

Citation Ranking: Hiroyuki Sasaki Papers

(Scopus, February 22, 2024)

h-Index=72

Times cited (/years since publication)

- 1. 1069 times (/20 years):** Kaneda, M., Okano, M., Hata, K., Sado, T., Tsujimoto, N., Li, E. & Sasaki, H. Essential role for *de novo* DNA methyltransferase Dnmt3a in paternal and maternal imprinting. **Nature** 429, 900-903 (2004).
- 2. 922 times (/16 years):** Watanabe, T., Totoki, Y., Toyoda, A., Kaneda, M., Kuramochi-Miyagawa, S., Obata, Y., Chiba, H., Kohara, Y., Kono, T., Nakano, T., Surani, M.A., Sakaki, Y. & Sasaki, H. Endogenous siRNAs from naturally formed dsRNAs regulate transcripts in mouse oocytes. **Nature** 453, 539-543 (2008).
- 3. 730 times (/16 years):** Kuramochi-Miyagawa, S., Watanabe, T., Gotoh, K., Totoki, Y., Toyoda, A., Ikawa, M., Asada, N., Kojima, K., Yamaguchi, Y., Ijiri, T., Hata, K., Li, E., Matsuda, Y., Kimura, T., Okabe, M., Sakaki, Y., Sasaki, H. & Nakano, T. DNA methylation of retrotransposon genes is regulated by Piwi family members MILI and MIWI2 in murine fetal testes. **Genes Dev.** 22, 908-917 (2008).
- 4. 670 times (/16 years):** Sasaki, H. & Matsui, Y. Epigenetic events in mammalian germ-cell development: reprogramming and beyond. (Review) **Nat. Rev. Genet.** 9, 129-140 (2008).
- 5. 484 times (/14 years):** Borgel, J., Guibert, S., Li, Y., Chiba, H., Schuebeler, D., Sasaki, H., Forne, T. & Weber, M. Targets and dynamics of promoter DNA methylation during early mouse development. **Nat. Genet.** 42, 1093-1100 (2010).
- 6. 479 times (/6 years):** Okae, H., Toh, H., Sato, T., Hiura, H., Takahashi, S., Shirane, K., Kabayama, Y., Suyama, M., Sasaki, H. & Arima, T. Derivation of human trophoblast stem cells. **Cell Stem Cell** 22, 50-63 (2018).
- 7. 479 times (/18 years):** Watanabe, T., Takeda, A., Tsukiyama, T., Mise, K., Okuno, T., Sasaki, H., Minami, N. & Imai, H. Identification and characterization of two novel classes of small RNAs in the mouse germline: retrotransposon-derived siRNAs in oocytes and germline small RNAs in testes. **Genes Dev.** 20, 1732-1743 (2006).
- 8. 410 times (/17 years):** Kato, Y., Kaneda, M., Hata, K., Kumaki, K., Hisano, M., Kohara, Y., Okano, M., Li, E., Nozaki, M. & Sasaki, H. Role of the Dnmt3 family in *de novo* methylation of imprinted and repetitive sequences during male germ cell development in the mouse. **Hum. Mol. Genet.** 16, 2272-2280 (2007).
- 9. 388 times (/23 years):** Mizuno, S., Chijiwa, T., Okamura, T., Akashi, K., Fukumaki, Y., Niho, Y. & Sasaki, H. Expression of DNA methyltransferases DNMT1, 3A and 3B in normal hematopoiesis and in acute and chronic myelogenous leukemia. **Blood** 97, 1172-1179 (2001).
- 10. 379 times (/16 years):** Hirasawa, R., Chiba, H., Kaneda, M., Tajima, S., Li, E., Jaenisch, R. & Sasaki, H. Maternal and zygotic Dnmt1 are necessary and sufficient for the maintenance of DNA methylation imprints during preimplantation

development. *Genes Dev.* 22, 1607-1616 (2008).

