Stanford

Manuel Rivas

Assistant Professor of Biomedical Data Science

Department of Biomedical Data Science

NIH Biosketch available Online

Bio

ACADEMIC APPOINTMENTS

- Assistant Professor, Department of Biomedical Data Science
- Member, Bio-X
- Member, Stanford Medicine Children's Health Center for IBD and Celiac Disease

HONORS AND AWARDS

- Clarendon Scholar, University of Oxford (2010-2015)
- Osler Award, University of Oxford (2010-2015)
- Gates Millenium Scholar, Bill & Melinda Gates Foundation (2004-2008)

PROFESSIONAL EDUCATION

- DPhil, University of Oxford , Clinical Medicine (2015)
- B.S., Massachusetts Institute of Technology , Mathematics (2008)

LINKS

- My Lab Site: http://med.stanford.edu/rivaslab

Teaching

COURSES

2024-25

- Workshop in Biostatistics: BIODS 260C, STATS 260C (Spr)

2023-24

- Generative AI in Healthcare: BIODS 295, DESIGN 266 (Spr)
- Workshop in Biostatistics: BIODS 260A, STATS 260A (Aut)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Ashley Lewis, Min Sun

Postdoctoral Faculty Sponsor

Tuomo Kiiskinen

Publications

PUBLICATIONS

- **Efficient storage and regression computation for population-scale genome sequencing studies.** *Bioinformatics (Oxford, England)*
  Rivas, M. A., Chang, C.
  2025

- **Unified meta regression models for rare variant association studies.** *bioRxiv : the preprint server for biology*
  Lauer, L., Rivas, M. A.
  2025

- **Standardized Measurement of Type 1 Diabetes Polygenic Risk Across Multi-Ancestry Population Cohorts.** *medRxiv : the preprint server for health sciences*
  Luckett, A. M., Oram, R. A., Deutsch, A. J., Ortega, H. I., Fraser, D. P., Ashok, K., Manning, A. K., Mercader, J. M., Rivas, M., Udler, M. S., Weedon, M. N., Gloyn, A. L., Sharp, et al
  2025

- **Efficient storage and regression computation for population-scale genome sequencing studies.** *bioRxiv : the preprint server for biology*
  Rivas, M. A., Chang, C.
  2024

- **Survival Analysis on Rare Events Using Group-Regularized Multi-Response Cox Regression.** *Bioinformatics (Oxford, England)*
  Li, R., Tanigawa, Y., Justesen, J. M., Taylor, J., Hastie, T., Tibshirani, R., Rivas, M. A.
  2021

- **Polygenic risk modeling with latent trait-related genetic components.** *European journal of human genetics : EJHG*
  Aguirre, M., Tanigawa, Y., Venkataraman, G. R., Tibshirani, R., Hastie, T., Rivas, M. A.
  2021

- **Genetics of 35 blood and urine biomarkers in the UK Biobank.** *Nature genetics*
  Sinnott-Armstrong, N., Tanigawa, Y., Amar, D., Mars, N., Benner, C., Aguirre, M., Venkataraman, G. R., Wainberg, M., Ollila, H. M., Kiiskinen, T., Havulinna, A. S., Pirruccello, J. P., Qian, et al
  2021

- **Graphical analysis for phenome-wide causal discovery in genotyped population-scale biobanks.** *Nature communications*
  Amar, D., Sinnott-Armstrong, N., Ashley, E. A., Rivas, M. A.
  2021; 12 (1): 350

- **Sex-specific genetic effects across biomarkers.** *European journal of human genetics : EJHG*
  Flynn, E., Tanigawa, Y., Rodriguez, F., Altman, R. B., Sinnott-Armstrong, N., Rivas, M. A.
  2020

- **Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma** *PLOS GENETICS*
  Tanigawa, Y., Wainberg, M., Karjalainen, J., Kiiskinen, T., Venkataraman, G., Lemmela, S., Turunen, J. A., Graham, R. R., Havulinna, A. S., Perola, M., Palotie, A., Gen, F., Daly, et al
  2020; 16 (5)

