Curriculum Vitae Prof. Dr W.L. de Laat (1970)

Training and career

1988-1993: Masters Degree in Biology, Utrecht
1993-1998: Ph.D. in Genetics, Erasmus University Rotterdam (Hoeijmakers)
1998-2000: Post-doctoral Fellow, Dept. Cell Biology Erasmus University Rotterdam (Grosveld)
2000-2004: Staff scientist, Dept. Cell Biology Erasmus University Rotterdam
2004-2008: Assistant Professor, Dept. of Cell Biology, Erasmus University Medical Center, Rotterdam
2008- : Permanent Staff member Hubrecht Institute, Utrecht
2009- : Appointed Professor 'Biomedical Genomics' UMC Utrecht

Fellowships & Awards

2001 NWO Vernieuwingsimpuls (career grant 'VIDI', NWO Netherlands)
2008 ERC Starting Grant (career grant EU)
2009 Elected EMBO member
2013 NWO VICI grant (career grant 'VICI' NWO Netherlands)

Patents

- De Laat, Grosveld '4C technology' WO/2007/004057
- De Laat, Grosveld 'multiplex 4C' WO 2008/084405
- De Laat, van Min 'Targeted Locus Amplification' WO 2012/005595
- De Laat, Vermeulen, 'Targeted Locus Cloning' WO 2017/061861

Spin-off company (Founder)

Founder of Cergentis (founded July 2012), a biotech start-up that provides services and kits for complete gene sequencing based on its proprietary Targeted Locus Amplification (TLA) Technology: www.cergentis.com

Board Memberships

- Scientific Board Member KWF (Dutch Cancer Society)
- Supervisory Board Member HUB (Hubrecht Organoid Technology)

International Networks

- member FP7 international training network 'InteGer' (http://www.integer-itn.org/)
- WP leader FP7 Large scale Integrating Project 'MODHEP' (MODelling HEPatocellular carcinoma)
- Leducq Trans-Atlantic Network of Excellence ('AF, genetics in 4 dimensions')

Invited Lectures

Over the last 12 years I have given an average of 10 international invited lectures per year, in Europe, the US, Japan and Singapore, at major conferences and research institutes.

Scientific Grants

2017	4D Nucleome (NIH TCPA)	(400K$)
2017	ALS modifiers	(395K€)
2014	Leducq Trans-Atlantic NoE	(800K€)
2013	VICI (Dutch Career grant)	(1.5M€)
2012	TOP grant NWO (topic: pericentromeric heterochromatin)	(755K€)
2011	NanonextNL. Breast Cancer (with Philips, ErasmusMC)	(325K€)
2011	EU FP7 Collaborative project on liver cancer. 'ModHep'	(800K€)
2011	NGI PreSeed grant. 4C in DNA Diagnostics	(250K€)
2011	CGC PoC grant 4C in DNA Diagnostics	(80K€)
2009	KWF grant on Breast Cancer (with ErasmusMC)	(250K€)
2008	ERC Starting Grant. 4C technology to study the 3D genome	(1.25M€)
2008	NGI Horizon grant. Proteins folding the genome	(500K€)
2008	EU International Training Network ITN 'InteGer'	(250K€)
2007	MRace (Erasmus grant).	(150K€)
2005	ALW open program grant, NWO	(300K€)
2004	ZonMW open program grant, NWO	(500K€)
2004	NGI Horizon Breakthrough Project	(100K€)
2000	NWO Vernieuwingsimpuls (VIDI), career grant	(650K€)

Research Summary

Our research has made seminal contributions to the field that studies gene regulation and chromatin architecture in health, development and disease (cancer). We are world-wide recognized for the pioneering application and further development of novel functional genomics tools.

Highlights:

- first to adapt 3C technology and demonstrate that distant enhancers and promoters contact each other for gene regulation (Tolhuis, 2002; Palstra, 2003).
- first to demonstrate that transcription factors mediate chromatin loops (Drissen, 2004)
- first to show that the key transcription factor CTCF forms chromatin loops in vivo (Splinter, 2006).
- developed 4C technology, the first genomics technique that allows to screen the genome for sites that contact a selected gene in the nucleus (Simonis, 2006).
- first to realize that 3C technologies are very suitable as diagnostics tools, enabling high-resolution identification of genomic rearrangements near loci of interest. This resulted a.o. in the discovery of new oncogenes in leukemia (Simonis, 2009; Homminga, 2011).
- first to show that non-coding RNA molecules can change chromosome topology (Splinter et al., 2011).
- first genetic evidence that an enhancer can *trans* activate a gene on another chromosome (Noordermeer, 2011).
- developed TLA technology, a robust novel gene sequencing method, which enabled identifying previously missed mutations in cancer genes (de Vree et al., 2014)

Collectively, our work has given unprecedented insight into genome structure and gene regulation and has delivered invaluable genomics tools to the research community. In addition, we develop novel diagnostic tools that promise to facilitate development and implementation of personalized medicine in cancer.

