

# Fred van Leeuwen

## List of Publications by Year in descending order

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74  
papers

4,802  
citations

126907

33  
h-index

98798

67  
g-index

82  
all docs

82  
docs citations

82  
times ranked

4796  
citing authors

#	ARTICLE	IF	CITATIONS
1	Dot1p Modulates Silencing in Yeast by Methylation of the Nucleosome Core. <i>Cell</i> , 2002, 109, 745-756.	28.9	771
2	The histone modification pattern of active genes revealed through genome-wide chromatin analysis of a higher eukaryote. <i>Genes and Development</i> , 2004, 18, 1263-1271.	5.9	706
3	Antigenic variation in malaria. <i>Cell</i> , 1995, 82, 1-4.	28.9	192
4	Î²-d-glucosyl-hydroxymethyluracil: A novel modified base present in the DNA of the parasitic protozoan <i>T. brucei</i> . <i>Cell</i> , 1993, 75, 1129-1136.	28.9	191
5	Nonprocessive methylation by Dot1 leads to functional redundancy of histone H3K79 methylation states. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 550-557.	8.2	163
6	Localized H3K36 methylation states define histone H4K16 acetylation during transcriptional elongation in <i>Drosophila</i> . <i>EMBO Journal</i> , 2007, 26, 4974-4984.	7.8	153
7	Patterns and Mechanisms of Ancestral Histone Protein Inheritance in Budding Yeast. <i>PLoS Biology</i> , 2011, 9, e1001075.	5.6	136
8	Â-D-Glucosyl-hydroxymethyluracil is a conserved DNA modification in kinetoplastid protozoans and is abundant in their telomeres. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 2366-2371.	7.1	114
9	Localization of the modified base J in telomeric<i>VSG</i> gene expression sites of<i>Trypanosomaâ€%brucei</i>. <i>Genes and Development</i> , 1997, 11, 3232-3241.	5.9	113
10	CD4+ T cell help creates memory CD8+ T cells with innate and help-independent recall capacities. <i>Nature Communications</i> , 2019, 10, 5531.	12.8	106
11	The emerging roles of DOT1L in leukemia and normal development. <i>Leukemia</i> , 2014, 28, 2131-2138.	7.2	104
12	Reconstitution of Yeast Silent Chromatin: Multiple Contact Sites and O-AADPR Binding Load SIR Complexes onto Nucleosomes In Vitro. <i>Molecular Cell</i> , 2009, 33, 323-334.	9.7	103
13	Recombination-induced tag exchange to track old and new proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 64-68.	7.1	92
14	The upstreams and downstreams of H3K79 methylation by DOT1L. <i>Chromosoma</i> , 2016, 125, 593-605.	2.2	86
15	The telomeric GGTTA repeats of <i>Trypanosoma brucei</i> contain the hypermodified base J in both strands. <i>Nucleic Acids Research</i> , 1996, 24, 2476-2482.	14.5	80
16	Control of VSG gene expression sites in <i>Trypanosoma brucei</i> . <i>Molecular and Biochemical Parasitology</i> , 1998, 91, 67-76.	1.1	78
17	An N-terminal acidic region of Sgs1 interacts with Rpa70 and recruits Rad53 kinase to stalled forks. <i>EMBO Journal</i> , 2012, 31, 3768-3783.	7.8	74
18	Genome-wide histone modifications: gaining specificity by preventing promiscuity. <i>Current Opinion in Cell Biology</i> , 2002, 14, 756-762.	5.4	73

