

## PUBLICACIONES

- Achour, M. et al. (2015) Neuronal Identity Genes Regulated by Super-Enhancers Are Preferentially Down-Regulated in the Striatum of Huntington's Disease Mice. *Hum. Mol. Genet.* 2015 : ddv099v1-ddv099.
- Auclair, G., et al. (2015) EHMT2 directs DNA methylation for efficient gene silencing in mouse embryos. *Genome Res.* 26: 192-202. doi: 10.1101/gr.198291.115.
- Baker, C. L., et al. (2015) Multimer Formation Explains Allelic Suppression of PRDM9 Recombination Hotspots. *PLOS Genetics.* doi: 10.1371/journal.pgen.1005512.
- Baker, C. L., et al. (2015) PRDM9 Drives Evolutionary Erosion of Hotspots in *Mus musculus* through Haplotype-Specific Initiation of Meiotic Recombination. *PLOS Genetics.* doi: 10.1371/journal.pgen.1004916.
- Baker, C. L., et al. (2014) PRDM9 binding organizes hotspot nucleosomes and limits Holliday junction migration. *Genome Res.* 24(5):724-32.
- Bjorn-Mortensen, K., et al. (2015) Direct DNA Extraction from *Mycobacterium tuberculosis* Frozen Stocks as a Reculture-Independent Approach to Whole-Genome Sequencing. *J. Clin. Microbiol.* 53:8 2716-2719. doi:10.1128/JCM.00662-15.
- Boo, K., et al. (2015) Pontin functions as an essential coactivator for Oct4-dependent lincRNA expression in mouse embryonic stem cells. *Nature Communications* 6:6810. doi:10.1038/ncomms7810.
- Bubier, J. et al. (2014) Identification of a QTL in *Mus musculus* for Alcohol Preference, Withdrawal, and Ap3m2 Expression Using Integrative Functional Genomics and Precision Genetics. *Genetics* 197(4): 1377-1393.
- Chiu, W. T. et. al. (2014) Genome-wide view of TGF $\beta$ /Foxh1 regulation of the early mesendoderm program. *Development.* 141:4537-4547.
- Clop A, Bertoni A, Spain SL, Simpson MA, Pullabhatla V, et al. (2013) An In-Depth Characterization of the Major Psoriasis Susceptibility Locus Identifies Candidate Susceptibility Alleles within an HLA-C Enhancer Element. *PLoS ONE* 8(8): e71690. doi:10.1371/journal.pone.0071690
- Cvejic A, Haer-Wigman L, Stephens JC et al. (2013) SMIM1 underlies the Vel blood group and influences red blood cell traits. *Nature Genetics.* doi:10.1038/ng.2603
- Deng, X. et al. (2014) Molecular mechanisms of two-component system RhpRS regulating type III secretion system in *Pseudomonas syringae*. *Nucl. Acids Res.* 42 (18): 11472-11486 doi: 10.1093/nar/gku865
- Derboven, E., Ekker, H., Kusenda, B., Bulankova, P., Riha K. (2014) Role of STN1 and DNA Polymerase  $\alpha$  in Telomere Stability and Genome-Wide Replication in *Arabidopsis*. *PLoS Genetics.* DOI: 10.1371/journal.pgen.1004682.

