

- Musa A, Tripathi S, Dehmer M, Emmert-Streib F. 2019. L1000 viewer: A search engine and Web interface for the LINCS data repository. *Frontiers in Genetics*. 10(JUN). <https://doi.org/10.3389/fgene.2019.00557>
- Moore D, Simoes RDM, Dehmer M, Emmert-Streib F. 2019. Prostate cancer gene regulatory network inferred from RNA-seq data. *CURRENT GENOMICS*. 20(1):38-48. <https://doi.org/10.2174/1389202919666181107122005>
- Gumulya Y, Boxall NJ, Khaleque HN, Santala V, Carlson RP, Kaksonen AH. 2018. In a quest for engineering acidophiles for biomining applications: Challenges and opportunities. *Genes*. 9(2). <https://doi.org/10.3390/genes9020116>
- Emmert-Streib F, Dehmer M, Yli-Harja O. 2017. Lessons from the human genome project: Modesty, honesty, and realism. *Frontiers in Genetics*. 8(NOV). <https://doi.org/10.3389/fgene.2017.00184>
- Emmert-Streib F, Dehmer M, Yli-Harja O. 2016. Against dataism and for data sharing of big biomedical and clinical data with research parasites. *Frontiers in Genetics*. 7(AUG). <https://doi.org/10.3389/fgene.2016.00154>
- Emmert-Streib F, Tuomisto L, Yli-Harja O. 2016. The need for formally defining "modern medicine" by means of experimental design. *Frontiers in Genetics*. 7(APR). <https://doi.org/10.3389/fgene.2016.00060>
- Al Olama AA, Dadaev T, Hazelett DJ, Li Q, Leongamornlert D, Saunders EJ, Stephens S, Cieza-Borrella C, Whitmore I, Garcia SB, Giles GG, Southey MC, Fitzgerald L, Gronberg H, Wiklund F, Aly M, Henderson BE, Schumacher F, Haiman CA, Schleutker J, Wahlfors T, Tammela TL, Nordestgaard BG, Key TJ, Travis RC, Neal DE, Donovan JL, Hamdy FC, Pharoah P, Pashayan N, Khaw KT, Stanford JL, Thibodeau SN, McDonnell SK, Schaid DJ, Maier C, Vogel W, Luedeke M, Herkommer K, Kibel AS, Cybulski C, Wokolorczyk D, Kluzniak W, Cannon-Albright L, Brenner H, Butterbach K, Arndt V, Park JY, Sellers T, Lin HY, Slavov C, Kaneva R, Mitev V, Batra J, Clements JA, Spurdle A, Teixeira MR, Paulo P, Maia S, Pandha H, Michael A, Kierzek A, Govindasami K, Guy M, Lophatonanon A, Muir K, Viñuela A, Brown AA, Freedman M, Conti DV, Easton D, Coetzee GA, Eeles RA, Kote-Jarai Z. 2015. Multiple novel prostate cancer susceptibility signals identified by fine-mapping of known risk loci among Europeans. *HUMAN MOLECULAR GENETICS*. 24(19):5589-5602. <https://doi.org/10.1093/hmg/ddv203>
- Turpeinen H, Seppälä I, Lyytikäinen LP, Raitoharju E, Hutri-Kähönen N, Levula M, Oksala N, Waldenberger M, Klopp N, Illig T, Mononen N, Laaksonen R, Raitakari O, Kähönen M, Lehtimäki T, Pesu M. 2015. A genome-wide expression quantitative trait loci analysis of proprotein convertase subtilisin/kexin enzymes identifies a novel regulatory gene variant for FURIN expression and blood pressure. *HUMAN GENETICS*. 134(6):627-636. <https://doi.org/10.1007/s00439-015-1546-5>
- Teerlink CC, Thibodeau SN, McDonnell SK, Schaid DJ, Rinckleb A, Maier C, Vogel W, Cancel-Tassin G, Egrot C, Cussenot O, Foulkes WD, Giles GG, Hopper JL, Severi G, Eeles R, Easton D, Kote-Jarai Z, Guy M, Cooney KA, Ray AM, Zuhlke KA, Lange EM, Fitzgerald LM, Stanford JL, Ostrander EA, Wiley KE, Isaacs SD, Walsh PC, Isaacs WB, Wahlfors T, Tammela T, Schleutker J, Wiklund F, Grönberg H, Emanuelsson M, Carpten J, Bailey-Wilson J, Whittemore AS, Oakley-Girvan I, Hsieh CL, Catalona WJ, Zheng SL, Jin G, Lu L, Xu J, Camp NJ, Cannon-Albright LA. 2014. Association analysis of 9,560 prostate cancer cases from the International Consortium of Prostate Cancer Genetics confirms the role of reported prostate cancer associated SNPs for familial disease. *HUMAN GENETICS*. 133(3):347-356. <https://doi.org/10.1007/s00439-013-1384-2>
- Traylor M, Mäkelä KM, Kilarski LL, Holliday EG, Devan WJ, Nalls MA, Wiggins KL, Zhao W, Cheng YC, Achterberg S, Malik R, Sudlow C, Bevan S, Raitoharju E, Oksala N, Thijs V, Lemmens R, Lindgren A, Slowik A, Maguire JM, Walters M, Algra A, Sharma P, Attia JR, Boncoraglio GB, Rothwell PM, de Bakker PIW, Bis JC, Saleheen D, Kittner SJ, Mitchell BD, Rosand J, Meschia JF, Levi C, Dichgans M, Lehtimäki T, Lewis CM, Markus HS. 2014. A Novel MMP12 Locus Is Associated with Large Artery Atherosclerotic Stroke Using a Genome-Wide Age-at-Onset Informed Approach. *PLOS GENETICS*. 10(7). <https://doi.org/10.1371/journal.pgen.1004469>
- Emmert-Streib F. 2014. Enhancing our understanding of ways to analyze metagenomes. *Frontiers in Genetics*. 5(APR). <https://doi.org/10.3389/fgene.2014.00108>
- Olsen C, Bontempi G, Emmert-Streib F, Quackenbush J, Haibe-Kains B. 2014. Relevance of different prior knowledge sources for inferring gene interaction networks. *Frontiers in Genetics*. 5(JUN). <https://doi.org/10.3389/fgene.2014.00177>

