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## # 감사의 글

### ## Reference List

1. R. Stein, L. Razin, E. Fried, In vitro methylation of hamster adenine phosphoribosyltransferase gene inhibits its expression in mouse L cells. *Proc. Natl. Acad. Sci. USA.* 89, 623-627 (1992).
2. M. Busslinger, J. Hurst, P. R. Flavell, DNA methylation regulates expression of the insulin gene. *Cell.* 39, 179-186 (1984).
3. M. Wigler, D. Levy, M. Peruccchio, The somatic repair of DNA by human bone marrow cells. *Nature.* 241, 33-40 (1981).
4. C. K. Meloni, N. Chaille, T. H. Bestor, Transcription of L1AP endogenous retroviruses is constrained by cytosine methylation. *Nature.* 395, 113-117 (1998).
5. E. J. Bérard, P. Jaenisch, Role for DNA methylation in genomic imprinting. *Nature.* 386, 550-553 (1997).
6. S. J. Koss, N. Landsberger, A. P. Wolffe, DNA methylation controls cell type-dependent repression of transcription initiation. *Curr. Biol.* 7, 157-165 (1997).
7. C. Bujard, J. Strahl, F. Rethig, M. Graessmann, A. Graessmann, Chromatin structure is read and altered by transcription in the methylated herpes simplex virus thymidine kinase gene. *Proc. Natl. Acad. Sci. U.S.A.* 91, 1020-1024 (1994).
8. I. M. Caballero, J. Hansen, D. Lierdall, S. M. Thomsen, S. H. Merlie, The MeCP2, Mbd2 and Kaiso are dispensable for mouse embryogenesis but play crucial roles in neural development and differentiation. *Proc. Natl. Acad. Sci. U.S.A.* 102, 1020-1024 (2005).
9. M. O'Geen et al., Histone-modifying enzymes interact with DNA methyltransferases. *Annu. Rev. Biochem.* 74, 481-514 (2005).
10. M. Zhang, A. Zill, Controls endogenous retrovirus in embryonic stem cells. *Nature.* 465, 297-301 (2010).
11. K. Mandado, Y. Wang, M. Shintata, A. G. Clark, M. J. Garcia-Garcia, TRIM28 controls germ line inheritance of X chromosome dissort mechanisms during and after early embryonic-wide reprogramming. *Proc. Natl. Acad. Sci. U.S.A.* 111, E1542-E1551 (2014).
12. G. S. Gopal et al., Structure of KAP1 triple-zipper domain reveals molecular interfaces required for retroelement silencing. *Proc. Natl. Acad. Sci. U.S.A.* 111, E1542-E1551 (2014).
13. D. Wolf, S. F. Goff, Embryonic stem cells use two types of silencing viral DNAs. *Nature.* 458, 1201-1204 (2009).
14. N. Zacharias, Y. Akimoto, G. Hart, The O-GlcNAc modification in histone H3. *Glycobiology*, A. Varki, Ed. (Cold Spring Harbor Laboratory Press, NY, 3 ed. 2017), pp. 358-376.
15. G. Magdalà, R. J. Clifford, L. Katozurski, J. Tabernero, T. S. Bestor, Envirotype-specific endogenous retroviruses are genomic suppressors. *Proc. Natl. Acad. Sci. U.S.A.* 106, 9020-9025 (2009).
16. T. S. Macfarlan et al., Endogenous non-LTR retroelements and L1s are coordinately repressed by LSD1/KDM1A. *Genome Res.* 25, 594-607 (2011).
17. C. O. C. Yee, Y. Liu, L. Feng, Utilizes the L1-ORF1bST-PAD1 complex and controls the function of L1-type zinc fingers. *PLoS One* 3, e3255 (2008).
18. S. P. Rowbotham et al., Maintenance of silent chromatin through replication requires SWI/SNF-like chromatin remodeler SMARCA5. *Genes Dev.* 25, 1086-1098 (2011).
19. S. Covellino, P. Asp, R. Percipalle, A. J.-O. Farrant, The WSTF-SNF2h chromatin remodeling complex recruits several nuclear proteins in transcription. *J. Biol. Chem.* 281, 16261-16271 (2006).
20. M. O'Geen, A. Meissner, J. Müller, Essential role of the glycosyltransferase superfamily in polycomb repression. *Science* 325, 93-96 (2009).
21. J. Reichmann et al., Microarray analysis of LTR-retrotransposon silencing identifies Head as a regulator of retrotransposon expression in mouse embryonic stem cells. *BMC Genomics* 8, e1002465 (2007).
22. X. Lu et al., The MOV10 helicase inhibits LINE mobility in vivo. *Nature.* 489, 2149-2150 (2013).
23. L. Zhou et al., ENU mutagenesis screen identifies novel and known genes involved in epigenetic processes in the mouse. *Genome Biol.* 13, R81 (2012).
24. Y. Zhang, L. LeRoy, H.-P. Seelig, W. S. Lane, D. Reinberg, The dermatomyositis-specific autoantigen Mi2 is a component of a complex containing histone deacetylase and nucleosome remodeling activity. *Genes Dev.* 25, 1086-1098 (2011).
25. X. Zhu et al., O-GlcNAcylation of histone deacetylases 1 in hepatocellular carcinoma progression. *Glycobiology* 26, 820-833 (2016).