- **A fast and scalable framework for large-scale and ultrahigh-dimensional sparse regression with application to the UK Biobank.** *PLoS genetics*
  Qian, J. n., Tanigawa, Y. n., Du, W. n., Aguirre, M. n., Chang, C. n., Tibshirani, R. n., Rivas, M. A., Hastie, T. n.
  2020; 16 (10): e1009141

- **Assessing Digital Phenotyping to Enhance Genetic Studies of Human Diseases.** *American journal of human genetics*
  DeBoever, C. n., Tanigawa, Y. n., Aguirre, M. n., McInnes, G. n., Lavertu, A. n., Rivas, M. A.
  2020

- **Fast Lasso method for large-scale and ultrahigh-dimensional Cox model with applications to UK Biobank.** *Biostatistics (Oxford, England)*
  Li, R. n., Chang, C. n., Justesen, J. M., Tanigawa, Y. n., Qiang, J. n., Hastie, T. n., Rivas, M. A., Tibshirani, R. n.
  2020

- **Homogeneity in the association of body mass index with type 2 diabetes across the UK Biobank: A Mendelian randomization study.** *PLoS medicine*
  Wainberg, M., Mahajan, A., Kundaje, A., McCarthy, M. I., Ingelsson, E., Sinnott-Armstrong, N., Rivas, M. A.
  2019; 16 (12): e1002982
- **Rare and common variant discovery in complex disease: the IBD case study.** *Human molecular genetics*
  Venkataraman, G. R., Rivas, M. A.
  2019
- **Phenome-wide Burden of Copy-Number Variation in the UK Biobank.** *American journal of human genetics*
  Aguirre, M., Rivas, M. A., Priest, J.
  2019
- **Global Biobank Engine: enabling genotype-phenotype browsing for biobank summary statistics** *BIOINFORMATICS*
  McInnes, G., Tanigawa, Y., DeBoever, C., Lavertu, A., Olivieri, J., Aguirre, M., Rivas, M. A.
  2019; 35 (14): 2495–97
- **Opportunities and challenges for transcriptome-wide association studies.** *Nature genetics*
  Wainberg, M., Sinnott-Armstrong, N., Mancuso, N., Barbeira, A. N., Knowles, D. A., Golan, D., Ermel, R., Ruusalepp, A., Quertermous, T., Hao, K., Björkegren, J. L., Im, H. K., Pasaniuc, et al
  2019; 51 (4): 592-599
- **Opportunities and challenges for transcriptome-wide association studies** *NATURE GENETICS*
  Wainberg, M., Sinnott-Armstrong, N., Mancuso, N., Barbeira, A. N., Knowles, D. A., Golan, D., Ermel, R., Ruusalepp, A., Quertermous, T., Hao, K., Bjorkegren, J. M., Im, H., Pasaniuc, et al
  2019; 51 (4): 592–99
- **Significant shared heritability underlies suicide attempt and clinically predicted probability of attempting suicide.** *Molecular psychiatry*
  Ruderfer, D. M., Walsh, C. G., Aguirre, M. W., Tanigawa, Y., Ribeiro, J. D., Franklin, J. C., Rivas, M. A.
  2019
- **Components of genetic associations across 2,138 phenotypes in the UK Biobank highlight adipocyte biology.** *Nature communications*
  Tanigawa, Y. n., Li, J. n., Justesen, J. M., Horn, H. n., Aguirre, M. n., DeBoever, C. n., Chang, C. n., Narasimhan, B. n., Lage, K. n., Hastie, T. n., Park, C. Y., Bejerano, G. n., Ingelsson, et al
  2019; 10 (1): 4064
- **Global Biobank Engine: enabling genotype-phenotype browsing for biobank summary statistics.** *Bioinformatics (Oxford, England)*
  McInnes, G., Tanigawa, Y., DeBoever, C., Lavertu, A., Olivieri, J. E., Aguirre, M., Rivas, M. A.
  2018
- **DeepTag: inferring diagnoses from veterinary clinical notes.** *NPJ digital medicine*
  Nie, A., Zehnder, A., Page, R. L., Zhang, Y., Pineda, A. L., Rivas, M. A., Bustamante, C. D., Zou, J.
  2018; 1: 60
- **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
- **Insights into the genetic epidemiology of Crohn's and rare diseases in the Ashkenazi Jewish population.** *PLoS genetics*
  Rivas, M. A., Avila, B. E., Koskela, J., Huang, H., Stevens, C., Pirinen, M., Haritunians, T., Neale, B. M., Kurki, M., Ganna, A., Graham, D., Glaser, B., Peter, et al
  2018; 14 (5): e1007329
- **A protein-truncating R179X variant in RNF186 confers protection against ulcerative colitis** *NATURE COMMUNICATIONS*
  Rivas, M. A., Graham, D., Sulem, P., Stevens, C., Desch, A. N., Goyette, P., Gudbjartsson, D., Jonsdottir, I., Thorsteinsdottir, U., Degenhardt, F., Mucha, S., Kurki, M. I., Li, et al
  2016; 7
- **Discovery of rare variants for complex phenotypes** *HUMAN GENETICS*
  Kosmicki, J. A., Churchhouse, C. L., Rivas, M. A., Neale, B. M.