Emmert-Streib F, Simoes RDM, Mullan P, Haibe-Kains B, Dehmer M. 2014. The gene regulatory network for breast cancer: Integrated regulatory landscape of cancer hallmarks. *Frontiers in Genetics*. 5(FEB). <https://doi.org/10.3389/fgene.2014.00015>

Emmert-Streib F, Dehmer M, Haibe-Kains B. 2014. Untangling statistical and biological models to understand network inference: The need for a genomics network ontology. *Frontiers in Genetics*. 5(AUG). <https://doi.org/10.3389/fgene.2014.00299>

Oksala N, Pärssinen J, Seppälä I, Raitoharju E, Ivana K, Hernesniemi J, Lyytikäinen LP, Levula M, Mäkelä KM, Sioris T, Kähönen M, Laaksonen R, Hytönen V, Lehtimäki T. 2013. Association of neuroimmune guidance cue netrin-1 and its chemorepulsive receptor UNC5B with atherosclerotic plaque expression signatures and stability in human(s) Tampere Vascular Study (TVS). *Circulation: Cardiovascular Genetics*. 6(6):579-587. <https://doi.org/10.1161/CIRCGENETICS.113.000141>

Kleber ME, Seppälä I, Pilz S, Hoffmann MM, Tomaschitz A, Oksala N, Raitoharju E, Lyytikäinen LP, Mäkelä KM, Laaksonen R, Kähönen M, Raitakari OT, Huang J, Kienreich K, Fahrleitner-Pammer A, Drechsler C, Krane V, Boehm BO, Koenig W, Wanner C, Lehtimäki T, März W, Meinitzer A. 2013. Genome-wide association study identifies 3 genomic loci significantly associated with serum levels of homoarginine: The atheroremo consortium. *Circulation: Cardiovascular Genetics*. 6(5):505-513. <https://doi.org/10.1161/CIRCGENETICS.113.000108>

Nickerson ML, Im KM, Misner KJ, Tan W, Lou H, Gold B, Wells DW, Bravo HC, Fredrikson KM, Harkins TT, Milos P, Zbar B, Linehan WM, Yeager M, Andersson T, Dean M, Bova GS. 2013. Somatic alterations contributing to metastasis of a castration-resistant prostate cancer. *HUMAN MUTATION*. 34(9):1231-1241. <https://doi.org/10.1002/humu.22346>

Simpson CL, Cropp CD, Wahlfors T, George A, Jones MS, Harper U, Ponciano-Jackson D, Tammela T, Schleutker J, Bailey-Wilson JE. 2013. Genetic heterogeneity in Finnish hereditary prostate cancer using ordered subset analysis. *EUROPEAN JOURNAL OF HUMAN GENETICS*. 21(4):437-443. <https://doi.org/10.1038/ejhg.2012.185>