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19	Biosynthesis and Function of the Modified DNA Base $\hat{\Gamma}$ -d-Glucosyl-Hydroxymethyluracil in <i>Trypanosoma brucei</i> . <i>Molecular and Cellular Biology</i> , 1998, 18, 5643-5651.	2.3	68
20	Assays for gene silencing in yeast. <i>Methods in Enzymology</i> , 2002, 350, 165-186.	1.0	68
21	The modified base J is the target for a novel DNA-binding protein in kinetoplastid protozoans. <i>EMBO Journal</i> , 1999, 18, 6573-6581.	7.8	67
22	Dot1-Dependent Histone H3K79 Methylation Promotes Activation of the Mek1 Meiotic Checkpoint Effector Kinase by Regulating the Hop1 Adaptor. <i>PLoS Genetics</i> , 2013, 9, e1003262.	3.5	67
23	Yeast PP4 Interacts with ATR Homolog Ddc2-Mec1 and Regulates Checkpoint Signaling. <i>Molecular Cell</i> , 2015, 57, 273-289.	9.7	63
24	A Key Role for Chd1 in Histone H3 Dynamics at the 3' Ends of Long Genes in Yeast. <i>PLoS Genetics</i> , 2012, 8, e1002811.	3.5	62
25	A Network Model of the Molecular Organization of Chromatin in <i>Drosophila</i> . <i>Molecular Cell</i> , 2013, 49, 759-771.	9.7	58
26	Progressive methylation of ageing histones by Dot1 functions as a timer. <i>EMBO Reports</i> , 2011, 12, 956-962.	4.5	56
27	Tandemly repeated DNA is a target for the partial replacement of thymine by $\hat{\Gamma}$ -d-glucosyl-hydroxymethyluracil in <i>Trypanosoma brucei</i> . <i>Molecular and Biochemical Parasitology</i> , 2000, 109, 133-145.	1.1	54
28	Synthetic Lethal Screens Identify Gene Silencing Processes in Yeast and Implicate the Acetylated Amino Terminus of Sir3 in Recognition of the Nucleosome Core. <i>Molecular and Cellular Biology</i> , 2008, 28, 3861-3872.	2.3	53
29	CD8 <sup>+</sup> dendritic cells preferentially cross-present <i>Saccharomyces cerevisiae</i> antigens. <i>European Journal of Immunology</i> , 2008, 38, 370-380.	2.9	51
30	$\hat{\Gamma}$ -d-glucosyl-hydroxymethyluracil, a novel base in African trypanosomes and other Kinetoplastida. <i>Molecular and Biochemical Parasitology</i> , 1997, 90, 1-8.	1.1	44
31	Spatiotemporal analysis of organelle and macromolecular complex inheritance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 175-180.	7.1	43
32	Mutational Analysis of the Sir3 BAH Domain Reveals Multiple Points of Interaction with Nucleosomes. <i>Molecular and Cellular Biology</i> , 2009, 29, 2532-2545.	2.3	42
33	Histone modifications: from genome-wide maps to functional insights. <i>Genome Biology</i> , 2005, 6, 113.	9.6	38
34	N-terminal acetylation and replicative age affect proteasome localization and cell fitness during aging. <i>Journal of Cell Science</i> , 2015, 128, 109-17.	2.0	36
35	Flexibility in crosstalk between H2B ubiquitination and H3 methylation <i>in vivo</i> . <i>EMBO Reports</i> , 2014, 15, 1077-1084.	4.5	34
36	The histone methyltransferase DOT1L prevents antigen-independent differentiation and safeguards epigenetic identity of CD8 <sup>+</sup> T cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 20706-20716.	7.1	32

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37	Control of Antigenic Variation in African Trypanosomas. Cold Spring Harbor Symposia on Quantitative Biology, 1993, 58, 105-114.	1.1	31
38	Dot1 binding induces chromatin rearrangements by histone methylation-dependent and -independent mechanisms. Epigenetics and Chromatin, 2011, 4, 2.	3.9	28
39	Conserved crosstalk between histone deacetylation and H3K79 methylation generates DOT1L dose dependency in HDAC1-deficient thymic lymphoma. EMBO Journal, 2019, 38, e101564.	7.8	28
40	Histone methyltransferase DOT1L controls state-specific identity during B cell differentiation. EMBO Reports, 2021, 22, e51184.	4.5	27
41	Multiple histone modifications in euchromatin promote heterochromatin formation by redundant mechanisms in Saccharomyces cerevisiae. BMC Molecular Biology, 2009, 10, 76.	3.0	25
42	A Barcode Screen for Epigenetic Regulators Reveals a Role for the NuB4/HAT-B Histone Acetyltransferase Complex in Histone Turnover. PLoS Genetics, 2011, 7, e1002284.	3.5	25
43	The Modified DNA Base $\hat{2}$ -d-Glucosylhydroxymethyluracil Confers Resistance to Micrococcal Nuclease and Is Incompletely Recovered by $^{32}$ P-Postlabeling. Analytical Biochemistry, 1998, 258, 223-229.	2.4	24
44	Dot1 promotes H2B ubiquitination by a methyltransferase-independent mechanism. Nucleic Acids Research, 2018, 46, 11251-11261.	14.5	24
45	Antigenic Variation in Trypanosomes. , 1983, , 621-659.		24
46	Direct screening for chromatin status on DNA barcodes in yeast delineates the regulome of H3K79 methylation by Dot1. ELife, 2016, 5, .	6.0	22
47	The modified DNA base $\hat{2}$ -d-glucosyl-hydroxymethyluracil is not found in the tsetse fly stages of Trypanosoma brucei. Molecular and Biochemical Parasitology, 1998, 94, 127-130.	1.1	18
48	A UV-Induced Genetic Network Links the RSC Complex to Nucleotide Excision Repair and Shows Dose-Dependent Rewiring. Cell Reports, 2013, 5, 1714-1724.	6.4	18
49	A Modified Epigenetics Toolbox to Study Histone Modifications on the Nucleosome Core. ChemBioChem, 2011, 12, 308-313.	2.6	17
50	The Histone Minority Report. Cell, 2003, 112, 591-593.	28.9	16
51	News about old histones: A role for histone age in controlling the epigenome. Cell Cycle, 2012, 11, 11-12.	2.6	16
52	Changes in expression site control and DNA modification in Trypanosoma brucei during differentiation of the bloodstream form to the procyclic form. Molecular and Biochemical Parasitology, 1998, 93, 115-130.	1.1	15
53	Recombination-Induced Tag Exchange (RITE) Cassette Series to Monitor Protein Dynamics in Saccharomyces cerevisiae. G3: Genes, Genomes, Genetics, 2013, 3, 1261-1272.	1.8	15
54	Dot1 histone methyltransferases share a distributive mechanism but have highly diverged catalytic properties. Scientific Reports, 2015, 5, 9824.	3.3	15