2016; 135 (6): 625-634

- **Assessing allele-specific expression across multiple tissues from RNA-seq read data** *BIOINFORMATICS*
  Pirinen, M., Lappalainen, T., Zaitlen, N. A., Dermitzakis, E. T., Donnelly, P., McCarthy, M. I., Rivas, M. A.
  2015; 31 (15): 2497-2504

- **Effect of predicted protein-truncating genetic variants on the human transcriptome** *SCIENCE*
  Rivas, M. A., Pirinen, M., Conrad, D. F., Lek, M., Tsang, E. K., Karczewski, K. J., Maller, J. B., Kukurba, K. R., DeLuca, D. S., Fromer, M., Ferreira, P. G., Smith, K. S., Zhang, et al
  2015; 348 (6235): 666-669

- **The Power of Gene-Based Rare Variant Methods to Detect Disease-Associated Variation and Test Hypotheses About Complex Disease** *PLOS GENETICS*
  Moutsianas, L., Agarwala, V., Fuchsberger, C., Flannick, J., Rivas, M. A., Gaulton, K. J., Albers, P. K., McVean, G., Boehnke, M., Altshuler, D., McCarthy, M. I.
  2015; 11 (4)

- **Choice of transcripts and software has a large effect on variant annotation** *GENOME MEDICINE*
  McCarthy, D. J., Humburg, P., Kanapin, A., Rivas, M. A., Gaulton, K., Cazier, J., Donnelly, P.
  2014; 6

- **Assessing association between protein truncating variants and quantitative traits** *BIOINFORMATICS*
  Rivas, M. A., Pirinen, M., Neville, M. J., Gaulton, K. J., Moutsianas, L., Lindgren, C. M., Karpe, F., McCarthy, M. I., Donnelly, P.
  2013; 29 (19): 2419-2426

- **Transcriptome and genome sequencing uncovers functional variation in humans.** *Nature*
  Lappalainen, T., Sammeth, M., Friedländer, M. R., 't Hoen, P. A., Monlong, J., Rivas, M. A., Gonzàlez-Porta, M., Kurbatova, N., Griebel, T., Ferreira, P. G., Barann, M., Wieland, T., Greger, et al
  2013; 501 (7468): 506-511

- **Deep Resequencing of GWAS Loci Identifies Rare Variants in CARD9, IL23R and RNF186 That Are Associated with Ulcerative Colitis** *PLOS GENETICS*
  Beaudoin, M., Goyette, P., Boucher, G., Lo, K. S., Rivas, M. A., Stevens, C., Alikashani, A., Ladouceur, M., Ellinghaus, D., Torkvist, L., Goel, G., Lagace, C., Annese, et al
  2013; 9 (9)

