

PEER REVIEWED PUBLICATIONS

1. Rigel DS, **Whitaker JW**, Skelsey MK, Peck G, Howell MD, Jansen B (2021) Response to Marchetti et al. *Journal of Investigative Dermatology*. 142: 232-234.
2. The ENCODE Consortium (2020) Perspectives on ENCODE. *Nature*. 583: 693-698
3. The ENCODE Consortium (2020) Expanded encyclopedias of DNA elements in the human and mouse genomes. *Nature*. 583: 699-710
4. Wang M, Zhang K, Ngo V, Liu C, Fan S, **Whitaker JW**, Chen Y, Ai R, Chen Z, Wang J, Zheng L, Wang W (2019) Identification of DNA motifs that regulate DNA methylation. *Nucleic Acids Research*. 47: 6753-68
5. Ngo V, Chen Z, Zhang K, **Whitaker JW**, Wang M, Wang W (2019) Epigenomic analysis reveals DNA motifs regulating histone modifications in human and mouse. *PNAS*. 116: 3668-3677
6. Ai R, (8 more authors) **Whitaker JW**, Bai Y, Nagpal S, Bachman KE, Ainsworth RI, Wang M, Ding B, Gulko PS, Wang W, Firestein GS (2018) Comprehensive epigenetic landscape of rheumatoid arthritis fibroblast-like synoviocytes. *Nature Communications* 9: 1921
7. Maeshima K, (9 more authors) **Whitaker JW**, Zhang ZY, Wang W, Bottini N, Firestein GS (2016) Abnormal DNA methylation in a novel PTPN11 enhancer increases destructive potential of rheumatoid arthritis fibroblast-like synoviocytes and joint inflammation. *JCI insight* 19: e86580
8. Spreafico R, Rossetta M, **Whitaker JW**, Wang W, Lovell DJ, Albani S (2016) Epipolymorphisms associated with the clinical outcome of autoimmune arthritis affect CD4+ T cell activation pathways. *PNAS* 113: 13845-50
9. Kamisugi Y, **Whitaker JW**, Cuming AC (2016) The DNA double-strand break transcriptome of *Physcomitrella patens*. *PLoS ONE* 11: e0161204
10. Hammaker D, **Whitaker JW**, Maeshima K, Boyle DL, Ekwall AKH, Wang W, Firestein GS (2016) Limb Bud and Heart Development (LBH) transcription is regulated by the interplay of an enhancer risk allele and DNA methylation in rheumatoid arthritis. *Arthritis & Rheumatology* 68: 2637-45
11. Walsh AM*, **Whitaker JW***, Huang CC, Cherkas Y, Lamberth S, Brodmerkel C, Curran M, Dobrin R (2016) Integrative genomic deconvolution of rheumatoid arthritis GWAS loci into protein and cell type associations. *Genome Biology* 17: 1 (*=these authors contributed equally)
12. Zhu Y, Chen Z, Zhang K, Medovoy D, **Whitaker JW**, Ding B, Li N, Zheng L, Wang W (2016) Constructing 3D interaction maps from 1D epigenomes. *Nature Communications* 7: 10812
13. Schultz MD, He Y, **Whitaker JW**, Hariharan M, Mukamel EA, Leung D, Rajagopal N, Nery JR, Urich MA, Chen H, Lin S, Lin Y, Ren B, Sejnowski TJ, Wang W, Ecker JR (2015) Human body epigenome maps reveal noncanonical DNA methylation variation. *Nature* 523: 212-6
14. Ai R, **Whitaker JW**, Boyle DL, Tak PP, Gerlag DM, Wang W, Firestein GS (2015) DNA methylome signature in early rheumatoid arthritis synoviocytes compared with longstanding rheumatoid arthritis synoviocytes. *Arthritis & Rheumatology* 67: 1978-80
15. Ekwall AKH, **Whitaker JW**, Hammaker D, Bugbee W, Wang W, Firestein GS (2015) The rheumatoid arthritis risk gene, LBH, regulates growth in synoviocytes. *Arthritis & Rheumatology* 67: 1193-202
16. Roadmap Epigenomics Consortium, Kundaje A*, Meuleman W*, Ernst J*, Bilenky M*, Yen A#, Heravi-Moussavi A#, Kheradpour P#, Zhang Z#, Wang J#, Ziller MJ#, Amin V#, **Whitaker JW**#, Schultz MD#, Ward LD#, Sarkar A#, Quon G#, Sandstrom RS#, Eaton ML#, Wu Y#, Pfenning AR#,

