  
Lins, L. F., Trojahn, S., Sockell, A., Yee, M., Tatarenkov, A., Bustamante, C. D., Earley, R. L., Kelley, J. L.  
2018; 61 (4): 241–47
- **Origins and genetic legacies of the Caribbean Taino** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Schroeder, H., Sikora, M., Gopalakrishnan, S., Cassidy, L. M., Delsere, P., Velasco, M., Schraiber, J. G., Rasmussen, S., Homburger, J. R., Avila-Arcos, M. C., Allentoft, M. E., Moreno-Mayar, J., Renaud, et al  
2018; 115 (10): 2341–46
- **A genome-wide association study identifies only two ancestry specific variants associated with spontaneous preterm birth** *SCIENTIFIC REPORTS*  
Rappoport, N., Toung, J., Hadley, D., Wong, R. J., Fujioka, K., Reuter, J., Abbott, C. W., Oh, S., Hu, D., Eng, C., Huntsman, S., Bodian, D. L., Niederhuber, et al  
2018; 8: 226

- **Population genomic analyses of the chocolate tree, *Theobroma cacao* L., provide insights into its domestication process.** *Communications biology*  
Cornejo, O. E., Yee, M., Dominguez, V., Andrews, M., Sockell, A., Strandberg, E., Livingstone, D. 3., Stack, C., Romero, A., Umaharan, P., Royaert, S., Tawari, N. R., Ng, et al  
2018; 1: 167
- **Gut microbiome transition across a lifestyle gradient in Himalaya.** *PLoS biology*  
Jha, A. R., Davenport, E. R., Gautam, Y., Bhandari, D., Tandukar, S., Ng, K. M., Fragiadakis, G. K., Holmes, S., Gautam, G. P., Leach, J., Sherchand, J. B., Bustamante, C. D., Sonnenburg, et al  
2018; 16 (11): e2005396
- **An admixture mapping meta-analysis implicates genetic variation at 18q21 with asthma susceptibility in Latinos** *THE JOURNAL OF ALLERGY AND CLINICAL IMMUNOLOGY*  
Gignoux, C. R., Torgerson, D. G., Pino-Yanes, M., Uricchio, L. H., Galanter, J., et al  
2018; in press
- **Complexities of gene expression patterns in natural populations of an extremophile fish (*Poecilia mexicana*, Poeciliidae)** *MOLECULAR ECOLOGY*  
Passow, C. N., Brown, A. P., Arias-Rodriguez, L., Yee, M., Sockell, A., Schartl, M., Warren, W. C., Bustamante, C., Kelley, J. L., Tobler, M.  
2017; 26 (16): 4211–25
- **Dispersals and genetic adaptation of Bantu-speaking populations in Africa and North America** *SCIENCE*  
Patin, E., Lopez, M., Grollemund, R., Verdu, P., Harmant, C., Quach, H., Laval, G., Perry, G. H., Barreiro, L. B., Froment, A., Heyer, E., Massougbdji, A., Fortes-Lima, et al  
2017; 356 (6337): 543-546
- **Identifying tagging SNPs for African specific genetic variation from the African Diaspora Genome** *SCIENTIFIC REPORTS*  
Johnston, H. R., Hu, Y., Gao, J., O'Connor, T. D., Abecasis, G. R., Wojcik, G. L., Gignoux, C. R., Gourraud, P., Lizee, A., Hansen, M., Genuario, R., Bullis, D., Lawley, et al  
2017; 7
- **Using genotype array data to compare multi- and single-sample variant calls and improve variant call sets from deep coverage whole-genome sequencing data** *BIOINFORMATICS*  
Shringarpure, S. S., Mathias, R. A., Hernandez, R. D., O'Connor, T. D., Szpiech, Z. A., Torres, R., De La Vega, F. M., Bustamante, C. D., Barnes, K. C., Taub, M. A.  
