

Mathieu Lupien

List of Publications by Citations

Source: <https://exaly.com/author-pdf/7626538/mathieu-lupien-publications-by-citations.pdf>

Version: 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

123
papers

9,469
citations

49
h-index

96
g-index

139
ext. papers

11,713
ext. citations

15.7
avg, IF

5.62
L-index

#	Paper	IF	Citations
123	FoxA1 translates epigenetic signatures into enhancer-driven lineage-specific transcription. <i>Cell</i> , 2008 , 132, 958-70	56.2	746
122	Androgen receptor regulates a distinct transcription program in androgen-independent prostate cancer. <i>Cell</i> , 2009 , 138, 245-56	56.2	691
121	Epigenomic alterations define lethal CIMP-positive ependymomas of infancy. <i>Nature</i> , 2014 , 506, 445-50	50.4	434
120	Nucleosome dynamics define transcriptional enhancers. <i>Nature Genetics</i> , 2010 , 42, 343-7	36.3	382
119	Genomic hallmarks of localized, non-indolent prostate cancer. <i>Nature</i> , 2017 , 541, 359-364	50.4	320
118	Breast cancer risk-associated SNPs modulate the affinity of chromatin for FOXA1 and alter gene expression. <i>Nature Genetics</i> , 2012 , 44, 1191-8	36.3	287
117	Positive cross-regulatory loop ties GATA-3 to estrogen receptor alpha expression in breast cancer. <i>Cancer Research</i> , 2007 , 67, 6477-83	10.1	274
116	Combinatorial effects of multiple enhancer variants in linkage disequilibrium dictate levels of gene expression to confer susceptibility to common traits. <i>Genome Research</i> , 2014 , 24, 1-13	9.7	258
115	Epigenomic enhancer profiling defines a signature of colon cancer. <i>Science</i> , 2012 , 336, 736-9	33.3	255
114	Estrogen-dependent signaling in a molecularly distinct subclass of aggressive prostate cancer. <i>Journal of the National Cancer Institute</i> , 2008 , 100, 815-25	9.7	251
113	Fate mapping of human glioblastoma reveals an invariant stem cell hierarchy. <i>Nature</i> , 2017 , 549, 227-232	50.4	197
112	Intratumor DNA methylation heterogeneity reflects clonal evolution in aggressive prostate cancer. <i>Cell Reports</i> , 2014 , 8, 798-806	10.6	177
111	Epigenetic switch involved in activation of pioneer factor FOXA1-dependent enhancers. <i>Genome Research</i> , 2011 , 21, 555-65	9.7	172
110	Modulation of long noncoding RNAs by risk SNPs underlying genetic predispositions to prostate cancer. <i>Nature Genetics</i> , 2016 , 48, 1142-50	36.3	158
109	CARM1 regulates estrogen-stimulated breast cancer growth through up-regulation of E2F1. <i>Cancer Research</i> , 2008 , 68, 301-6	10.1	156
108	Risk SNP-Mediated Promoter-Enhancer Switching Drives Prostate Cancer through lncRNA PCAT19. <i>Cell</i> , 2018 , 174, 564-575.e18	56.2	154
107	Overexpression of activated murine Notch1 and Notch3 in transgenic mice blocks mammary gland development and induces mammary tumors. <i>American Journal of Pathology</i> , 2006 , 168, 973-90	5.8	148