- **A Flexible Approach for the Analysis of Rare Variants Allowing for a Mixture of Effects on Binary or Quantitative Traits** *PLOS GENETICS*
  Clarke, G. M., Rivas, M. A., Morris, A. P.
  2013; 9 (8)

- **Deep resequencing of GWAS loci identifies independent rare variants associated with inflammatory bowel disease** *NATURE GENETICS*
  Rivas, M. A., Beaudoin, M., Gardet, A., Stevens, C., Sharma, Y., Zhang, C. K., Boucher, G., Ripke, S., Ellinghaus, D., Burtt, N., Fennell, T., Kirby, A., Latiano, et al
  2011; 43 (11): 1066-U50

- **A framework for variation discovery and genotyping using next-generation DNA sequencing data** *NATURE GENETICS*
  DePristo, M. A., Banks, E., Poplin, R., Garimella, K. V., Maguire, J. R., Hartl, C., Philippakis, A. A., del Angel, G., Rivas, M. A., Hanna, M., McKenna, A., Fennell, T. J., Kernytsky, et al
  2011; 43 (5): 491-?

- **Testing for an Unusual Distribution of Rare Variants** *PLOS GENETICS*
  Neale, B. M., Rivas, M. A., Voight, B. F., Altshuler, D., Devlin, B., Orho-Melander, M., Kathiresan, S., Purcell, S. M., Roeder, K., Daly, M. J.
  2011; 7 (3)

- **Panel stacking is a threat to consensus statement validity.** *Journal of clinical epidemiology*
  Kepp, K. P., Aavitsland, P., Ballin, M., Balloux, F., Baral, S., Bardosh, K., Bauchner, H., Bendavid, E., Bhopal, R., Blumstein, D. T., Boffetta, P., Bourgeois, F., Brufsky, et al
  2024: 111428

- **Integrative machine learning approaches for predicting disease risk using multi-omics data from the UK Biobank.** *bioRxiv : the preprint server for biology*
  Aguilar, O., Chang, C., Bismuth, E., Rivas, M. A.

2024

- **Comprehensive Inherited Risk Estimation for Risk-Based Breast Cancer Screening in Women.** *Journal of clinical oncology : official journal of the American Society of Clinical Oncology*
  Mars, N., Kerminen, S., Tamlander, M., Pirinen, M., Jakkula, E., Aaltonen, K., Meretoja, T., Heinavaara, S., Widen, E., Ripatti, S., FinnGen, Palotie, A., Daly, M., et al
  2024: JCO2300295

- **Narcolepsy risk loci outline role of T cell autoimmunity and infectious triggers in narcolepsy.** *Nature communications*
  Ollila, H. M., Sharon, E., Lin, L., Sinnott-Armstrong, N., Ambati, A., Yogeshwar, S. M., Hillary, R. P., Jolanki, O., Faraco, J., Einen, M., Luo, G., Zhang, J., Han, et al
  2023; 14 (1): 2709

- **SGLT2 inhibitor ameliorates endothelial dysfunction associated with the common ALDH2 alcohol flushing variant.** *Science translational medicine*
  Guo, H., Yu, X., Liu, Y., Paik, D. T., Justesen, J. M., Chandy, M., Jahng, J. W., Zhang, T., Wu, W., Rwere, F., Zhao, S. R., Pokhrel, S., Shivnaraine, et al
  2023; 15 (680): eabp9952

- **LARGE-SCALE MULTIVARIATE SPARSE REGRESSION WITH APPLICATIONS TO UK BIOBANK** *ANNALS OF APPLIED STATISTICS*
  Qian, J., Tanigawa, Y., Li, R., Tibshirani, R., Rivas, M. A., Hastie, T.
  2022; 16 (3): 1891-1918