2017; 33 (8): 1147-1153
- **Human Demographic History Impacts Genetic Risk Prediction across Diverse Populations** *AMERICAN JOURNAL OF HUMAN GENETICS*  
Martin, A. R., Gignoux, C. R., Walters, R. K., Wojcik, G. L., Neale, B. M., Gravel, S., Daly, M. J., Bustamante, C. D., Kenny, E. E.  
2017; 100 (4): 635-649
- **A Complex, Polygenic Architecture for Lightened Skin Pigmentation in the Southern African KhoeSan**  
Martin, A. R., Gignoux, C. R., Lin, M., Granka, J. M., Adams, A., Liu, X., Atkinson, E. G., Guenther, C. A., Beleza, S., Werely, C. J., Myrick, J., Moller, M., Kingsley, et al  
WILEY.2017: 277
- **High Heritability and Ancestry Dominance are behind the Genetics of Short Stature in South African KhoeSan Populations**  
Lin, M., Granka, J. M., Martin, A. R., Myrick, J., Atkinson, E. G., Werely, C. J., Gurdasani, D., Pomilla, C., Carstensen, T., Scelza, B., Moller, M., Sandhu, M., Bustamante, et al  
WILEY.2017: 263–64
- **Population genetic analysis of the DARC locus (Duffy) reveals adaptation from standing variation associated with malaria resistance in humans** *PLOS GENETICS*  
McManus, K. F., Taravella, A. M., Henn, B. M., Bustamante, C. D., Sikora, M., Cornejo, O. E.  
2017; 13 (3)
- **Genetic effects on gene expression across human tissues.** *Nature*  
Battle, A., Brown, C. D., Engelhardt, B. E., Montgomery, S. B.  
2017; 550 (7675): 204–13
- **An Unexpectedly Complex Architecture for Skin Pigmentation in Africans.** *Cell*  
Martin, A. R., Lin, M., Granka, J. M., Myrick, J. W., Liu, X., Sockell, A., Atkinson, E. G., Werely, C. J., Möller, M., Sandhu, M. S., Kingsley, D. M., Hoal, E. G., Liu, et al

2017; 171 (6): 1340–53.e14

- **FIRE: functional inference of genetic variants that regulate gene expression.** *Bioinformatics (Oxford, England)*  
Ioannidis, N. M., Davis, J. R., DeGorter, M. K., Larson, N. B., McDonnell, S. K., French, A. J., Battle, A. J., Hastie, T. J., Thibodeau, S. N., Montgomery, S. B., Bustamante, C. D., Sieh, W., Whittemore, et al  
2017; 33 (24): 3895–3901
- **Using genotype array data to compare multi- and single-sample variant calls and improve variant call sets from deep coverage whole-genome sequencing data.** *Bioinformatics*  
Shringarpure, S. S., Mathias, R. A., Hernandez, R. D., O'Connor, T. D., Szpiech, Z. A., Torres, R., De La Vega, F. M., Bustamante, C. D., Barnes, K. C., Taub, M. A.  
