

# Mathieu Lupien

## List of Publications by Year in Descending Order

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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	ecDNAs personify cancer gangsters.. <i>Molecular Cell</i> , <b>2022</b> , 82, 500-502	17.6	0
122	PRMT5 regulates ATF4 transcript splicing and oxidative stress response.. <i>Redox Biology</i> , <b>2022</b> , 51, 102282	11.3	1
121	Cancer-associated chromatin variants uncover the oncogenic role of transposable elements.. <i>Current Opinion in Genetics and Development</i> , <b>2022</b> , 74, 101911	4.9	1
120	PRMT inhibition induces a viral mimicry response in triple-negative breast cancer.. <i>Nature Chemical Biology</i> , <b>2022</b> ,	11.7	3
119	Copy-scAT: Deconvoluting single-cell chromatin accessibility of genetic subclones in cancer. <i>Science Advances</i> , <b>2021</b> , 7, eabg6045	14.3	0
118	Reorganization of the 3D Genome Pinpoints Noncoding Drivers of Primary Prostate Tumors. <i>Cancer Research</i> , <b>2021</b> , 81, 5833-5848	10.1	2
117	CRISPRi screens reveal a DNA methylation-mediated 3D genome dependent causal mechanism in prostate cancer. <i>Nature Communications</i> , <b>2021</b> , 12, 1781	17.4	6
116	The Transition from Quiescent to Activated States in Human Hematopoietic Stem Cells Is Governed by Dynamic 3D Genome Reorganization. <i>Cell Stem Cell</i> , <b>2021</b> , 28, 488-501.e10	18	11
115	Pioneer of prostate cancer: past, present and the future of FOXA1. <i>Protein and Cell</i> , <b>2021</b> , 12, 29-38	7.2	18
114	Gradient of Developmental and Injury Response transcriptional states defines functional vulnerabilities underpinning glioblastoma heterogeneity.. <i>Nature Cancer</i> , <b>2021</b> , 2, 157-173	15.4	31
113	Single-cell chromatin accessibility profiling of glioblastoma identifies an invasive cancer stem cell population associated with lower survival. <i>ELife</i> , <b>2021</b> , 10,	8.9	9
112	Large organized chromatin lysine domains help distinguish primitive from differentiated cell populations. <i>Nature Communications</i> , <b>2021</b> , 12, 499	17.4	3
111	PRMT5 inhibition disrupts splicing and stemness in glioblastoma. <i>Nature Communications</i> , <b>2021</b> , 12, 979	17.4	23
110	Biological and therapeutic implications of a unique subtype of NPM1 mutated AML. <i>Nature Communications</i> , <b>2021</b> , 12, 1054	17.4	7
109	TFEB-mediated endolysosomal activity controls human hematopoietic stem cell fate. <i>Cell Stem Cell</i> , <b>2021</b> , 28, 1838-1850.e10	18	4
108	Epigenetic Switch-Induced Viral Mimicry Evasion in Chemotherapy-Resistant Breast Cancer. <i>Cancer Discovery</i> , <b>2020</b> , 10, 1312-1329	24.4	34
107	Candidate Cancer Driver Mutations in Distal Regulatory Elements and Long-Range Chromatin Interaction Networks. <i>Molecular Cell</i> , <b>2020</b> , 77, 1307-1321.e10	17.6	20