- **Deconvoluting complex correlates of COVID-19 severity with a multi-omic pandemic tracking strategy.** *Nature communications*
  Parikh, V. N., Ioannidis, A. G., Jimenez-Morales, D., Gorzynski, J. E., De Jong, H. N., Liu, X., Roque, J., Cepeda-Espinoza, V. P., Osoegawa, K., Hughes, C., Sutton, S. C., Youlton, N., Joshi, et al
  2022; 13 (1): 5107

- **Large-scale sequencing identifies multiple genes and rare variants associated with Crohn's disease susceptibility.** *Nature genetics*
  Sazonovs, A., Stevens, C. R., Venkataraman, G. R., Yuan, K., Avila, B., Abreu, M. T., Ahmad, T., Allez, M., Ananthakrishnan, A. N., Atzmon, G., Baras, A., Barrett, J. C., Barzilai, et al
  2022

- **High heritability of ascending aortic diameter and trans-ancestry prediction of thoracic aortic disease.** *Nature genetics*
  Tcheandjieu, C., Xiao, K., Tejeda, H., Lynch, J. A., Ruotsalainen, S., Bellomo, T., Palnati, M., Judy, R., Klarin, D., Kember, R. L., Verma, S., Palotie, A., Daly, et al
  2022

- **Opportunities and challenges for the use of common controls in sequencing studies.** *Nature reviews. Genetics*
  Wojcik, G. L., Murphy, J., Edelson, J. L., Gignoux, C. R., Ioannidis, A. G., Manning, A., Rivas, M. A., Buyske, S., Hendricks, A. E.
  2022

- **Integration of rare expression outlier-associated variants improves polygenic risk prediction.** *American journal of human genetics*
  Smail, C., Ferraro, N. M., Hui, Q., Durrant, M. G., Aguirre, M., Tanigawa, Y., Keever-Keigher, M. R., Rao, A. S., Justesen, J. M., Li, X., Gloudemans, M. J., Assimes, T. L., Kooperberg, et al
  2022

- **Cannabinoid receptor 1 antagonist genistein attenuates marijuana-induced vascular inflammation.** *Cell*
  Wei, T. T., Chandy, M., Nishiga, M., Zhang, A., Kumar, K. K., Thomas, D., Manhas, A., Rhee, S., Justesen, J. M., Chen, I. Y., Wo, H. T., Khanamiri, S., Yang, et al
  2022

- **Significant sparse polygenic risk scores across 813 traits in UK Biobank.** *PLoS genetics*
  Tanigawa, Y., Qian, J., Venkataraman, G., Justesen, J. M., Li, R., Tibshirani, R., Hastie, T., Rivas, M. A.
  2022; 18 (3): e1010105

- **Bayesian model comparison for rare-variant association studies.** *American journal of human genetics*
  Venkataraman, G. R., DeBoever, C., Tanigawa, Y., Aguirre, M., Ioannidis, A. G., Mostafavi, H., Spencer, C. C., Poterba, T., Bustamante, C. D., Daly, M. J., Pirinen, M., Rivas, M. A.
  2021

- **A cross-population atlas of genetic associations for 220 human phenotypes.** *Nature genetics*
  Sakaue, S., Kanai, M., Tanigawa, Y., Karjalainen, J., Kurki, M., Koshiba, S., Narita, A., Konuma, T., Yamamoto, K., Akiyama, M., Ishigaki, K., Suzuki, A., Suzuki, et al
  2021

- **APOC3 genetic variation, serum triglycerides, and risk of coronary artery disease in Asian Indians, Europeans, and other ethnic groups.** *Lipids in health and disease*
  Goyal, S., Tanigawa, Y., Zhang, W., Chai, J., Almeida, M., Sim, X., Lerner, M., Chainakul, J., Ramiu, J. G., Seraphin, C., Apple, B., Vaughan, A., Muniu, et al
  2021; 20 (1): 113

- **Mapping the human genetic architecture of COVID-19.** *Nature*
  COVID-19 Host Genetics Initiative
  2021