- De Nardo, D, et. al. (2014) High-density lipoprotein mediates anti-inflammatory reprogramming of macrophages via the transcriptional regulator ATF3 *Nature Immunology* 15:152-60.
- Dong, Q., Fang, M., Roychowdhury, S. and Bauer, C. E. (2015) Mapping the CgrA regulon of *Rhodospirillum centenum* reveals a hierarchical network controlling Gram-negative cyst development. *BMC Genomics*. 16:1066. doi:10.1186/s12864-015-2248-z.
- Filletton, F., Chuffart, F., Nagarajan, M., Bottin-Duplus, H. and Yvert, G. (2015) The complex pattern of epigenomic variation between natural yeast strains at single-nucleosome resolution. *Epigenetics Chromatin*. 8:26. doi: 10.1186/s13072-015-0019-3.
- Fischer, N., et al. (2014) Rapid metagenomic diagnostics for suspected outbreak of severe pneumonia [letter]. *Emerg Infect Dis*. doi: 10.3201/eid2006.131526.
- Garrido, D., et al. (2015) Comparative transcriptomics reveals key differences in the response to milk oligosaccharides of infant gut-associated bifidobacteria. *Scientific Reports*. 5:13517. doi:10.1038/srep13517.
- Golomb, B. L., Hirao, L. A., Dandekar, S. and Marco, M. L. (2016) Gene expression of *Lactobacillus plantarum* and the commensal microbiota in the ileum of healthy and early SIV-infected rhesus macaques. *Scientific Reports* 6:24723. doi:10.1038/srep24723.
- Gosselin, D. et al. (2014) Environment Drives Selection and Function of Enhancers Controlling Tissue-Specific Macrophage Identities. *Cell*. 159:6, 1327–1340. doi:10.1016/j.cell.2014.11.023.
- Gregor, A. et al. (2013) De Novo Mutations in the Genome Organizer CTCF Cause Intellectual Disability. *AJHG*. 93:1. 124–131.
- Jiang, L. et al. (2014) ZBED6 Modulates the Transcription of Myogenic Genes in Mouse Myoblast Cells. *PLoS ONE* 9(4): e94187. doi: 10.1371/journal.pone.0094187.
- Jones, C.J. et. al. (2014) ChIP-Seq and RNA-Seq reveal an AmrZ-mediated mechanism for cyclic di-GMP synthesis and biofilm development by *Pseudomonas aeruginosa*. *PLoS Pathog*. e1003984.
- Juntawong, P., Girke, T., Bazin, J. and Bailey-Serres, J. (2014) Translational dynamics revealed by genome-wide profiling of ribosome footprints in *Arabidopsis*. *Proc. Natl. Acad. Sci. U.S.A.* 111:1, E203-12.
- Kieffer-Kwon, KR, et. al. (2013) Interactome maps of mouse gene regulatory domains reveal basic principles of transcriptional regulation. *Cell* 155:1507-20.
- Kong, W., et al. (2015) ChIP-seq reveals the global regulator AlgR mediating cyclic di-GMP synthesis in *Pseudomonas aeruginosa*. *Nucl. Acids Res*. 43:17. 8268-8282, doi: 10.1093/nar/gkv747.
- Le Billan, F., et al. (2015) Cistrome of the aldosterone-activated mineralocorticoid receptor in human renal cells. *FASEB J*. 29: 3977 - 3989.

- Lelandais, G., Blugeon, C. and Merhej, J. (2016) ChIPseq in Yeast Species: From Chromatin Immunoprecipitation to High-Throughput Sequencing and Bioinformatics Data Analyses. *Yeast Functional Genomics: Methods and Protocols*, Methods in Molecular Biology, 1361. Pg 1-11. Springer Science+Business Media New York. Doi: 10.1007/978-1-4939-3079.
- Liang, H., et. al. (2014) Molecular mechanisms of master regulator VqsM mediating quorum-sensing and antibiotic resistance in *Pseudomonas aeruginosa*. *Nucleic Acids Research*. doi: 10.1093/nar/gku586.
- Lam MTY, Cho H, Lesch HP et al. (2013) Rev-Erbs repress macrophage gene expression by inhibiting enhancer-directed transcription. *Nature*. doi:10.1038/nature12209.
- Malysheva, V., Mendoza-Parra, M. A., Saleem, M.-A. M. and Gronemeyer, H. (2016) Reconstruction of gene regulatory networks reveals chromatin remodelers and key transcription factors in tumorigenesis. *Genome Medicine*. 8:57. doi: 10.1186/s13073-016-0310-3.
- Mendoza-Parra, M.-A., et al. (2016) Antibody performance in ChIP-sequencing assays: From quality scores of public data sets to quantitative certification. *F1000 Research*. doi: 10.12688/f1000research.7637.1v1.
- Parobek, C. M., Bailey, J. A., Hathaway, N. J., Socheat, D., Rogers, W. O. and Juliano, J. J. (2014) Differing Patterns of Selection and Geospatial Genetic Diversity within Two Leading *Plasmodium vivax* Candidate Vaccine Antigens. *PLoS Neglected Tropical Diseases*. doi: 10.1371/journal.pntd.0002796.
- Pfeiffer, A., Shia, H., Teppermana, J. M., Zhanga, Y. and Quaila, P. H. (2014) Combinatorial Complexity in a Transcriptionally Centered Signaling Hub in *Arabidopsis*. *Mol. Plant* 7 (11): 1598-1618. doi: 10.1093/mp/ssu087.
- Proudhon, C., et al. (2016) 1Active and Inactive Enhancers Cooperate to Exert Localized and Long-Range Control of Gene Regulation. *Cell Reports*. 15:10, 2159–2169. doi: 10.1016/j.celrep.2016.04.087.
- Rosario, R. C. H., et. al. (2015) Sensitive detection of chromatin-altering polymorphisms reveals autoimmune disease mechanisms. *Nature Methods*. doi:10.1038/nmeth.3326.
- Rossetto CC, Tarrant-Elorza M, Pari GS (2013) Cis and Trans Acting Factors Involved in Human Cytomegalovirus Experimental and Natural Latent Infection of CD14 (+) Monocytes and CD34 (+) Cells. *PLoS Pathog* 9(5): e1003366. doi:10.1371/journal.ppat.1003366.
- Rube, H. T., et al. (2016) Sequence features accurately predict genome-wide MeCP2 binding in vivo. *Nature Communications*. 7:11025. doi:10.1038/ncomms11025.
- Sakashita, A., et al. (2015) Sex Specification and Heterogeneity of Primordial Germ Cells in Mice. *PLoS ONE*. 10:12. doi:10.1371/journal.pone.0144836.
- Salehi, F., et al. (2015) CHOPER Filters Enable Rare Mutation Detection in Complex Mutagenesis Populations by Next-Generation Sequencing. *PLoS ONE*. Doi: 10.1371/journal.pone.0116877.