106	Noncoding mutations target cis-regulatory elements of the FOXA1 plexus in prostate cancer. <i>Nature Communications</i> , <b>2020</b> , 11, 441	17.4	21
105	Telomere dysfunction cooperates with epigenetic alterations to impair murine embryonic stem cell fate commitment. <i>ELife</i> , <b>2020</b> , 9,	8.9	5
104	Metabolic Regulation of the Epigenome Drives Lethal Infantile Ependymoma. <i>Cell</i> , <b>2020</b> , 181, 1329-1345.e24	56.2	40
103	GLUT1 inhibition blocks growth of RB1-positive triple negative breast cancer. <i>Nature Communications</i> , <b>2020</b> , 11, 4205	17.4	41
102	Identifying clusters of -regulatory elements underpinning TAD structures and lineage-specific regulatory networks. <i>Genome Research</i> , <b>2019</b> , 29, 1733-1743	9.7	9
101	Genome-wide germline correlates of the epigenetic landscape of prostate cancer. <i>Nature Medicine</i> , <b>2019</b> , 25, 1615-1626	50.5	25
100	Pervasive H3K27 Acetylation Leads to ERV Expression and a Therapeutic Vulnerability in H3K27M Gliomas. <i>Cancer Cell</i> , <b>2019</b> , 35, 782-797.e8	24.3	52
99	A chemical toolbox for the study of bromodomains and epigenetic signaling. <i>Nature Communications</i> , <b>2019</b> , 10, 1915	17.4	43
98	The Proteogenomic Landscape of Curable Prostate Cancer. <i>Cancer Cell</i> , <b>2019</b> , 35, 414-427.e6	24.3	97
97	The Mitochondrial Transacylase, Tafazzin, Regulates for AML Stemness by Modulating Intracellular Levels of Phospholipids. <i>Cell Stem Cell</i> , <b>2019</b> , 24, 621-636.e16	18	19
96	Targeting bivalency de-represses Indian Hedgehog and inhibits self-renewal of colorectal cancer-initiating cells. <i>Nature Communications</i> , <b>2019</b> , 10, 1436	17.4	21
95	High-resolution structural genomics reveals new therapeutic vulnerabilities in glioblastoma. <i>Genome Research</i> , <b>2019</b> , 29, 1211-1222	9.7	31
94	Cistrome Partitioning Reveals Convergence of Somatic Mutations and Risk Variants on Master Transcription Regulators in Primary Prostate Tumors. <i>Cancer Cell</i> , <b>2019</b> , 36, 674-689.e6	24.3	21
93	Functional Enhancers Shape Extrachromosomal Oncogene Amplifications. <i>Cell</i> , <b>2019</b> , 179, 1330-1341.e13	36.2	87
92	C3D: a tool to predict 3D genomic interactions between cis-regulatory elements. <i>Bioinformatics</i> , <b>2019</b> , 35, 877-879	7.2	8
91	Characterization of inv(3) cell line OCI-AML-20 with stroma-dependent CD34 expression. <i>Experimental Hematology</i> , <b>2019</b> , 69, 27-36	3.1	2
90	A Myc enhancer cluster regulates normal and leukaemic haematopoietic stem cell hierarchies. <i>Nature</i> , <b>2018</b> , 553, 515-520	50.4	142
89	Therapeutic targeting of ependymoma as informed by oncogenic enhancer profiling. <i>Nature</i> , <b>2018</b> , 553, 101-105	50.4	116