2016
- **Strategies for Enriching Variant Coverage in Candidate Disease Loci on a Multiethnic Genotyping Array** *PLOS ONE*  
Bien, S. A., Wojcik, G. L., Zubair, N., Gignoux, C. R., Martin, A. R., Kocarnik, J. M., Martin, L. W., Buyske, S., Haessler, J., Walker, R. W., Cheng, I., Graff, M., Xia, et al  
2016; 11 (12)
- **A continuum of admixture in the Western Hemisphere revealed by the African Diaspora genome** *NATURE COMMUNICATIONS*  
Mathias, R. A., Taub, M. A., Gignoux, C. R., Fu, W., Musharoff, S., O'Connor, T. D., Vergara, C., Torgerson, D. G., Pino-Yanes, M., Shringarpure, S. S., Huang, L., Rafaels, N., Boorgula, et al  
2016; 7
- **REVEL: An Ensemble Method for Predicting the Pathogenicity of Rare Missense Variants** *AMERICAN JOURNAL OF HUMAN GENETICS*  
Ioannidis, N. M., Rothstein, J. H., Pejaver, V., Middha, S., McDonnell, S. K., Baheti, S., Musolf, A., Li, Q., Holzinger, E., Karyadi, D., Cannon-Albright, L. A., Teerlink, C. C., Stanford, et al  
2016; 99 (4): 877-885
- **Multidimensional structure-function relationships in human beta-cardiac myosin from population-scale genetic variation** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Homburger, J. R., Green, E. M., Caleshu, C., Sunitha, M. S., Taylor, R. E., Ruppel, K. M., Metpally, R. P., Colan, S. D., Michels, M., Day, S. M., Olivotto, I., Bustamante, C. D., Dewey, et al  
2016; 113 (24): 6701-6706
- **Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences** *NATURE GENETICS*  
Poznik, G. D., Xue, Y., Mendez, F. L., Willems, T. F., Massaia, A., Sayres, M. A., Ayub, Q., McCarthy, S. A., Narechania, A., Kashin, S., Chen, Y., Banerjee, R., Rodriguez-Flores, et al  
2016; 48 (6): 593-?
- **Mechanisms Underlying Adaptation to Life in Hydrogen Sulfide-Rich Environments** *MOLECULAR BIOLOGY AND EVOLUTION*  
Kelley, J. L., Arias-Rodriguez, L., Martin, D. P., Yee, M., Bustamante, C. D., Tobler, M.  
2016; 33 (6): 1419-1434
- **Efficient analysis of large datasets and sex bias with ADMIXTURE** *BMC BIOINFORMATICS*  
Shringarpure, S. S., Bustamante, C. D., Lange, K., Alexander, D. H.  
2016; 17
- **The Great Migration and African-American Genomic Diversity** *PLOS GENETICS*  
Baharian, S., Barakatt, M., Gignoux, C. R., Shringarpure, S., Errington, J., Blot, W. J., Bustamante, C. D., Kenny, E. E., Williams, S. M., Aldrich, M. C., Gravel, S.  
2016; 12 (5)
- **A research roadmap for next-generation sequencing informatics** *SCIENCE TRANSLATIONAL MEDICINE*  
Altman, R. B., Prabhu, S., Sidow, A., Zook, J. M., Goldfeder, R., Litwack, D., Ashley, E., Asimenos, G., Bustamante, C. D., Donigan, K., Giacomini, K. M., Johansen, E., Khuri, et al  
2016; 8 (335)
- **The Time Scale of Recombination Rate Evolution in Great Apes.** *Molecular biology and evolution*  
Stevison, L. S., Woerner, A. E., Kidd, J. M., Kelley, J. L., Veeramah, K. R., McManus, K. F., Bustamante, C. D., Hammer, M. F., Wall, J. D.  
2016; 33 (4): 928-945
- **Demographically-Based Evaluation of Genomic Regions under Selection in Domestic Dogs** *PLOS GENETICS*

- Freedman, A. H., Schweizer, R. M., Ortega-Del Vecchyo, D., Han, E., Davis, B. W., Gronau, I., Silva, P. M., Galaverni, M., Fan, Z., Marx, P., Lorente-Galdos, B., Ramirez, O., Hormozdiari, et al  
2016; 12 (3)
- **GBStools: A Statistical Method for Estimating Allelic Dropout in Reduced Representation Sequencing Data** *PLOS GENETICS*  
Cooke, T. F., Yee, M., Muzzio, M., Sockell, A., Bell, R., Cornejo, O. E., Kelley, J. L., Bailliet, G., Bravi, C. M., Bustamante, C. D., Kenny, E. E.  
2016; 12 (2)
  - **GBStools: A Statistical Method for Estimating Allelic Dropout in Reduced Representation Sequencing Data.** *PLoS genetics*  
Cooke, T. F., Yee, M., Muzzio, M., Sockell, A., Bell, R., Cornejo, O. E., Kelley, J. L., Bailliet, G., Bravi, C. M., Bustamante, C. D., Kenny, E. E.  