11. 373 times (/31 years): Ferguson-Smith, A.C., Sasaki, H., Cattanach, B.M. & Surani, M.A. Parental-origin-specific epigenetic modification of the mouse *H19* gene. *Nature* 362, 751-755 (1993).

12. 354 times (/17 years) Kobayashi, H., Sato, A., Otsu, E., Hiura, H., Tomatsu, C., Utsunomiya, T., Sasaki, H., Yaegashi, N. & Arima, T. Aberrant DNA methylation of imprinted loci in sperm from oligospermic patients. *Hum. Mol. Genet.* 16, 2542-2551 (2007).

13. 313 times (/13 years): Watanabe, T., Tomizawa, S., Mitsuya, K., Totoki, Y., Yamamoto, Y., Kuramochi-Miyagawa, S., Iida, N., Hoki, Y., Murphy, P.J., Toyoda, A., Gotoh, K., Hiura, H., Arima, T., Fujiyama, A., Sado, T., Shibata, T., Nakano, T., Lin, H., Ichianagi, K., Soloway, P.D. & Sasaki, H. Role for piRNAs and non-coding RNA in *de novo* DNA methylation of the imprinted mouse *Rasgrf1* locus. *Science* 332, 848-852 (2011).

14. 282 times (/5 years): Tucci, V., Isles, A., Kelsey, G., Ferguson-Smith, A.C. & The Erice Imprinting Group (including Sasaki, H.). Genomic imprinting and physiological processes in mammals. (Review) *Cell* 176, 952-965 (2019).

15. 279 times (/8 years): Stunnenberg, H.G., The International Human Epigenome Consortium (including Sasaki, H.) & Hirst, M. The International Human Epigenome Consortium: a blueprint for scientific collaboration and discovery. (Review) *Cell* 167, 1145-1149 (2016).

16. 268 times (/23 years): Sado, T., Wang, Z., Sasaki, H. & Li, E. Regulation of imprinted X-chromosome inactivation in mice by *Tsix*. *Development* 128, 1275-1286 (2001).

17. 266 times (/30 years): Sumimoto, H., Kage, Y., Nunoi, H., Sasaki, H., Nose, T., Fukumaki, Y., Ohno, M., Minakami, S. & Takeshige, K. Role of Src homology 3 domains in assembly and activation of the phagocyte NADPH oxidase. *Proc. Natl. Acad. Sci. USA* 91, 5345-5349 (1994).

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19. 253 times (/15 years): Shoji, M., Tanaka, T., Hosokawa, M., Reuter, M., Stark, A., Kato, Y., Kondoh, G., Okawa, K., Chujo, T., Suzuki, T., Hata, K., Martin, S.L., Noce, T., Kuramochi-Miyagawa, S., Nakano, T., Sasaki, H., Pillai, R.S., Nakatsuji, N. & Chuma, S. The TDRD9-MIWI2 complex is essential for piRNA-mediated retrotransposon silencing in the mouse male germline. *Dev. Cell* 17, 775-787 (2009).

20. 242 times (/32 years): Sasaki, H., Jones, P.A., Chaillet, J.R., Ferguson-Smith, A.C., Barton, S.C., Reik, W. & Surani, M.A. Parental imprinting: potentially active chromatin of the repressed maternal allele of the mouse insulin-like growth factor II (*Igf2*) gene. *Genes Dev.* 6, 1843-1856 (1992).