26. P. G. Murray et al., 3-M syndrome: A growth hormone-releasing peptide receptor mutation. *Endocr. Connect.* 2, 225-235 (2013).
27. C. Stadler et al., O-GlcNAcase maintains microtubule and genome integrity. *Mol. Cell* 54, 91-94 (2014).
28. C. Schmiedt, J. Müller, A critical perspective of the diverse roles of O-GlcNAc transferase on chromatin. *Chromosomes* 124, 429-442 (2015).
29. K. Shafi et al., The O-GlcNAc transferase encoded by Gm13056 on the X chromosome and is essential for embryonic stem cell viability and mouse ontogeny. *Proc. Natl. Acad. Sci. U.S.A.* 107, 7251-7256 (2010).
30. R. L. Dennis et al., Structure and mechanism of an O-GlcNAc transferase lacking O-GlcNACase activity. *Nat. Struct. Mol. Biol.* 13, 365-371 (2006).
31. M. A. DeBenedictis, P. Reber-Palacios, D. Bourcis, An epigenetic switch ensures permanent repression via dynamic loss of DNA methylation in embryonic stem cells. *eLife* 5, R87 (2016).
32. A. S. Tey et al., O-GlcNAc transferase suppresses necroptosis and liver fibrosis. *JCI Insight* 2, 90505 (2017).
33. A. Skinner et al., Conserved serine-rich phosphoprotein triggered by phosphorylation controls differential gene expression. *Proc. Natl. Acad. Sci. U.S.A.* 114, 13453-13458 (2017).
34. H. Muñoz et al., PGL2 is regulated by O-linked N-acetylgalactosamine (O-GlcNAc). *J. Biol. Chem.* 278, 14046-14052 (2003).
35. M. R. Cooper et al., The cAMP-responsive transcription (CBP) binding protein interacts preferentially with the glycosylated form of CBP. *Mol. Cell. Biol.* 24, 5152-5162 (2004).
36. J. O'Donnell, O-GlcNAc regulates RNA polymerase II transcription by directly acting on large components of the pluripotency network. *Cell Stem Cell* 11, 62-74 (2012).
37. E. T. Comer, G. W. Hart, Reciprocity between the lysine acetyltransferase GCN5 and the carboxy-terminal domain of RNA polymerase II. *Biochemistry* 40, 7845-7852 (2001).
38. R. G. Warren, T. B. Hahnerman, W. W. Hart, B. A. Lewis, Evidence for the involvement of O-GlcNAcylation of human RNA polymerases II CTD in transcription in vitro and in vivo. *J. Biol. Chem.* 287, 393-416 (2019).
39. R. Bruno, M. Mahgoub, T. S. Macfarian, The arms race between KRAB-zinc finger proteins and RNA polymerase II: the impact on mammalian gene regulation. *Annu. Rev. Genet.* 53, 393-416 (2019).
40. Y. Li, L. Zhang, M. Blumenkach, W. Cheng, A common mode of recognition for methylated DNA by bromodomain proteins. *Nucleic Acids Res.* 41, 1504-1513 (2013).
41. S. Dume et al., A Pelicanret growth factor is inserted in mouse embryos by the zinc finger protein ZFP568. *Science* 356, 767-759 (2017).
42. H. Lei et al., De novo DNA cytosine methylation in mouse embryonic stem cells. *Development* 121, 319-325 (1995).
43. A. L. Edwards, T. S. Bestor, RXL1 protects Polycomb-bound genes from hypermethylation. *Nat. Genet.* 47, 479-485 (2015).
44. Y. Zhang et al., Model-based analysis of Massively Parallel Sequencing (MASS). *Genome Biol.* 9, R137 (2008).
45. S. J. Elissa, E. N. Non, N. Diaz, O. C. Allis, A. L. Parnesky, Histone H3K9me2 is required for endogenous retroviral element silencing in embryonic stem cells. *Proc. Natl. Acad. Sci. U.S.A.* 112, 1211-1221 (2014).
46. W. Xie et al., Base-resolution analyses of de novo and parent-of-origin dependent DNA methylation in the mouse genome. *Cell* 149, 1211-1221 (2014).
47. S. P. Jackson, K. Tjian, Purification and analysis of RNA polymerase II transcription factors by using gel filtration and affinity chromatography. *Proc. Natl. Acad. Sci. U.S.A.* 84, 7643-7647 (1987).
48. D. T. Trig, M. Kyba, G. Q. Daley, Inducible transgene expression in mouse stem cells. *Methods Mol. Biol.* 261, 15-26 (2005).
49. S. K. Ooi et al., Dynamic instability of gene expression patterns in pluripotent stem cells. *Epigenetics Chromatin* 3, 17 (2010).
50. J. Kingsmead, S. L. Salzberg, Fast gapped-read realignment with Bowtie 2. *Nat. Methods* 9, 357-359 (2012).
51. Y. Kim et al., Randal2: Accurate alignment of transcriptomes in the presence of insertions, deletions and gene fusions. *Genome Biol.* 14, R36 (2013).
52. Y. Liao, G. K. Smyth, W. Shi, FeatureCounts: gene-wise comparison of Illumina whole-genome shotgun reads to genomic features. *Bioinformatics* 30, 923-930 (2014).

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