

# Fred van Leeuwen

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5873487/publications.pdf>

Version: 2024-02-01

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	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
2	SETD2: from chromatin modifier to multipronged regulator of the genome and beyond. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, .	5.4	15
3	Histone methyltransferase DOT1L controls state-specific identity during B cell differentiation. <i>EMBO Reports</i> , 2021, 22, e51184.	4.5	27
4	Epigenetics Identifier screens reveal regulators of chromatin acylation and limited specificity of acylation antibodies. <i>Scientific Reports</i> , 2021, 11, 12795.	3.3	1
5	Signals for antigen-independent differentiation of memory CD8+ T cells. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 6395-6408.	5.4	4
6	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
7	Strategy for Development of Site-Specific Ubiquitin Antibodies. <i>Frontiers in Chemistry</i> , 2020, 8, 111.	3.6	7
8	Inhibition of transcription leads to rewiring of locus-specific chromatin proteomes. <i>Genome Research</i> , 2020, 30, 635-646.	5.5	10
9	Application of Recombination-Induced Tag Exchange (RITE) to study histone dynamics in human cells. <i>Epigenetics</i> , 2020, 15, 901-913.	2.7	6
10	A genetic interaction map centered on cohesin reveals auxiliary factors in sister chromatid cohesion. <i>Journal of Cell Science</i> , 2020, 133, .	2.0	5
11	Chromatin modified in a molecular reaction chamber. <i>Nature</i> , 2020, 579, 503-504.	27.8	2
12	Conserved crosstalk between histone deacetylation and H3K79 methylation generates DOT1L-dose dependency in HDAC1-deficient thymic lymphoma. <i>EMBO Journal</i> , 2019, 38, e101564.	7.8	28
13	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
14	A novel germline variant in the DOT1L gene co-segregating in a Dutch family with a history of melanoma. <i>Melanoma Research</i> , 2019, 29, 582-589.	1.2	7
15	Epi-ID: Systematic and Direct Screening for Chromatin Regulators in Yeast by Barcode-ChIP-Seq. <i>Methods in Molecular Biology</i> , 2019, 2049, 87-103.	0.9	3
16	Drug toxicity profiling of a <i>Saccharomyces cerevisiae</i> deubiquitinase deletion panel shows that acetaminophen mimics tyrosine. <i>Toxicology in Vitro</i> , 2018, 47, 259-268.	2.4	5
17	Dot1 promotes H2B ubiquitination by a methyltransferase-independent mechanism. <i>Nucleic Acids Research</i> , 2018, 46, 11251-11261.	14.5	24
18	Decoding the chromatin proteome of a single genomic locus by DNA sequencing. <i>PLoS Biology</i> , 2018, 16, e2005542.	5.6	14

#	ARTICLE	IF	CITATIONS
19	Modeling Distributive Histone Modification by Dot1 Methyltransferases. , 2017, , 117-141.		2
20	The effect of acetaminophen on ubiquitin homeostasis in <i>Saccharomyces cerevisiae</i> . PLoS ONE, 2017, 12, e0173573.	2.5	4
21	The upstreams and downstreams of H3K79 methylation by DOT1L. Chromosoma, 2016, 125, 593-605.	2.2	86
22	Direct screening for chromatin status on DNA barcodes in yeast delineates the regulome of H3K79 methylation by Dot1. ELife, 2016, 5, .	6.0	22
23	N-terminal acetylation and replicative age affect proteasome localization and cell fitness during aging. Journal of Cell Science, 2015, 128, 109-17.	2.0	36
24	Dot1 histone methyltransferases share a distributive mechanism but have highly diverged catalytic properties. Scientific Reports, 2015, 5, 9824.	3.3	15
25	Yeast PP4 Interacts with ATR Homolog Ddc2-Mec1 and Regulates Checkpoint Signaling. Molecular Cell, 2015, 57, 273-289.	9.7	63
26	The emerging roles of DOT1L in leukemia and normal development. Leukemia, 2014, 28, 2131-2138.	7.2	104
27	Flexibility in crosstalk between H2B ubiquitination and H3 methylation <i>in vivo</i> . EMBO Reports, 2014, 15, 1077-1084.	4.5	34
28	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
29	Histone exchange: sculpting the epigenome. Frontiers in Life Science: Frontiers of Interdisciplinary Research in the Life Sciences, 2013, 7, 63-79.	1.1	7
30	A Network Model of the Molecular Organization of Chromatin in <i>Drosophila</i> . Molecular Cell, 2013, 49, 759-771.	9.7	58
31	Spatiotemporal analysis of organelle and macromolecular complex inheritance. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 175-180.	7.1	43
32	Recombination-Induced Tag Exchange (RITE) Cassette Series to Monitor Protein Dynamics in <i>Saccharomyces cerevisiae</i> . G3: Genes, Genomes, Genetics, 2013, 3, 1261-1272.	1.8	15
33	Dot1-Dependent Histone H3K79 Methylation Promotes Activation of the Mek1 Meiotic Checkpoint Effector Kinase by Regulating the Hop1 Adaptor. PLoS Genetics, 2013, 9, e1003262.	3.5	67
34	News about old histones: A role for histone age in controlling the epigenome. Cell Cycle, 2012, 11, 11-12.	2.6	16
35	A Key Role for Chd1 in Histone H3 Dynamics at the 3' Ends of Long Genes in Yeast. PLoS Genetics, 2012, 8, e1002811.	3.5	62
36	An N-terminal acidic region of Sgs1 interacts with Rpa70 and recruits Rad53 kinase to stalled forks. EMBO Journal, 2012, 31, 3768-3783.	7.8	74