Al Olama AA, Kote-Jarai Z, Schumacher FR, Wiklund F, Berndt SI, Benlloch S, Giles GG, Severi G, Neal DE, Hamdy FC, Donovan JL, Hunter DJ, Henderson BE, Thun MJ, Gaziano M, Giovannucci EL, Siddiq A, Travis RC, Cox DG, Canzian F, Riboli E, Key TJ, Andriole G, Albanes D, Hayes RB, Schleutker J, Auvinen A, Tammela TLJ, Weischer M, Stanford JL, Ostrander EA, Cybulski C, Lubinski J, Thibodeau SN, Schaid DJ, Sorensen KD, Batra J, Clements JA, Chambers S, Aitken J, Gardiner RA, Maier C, Vogel W, Dörk T, Brenner H, Habuchi T, Ingles S, John EM, Dickinson JL, Cannon-Albright L, Teixeira MR, Kaneva R, Zhang HW, Lu YJ, Park JY, Cooney KA, Muir KR, Leongamornlert DA, Saunders E, Tymrakiewicz M, Mahmud N, Guy M, Govindasami K, O'Brien LT, Wilkinson RA, Hall AL, Sawyer EJ, Dadaev T, Morrison J, Dearnaley DP, Horwich A, Huddart RA, Khoo VS, Parker CC, Van As N, Woodhouse CJ, Thompson A, Dudderidge T, Ogden C, Cooper CS, Lophatonanon A, Southey MC, Hopper JL, English D, Virtamo J, Marchand LL, Campa D, Kaaks R, Lindstrom S, Diver WR, Gapstur S, Yeager M, Cox A, Stern MC, Corral R, Aly M, Isaacs W, Adolfsson J, Xu J, Zheng SL, Wahlfors T, Taari K, Kujala P, Klarskov P, Nordestgaard BG, Røder MA, Frikke-Schmidt R, Bojesen SE, FitzGerald LM, Kolb S, Kwon EM, Karyadi DM, Orntoft TF, Borre M, Rinckleb A, Luedeke M, Herkommer K, Meyer A, Serth JR, Marthick JR, Patterson B, Wokolorczyk D, Spurdle A, Lose F, McDonnell SK, Joshi AD, Shahabi A, Pinto P, Santos J, Ray A, Sellers TA, Lin HY, Stephenson RA, Teerlink C, Muller H, Rothenbacher D, Tsuchiya N, Narita S, Cao GW, Slavov C, Mitev V, Chanock S, Gronberg H, Haiman CA, Kraft P, Easton DF, Eeles RA. 2013. A meta-analysis of genome-wide association studies to identify prostate cancer susceptibility loci associated with aggressive and non-aggressive disease. *HUMAN MOLECULAR GENETICS*. 22(2):408-415. <https://doi.org/10.1093/hmg/dds425>

Xu J, Lange EM, Lu L, Zheng SL, Wang Z, Thibodeau SN, Cannon-Albright LA, Teerlink CC, Camp NJ, Johnson AM, Zuhlke KA, Stanford JL, Ostrander EA, Wiley KE, Isaacs SD, Walsh PC, Maier C, Luedeke M, Vogel W, Schleutker J, Wahlfors T, Tammela T, Schaid D, McDonnell SK, Derycke MS, Cancel-Tassin G, Cussenot O, Wiklund F, Grönberg H, Eeles R, Easton D, Kote-Jarai Z, Whittemore AS, Hsieh CL, Giles GG, Hopper JL, Severi G, Catalona WJ, Mandal D, Ledet E, Foulkes WD, Hamel N, Mahle L, Moller P, Powell I, Bailey-Wilson JE, Carpten JD, Seminara D, Cooney KA, Isaacs WB. 2013. HOXB13 is a susceptibility gene for prostate cancer: Results from the International Consortium for Prostate Cancer Genetics (ICPCG). *HUMAN GENETICS*. 132(1):5-14. <https://doi.org/10.1007/s00439-012-1229-4>

Simoes RDM, Dehmer M, Emmert-Streib F. 2013. B-cell lymphoma gene regulatory networks: Biological consistency among inference methods. *Frontiers in Genetics*. 4(DEC). <https://doi.org/10.3389/fgene.2013.00281>

Emmert-Streib F. 2013. Personalized medicine: Has it started yet? A reconstruction of the early history. *Frontiers in Genetics*. 3(JAN). <https://doi.org/10.3389/fgene.2012.00313>

Avikko M, Li SP, Saarinen S, Alhopuro P, Kaasinen E, Morgunova E, Li Y, Vesanen K, Smith MJ, Evans DGR, Pöyhönen M, Kiuru A, Auvinen A, Aaltonen LA, Taipale J, Vahteristo P. 2012. Loss of SUFU function in familial multiple meningioma. *AMERICAN JOURNAL OF HUMAN GENETICS*. 91(3):520-526. <https://doi.org/10.1016/j.ajhg.2012.07.015>

Inouye M, Ripatti S, Kettunen J, Lyytikäinen LP, Oksala N, Laurila PP, Kangas AJ, Soininen P, Savolainen MJ, Viikari J, Kähönen M, Perola M, Salomaa V, Raitakari O, Lehtimäki T, Taskinen MR, Järvelin MR, Ala-Korpela M, Palotie A, de Bakker PIW. 2012. Novel Loci for Metabolic Networks and Multi-Tissue Expression Studies Reveal Genes for Atherosclerosis. *PLOS GENETICS*. 8(8). <https://doi.org/10.1371/journal.pgen.1002907>