88	Risk SNP-Mediated Promoter-Enhancer Switching Drives Prostate Cancer through lncRNA PCAT19. <i>Cell</i> , <b>2018</b> , 174, 564-575.e18	56.2	154
87	Reporters to mark and eliminate basal or luminal epithelial cells in culture and in vivo. <i>PLoS Biology</i> , <b>2018</b> , 16, e2004049	9.7	10
86	Mammary molecular portraits reveal lineage-specific features and progenitor cell vulnerabilities. <i>Journal of Cell Biology</i> , <b>2018</b> , 217, 2951-2974	7.3	20
85	Organizing combinatorial transcription factor recruitment at cis-regulatory modules. <i>Transcription</i> , <b>2018</b> , 9, 233-239	4.8	5
84	SMuRF: a novel tool to identify regulatory elements enriched for somatic point mutations. <i>BMC Bioinformatics</i> , <b>2018</b> , 19, 454	3.6	3
83	Genomic hallmarks of localized, non-indolent prostate cancer. <i>Nature</i> , <b>2017</b> , 541, 359-364	50.4	320
82	The logic of transcriptional regulator recruitment architecture at -regulatory modules controlling liver functions. <i>Genome Research</i> , <b>2017</b> , 27, 985-996	9.7	13
81	Early-life antibiotic treatment enhances the pathogenicity of CD4 T cells during intestinal inflammation. <i>Journal of Leukocyte Biology</i> , <b>2017</b> , 101, 893-900	6.5	19
80	Gene isoforms as expression-based biomarkers predictive of drug response in vitro. <i>Nature Communications</i> , <b>2017</b> , 8, 1126	17.4	34
79	Fate mapping of human glioblastoma reveals an invariant stem cell hierarchy. <i>Nature</i> , <b>2017</b> , 549, 227-232	50.4	197
78	ASCL1 Reorganizes Chromatin to Direct Neuronal Fate and Suppress Tumorigenicity of Glioblastoma Stem Cells. <i>Cell Stem Cell</i> , <b>2017</b> , 21, 209-224.e7	18	78
77	TMPRSS2-ERG fusion co-opts master transcription factors and activates NOTCH signaling in primary prostate cancer. <i>Nature Genetics</i> , <b>2017</b> , 49, 1336-1345	36.3	105
76	Convergence of BMI1 and CHD7 on ERK Signaling in Medulloblastoma. <i>Cell Reports</i> , <b>2017</b> , 21, 2772-2784	10.6	19
75	Variant Set Enrichment: an R package to identify disease-associated functional genomic regions. <i>BioData Mining</i> , <b>2017</b> , 10, 9	4.3	16
74	Noncoding somatic and inherited single-nucleotide variants converge to promote ESR1 expression in breast cancer. <i>Nature Genetics</i> , <b>2016</b> , 48, 1260-6	36.3	53
73	Modulation of long noncoding RNAs by risk SNPs underlying genetic predispositions to prostate cancer. <i>Nature Genetics</i> , <b>2016</b> , 48, 1142-50	36.3	158
72	Mutant IDH1 Downregulates ATM and Alters DNA Repair and Sensitivity to DNA Damage Independent of TET2. <i>Cancer Cell</i> , <b>2016</b> , 30, 337-348	24.3	121
71	Emergence of the Noncoding Cancer Genome: A Target of Genetic and Epigenetic Alterations. <i>Cancer Discovery</i> , <b>2016</b> , 6, 1215-1229	24.4	41

70	Blockade of AP-1 Potentiates Endocrine Therapy and Overcomes Resistance. <i>Molecular Cancer Research</i> , <b>2016</b> , 14, 470-81	6.6	27
69	PharmacGx: an R package for analysis of large pharmacogenomic datasets. <i>Bioinformatics</i> , <b>2016</b> , 32, 1244-6	7.2	127
68	Transcriptome-wide characterization of the endogenous miR-34A-p53 tumor suppressor network. <i>Oncotarget</i> , <b>2016</b> , 7, 49611-49622	3.3	8
67	Pre-neoplastic epigenetic disruption of transcriptional enhancers in chronic inflammation. <i>Oncotarget</i> , <b>2016</b> , 7, 15772-86	3.3	19
66	Integrated (epi)-Genomic Analyses Identify Subgroup-Specific Therapeutic Targets in CNS Rhabdoid Tumors. <i>Cancer Cell</i> , <b>2016</b> , 30, 891-908	24.3	135
65	Molecular Insights of Pathways Resulting from Two Common PIK3CA Mutations in Breast Cancer. <i>Cancer Research</i> , <b>2016</b> , 76, 3989-4001	10.1	17
64	The Transcriptional Repressor Polycomb Group Factor 6, PCGF6, Negatively Regulates Dendritic Cell Activation and Promotes Quiescence. <i>Cell Reports</i> , <b>2016</b> , 16, 1829-37	10.6	17
63	The histone variant H2A.Z is an important regulator of enhancer activity. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, 9742-56	20.1	52
62	MLL5 Orchestrates a Cancer Self-Renewal State by Repressing the Histone Variant H3.3 and Globally Reorganizing Chromatin. <i>Cancer Cell</i> , <b>2015</b> , 28, 715-729	24.3	64
61	BioID identifies novel c-MYC interacting partners in cultured cells and xenograft tumors. <i>Journal of Proteomics</i> , <b>2015</b> , 118, 95-111	3.9	83
60	Personalized diagnosis of medulloblastoma subtypes across patients and model systems. <i>Genomics</i> , <b>2015</b> , 106, 96-106	4.3	7
59	ABC: a tool to identify SNVs causing allele-specific transcription factor binding from ChIP-Seq experiments. <i>Bioinformatics</i> , <b>2015</b> , 31, 3057-9	7.2	11
58	ZNF143 provides sequence specificity to secure chromatin interactions at gene promoters. <i>Nature Communications</i> , <b>2015</b> , 2, 6186	17.4	123
57	The pioneer factor PBX1 is a novel driver of metastatic progression in ER $\beta$ -positive breast cancer. <i>Oncotarget</i> , <b>2015</b> , 6, 21878-91	3.3	28
56	Laying a solid foundation for Manhattan--Getting the functional basis for the post-GWAS eraU	8.5	68
55	Epigenomic alterations define lethal CIMP-positive ependymomas of infancy. <i>Nature</i> , <b>2014</b> , 506, 445-50	50.4	434
54	Combinatorial effects of multiple enhancer variants in linkage disequilibrium dictate levels of gene expression to confer susceptibility to common traits. <i>Genome Research</i> , <b>2014</b> , 24, 1-13	9.7	258
53	Enhancer alterations in cancer: a source for a cell identity crisis. <i>Genome Medicine</i> , <b>2014</b> , 6, 77	14.4	36