21. 241 times (/34 years): Yoshikai, S., Sasaki, H., Doh-ura, K., Furuya, H. & Sakaki,

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- 22. 240 times (/11 years):** Shirane, K., Toh, H., Kobayashi, H., Miura, F., Chiba, H., Ito, T., Kono, T. & Sasaki, H. Mouse oocyte methylomes at base resolution reveal genome-wide accumulation of non-CpG methylation and role of DNA methyltransferases. *PLoS Genet.* 9, e1003439 (2013).
- 23. 235 times (/27 years):** Moore, T., Constancia, M., Zubair, M., Bailleul, B., Feil, R., Sasaki, H. & Reik, W. Multiple imprinted sense and antisense transcripts, differential methylation and tandem repeats in a putative imprinting control region upstream of mouse *Igf2*. *Proc. Natl. Acad. Sci. USA* 94, 12509-12514 (1997).
- 24. 226 times (/13 years):** Watanabe, T., Chuma, S., Yamamoto, Y., Kuramochi-Miyagawa, S., Totoki, Y., Toyoda, A., Hoki, Y., Fujiyama, A., Shibata, T., Sado, T., Noce, T., Nakano, T., Nakatsuji, N., Lin, H. & Sasaki, H. MitoPLD is a mitochondrial protein essential for nuage formation and piRNA biogenesis in the mouse germline. *Dev. Cell* 20, 364-375 (2011).
- 25. 205 times (/30 years):** Hayashizaki, Y., Shibata, H., Hirotsune, S., Sugino, H., Okazaki, Y., Sasaki, N., Hirose, K., Imoto, H., Okuzumi, H., Muramatsu, M., Komatsubara, H., Shiroishi, T., Moriwaki, K., Matsuki, M., Hatano, N., Sasaki, H., Ueda, T., Mise, N., Takagi, N., Plass, C. & Chapman, V.M. Identification and characterization of an imprinted U2af binding protein related sequence on mouse chromosome 11 detected by efficient genomic screening using restriction landmark genomic scanning (RLGS-M). *Nat. Genet.* 6, 33-40 (1994).
- 26. 202 times (/14 years):** Kuramochi-Miyagawa, S., Watanabe, T., Gotoh, K., Takamatsu, K., Chuma, S., Kojima-Kita, K., Shiromoto, Y., Asada, N., Kimura, T., Nakatsuji, N., Noce, T., Sasaki, H. & Nakano, T. MVH in piRNA processing and gene silencing of retrotransposons. *Genes Dev.* 24, 887-892 (2010).
- 27. 199 times (/17 years):** Li, J.-Y., Pu, M.-T., Hirasawa, R., Li, B.-Z., Huang, Y.-N., Zeng, R., Jing, N.-H., Chen, T., Li, E., Sasaki, H. & Xu, G.-L. Synergistic function of DNA methyltransferases Dnmt3a and Dnmt3b in the methylation of Oct4 and Nanog. *Mol. Cell. Biol.* 27, 8748-8759 (2007).
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- 29. 189 times (/13 years):** Tomizawa, S., Kobayashi, H., Watanabe, T., Andrews, S., Hata, K., Kelsey, G. & Sasaki, H. Dynamic stage-specific changes of imprinted differentially methylated regions during early mammalian development and prevalence of non-CpG methylation in oocytes. *Development* 138, 811-829 (2011)..
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- 31. 180 times (/24 years):** Ueda, T., Abe, K., Miura, A., Yuzuriha, M., Zubair M., Noguchi, M., Niwa, K., Kawase, Y., Kono, T., Matsuda, Y., Fujimoto, H., Shibata, H., Hayashizaki, Y. & Sasaki, H. The paternal methylation imprint of the mouse *H19* locus is acquired in the gonocyte stage during fetal testis development. *Genes*

Cells 5, 649-659 (2000).