- **Fast Numerical Optimization for Genome Sequencing Data in Population Biobanks.** *Bioinformatics (Oxford, England)*
  Li, R., Chang, C., Tanigawa, Y., Narasimhan, B., Hastie, T., Tibshirani, R., Rivas, M. A.
  2021

- **Exome Sequencing in Patient-Parent Trios Suggests New Candidate Genes for Early-onset Primary Sclerosing Cholangitis.** *Liver international : official journal of the International Association for the Study of the Liver*
  Haisma, S., Weersma, R. K., Joosse, M. E., de Koning, B. A., de Meij, T., Koot, B. G., Wolters, V., Norbruis, O., Daly, M. J., Stevens, C., Xavier, R. J., Koskela, J., Rivas, et al
  2021

- **GWAS of three molecular traits highlights core genes and pathways alongside a highly polygenic background.** *eLife*
  Sinnott-Armstrong, N., Naqvi, S., Rivas, M., Pritchard, J. K.
  2021; 10

- **A regulatory variant at 3q21.1 confers an increased pleiotropic risk for hyperglycemia and altered bone mineral density.** *Cell metabolism*
  Sinnott-Armstrong, N., Sousa, I. S., Laber, S., Rendina-Ruedy, E., Nitter Dankel, S. E., Ferreira, T., Mellgren, G., Karasik, D., Rivas, M., Pritchard, J., Guntur, A. R., Cox, R. D., Lindgren, et al
  2021

- **Sleep apnoea is a risk factor for severe COVID-19.** *BMJ open respiratory research*
  Strausz, S., Kiiskinen, T., Broberg, M., Ruotsalainen, S., Koskela, J., Bachour, A., FinnGen, Palotie, A., Palotie, T., Ripatti, S., Ollila, H. M., Palotie, A., Daly, M., et al
  2021; 8 (1)

- **Combining Clinical and Polygenic Risk Improves Stroke Prediction Among Individuals with Atrial Fibrillation.** *Circulation. Genomic and precision medicine*
  O'Sullivan, J. W., Shcherbina, A., Justesen, J. M., Turakhia, M., Perez, M., Wand, H., Tcheandjieu, C., Clarke, S. L., Rivas, M. A., Ashley, E. A.
  2021

- **Time trajectories in the transcriptomic response to exercise - a meta-analysis.** *Nature communications*
  Amar, D., Lindholm, M. E., Norrbom, J., Wheeler, M. T., Rivas, M. A., Ashley, E. A.
  2021; 12 (1): 3471

- **Association of accelerometer-derived sleep measures with lifetime psychiatric diagnoses: A cross-sectional study of 89,205 participants from the UK Biobank.** *PLoS medicine*
  Wainberg, M., Jones, S. E., Beaupre, L. M., Hill, S. L., Felsky, D., Rivas, M. A., Lim, A. S., Ollila, H. M., Tripathy, S. J.
  2021; 18 (10): e1003782

- **Efficient Computation and Analysis of Distributional Shapley Values**
  Kwon, Y., Rivas, M. A., Zou, J., Banerjee, A., Fukumizu, K.
  MICROTOME PUBLISHING.2021

- **Nonsense-mediated decay is highly stable across individuals and tissues.** *American journal of human genetics*
  Teran, N. A., Nachun, D. C., Eulalio, T., Ferraro, N. M., Smail, C., Rivas, M. A., Montgomery, S. B.
  2021

- **Significant shared heritability underlies suicide attempt and clinically predicted probability of attempting suicide** *MOLECULAR PSYCHIATRY*
  Ruderfer, D. M., Walsh, C. G., Aguirre, M. W., Tanigawa, Y., Ribeiro, J. D., Franklin, J. C., Rivas, M. A.
  2020; 25 (10): 2422–30

- **Race, socioeconomic deprivation, and hospitalization for COVID-19 in English participants of a national biobank.** *International journal for equity in health*
  Patel, A. P., Paranjpe, M. D., Kathiresan, N. P., Rivas, M. A., Khera, A. V.
  2020; 19 (1): 114