52	Human somatic cell mutagenesis creates genetically tractable sarcomas. <i>Nature Genetics</i> , <b>2014</b> , 46, 964-763	36.3	23
51	Human-chromatin-related protein interactions identify a demethylase complex required for chromosome segregation. <i>Cell Reports</i> , <b>2014</b> , 8, 297-310	10.6	46
50	Intratumor DNA methylation heterogeneity reflects clonal evolution in aggressive prostate cancer. <i>Cell Reports</i> , <b>2014</b> , 8, 798-806	10.6	177
49	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , <b>2014</b> , 4, 4999	17.4	87
48	Chromatin and epigenetic determinants of estrogen receptor alpha (ESR1) signaling. <i>Molecular and Cellular Endocrinology</i> , <b>2014</b> , 382, 633-641	4.4	41
47	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> , <b>2014</b> , 111, 4472-7	11.5	86
46	Chromatin profiling reveals regulatory network shifts and a protective role for hepatocyte nuclear factor 4 during colitis. <i>Molecular and Cellular Biology</i> , <b>2014</b> , 34, 3291-304	4.8	28
45	A global assessment of cancer genomic alterations in epigenetic mechanisms. <i>Epigenetics and Chromatin</i> , <b>2014</b> , 7, 29	5.8	46
44	Methyltransferase G9A regulates T cell differentiation during murine intestinal inflammation. <i>Journal of Clinical Investigation</i> , <b>2014</b> , 124, 1945-55	15.9	57
43	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> , <b>2013</b> , 110, E1490-9	11.5	120
42	Exploiting tumor epigenetics to improve oncolytic virotherapy. <i>Frontiers in Genetics</i> , <b>2013</b> , 4, 184	4.5	15
41	Inferring Human Phenotype Networks from Genome-Wide Genetic Associations. <i>Lecture Notes in Computer Science</i> , <b>2013</b> , 23-34	0.9	4
40	Breast cancer risk-associated SNPs modulate the affinity of chromatin for FOXA1 and alter gene expression. <i>Nature Genetics</i> , <b>2012</b> , 44, 1191-8	36.3	287
39	Cancer heterogeneity: origins and implications for genetic association studies. <i>Trends in Genetics</i> , <b>2012</b> , 28, 538-43	8.5	20
38	Integrative functional genomics identifies an enhancer looping to the SOX9 gene disrupted by the 17q24.3 prostate cancer risk locus. <i>Genome Research</i> , <b>2012</b> , 22, 1437-46	9.7	107
37	Chromatin landscape and endocrine response in breast cancer. <i>Epigenomics</i> , <b>2012</b> , 4, 675-83	4.4	12
36	Epigenomic enhancer profiling defines a signature of colon cancer. <i>Science</i> , <b>2012</b> , 336, 736-9	33.3	255
35	Dual suppression of the cyclin-dependent kinase inhibitors CDKN2C and CDKN1A in human melanoma. <i>Journal of the National Cancer Institute</i> , <b>2012</b> , 104, 1673-9	9.7	29