- 32. 179 times (/6 years):** Yamashiro, C., Sasaki, K., Yabuta, Y., Kojima, Y., Nakamura, T., Okamoto, I., Yokobayashi, S., Murase, Y., Ishikura, I., Shirane, K., Sasaki, H., Yamamoto, T. & Saitou, M. Generation of human oogonia from induced pluripotent stem cells in vitro. *Science* 362, 356-360 (2018).
- 33. 177 times (/8 years):** Amouroux, R., Nashun, B., Shirane, K., Nakagawa, S., Hill, P.W., D'Souza, Z., Nakayama, M., Matsuda, M., Turp, A., Ndjetehe, E., Encheva, V., Kudo, N.R., Koseki, H., Sasaki, H. & Hajkova, P. *De novo* DNA methylation drives 5hmC accumulation in mouse zygotes. *Nat. Cell Biol.* 18, 225-233 (2016).
- 34. 165 times (/28 years):** Plass, C., Shibata, H., Kalcheva, I., Mullins, L., Kotelevtseva, N., Mullins, J., Kato, R., Sasaki, H., Hirotsune, S., Okazaki, Y., Held, W.A., Hayashizaki, Y. & Chapman, V.M. Identification of *Grf1* on mouse chromosome 9 as an imprinted gene by RLGS-M. *Nat. Genet.* 14, 106-109 (1996).
- 35. 155 times (/33 years):** Kira, J., Koyanagi, Y., Yamada, T., Itaya, Y., Goto, I., Yamamoto, M., Sasaki, H. & Sakaki, Y. Increased HTLV-I proviral DNA in HTLV-I-associated myelopathy: a quantitative PCR study. *Ann. Neurol.* 29, 194-201 (1991).
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- 37. 138 times (/29 years):** Sasaki, H., Ferguson-Smith, A.C., Shum, A.S.W., Barton, S.C. & Surani, M.A. Temporal and spatial regulation of *H19* imprinting in normal and uniparental embryos. *Development* 121, 4195-4202 (1995).
- 38. 130 times (/37 years):** Yamada, T., Sasaki, H., Furuya, H., Miyata, T., Goto, I. & Sakaki, Y. Complementary DNA for the mouse homolog of the human amyloid \square protein precursor. *Biochem. Biophys. Res. Commun.* 149, 665-671 (1987).
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- 40. 118 times (/14 years):** Ohnishi, Y., Totoki, Y., Toyoda, A., Watanabe, T., Yamamoto, Y., Tokunaga, K., Sakaki, Y., Sasaki, H. & Hohjoh, H. Small RNA class transition from siRNA/piRNA to miRNA during pre-implantation mouse development. *Nucl. Acids Res.* 38, 5141-5151 (2010).
- 41. 117 times (/18 years):** Hatada, I., Fukasawa, M., Kimura, M., Morita, S., Yamada, K., Yoshikawa, T., Yamanaka, S., Endo, C., Sakurada, A., Sato, M., Kondo, T., Horii, A., Ushijima, T. & Sasaki, H. Genome-wide profiling of promoter methylation in human. *Oncogene* 25, 3059-3064 (2006).
- 42. 114 times (/8 years):** Ishikura, Y., Yabuta, Y., Ohta, H., Hayashi, K., Nakamura, T., Okamoto, I., Yamamoto, T., Kurimoto, K., Shirane, K., Sasaki, H. & Saitou, M. In

vitro derivation and propagation of spermatogonial stem cell activity from mouse pluripotent stem cells. *Cell Rep.* 17, 2789-2804 (2016).