- **Molecular Transducers of Physical Activity Consortium (MoTrPAC): Mapping the Dynamic Responses to Exercise.** *Cell*
  Sanford, J. A., Nogiec, C. D., Lindholm, M. E., Adkins, J. N., Amar, D., Dasari, S., Drugan, J. K., Fernandez, F. M., Radom-Aizik, S., Schenk, S., Snyder, M. P., Tracy, R. P., Vanderboom, et al
  2020; 181 (7): 1464–74

- **Race, Socioeconomic Deprivation, and Hospitalization for COVID-19 in English participants of a National Biobank.** *medRxiv : the preprint server for health sciences*
  Patel, A. P., Paranjpe, M. D., Kathiresan, N. P., Rivas, M. A., Khera, A. V.
  2020

- **Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma.** *PLoS genetics*
  Tanigawa, Y., Wainberg, M., Karjalainen, J., Kiiskinen, T., Venkataraman, G., Lemmela, S., Turunen, J. A., Graham, R. R., Havulinna, A. S., Perola, M., Palotie, A., FinnGen, Daly, M. J., et al
  2020; 16 (5): e1008682

- **Whole exome sequencing analyses reveal gene-microbiota interactions in the context of IBD.** *Gut*
  Hu, S. n., Vich Vila, A. n., Gacesa, R. n., Collij, V. n., Stevens, C. n., Fu, J. M., Wong, I. n., Talkowski, M. E., Rivas, M. A., Imhann, F. n., Bolte, L. n., van Dullemen, H. n., Dijkstra, et al
  2020

- **A phenome-wide association study of 26 mendelian genes reveals phenotypic expressivity of common and rare variants within the general population.** *PLoS genetics*
  Tcheandjieu, C. n., Aguirre, M. n., Gustafsson, S. n., Saha, P. n., Potiny, P. n., Haendel, M. n., Ingelsson, E. n., Rivas, M. A., Priest, J. R.
  2020; 16 (11): e1008802

- **FasTag: Automatic text classification of unstructured medical narratives.** *PloS one*
  Venkataraman, G. R., Pineda, A. L., Bear Don't Walk Iv, O. J., Zehnder, A. M., Ayyar, S., Page, R. L., Bustamante, C. D., Rivas, M. A.
  2020; 15 (6): e0234647

- **Cardiac Imaging of Aortic Valve Area from 34,287 UK Biobank Participants Reveal Novel Genetic Associations and Shared Genetic Comorbidity with Multiple Disease Phenotypes.** *Circulation. Genomic and precision medicine*
  Córdova-Palomera, A. n., Tcheandjieu, C. n., Fries, J. n., Varma, P. n., Chen, V. S., Fiterau, M. n., Xiao, K. n., Tejeda, H. n., Keavney, B. n., Cordell, H. J., Tanigawa, Y. n., Venkataraman, G. n., Rivas, et al
  2020

- **The role of polygenic risk and susceptibility genes in breast cancer over the course of life.** *Nature communications*
  Mars, N., Widen, E., Kerminen, S., Meretoja, T., Pirinen, M., Della Briotta Parolo, P., Palta, P., FinnGen, Palotie, A., Kaprio, J., Joensuu, H., Daly, M., Ripatti, S., et al
  2020; 11 (1): 6383

- **Genetic architecture of human plasma lipidome and its link to cardiovascular disease.** *Nature communications*
  Tabassum, R., Ramo, J. T., Ripatti, P., Koskela, J. T., Kurki, M., Karjalainen, J., Palta, P., Hassan, S., Nunez-Fontarnau, J., Kiiskinen, T. T., Soderlund, S., Matikainen, N., Gerl, et al
  2019; 10 (1): 4329

- **Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution** *NATURE GENETICS*
  Justice, A. E., Karaderi, T., Highland, H. M., Young, K. L., Graff, M., Lu, Y., Turcot, V., Auer, P. L., Fine, R. S., Guo, X., Schurmann, C., Lempradl, A., Marouli, et al
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