List of publications

Invited reviews:

a.o. Nature Reviews Molecular Cell Biology (2016), Genes and Development (2016), Genome Biology (2015), FEBS (2015), Nature (2013), Current Opinion in Genetics and Development (2012), Frontiers in Epigenomics (2012), Genes and Development (2011), EMBO J (2011), Methods in Enzymology (2011, 2003), Trends in Genetics (2010), Current Opinion in Genetics and Development (2007), Nature Methods (2007), Current Opinion in Cell Biology (2007), Chromosome Research (2003).

Scientific Book editor:
Methods (Elsevier): issue on Chromosome Conformation Capture Technologies (2012).

Publications

Vermeulen C, Geeven G, de Wit E, Verstegen MJAM, Jansen RPM, van Kranenburg M, de Bruijn E, Pulit SL, Kruisselbrink E, Shahsavari Z, Omrani D, Zeinali F, Najmabadi H, Katsila T, Vrettou C, Patrinos GP, Traeger-Synodinos J, Splinter E, Beekman JM, Kheradmand Kia S, Te Meerman GJ, Ploos van Amstel HK, de Laat W. (2017). Sensitive Monogenic Noninvasive Prenatal Diagnosis by Targeted Haplotyping. **Am J Hum Genet**. 101(3):326-339.

Gupta RM, Hadaya J, Trehan A, Zekavat SM, Roselli C, Klarin D, Emdin CA, Hilvering CRE, Bianchi V, Mueller C, Khera AV, Ryan RJH, Engreitz JM, Issner R, Shoresh N, Epstein CB, de Laat W, Brown JD, Schnabel RB, Bernstein BE, Kathiresan S. (2017). A Genetic Variant Associated with Five Vascular Diseases Is a Distal Regulator of Endothelin-1 Gene Expression. **Cell** 170(3):522-533.

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van de Werken HJG, Haan JC, Feodorova Y, Bijos D, Weuts A, Theunis K, Holwerda SJB, Meuleman W, Pagie L, Thanisch K, Kumar P, Leonhardt H, Marynen P, van Steensel B, Voet T, de Laat W, Solovei I, Joffe B. (2017). **Genome Res**. 27(6):922-933.

Dreijerink KMA, Groner AC, Vos ESM, Font-Tello A, Gu L, Chi D, Reyes J, Cook J, Lim E, Lin CY, de Laat W, Rao PK, Long HW, Brown M. (2017). Enhancer-Mediated Oncogenic Function of the Menin Tumor Suppressor in Breast Cancer. **Cell Rep.** 18(10):2359-2372

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Krijger PHL, Di Stefano B, de Wit E, Limone F, van Oevelen C, de Laat W, Graf T. (2016). Cell-of-origin specific 3D genome structure acquired during somatic cell reprogramming. **Cell Stem Cell**, 18(5):597-610.

Wijchers PJ, KrijgerPHL Geeven G, Zhu Y, Denker A, Verstegen MJAM, Valdes-Quezada C, Vermeulen C, Janssen M, Teunissen H, Anink-Groenen LCM, Verschure PJ, de Laat W. (2016). Cause and consequence of tethering a sub-TAD to different nuclear compartments. **Mol Cell**, 61(3):461-73.

Neijts R, Amin S, van Rooijen C, Tan S, Creyghton MP, de Laat W, Deschamps J. (2016). Polarized regulatory landscape and Wnt responsiveness underlie Hox activation in embryos. **Genes Dev.** 30(17):1937-42.

Kaaij LJ, Mokry M, Zhou M, Musheev M, Geeven G, Melquiond AS, de Jesus Domingues

AM, de Laat W, Niehrs C, Smith AD, Ketting RF. (2016). Enhancers reside in a unique epigenetic environment during early zebrafish development. **Genome Biol**. 5;17(1):146.

Denker A, de Laat W. (2016). The second decade of 3C technologies: detailed insights into nuclear organization. **Genes Dev**. 30:1357-82.

Wang X, Tucker NR, Rizki G, Mills R, Krijger PH, de Wit E, Subramanian V, Bartell E, Nguyen XX, Ye J, Leyton-Mange J, Dolmatova EV, van der Harst P, de Laat W, Ellinor PT, Newton-Cheh C, Milan DJ, Kellis M, Boyer LA. (2016). Discovery and validation of sub-threshold genome-wide association study loci using epigenomic signatures. **Elife**. 10;5. pii: e10557.

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