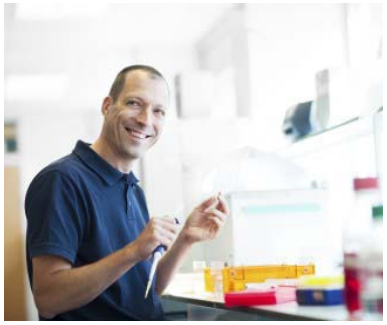
Fred van Leeuwen, PhD



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Website & Publications

Professional Experience

2010- present: Staff Member NKI-AVL, Tenured
2004 – 2010: Antoni van Leeuwenhoek Fellow (Tenure Track), The Netherlands Cancer Institute, Amsterdam
1998-2003: Post-doctoral fellow, Fred Hutchinson Cancer Res. Center, Seattle, USA. Lab: Dr. Daniel E. Gottschling; Histone methylation and gene silencing

Education

1993-1998: PhD student Division of Molecular Biology, Netherlands Cancer Institute, Amsterdam. Advisor: Dr. Piet Borst, Location, conservation and biosynthesis of J, an unusual DNA base in African trypanosomes.
1987-1992: BSc&MSc Biomedical Sciences, University of Leiden Medical School, The Netherlands. *Cum Laude*

Summary of research interests

The Van Leeuwen lab uses biochemical and genetic approaches to study mechanisms and principles of epigenetic regulation. Our general strategy is to develop new tools and technologies, taking advantage of yeast as a powerful model system. These novel tools enable us to discover and explore new areas of chromatin biology (e.g. histone dynamics) and to dissect specific chromatin processes in high molecular detail (e.g. histone methylation). In parallel, we are developing tools in mice and cultured human cells to translate our findings in yeast to mammals.

Career Development Funding

2013 VICI grant NWO Innovational Research Incentives Scheme
2005 Newly Established Team member of the EU Epigenome Network of Excellence
2003 Career Development Fellowship, Leukemia and Lymphoma Society,USA (LLS 3409-04)
2003 VIDI grant NWO Innovational Research Incentives Scheme
1999 Long term EMBO fellowship (ALTF178-1998) & Dutch Cancer Society Fellowship (1999)

Recent professional activities

- Board of Nucleic Acids study group of NWO-CW (2010-2013)
- Dean of NKI postdoctoral affairs (2013-present)
- Member of the NKI Faculty Council Board/Stafraadbestuur (2009-present)
- Member of NKI Education Committee (2011-present)

Selected Publications

- Stulemeijer IJE, De Vos D, van Harten K, Joshi OK, Blomberg O, van Welsem T, Terweij M, Vlaming H, de Graaf EL, Altelaar AFM, Bakker BM, and van Leeuwen F (2015). Dot1 histone methyltransferases share a distributive mechanism but have highly diverged catalytic properties. **Sci Rep** 5: 9824.
- Vlaming H, Van Welsem T, De Graaf EL, Ontoso D, Altelaar AFM, San-Segundo P, Heck AJ, and van Leeuwen F (2014). Flexibility in crosstalk between H2B ubiquitination and H3 methylation in vivo. **EMBO Rep** 15: 1077-1084.
- Radman-Livaja M, Verzijlbergen KF, Weiner A, van Welsem T, Friedman N, Rando OJ, and van Leeuwen F (2011). Patterns and mechanisms of ancestral histone protein inheritance in budding yeast. **PLoS Biol** 9: e1001075.
- De Vos D, Frederiks F, Terweij M, van Welsem T, Verzijlbergen KF, Iachina E, de Graaf EL, Altelaar AFM, Oudgenoeg G, Heck AJ, Krijgsveld J, Bakker BM, and van Leeuwen F (2011). Progressive methylation of ageing histones by Dot1 functions as a timer. **EMBO Rep** 12: 956-962.
- Verzijlbergen KF, van Welsem T, Sie D, Lenstra TL, Turner DJ, Holstege FCP, Kerkhoven RM, and van Leeuwen F (2011). A barcode screen for epigenetic regulators reveals a role for the NuB4/HAT-B histone acetyltransferase complex in histone turnover. **PLoS Genet** 7: e1002284.
- Verzijlbergen KF, Menendez-Benito V, van Welsem T, van Deventer SJ, Lindstrom DL, Ovaa H, Neefjes J, Gottschling DE, and van Leeuwen F (2010). Recombination-induced tag exchange to track old and new proteins. **Proc Natl Acad Sci USA** 107: 64-68.
- Frederiks F, Tzouros M, Oudgenoeg G, van Welsem T, Fornerod M, Krijgsveld J, and van Leeuwen F (2008). Nonprocessive methylation by Dot1 leads to functional redundancy of histone H3K79 methylation states. **Nature Struct Mol Biol** 15: 550-557.
- van Welsem T, Frederiks F, Verzijlbergen KF, Faber AW, Nelson ZW, Egan DA, Gottschling DE, and van Leeuwen F (2008). Synthetic lethal screens identify gene silencing processes in yeast and implicate the acetylated amino terminus of Sir3 in recognition of the nucleosome core. **Mol Cell Biol** 28: 3861-3872.