Jin G, Lu L, Cooney KA, Ray AM, Zuhlke KA, Lange EM, Cannon-Albright LA, Camp NJ, Teerlink CC, Fitzgerald LM, Stanford JL, Wiley KE, Isaacs SD, Walsh PC, Foulkes WD, Giles GG, Hopper JL, Severi G, Eeles R, Easton D, Kote-Jarai Z, Guy M, Rinckleb A, Maier C, Vogel W, Cancel-Tassin G, Egrot C, Cussenot O, Thibodeau SN, McDonnell SK, Schaid DJ, Wiklund F, Grönberg H, Emanuelsson M, Whittemore AS, Oakley-Girvan I, Hsieh CL, Wahlfors T, Tammela T, Schleutker J, Catalona WJ, Zheng SL, Ostrander EA, Isaacs WB, Xu J. 2012. Validation of prostate cancer risk-related loci identified from genome-wide association studies using family-based association analysis: Evidence from the International Consortium for Prostate Cancer Genetics (ICPCG). *HUMAN GENETICS*. 131(7):1095-1103. <https://doi.org/10.1007/s00439-011-1136-0>

Bailey-Wilson JE, Childs EJ, Cropp CD, Schaid DJ, Xu J, Camp NJ, Cannon-Albright LA, Farnham JM, George A, Powell I, Carpten JD, Giles GG, Hopper JL, Severi G, English DR, Foulkes WD, Mæhle L, Møller P, Eeles R, Easton D, Guy M, Edwards S, Badzioch MD, Whittemore AS, Oakley-Girvan I, Hsieh CL, Dimitrov L, Stanford JL, Karyadi DM, Deutsch K, McIntosh L, Ostrander EA, Wiley KE, Isaacs SD, Walsh PC, Thibodeau SN, McDonnell SK, Hebring S, Lange EM, Cooney KA, Tammela TLJ, Schleutker J, Maier C, Bochum S, Hoegel J, Grönberg H, Wiklund F, Emanuelsson M, Cancel-Tassin G, Valeri A, Cussenot O, Isaacs WB. 2012. Analysis of Xq27-28 linkage in the international consortium for prostate cancer genetics (ICPCG) families. *BMC MEDICAL GENETICS*. 13. <https://doi.org/10.1186/1471-2350-13-46>

Heikura T, Nieminen T, Roschier MM, Karvinen H, Kaikkonen MU, Mähönen AJ, Lesch HP, Rissanen TT, Laitinen OH, Airene KJ, Ylä-Herttua S. 2012. Baculovirus-mediated vascular endothelial growth factor-D $\Delta$ N $\Delta$ C gene transfer induces angiogenesis in rabbit skeletal muscle. *JOURNAL OF GENE MEDICINE*. 14(1):35-43. <https://doi.org/10.1002/jgm.1637>

Emmert-Streib F, Glazko GV, Altay G, Simoes RDM. 2012. Statistical inference and reverse engineering of gene regulatory networks from observational expression data. *Frontiers in Genetics*. 3(FEB). <https://doi.org/10.3389/fgene.2012.00008>

Sharma V, Dixit D, Koul N, Mehta VS, Sen E. 2011. Ras regulates interleukin-1 $\beta$ -induced HIF-1 $\alpha$  transcriptional activity in glioblastoma. *JOURNAL OF MOLECULAR MEDICINE: JMM*. 89(2):123-136. <https://doi.org/10.1007/s00109-010-0683-5>

Shaughnessy DT, Ohe T, Landi S, Warren SH, Richard AM, Munter T, Franzén R, Kronberg L, DeMarini DM. 2000. Mutation spectra of the drinking water mutagen 3-chloro-4-methyl-5-hydroxy-2(5H)-furanone (MCF) in Salmonella TA100 and TA104: Comparison to MX. *Environmental and Molecular Mutagenesis*. 35(2):106-113. [https://doi.org/10.1002/\(SICI\)1098-2280\(2000\)35:2<106::AID-EM5>3.0.CO;2-U](https://doi.org/10.1002/(SICI)1098-2280(2000)35:2<106::AID-EM5>3.0.CO;2-U)

Fekadu K, Parzefall W, Kronberg L, Franzen R, Schulte-Hermann R, Knasmüller S. 1994. Induction of genotoxic effects by chlorohydroxyfuranones, byproducts of water disinfection, in E. coli K-12 cells recovered from various organs of mice. *Environmental and Molecular Mutagenesis*. 24(4):317-324. <https://doi.org/10.1002/em.2850240409>