106	A Myc enhancer cluster regulates normal and leukaemic haematopoietic stem cell hierarchies. <i>Nature</i> , 2018 , 553, 515-520	50.4	142
105	Growth factor stimulation induces a distinct ER(alpha) cistrome underlying breast cancer endocrine resistance. <i>Genes and Development</i> , 2010 , 24, 2219-27	12.6	136
104	Integrated (epi)-Genomic Analyses Identify Subgroup-Specific Therapeutic Targets in CNS Rhabdoid Tumors. <i>Cancer Cell</i> , 2016 , 30, 891-908	24.3	135
103	MYC regulation of a "poor-prognosis" metastatic cancer cell state. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 3698-703	11.5	134
102	PBX1 genomic pioneer function drives ER signaling underlying progression in breast cancer. <i>PLoS Genetics</i> , 2011 , 7, e1002368	6	130
101	PharmacoGx: an R package for analysis of large pharmacogenomic datasets. <i>Bioinformatics</i> , 2016 , 32, 1244-6	7.2	127
100	ZNF143 provides sequence specificity to secure chromatin interactions at gene promoters. <i>Nature Communications</i> , 2015 , 2, 6186	17.4	123
99	Mutant IDH1 Downregulates ATM and Alters DNA Repair and Sensitivity to DNA Damage Independent of TET2. <i>Cancer Cell</i> , 2016 , 30, 337-348	24.3	121
98	Genome-wide reprogramming of the chromatin landscape underlies endocrine therapy resistance in breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, E1490-9	11.5	120
97	Pioneer factors: directing transcriptional regulators within the chromatin environment. <i>Trends in Genetics</i> , 2011 , 27, 465-74	8.5	120
96	Therapeutic targeting of ependymoma as informed by oncogenic enhancer profiling. <i>Nature</i> , 2018 , 553, 101-105	50.4	116
95	Unique ERalpha cistromes control cell type-specific gene regulation. <i>Molecular Endocrinology</i> , 2008 , 22, 2393-406		110
94	Elucidation of the ELK1 target gene network reveals a role in the coordinate regulation of core components of the gene regulation machinery. <i>Genome Research</i> , 2009 , 19, 1963-73	9.7	108
93	Integrative functional genomics identifies an enhancer looping to the SOX9 gene disrupted by the 17q24.3 prostate cancer risk locus. <i>Genome Research</i> , 2012 , 22, 1437-46	9.7	107
92	TMPRSS2-ERG fusion co-opts master transcription factors and activates NOTCH signaling in primary prostate cancer. <i>Nature Genetics</i> , 2017 , 49, 1336-1345	36.3	105
91	A comprehensive view of nuclear receptor cancer cistromes. <i>Cancer Research</i> , 2011 , 71, 6940-7	10.1	99
90	Genomic collaboration of estrogen receptor alpha and extracellular signal-regulated kinase 2 in regulating gene and proliferation programs. <i>Molecular and Cellular Biology</i> , 2011 , 31, 226-36	4.8	99
89	The Proteogenomic Landscape of Curable Prostate Cancer. <i>Cancer Cell</i> , 2019 , 35, 414-427.e6	24.3	97

88	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , 2014 , 4, 4999	17.4	87
87	Functional Enhancers Shape Extrachromosomal Oncogene Amplifications. <i>Cell</i> , 2019 , 179, 1330-1341.e1362	36.2	87
86	Estrogen controls the survival of BRCA1-deficient cells via a PI3K-NRF2-regulated pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 4472-7	11.5	86
85	BioID identifies novel c-MYC interacting partners in cultured cells and xenograft tumors. <i>Journal of Proteomics</i> , 2015 , 118, 95-111	3.9	83
84	Cell-type selective chromatin remodeling defines the active subset of FOXA1-bound enhancers. <i>Genome Research</i> , 2009 , 19, 372-80	9.7	83
83	ASCL1 Reorganizes Chromatin to Direct Neuronal Fate and Suppress Tumorigenicity of Glioblastoma Stem Cells. <i>Cell Stem Cell</i> , 2017 , 21, 209-224.e7	18	78
82	Cistromics of hormone-dependent cancer. <i>Endocrine-Related Cancer</i> , 2009 , 16, 381-9	5.7	69
81	Laying a solid foundation for Manhattan--Getting the functional basis for the post-GWAS eraU <i>Trends in Genetics</i> , 2014 , 30, 140-9	8.5	68
80	Coactivator function defines the active estrogen receptor alpha cistrome. <i>Molecular and Cellular Biology</i> , 2009 , 29, 3413-23	4.8	65
79	MLL5 Orchestrates a Cancer Self-Renewal State by Repressing the Histone Variant H3.3 and Globally Reorganizing Chromatin. <i>Cancer Cell</i> , 2015 , 28, 715-729	24.3	64
78	Methyltransferase G9A regulates T cell differentiation during murine intestinal inflammation. <i>Journal of Clinical Investigation</i> , 2014 , 124, 1945-55	15.9	57
77	Noncoding somatic and inherited single-nucleotide variants converge to promote ESR1 expression in breast cancer. <i>Nature Genetics</i> , 2016 , 48, 1260-6	36.3	53
76	Pervasive H3K27 Acetylation Leads to ERV Expression and a Therapeutic Vulnerability in H3K27M Gliomas. <i>Cancer Cell</i> , 2019 , 35, 782-797.e8	24.3	52
75	The histone variant H2A.Z is an important regulator of enhancer activity. <i>Nucleic Acids Research</i> , 2015 , 43, 9742-56	20.1	52
74	Human-chromatin-related protein interactions identify a demethylase complex required for chromosome segregation. <i>Cell Reports</i> , 2014 , 8, 297-310	10.6	46
73	A global assessment of cancer genomic alterations in epigenetic mechanisms. <i>Epigenetics and Chromatin</i> , 2014 , 7, 29	5.8	46
72	A chemical toolbox for the study of bromodomains and epigenetic signaling. <i>Nature Communications</i> , 2019 , 10, 1915	17.4	43
71	Emergence of the Noncoding Cancer Genome: A Target of Genetic and Epigenetic Alterations. <i>Cancer Discovery</i> , 2016 , 6, 1215-1229	24.4	41

