

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), [557]. <https://doi.org/10.3389/fgene.2019.00557>

Moore, D., Simoes, R. D. M., 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, N. J., Khaleque, H. N., Santala, V., Carlson, R. P., & Kaksonen, A. H. (2018). In a quest for engineering acidophiles for biomining applications: Challenges and opportunities. *Genes*, 9(2), [116]. <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), [184]. <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), [154]. <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), [60]. <https://doi.org/10.3389/fgene.2016.00060>

Al Olama, A. A., Dadaev, T., Hazelett, D. J., Li, Q., Leongamornlert, D., Saunders, E. J., ... 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. [ddv203]. <https://doi.org/10.1093/hmg/ddv203>

Turpeinen, H., Seppälä, I., Lyytikäinen, L. P., Raitoharju, E., Hutri-Kähönen, N., Levula, M., ... 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, C. C., Thibodeau, S. N., McDonnell, S. K., Schaid, D. J., Rinckleb, A., Maier, C., ... Cannon-Albright, L. A. (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, K. M., Kilarski, L. L., Holliday, E. G., Devan, W. J., Nalls, M. A., ... Markus, H. S. (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), [e1004469]. <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), [Article 108]. <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), [Article 177]. <https://doi.org/10.3389/fgene.2014.00177>

Emmert-Streib, F., Simoes, R. D. M., 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), [Article 15]. <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), [article 229]. <https://doi.org/10.3389/fgene.2014.00299>

- Oksala, N., Pärssinen, J., Seppälä, I., Raitoharju, E., Ivana, K., Hernesniemi, J., ... 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, M. E., Seppälä, I., Pilz, S., Hoffmann, M. M., Tomaschitz, A., Oksala, N., ... Meitner, 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, M. L., Im, K. M., Misner, K. J., Tan, W., Lou, H., Gold, B., ... Bova, G. S. (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, C. L., Cropp, C. D., Wahlfors, T., George, A., Jones, M. S., Harper, U., ... Bailey-Wilson, J. E. (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, A. A., Kote-Jarai, Z., Schumacher, F. R., Wiklund, F., Berndt, S. I., Benlloch, S., ... Eeles, R. A. (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. [dds425]. <https://doi.org/10.1093/hmg/dds425>
- Xu, J., Lange, E. M., Lu, L., Zheng, S. L., Wang, Z., Thibodeau, S. N., ... Isaacs, W. B. (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, R. D. M., Dehmer, M., & Emmert-Streib, F. (2013). B-cell lymphoma gene regulatory networks: Biological consistency among inference methods. *Frontiers in Genetics*, 4(DEC), [00281]. <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), [Article 313]. <https://doi.org/10.3389/fgene.2012.00313>
- Aavikko, M., Li, S. P., Saarinen, S., Alhopuro, P., Kaasinen, E., Morgunova, E., ... 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, L. P., Oksala, N., Laurila, P. P., ... de Bakker, P. I. W. (2012). Novel Loci for Metabolic Networks and Multi-Tissue Expression Studies Reveal Genes for Atherosclerosis. *PLOS GENETICS*, 8(8), [e1002907]. <https://doi.org/10.1371/journal.pgen.1002907>
- Jin, G., Lu, L., Cooney, K. A., Ray, A. M., Zuhlke, K. A., Lange, E. M., ... 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, J. E., Childs, E. J., Cropp, C. D., Schaid, D. J., Xu, J., Camp, N. J., ... Isaacs, W. B. (2012). Analysis of Xq27-28 linkage in the international consortium for prostate cancer genetics (ICPCG) families. *BMC MEDICAL GENETICS*, 13, [46]. <https://doi.org/10.1186/1471-2350-13-46>
- Heikura, T., Nieminen, T., Roschier, M. M., Karvinen, H., Kaikkonen, M. U., Mähönen, A. J., ... Ylä-Herttua, S. (2012). Baculovirus-mediated vascular endothelial growth factor-DΔNΔC 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, G. V., Altay, G., & Simoes, R. D. M. (2012). Statistical inference and reverse engineering of gene regulatory networks from observational expression data. *Frontiers in Genetics*, 3(FEB), [Article 8]. <https://doi.org/10.3389/fgene.2012.00008>

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

Shaughnessy, D. T., Ohe, T., Landi, S., Warren, S. H., Richard, A. M., Munter, T., ... DeMarini, D. M. (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>