

王志斌

代表性论文

- (1)Huang M, Lou D, Charli A, Kong D, Jin H, Anantharam V, Kanthasamy A, **Wang Z**, and Kanthasamy AG[†]. Mitochondrial dysfunction induces epigenetic dysregulation by H3K27 hyperacetylation to perturb active enhancers in Parkinson's disease models. *JCI insight* 2021 Sep 8; 6(17):e138088. doi: 10.1172/jci.insight.138088. PMID: [34494552](#) PMCID: [PMC8492320](#) ([†]co-correspondence author)
- (2)Freeman DM, Lou D, Li Y, Martos, SN, and **Wang Z**. The conserved DNMT1-dependent methylation regions in human cells are vulnerable to neurotoxicant rotenone exposure. *Epigenetics and Chromatin* 2020 Mar 16; 13(1):17. doi: 10.1186/s13072-020-00338-8 PMID: [32178731](#) [PMC7076959](#)
- (3)Freeman DM, O'Neal R, Zhang Q, Bouwer E, and **Wang Z**. Manganese-induced Parkinsonism in mice is reduced using a novel contaminated water sediment exposure model. *Environmental Toxicology and Pharmacology* 2020 Aug;78:103399. doi: 10.1016/j.etap.2020.103399. PMID: 32380377
- (4)Wu S, Lei L, Liu M, Song Y, Lu S, Lou D, Shi Y, **Wang Z**[†], and He D[†]. Mutation of *hop-1* and *pink-1* attenuates vulnerability of neurotoxicity in *C. elegans*: the role of mitochondria-associated membrane proteins in Parkinsonism. *Experimental Neurology* 2018 Nov;309:67-78. doi: 10.1016/j.expneurol.2018.07.018. PMID:30076829 PMCID: [PMC6579610](#) ([†]co-correspondence author)
- (5)Wang T, Pehrsson EC, Purushotham D, Li D, Zhang B, Lawson HA, Province MA, Krapp C, Lan Y, Coarfa C, Katz TA, Tang, WY, **Wang Z**, Biswal S, Rajagopalan S, Colacino J, Sartor M, Neier K, Dolinoy D, Pinto J, Hamanaka R, Mutlu G, Patisaul HB, Aylor DL, Crawford GE, Chadwick LH, Duncan CG, Garton AE, McAllister KA, (6)TaRGET II Consortium, Bartolomei MS, Walker CL, Tyson FL. The NIEHS TaRGET II Consortium and environmental epigenomes. *Nature Biotechnology* 2018, 36, 225-227; PMID: [29509741](#); PMCID: [PMC5991835](#); DOI: [10.1038/nbt.4099](#)
- (7)Zhu Y, Li Y, Lou D, Gao Y, Yu J, Kong D, Zhang Q, Jia Y, Zhang H, and **Wang Z**. Sodium arsenite exposure inhibits histone acetyltransferase p300 for attenuating H3K27ac at enhancers in mouse embryonic fibroblast cells. *Toxicology and Applied Pharmacology* 2018 Oct 15; 357:70-79. doi: 10.1016/j.taap.2018.08.011 PMID: 30130555 PMCID: [PMC6526104](#)
- (8)Martos SN, Li T, Bossardi R, Lou D, Dai H, Xu J, Gao G, Wang Q, An C, Zhang X, Jia Y, Dawson V, Dawson TM, Ji HK, and **Wang Z**. Two approaches revealed a

new paradigm of ‘switchable or genetics-influenced allele-specific DNA methylation (ASM)’ with potential in human disease. *Cell Discovery* 2017 Nov 14; 3:17038. doi: 10.1038/celldisc.2017.38. PMID: 29387450, PMCID: [PMC5787696](#)

(9)Dhar S, Lee SH, Chen K, Zhu G, Oh WK, Alton K, Gafni O, Kim YZ, Barton M, Hanna JH, **Wang Z**[†], Li W[†], Lee MG[†]. An essential role for UTX in resolution and activation of bivalent promoters. *Nucleic Acids Research*. 2016 May 5; 44(8):3659-74. doi: 10.1093/nar/gkv1516. ([†]co-correspondence author) [PMC4856969](#)

(10)Li N, Li Y, Lv J, Zheng X, Wen H, Shen H, Zhu G°, Chen T-Y, Dhar SS, Kan PY, **Wang Z**, Shiekhattar R, Shi X, Lan F, Chen K, Li W, Li H, Lee MG. ZMYND8 reads the dual histone mark H3K4me1-H3K14ac to antagonize the expression of metastasis-linked genes. *Molecular Cell* 2016 Aug 4; 63(3):470-84. doi: 10.1016/j.molcel.2016.06.035 PMID: 27477906