70	Chromatin and epigenetic determinants of estrogen receptor alpha (ESR1) signaling. <i>Molecular and Cellular Endocrinology</i> , 2014 , 382, 633-641	4.4	41
69	GLUT1 inhibition blocks growth of RB1-positive triple negative breast cancer. <i>Nature Communications</i> , 2020 , 11, 4205	17.4	41
68	Metabolic Regulation of the Epigenome Drives Lethal Infantile Ependymoma. <i>Cell</i> , 2020 , 181, 1329-1345	5.24	40
67	Raloxifene and ICI182,780 increase estrogen receptor-alpha association with a nuclear compartment via overlapping sets of hydrophobic amino acids in activation function 2 helix 12. <i>Molecular Endocrinology</i> , 2007 , 21, 797-816		37
66	Enhancer alterations in cancer: a source for a cell identity crisis. <i>Genome Medicine</i> , 2014 , 6, 77	14.4	36
65	Gene isoforms as expression-based biomarkers predictive of drug response in vitro. <i>Nature Communications</i> , 2017 , 8, 1126	17.4	34
64	Epigenetic Switch-Induced Viral Mimicry Evasion in Chemotherapy-Resistant Breast Cancer. <i>Cancer Discovery</i> , 2020 , 10, 1312-1329	24.4	34
63	High-resolution structural genomics reveals new therapeutic vulnerabilities in glioblastoma. <i>Genome Research</i> , 2019 , 29, 1211-1222	9.7	31
62	Layers of epistasis: genome-wide regulatory networks and network approaches to genome-wide association studies. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2011 , 3, 513-26	6.6	31
61	Gradient of Developmental and Injury Response transcriptional states defines functional vulnerabilities underpinning glioblastoma heterogeneity.. <i>Nature Cancer</i> , 2021 , 2, 157-173	15.4	31
60	Dual suppression of the cyclin-dependent kinase inhibitors CDKN2C and CDKN1A in human melanoma. <i>Journal of the National Cancer Institute</i> , 2012 , 104, 1673-9	9.7	29
59	Chromatin profiling reveals regulatory network shifts and a protective role for hepatocyte nuclear factor 4 during colitis. <i>Molecular and Cellular Biology</i> , 2014 , 34, 3291-304	4.8	28
58	Tamoxifen and raloxifene differ in their functional interactions with aspartate 351 of estrogen receptor alpha. <i>Molecular Pharmacology</i> , 2006 , 70, 579-88	4.3	28
57	The pioneer factor PBX1 is a novel driver of metastatic progression in ER-positive breast cancer. <i>Oncotarget</i> , 2015 , 6, 21878-91	3.3	28
56	Blockade of AP-1 Potentiates Endocrine Therapy and Overcomes Resistance. <i>Molecular Cancer Research</i> , 2016 , 14, 470-81	6.6	27
55	Expression of constitutively active Notch1 in male genital tracts results in ectopic growth and blockage of efferent ducts, epididymal hyperplasia and sterility. <i>Developmental Biology</i> , 2006 , 300, 497-511	3.1	26
54	Identification of PBX1 target genes in cancer cells by global mapping of PBX1 binding sites. <i>PLoS ONE</i> , 2012 , 7, e36054	3.7	26
53	Genome-wide germline correlates of the epigenetic landscape of prostate cancer. <i>Nature Medicine</i> , 2019 , 25, 1615-1626	50.5	25