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55	SETD2: from chromatin modifier to multipronged regulator of the genome and beyond. Cellular and Molecular Life Sciences, 2022, 79, .	5.4	15
56	Decoding the chromatin proteome of a single genomic locus by DNA sequencing. PLoS Biology, 2018, 16, e2005542.	5.6	14
57	Chemical Biology Approaches to Probe the Proteome. ChemBioChem, 2008, 9, 2913-2919.	2.6	12
58	Heterologous expression reveals distinct enzymatic activities of two DOT1 histone methyltransferases of <i>Trypanosoma brucei</i> . Journal of Cell Science, 2010, 123, 4019-4023.	2.0	12
59	Crosstalk between aging and the epigenome. Epigenomics, 2012, 4, 5-7.	2.1	11
60	Two Dot1 isoforms in <i>Saccharomyces cerevisiae</i> as a result of leaky scanning by the ribosome. Nucleic Acids Research, 2009, 37, 7047-7058.	14.5	10
61	Inhibition of transcription leads to rewiring of locus-specific chromatin proteomes. Genome Research, 2020, 30, 635-646.	5.5	10
62	Histone exchange: sculpting the epigenome. Frontiers in Life Science: Frontiers of Interdisciplinary Research in the Life Sciences, 2013, 7, 63-79.	1.1	7
63	A novel germline variant in the DOT1L gene co-segregating in a Dutch family with a history of melanoma. Melanoma Research, 2019, 29, 582-589.	1.2	7
64	Strategy for Development of Site-Specific Ubiquitin Antibodies. Frontiers in Chemistry, 2020, 8, 111.	3.6	7
65	Application of Recombination -Induced Tag Exchange (RITE) to study histone dynamics in human cells. Epigenetics, 2020, 15, 901-913.	2.7	6
66	Drug toxicity profiling of a <i>Saccharomyces cerevisiae</i> deubiquitinase deletion panel shows that acetaminophen mimics tyrosine. Toxicology in Vitro, 2018, 47, 259-268.	2.4	5
67	A genetic interaction map centered on cohesin reveals auxiliary factors in sister chromatid cohesion. Journal of Cell Science, 2020, 133, .	2.0	5
68	Signals for antigen-independent differentiation of memory CD8+ T cells. Cellular and Molecular Life Sciences, 2021, 78, 6395-6408.	5.4	4
69	The effect of acetaminophen on ubiquitin homeostasis in <i>Saccharomyces cerevisiae</i> . PLoS ONE, 2017, 12, e0173573.	2.5	4
70	Epi-ID: Systematic and Direct Screening for Chromatin Regulators in Yeast by Barcode-ChIP-Seq. Methods in Molecular Biology, 2019, 2049, 87-103.	0.9	3
71	Modeling Distributive Histone Modification by Dot1 Methyltransferases. , 2017, , 117-141.		2
72	Chromatin modified in a molecular reaction chamber. Nature, 2020, 579, 503-504.	27.8	2

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73	Epi-Decoder: Decoding the Local Proteome of a Genomic Locus by Massive Parallel Chromatin Immunoprecipitation Combined with DNA-Barcode Sequencing. <i>Methods in Molecular Biology</i> , 2022, 2458, 123-150.	0.9	2
74	Epigenetics Identifier screens reveal regulators of chromatin acylation and limited specificity of acylation antibodies. <i>Scientific Reports</i> , 2021, 11, 12795.	3.3	1