2016; 12 (2)
  - **Distance from sub-Saharan Africa predicts mutational load in diverse human genomes** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Henn, B. M., Botigue, L. R., Peischl, S., Dupanloup, I., Lipatov, M., Maples, B. K., Martin, A. R., Musharoff, S., Cann, H., Snyder, M. P., Excoffier, L., Kidd, J. M., Bustamante, et al  
2016; 113 (4): E440-E449
  - **An Efficient Multiple-Testing Adjustment for eQTL Studies that Accounts for Linkage Disequilibrium between Variants** *AMERICAN JOURNAL OF HUMAN GENETICS*  
Davis, J. R., Fresard, L., Knowles, D. A., Pala, M., Bustamante, C. D., Battle, A., Montgomery, S. B.  
2016; 98 (1): 216-224
  - **The Genome of the Self-Fertilizing Mangrove Rivulus Fish, *Kryptolebias marmoratus*: A Model for Studying Phenotypic Plasticity and Adaptations to Extreme Environments.** *Genome biology and evolution*  
Kelley, J. L., Yee, M., Brown, A. P., Richardson, R. R., Tatarenkov, A., Lee, C. C., Harkins, T. T., Bustamante, C. D., Earley, R. L.  
2016; 8 (7): 2145-2154
  - **The African Turquoise Killifish Genome Provides Insights into Evolution and Genetic Architecture of Lifespan** *CELL*  
Valenzano, D. R., Benayoun, B. A., Singh, P. P., Zhang, E., Etter, P. D., Hu, C., Clement-Ziza, M., Willemsen, D., Cui, R., Harel, I., Machado, B. E., Yee, M., Sharp, et al  
2015; 163 (6): 1539-1554
  - **Genomic Insights into the Ancestry and Demographic History of South America.** *PLoS genetics*  
Homburger, J. R., Moreno-Estrada, A., Gignoux, C. R., Nelson, D., Sanchez, E., Ortiz-Tello, P., Pons-Estel, B. A., Acevedo-Vasquez, E., Miranda, P., Langefeld, C. D., Gravel, S., Alarcón-Riquelme, M. E., Bustamante, et al  
2015; 11 (12)
  - **Genomic Insights into the Ancestry and Demographic History of South America** *PLOS GENETICS*  
Homburger, J. R., Moreno-Estrada, A., Gignoux, C. R., Nelson, D., Sanchez, E., Ortiz-Tello, P., Pons-Estel, B. A., Acevedo-Vasquez, E., Miranda, P., Langefeld, C. D., Gravel, S., Alarcon-Riquelme, M. E., Bustamante, et al  
2015; 11 (12)
  - **Discovery and functional characterization of a neomorphic PTEN mutation** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Costa, H. A., Leitner, M. G., Sos, M. L., Mavrantoni, A., Rychkova, A., Johnson, J. R., Newton, B. W., Yee, M., De La Vega, F. M., Ford, J. M., Krogan, N. J., Shokat, K. M., Oliver, et al  
2015; 112 (45): 13976-13981
  - **Privacy Risks from Genomic Data-Sharing Beacons** *AMERICAN JOURNAL OF HUMAN GENETICS*  
Shringarpure, S. S., Bustamante, C. D.  
2015; 97 (5): 631-646
  - **Genetic structure in village dogs reveals a Central Asian domestication origin** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Shannon, L. M., Boyko, R. H., Castelhanos, M., Corey, E., Hayward, J. J., McLean, C., White, M. E., Said, M. A., Anita, B. A., Bondjengo, N. I., Calero, J., Galov, A., Hedimbi, et al  
2015; 112 (44): 13639-13644
  - **Chemically tunable mucin chimeras assembled on living cells** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Kramer, J. R., Onoa, B., Bustamante, C., Bertozzi, C. R.

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