- Wang X#, Claussnitzer M#, Liu Y#, (62 more authors), Bernstein BE, Costello JF, Ecker JR, Hirst M, Meissner A, Milosavljevic A, Ren B, Stamatoyannopoulos JA, Wang T, Kellis M (2015) Integrative analysis of 111 reference human epigenomes. *Nature* 518: 317-30 (equal contributors: * = to integrative analysis coordination; # = to integrative analysis)
17. **Whitaker JW**, Tung TN, Zhu Y, Wildberg A, Wang W (2015) Computational schemes for the prediction and annotation of enhancers from epigenomic assays. *Methods* 72: 86-94
 18. **Whitaker JW**, Boyle DL, Bartok B, Ball ST, Gay S, Wang W, Firestein GS (2015) Integrative omics analysis of rheumatoid arthritis identifies non-obvious therapeutic targets. *PLoS ONE* 10: e0124254
 19. **Whitaker JW**, Chen Z, Wang W (2014) Predicting the human epigenome from DNA motifs. *Nature Methods* 12: 265-72
 20. Wang T, Liu J, Shen L, Tonti-Filippini J, Zhu Y, Jia H, Lister R, Whitaker JW, Ecker JR, Millar AH, Ren B, Wang W (2013) STAR: An Integrated Solution to Management and Visualization of Sequencing Data. *Bioinformatics* 29:3204-10
 21. Zhu Y, Sun L, Chen Z, **Whitaker JW**, Wang T, Wang W (2013) Predicting enhancer transcription and activity from chromatin modifications. *Nucleic Acids Research* 41: 10032-43
 22. Xie W, Schultz MD*, Lister R*, Hou Z*, Rajagopal N*, Ray P*, **Whitaker JW***, Tian S*, Hawkins RD*, Leung D*, (27 more authors), Zhang MQ, Wang W, Thomson JA, Ecker JR, Ren B (2013) Epigenomic analysis of multi-lineage differentiation of human embryonic stem cells. *Cell* 153: 1134-48 (*=these authors contributed equally)
 23. **Whitaker JW**, Shoemaker R, Boyle DL, Hillman J, Anderson D, Wang W, Firestein GS (2013) An imprinted rheumatoid arthritis methylome signature reflects pathogenic phenotype. *Genome Medicine* 5: 40
 24. Nakano K, **Whitaker JW**, Wang W, Boyle DL, Firestein GS (2013) DNA methylome signature in rheumatoid arthritis. *Annals of the Rheumatic Diseases* 72: 110-7
 25. Won KJ, Xu Z, Zhang X, **Whitaker JW**, Shoemaker R, Ren B, Xu Y, Wang W (2012) Global identification of transcriptional regulators of pluripotency and differentiation in embryonic stem cells. *Nucleic Acids Research* 40: 8199
 26. Ward WO, Swartz CD, Hanley NM, **Whitaker JW**, Franzén R, DeMarini DM (2010) Mutagen structure and transcriptional response: induction of distinct transcriptional profiles by the drinking-water mutagen MX and its homologues in *Salmonella* TA100. *Environmental and Molecular Mutagenesis* 51: 69-79
 27. **Whitaker JW**, Westhead DR, McConkey GA (2009) *Alio intuitu*: the automated reconstruction of the metabolic networks of parasites. *Trends in Parasitology* 25: 396-7
 28. **Whitaker JW**, McConkey GA, Westhead DR (2009) Prediction of horizontal gene transfers in eukaryotes: approaches and challenges. *Biochemical Society Transactions* 37: 792-5
 29. **Whitaker JW**, McConkey GA, Westhead DR (2009) The transferome of metabolic genes explored: analysis of the horizontal transfer of enzyme encoding genes in unicellular eukaryotes. *Genome Biology* 10: R36
 30. **Whitaker JW**, Letunic I, McConkey GA, Westhead DR (2009) metaTIGER: a metabolic evolution resource. *Nucleic Acids Research* 37: D531-8