- Scharer, C. D., et al. (2015) Genome-wide CIITA-binding profile identifies sequence preferences that dictate function versus recruitment. *Nuc. Acids Res.* doi: 10.1093/nar/gkv182.
- Shin, H.-J., R., et al. (2016) AMPK–SKP2–CARM1 signalling cascade in transcriptional regulation of autophagy. *Nature*, doi:10.1038/nature18014.
- Stelloh, C., et al. (2016) The cohesin-associated protein Wapal is required for proper Polycomb-mediated gene silencing. *Epigenetics & Chromatin*. 9:14, doi: 10.1186/s13072-016-0063-7.
- Stenzig, J., et al. (2016) DNA methylation in an engineered heart tissue model of cardiac hypertrophy: common signatures and effects of DNA methylation inhibitors. *Basic Research in Cardiology*. 111:9. doi: 10.1007/s00395-015-0528-z.
- Thakur J. and Sanyal K. (Feb 2013) Efficient neocentromere formation is suppressed by gene conversion to maintain centromere function at native physical chromosomal loci in *Candida albicans*. *Genome Research*. doi: 10.1101/gr.141614.11
- Watson E., MacNeil L.T. et al. (2013) Integration of Metabolic and Gene Regulatory Networks Modulates the *C. elegans* Dietary Response. *Cell*.
- Wu, Y, et al. (2014) Phosphorylation of p53 by TAF1 inactivates p53-dependent transcription in the DNA damage response. *Mol. Cell* 53(1):63-74.
- Xiong, W., Li, J. Zhang, E. and Huang, H. (2016) BMAL1 regulates transcription initiation and activates circadian clock gene expression in mammals. *Biochemical and Biophysical Research Communications*. doi:10.1016/j.bbrc.2016.04.009.
- Xu, Z., Chen, H., Ling, J., Yu, D., Struffi, P., and Small, S. (2014) Impacts of the ubiquitous factor Zelda on Bicoid-dependent DNA binding and transcription in *Drosophila*. *Genes & Dev*. 28: 608 - 621.
- Xue, X., et al. (2015) LncRNA HOTAIR enhances ER signaling and confers tamoxifen resistance in breast cancer. *Oncogene*. doi:10.1038/onc.2015.340.
- Yamane A., et al. (2013) RPA Accumulation during Class Switch Recombination Represents 5'–3' DNA-End Resection during the S–G2/M Phase of the Cell Cycle. *Cell Reports*.
- Yang, H., Kwon, C. S., Choi, Y. and Lee, D. (2016) Both H4K20 mono-methylation and H3K56 acetylation mark transcription-dependent histone turnover in fission yeast. *Biochemical and Biophysical Research Communications*. doi: 10.1016/j.bbrc.2016.05.155.
- Zhao, J., et al. (2016) Structural and Molecular Mechanism of CdpR Involved in Quorum-Sensing and Bacterial Virulence in *Pseudomonas aeruginosa*. doi: 10.1371/journal.pbio.1002449.