52	Antibodies against the PER protein of <i>Drosophila</i> label neurons in the optic lobe, central brain, and thoracic ganglia of the crickets <i>Teleogryllus commodus</i> and <i>Teleogryllus oceanicus</i> . <i>Cell and Tissue Research</i> , 2003 , 312, 377-91	4.2	25
51	Human somatic cell mutagenesis creates genetically tractable sarcomas. <i>Nature Genetics</i> , 2014 , 46, 964-73	3.3	23
50	Multimodal regulation of E2F1 gene expression by progestins. <i>Molecular and Cellular Biology</i> , 2010 , 30, 1866-77	4.8	23
49	PRMT5 inhibition disrupts splicing and stemness in glioblastoma. <i>Nature Communications</i> , 2021 , 12, 979	17.4	23
48	Targeting bivalency de-represses Indian Hedgehog and inhibits self-renewal of colorectal cancer-initiating cells. <i>Nature Communications</i> , 2019 , 10, 1436	17.4	21
47	Noncoding mutations target cis-regulatory elements of the FOXA1 plexus in prostate cancer. <i>Nature Communications</i> , 2020 , 11, 441	17.4	21
46	Cistrome Partitioning Reveals Convergence of Somatic Mutations and Risk Variants on Master Transcription Regulators in Primary Prostate Tumors. <i>Cancer Cell</i> , 2019 , 36, 674-689.e6	24.3	21
45	Candidate Cancer Driver Mutations in Distal Regulatory Elements and Long-Range Chromatin Interaction Networks. <i>Molecular Cell</i> , 2020 , 77, 1307-1321.e10	17.6	20
44	Mammary molecular portraits reveal lineage-specific features and progenitor cell vulnerabilities. <i>Journal of Cell Biology</i> , 2018 , 217, 2951-2974	7.3	20
43	Cancer heterogeneity: origins and implications for genetic association studies. <i>Trends in Genetics</i> , 2012 , 28, 538-43	8.5	20
42	Early-life antibiotic treatment enhances the pathogenicity of CD4 T cells during intestinal inflammation. <i>Journal of Leukocyte Biology</i> , 2017 , 101, 893-900	6.5	19
41	The Mitochondrial Transacylase, Tafazzin, Regulates for AML Stemness by Modulating Intracellular Levels of Phospholipids. <i>Cell Stem Cell</i> , 2019 , 24, 621-636.e16	18	19
40	Convergence of BMI1 and CHD7 on ERK Signaling in Medulloblastoma. <i>Cell Reports</i> , 2017 , 21, 2772-2784	10.6	19
39	Pre-neoplastic epigenetic disruption of transcriptional enhancers in chronic inflammation. <i>Oncotarget</i> , 2016 , 7, 15772-86	3.3	19
38	Pioneer of prostate cancer: past, present and the future of FOXA1. <i>Protein and Cell</i> , 2021 , 12, 29-38	7.2	18
37	Molecular Insights of Pathways Resulting from Two Common PIK3CA Mutations in Breast Cancer. <i>Cancer Research</i> , 2016 , 76, 3989-4001	10.1	17
36	The Transcriptional Repressor Polycomb Group Factor 6, PCGF6, Negatively Regulates Dendritic Cell Activation and Promotes Quiescence. <i>Cell Reports</i> , 2016 , 16, 1829-37	10.6	17
35	Variant Set Enrichment: an R package to identify disease-associated functional genomic regions. <i>BioData Mining</i> , 2017 , 10, 9	4.3	16