#	ARTICLE	IF	CITATIONS
37	Crosstalk between aging and the epigenome. <i>Epigenomics</i> , 2012, 4, 5-7.	2.1	11
38	Progressive methylation of ageing histones by Dot1 functions as a timer. <i>EMBO Reports</i> , 2011, 12, 956-962.	4.5	56
39	Dot1 binding induces chromatin rearrangements by histone methylation-dependent and -independent mechanisms. <i>Epigenetics and Chromatin</i> , 2011, 4, 2.	3.9	28
40	A Modified Epigenetics Toolbox to Study Histone Modifications on the Nucleosome Core. <i>ChemBioChem</i> , 2011, 12, 308-313.	2.6	17
41	Patterns and Mechanisms of Ancestral Histone Protein Inheritance in Budding Yeast. <i>PLoS Biology</i> , 2011, 9, e1001075.	5.6	136
42	A Barcode Screen for Epigenetic Regulators Reveals a Role for the NuB4/HAT-B Histone Acetyltransferase Complex in Histone Turnover. <i>PLoS Genetics</i> , 2011, 7, e1002284.	3.5	25
43	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
44	Heterologous expression reveals distinct enzymatic activities of two DOT1 histone methyltransferases of <i>Trypanosoma brucei</i> . <i>Journal of Cell Science</i> , 2010, 123, 4019-4023.	2.0	12
45	Two Dot1 isoforms in <i>Saccharomyces cerevisiae</i> as a result of leaky scanning by the ribosome. <i>Nucleic Acids Research</i> , 2009, 37, 7047-7058.	14.5	10
46	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
47	Multiple histone modifications in euchromatin promote heterochromatin formation by redundant mechanisms in <i>Saccharomyces cerevisiae</i> . <i>BMC Molecular Biology</i> , 2009, 10, 76.	3.0	25
48	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
49	Chemical Biology Approaches to Probe the Proteome. <i>ChemBioChem</i> , 2008, 9, 2913-2919.	2.6	12
50	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
51	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
52	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
53	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
54	Histone modifications: from genome-wide maps to functional insights. <i>Genome Biology</i> , 2005, 6, 113.	9.6	38

#	ARTICLE	IF	CITATIONS
55	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
56	The Histone Minority Report. <i>Cell</i> , 2003, 112, 591-593.	28.9	16
57	Assays for gene silencing in yeast. <i>Methods in Enzymology</i> , 2002, 350, 165-186.	1.0	68
58	Dot1p Modulates Silencing in Yeast by Methylation of the Nucleosome Core. <i>Cell</i> , 2002, 109, 745-756.	28.9	771
59	Genome-wide histone modifications: gaining specificity by preventing promiscuity. <i>Current Opinion in Cell Biology</i> , 2002, 14, 756-762.	5.4	73
60	Tandemly repeated DNA is a target for the partial replacement of thymine by $\hat{2}$ -d-glucosyl-hydroxymethyluracil in <i>Trypanosoma brucei</i> . <i>Molecular and Biochemical Parasitology</i> , 2000, 109, 133-145.	1.1	54
61	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
62	Control of VSG gene expression sites in <i>Trypanosoma brucei</i> . <i>Molecular and Biochemical Parasitology</i> , 1998, 91, 67-76.	1.1	78
63	Changes in expression site control and DNA modification in <i>Trypanosoma brucei</i> during differentiation of the bloodstream form to the procyclic form. <i>Molecular and Biochemical Parasitology</i> , 1998, 93, 115-130.	1.1	15
64	The modified DNA base $\hat{2}$ -d-glucosyl-hydroxymethyluracil is not found in the tsetse fly stages of <i>Trypanosoma brucei</i> . <i>Molecular and Biochemical Parasitology</i> , 1998, 94, 127-130.	1.1	18
65	The Modified DNA Base $\hat{2}$ -d-Glucosylhydroxymethyluracil Confers Resistance to Micrococcal Nuclease and Is Incompletely Recovered by $^{32}$ P-Postlabeling. <i>Analytical Biochemistry</i> , 1998, 258, 223-229.	2.4	24
66	$\hat{2}$ -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
67	Biosynthesis and Function of the Modified DNA Base $\hat{2}$ -d-Glucosyl-Hydroxymethyluracil in <i>Trypanosoma brucei</i> . <i>Molecular and Cellular Biology</i> , 1998, 18, 5643-5651.	2.3	68
68	Localization of the modified base J in telomeric VSG gene expression sites of <i>Trypanosoma brucei</i> . <i>Genes and Development</i> , 1997, 11, 3232-3241.	5.9	113
69	$\hat{2}$ -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
70	The telomeric GGGTTA 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
71	Antigenic variation in malaria. <i>Cell</i> , 1995, 82, 1-4.	28.9	192
72	$\hat{2}$ -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

#	ARTICLE	IF	CITATIONS
73	Control of Antigenic Variation in African Trypanosomas. Cold Spring Harbor Symposia on Quantitative Biology, 1993, 58, 105-114.	1.1	31
74	Antigenic Variation in Trypanosomes. , 1983, , 621-659.		24