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- 44. 109 times (/11 years):** Unoki, M., Masuda, A., Dohmae, N., Arita, K., Yoshimatsu, M., Iwai, Y., Fukui, Y., Ueda, K., Hamamoto, R., Shirakawa, M., Sasaki, H. & Nakamura, Y. Lysyl 5-hydroxylation, a novel histone modification, by Jumonji domain containing 6 (JMJD6). *J. Biol. Chem.* 288, 6053-6062 (2013).
- 45. 108 times (/12 years):** Liu, Y., Toh, H., Sasaki, H., Zhang, X. & Cheng, X. An atomic model of ZFP57 recognition of CpG methylation within a specific DNA sequence. *Genes Dev.* 26, 2374-2379 (2012).
- 46. 107 times (/13 years):** Li, Y. & Sasaki, H. Genomic imprinting in mammals: its life cycle, molecular mechanisms and reprogramming. (Review) *Cell Res.* 21, 466-473 (2011).
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- 48. 106 times (/15 years):** Yamaguchi, S., Kurimoto, K., Yabuta, Y., Sasaki, H., Nakatsuji, N., Saitou, M. & Tada, T. Conditional knockdown of *Nanog* induces apoptotic cell death in mouse migrating primordial germ cells. *Development* 136, 4011-4020 (2009).
- 49. 103 times (/24 years):** Sasaki, H., Ishihara, K. & Kato, R. Mechanisms of Igf2/H19 imprinting: DNA methylation, chromatin and long-distance gene regulation. (Review) *J. Biochem.* 127, 711-715 (2000).
- 50. 102 times (/15 years):** Hoki, Y., Kimura, N., Kanbayashi, M., Amakawa, Y., Ohhata, T., Sasaki, H. & Sado, T. A proximal conserved repeat in the *Xist* gene is essential as a genomic element for X-inactivation in mouse. *Development* 136, 139-146 (2009).
- 51. 102 times (/17 years):** Yakushiji, N., Suzuki, M., Satoh, A., Shiroishi, T., Kobayashi, H., Sasaki, H., Ide, H. & Tamura, K. Correlation between Shh expression and DNA methylation status of the limb-specific Shh enhancer region during limb regeneration in amphibians. *Dev. Biol.* 312, 171-182 (2007).
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- 54. 94 times (/10 years):** Yokomizo, H., Inoguchi, T., Sonoda, N., Sakaki, Y., Maeda,

Y., Inoue, T., Hirata, E., Takei, R., Ikeda, N., Fujii, M., Fukuda, K., Sasaki, H. & Takayanagi, R. Maternal high fat diet induces insulin resistance and deterioration of pancreatic β cell function in adult offspring with gender differences in mice. *Am. J. Physiol. Endocrinol. Metab.* 306, E1163-1175 (2014).

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59. 88 times (/18 years): Fukasawa, M., Kimura, M., Morita, S., Matsubara, K., Yamanaka, S., Endo, C., Sakurada, A., Sato, M., Kondo, T., Horii, A., Sasaki, H. & Hatada, I. Microarray analysis of promoter methylation in lung cancers. *J. Hum. Genet.* 51, 368-374 (2006).

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61. 87 times (/12 years): Okae, H., Hiura, H., Miyauchi, N., Abe, C., Nishida, Y., Funayama, R., Tanaka, S., Chiba, H., Yaegashi, N., Nakayama, K., Sasaki, H. & Arima, T. Re-investigation and RNA sequencing-based identification of genes with placenta-specific imprinted expression. *Hum. Mol. Genet.* 21, 548-558 (2012).

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65. 82 times (/7 years): Maenohara, S., Unoki, M., Toh, H., Ohishi, H., Sharif, J., Koseki, H. & Sasaki, H. Role of UHRF1 in de novo DNA methylation in oocytes and

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- 69. 77 times (/12 years):** Tomizawa, S. & Sasaki, H. Genomic imprinting and its relevance to congenital disease, infertility, molar pregnancy and induced pluripotent stem cells. (Review) *J. Hum. Genet.* 57, 84-91 (2012).
- 70. 76 times (/35years):** Yoshioka, K., Furuya, H., Sasaki, H., Saraiva, M.J.M., Costa, P.P. & Sakaki, Y. Haplotype analysis of familial amyloidotic polyneuropathy: evidence for multiple origins of the Val to Met mutation most common to the disease. *Hum. Genet.* 82, 9-13 (1989).
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- 72. 73 times (/17 years):** Parker-Katiraei, L., Carson, A.R., Yamada, T., Arnaud, P., Feil, R., Abu-Amero, S.N., Moore, G.E., Kaneda, M., Perry, G.H., Stone, A.C., Lee, C., Meguro-Horiike, M., Sasaki, H., Kobayashi, K., Nakabayashi, K. & Scherer S.W. Identification of the imprinted KLF14 transcription factor undergoing human-specific accelerated evolution. *PLoS Genet.* 3, 665-678 (2007).
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