34	Exploiting tumor epigenetics to improve oncolytic virotherapy. <i>Frontiers in Genetics</i> , 2013 , 4, 184	4.5	15
33	The logic of transcriptional regulator recruitment architecture at -regulatory modules controlling liver functions. <i>Genome Research</i> , 2017 , 27, 985-996	9.7	13
32	Chromatin landscape and endocrine response in breast cancer. <i>Epigenomics</i> , 2012 , 4, 675-83	4.4	12
31	ABC: a tool to identify SNVs causing allele-specific transcription factor binding from ChIP-Seq experiments. <i>Bioinformatics</i> , 2015 , 31, 3057-9	7.2	11
30	The Transition from Quiescent to Activated States in Human Hematopoietic Stem Cells Is Governed by Dynamic 3D Genome Reorganization. <i>Cell Stem Cell</i> , 2021 , 28, 488-501.e10	18	11
29	Reporters to mark and eliminate basal or luminal epithelial cells in culture and in vivo. <i>PLoS Biology</i> , 2018 , 16, e2004049	9.7	10
28	Identifying clusters of -regulatory elements underpinning TAD structures and lineage-specific regulatory networks. <i>Genome Research</i> , 2019 , 29, 1733-1743	9.7	9
27	Single-cell chromatin accessibility profiling of glioblastoma identifies an invasive cancer stem cell population associated with lower survival. <i>ELife</i> , 2021 , 10,	8.9	9
26	Transcriptome-wide characterization of the endogenous miR-34A-p53 tumor suppressor network. <i>Oncotarget</i> , 2016 , 7, 49611-49622	3.3	8
25	C3D: a tool to predict 3D genomic interactions between cis-regulatory elements. <i>Bioinformatics</i> , 2019 , 35, 877-879	7.2	8
24	Personalized diagnosis of medulloblastoma subtypes across patients and model systems. <i>Genomics</i> , 2015 , 106, 96-106	4.3	7
23	Biological and therapeutic implications of a unique subtype of NPM1 mutated AML. <i>Nature Communications</i> , 2021 , 12, 1054	17.4	7
22	CRISPRi screens reveal a DNA methylation-mediated 3D genome dependent causal mechanism in prostate cancer. <i>Nature Communications</i> , 2021 , 12, 1781	17.4	6
21	Telomere dysfunction cooperates with epigenetic alterations to impair murine embryonic stem cell fate commitment. <i>ELife</i> , 2020 , 9,	8.9	5
20	Candidate cancer driver mutations in superenhancers and long-range chromatin interaction networks		5
19	Organizing combinatorial transcription factor recruitment at cis-regulatory modules. <i>Transcription</i> , 2018 , 9, 233-239	4.8	5
18	CREAM: Clustering of genomic REgions Analysis Method		4
17	Inferring Human Phenotype Networks from Genome-Wide Genetic Associations. <i>Lecture Notes in Computer Science</i> , 2013 , 23-34	0.9	4

16	Convergence of dispersed regulatory mutations predicts driver genes in prostate cancer		4
15	TFEB-mediated endolysosomal activity controls human hematopoietic stem cell fate. <i>Cell Stem Cell</i> , 2021 , 28, 1838-1850.e10	18	4
14	Combining chromatin immunoprecipitation and oligonucleotide tiling arrays (ChIP-Chip) for functional genomic studies. <i>Methods in Molecular Biology</i> , 2009 , 556, 155-64	1.4	3
13	Gene isoforms as expression-based biomarkers predictive of drug response in vitro		3
12	Large organized chromatin lysine domains help distinguish primitive from differentiated cell populations. <i>Nature Communications</i> , 2021 , 12, 499	17.4	3
11	SMuRF: a novel tool to identify regulatory elements enriched for somatic point mutations. <i>BMC Bioinformatics</i> , 2018 , 19, 454	3.6	3
10	PRMT inhibition induces a viral mimicry response in triple-negative breast cancer.. <i>Nature Chemical Biology</i> , 2022 ,	11.7	3
9	Somatic Mutations and Risk-Variants Converge on Cis-Regulatory Elements to Reveal the Cancer Driver Transcription Regulators in Primary Prostate Tumors. <i>SSRN Electronic Journal</i> ,	1	2
8	Reorganization of the 3D Genome Pinpoints Noncoding Drivers of Primary Prostate Tumors. <i>Cancer Research</i> , 2021 , 81, 5833-5848	10.1	2
7	Viral integration transforms chromatin to drive oncogenesis		2
6	Metabolic adaptations underlie epigenetic vulnerabilities in chemoresistant breast cancer		2
5	Characterization of inv(3) cell line OCI-AML-20 with stroma-dependent CD34 expression. <i>Experimental Hematology</i> , 2019 , 69, 27-36	3.1	2
4	PRMT5 regulates ATF4 transcript splicing and oxidative stress response.. <i>Redox Biology</i> , 2022 , 51, 102282	1.3	1
3	Cancer-associated chromatin variants uncover the oncogenic role of transposable elements.. <i>Current Opinion in Genetics and Development</i> , 2022 , 74, 101911	4.9	1
2	ecDNAs personify cancer gangsters.. <i>Molecular Cell</i> , 2022 , 82, 500-502	17.6	0
1	Copy-scAT: Deconvoluting single-cell chromatin accessibility of genetic subclones in cancer. <i>Science Advances</i> , 2021 , 7, eabg6045	14.3	0