(11)Li Z, Dai H, Martos SN, Xu B, Gao Y, Zhu G, Li T, Schones DE, and **Wang Z**. Distinct roles of DNMT1-dependent and DNMT1-independent methylation patterns in the genome of mouse embryonic stem cells. *Genome Biology* 2015 Jun 2; 16(1):115. doi: 10.1186/s13059-015-0685-2 PMID: 26032981 PMCID: [PMC4474455](#)

(12)Wu H, D'Alessio ACD, Ito S, Xia K, **Wang Z**, Cui K, Zhao K, Sun YE, and Zhang Y. Dual functions of Tet1 in transcriptional regulation in mouse embryonic stem cells. *Nature* 2011 May 19; 473(7347):389-93. doi: 10.1038/nature09934.

(13)Wu H, D'Alessio ACD, Ito S, **Wang Z**, Cui K, Zhao K, Sun YE, and Zhang Y. Genome-wide analysis of 5-hydroxymethylcytosine distribution reveals its dual function in transcriptional regulation in mouse embryonic stem cells. *Genes & Development* 2011 Apr 1; 25(7):679-84. doi: 10.1101/gad.2036011

(14)Qi HH, Sarkissian M, *Hu G-q, ***Wang Z**, Bhattacharjee A, Gordon DB, Lan F, Ongusaha PP, Huarte M, Yaghi NK, Lim H, Garcia BA, Brizuela L, Zhao K, Roberts TM, and Shi Y. Histone H3K9/H4K20 demethylase PHF8 regulates zebrafish brain and craniofacial development. *Nature* 2010 Jul 22; 466(7305):503-7. doi: 10.1038/nature09261 ([#] These authors contribute equally; * These authors contribute equally to ChIP-seq analyses) [PMC3072215](#)

(15)Daniel JA, *Santos MA, ***Wang Z**, *Zang C, **Jankovic M**, Gazumyan A, Kristopher R, Schwab KR, Yamane A, Filsuf D, Cho Y-W, Ge K, Nussenzweig MC, Casellas R, Dressler GR, Zhao K, and Nussenzweig A. PTIP promotes chromatin changes critical for immunoglobulin switch recombination. *Science* 2010 Aug 20;329(5994):917-23. doi: 10.1126/science.1187942. (*Co-second author) [PMC3008398](#)

- (16) Zhou J, Wang C, **Wang Z**, Dampier W, Wu K, Casimiro MC, Yu Z, Wang M, Liang B, Chepelev L, Popov VM, Sune C, Quong A, Lisanti MP, Tozeren A, Zhao K, and Pestell RG. Attenuation of forkhead signaling by the retinal determination factor DACH1. *Proceedings of the National Academy of Sciences USA* 2010 Apr 13;107(15):6864-9. doi: 10.1073/pnas.1002746107.
- (17) **Wang Z**, Zang C, Cui K, Schones DE, Barski A, Peng W, and Zhao K. Genome-wide mapping of HATs and HDACs reveals distinct functions in active and inactive genes. *Cell* 2009 Sep 4;138(5):1019-31. doi: 10.1016/j.cell.2009.06.049 PMID:19698979, [PMC2750862](#)
- (18) *Araki Y, ***Wang Z**, Zang C, Wood W III, Schones DE, Lhotsky B, Westo R, Peng W, Becker K, Zhao K, and Weng N-p. (2009) Genome-wide analysis of histone methylation reveals chromatin state-based complex regulation of gene transcription and function of memory CD8⁺ T cells. *Immunity* 2009 Jun 19;30(6):912-25. doi: 10.1016/j.jimmuni.2009.05.006 (* co-first author) PMID:19523850
- (19) **Wang Z**, Zang C, Rosenfeld JA, Schones DE, Barski A, Cuddapah S, Cui K, Roh T-y, Peng W, Zhang M, Zhao K. (2008). Combinatorial patterns of histone acetylations and methylations in the human genome. *Nature Genetics* 2008 Jul;40(7):897-903. doi: 10.1038/ng.154 PMID:18552846
- (20) Schones DE, Cui K, Cuddapah S, Roh T-y, Barski A, **Wang Z**, Wei G, Zhao K. Dynamic regulation of nucleosome positioning in the human genome. *Cell* 2008 Mar 7;132(5):887-98. doi: 10.1016/j.cell.2008.02.022
- (21) *Barski A, *Cuddapah S, *Cui K, *Roh T-y, *Schones DE, ***Wang Z**, *Wei G, Chepelev I, Zhao K. High-resolution profiling of histone methylations in the human genome. *Cell* 2007 May 18;129(4):823-37. doi: 10.1016/j.cell.2007.05.009. PMID:17512414 (*Contribute equally and are listed alphabetically)