34	Identification of PBX1 target genes in cancer cells by global mapping of PBX1 binding sites. <i>PLoS ONE</i> , <b>2012</b> , 7, e36054	3.7	26
33	Pioneer factors: directing transcriptional regulators within the chromatin environment. <i>Trends in Genetics</i> , <b>2011</b> , 27, 465-74	8.5	120
32	Layers of epistasis: genome-wide regulatory networks and network approaches to genome-wide association studies. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , <b>2011</b> , 3, 513-26	6.6	31
31	A comprehensive view of nuclear receptor cancer cistromes. <i>Cancer Research</i> , <b>2011</b> , 71, 6940-7	10.1	99
30	Epigenetic switch involved in activation of pioneer factor FOXA1-dependent enhancers. <i>Genome Research</i> , <b>2011</b> , 21, 555-65	9.7	172
29	Genomic collaboration of estrogen receptor alpha and extracellular signal-regulated kinase 2 in regulating gene and proliferation programs. <i>Molecular and Cellular Biology</i> , <b>2011</b> , 31, 226-36	4.8	99
28	PBX1 genomic pioneer function drives ER signaling underlying progression in breast cancer. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1002368	6	130
27	Nucleosome dynamics define transcriptional enhancers. <i>Nature Genetics</i> , <b>2010</b> , 42, 343-7	36.3	382
26	Multimodal regulation of E2F1 gene expression by progestins. <i>Molecular and Cellular Biology</i> , <b>2010</b> , 30, 1866-77	4.8	23
25	Growth factor stimulation induces a distinct ER(alpha) cistrome underlying breast cancer endocrine resistance. <i>Genes and Development</i> , <b>2010</b> , 24, 2219-27	12.6	136
24	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> , <b>2010</b> , 107, 3698-703	11.5	134
23	Combining chromatin immunoprecipitation and oligonucleotide tiling arrays (ChIP-Chip) for functional genomic studies. <i>Methods in Molecular Biology</i> , <b>2009</b> , 556, 155-64	1.4	3
22	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> , <b>2009</b> , 19, 1963-73	9.7	108
21	Cistromics of hormone-dependent cancer. <i>Endocrine-Related Cancer</i> , <b>2009</b> , 16, 381-9	5.7	69
20	Coactivator function defines the active estrogen receptor alpha cistrome. <i>Molecular and Cellular Biology</i> , <b>2009</b> , 29, 3413-23	4.8	65
19	Androgen receptor regulates a distinct transcription program in androgen-independent prostate cancer. <i>Cell</i> , <b>2009</b> , 138, 245-56	56.2	691
18	Cell-type selective chromatin remodeling defines the active subset of FOXA1-bound enhancers. <i>Genome Research</i> , <b>2009</b> , 19, 372-80	9.7	83
17	FoxA1 translates epigenetic signatures into enhancer-driven lineage-specific transcription. <i>Cell</i> , <b>2008</b> , 132, 958-70	56.2	746

16	Estrogen-dependent signaling in a molecularly distinct subclass of aggressive prostate cancer. <i>Journal of the National Cancer Institute</i> , <b>2008</b> , 100, 815-25	9.7	251
15	Unique ERalpha cistromes control cell type-specific gene regulation. <i>Molecular Endocrinology</i> , <b>2008</b> , 22, 2393-406		110
14	CARM1 regulates estrogen-stimulated breast cancer growth through up-regulation of E2F1. <i>Cancer Research</i> , <b>2008</b> , 68, 301-6	10.1	156
13	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> , <b>2007</b> , 21, 797-816		37
12	Positive cross-regulatory loop ties GATA-3 to estrogen receptor alpha expression in breast cancer. <i>Cancer Research</i> , <b>2007</b> , 67, 6477-83	10.1	274
11	Tamoxifen and raloxifene differ in their functional interactions with aspartate 351 of estrogen receptor alpha. <i>Molecular Pharmacology</i> , <b>2006</b> , 70, 579-88	4.3	28
10	Overexpression of activated murine Notch1 and Notch3 in transgenic mice blocks mammary gland development and induces mammary tumors. <i>American Journal of Pathology</i> , <b>2006</b> , 168, 973-90	5.8	148
9	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> , <b>2006</b> , 300, 497-511	3.1	26
8	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> , <b>2003</b> , 312, 377-91	4.2	25
7	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
6	CREAM: Clustering of genomic REgions Analysis Method		4
5	Convergence of dispersed regulatory mutations predicts driver genes in prostate cancer		4
4	Gene isoforms as expression-based biomarkers predictive of drug response in vitro		3
3	Viral integration transforms chromatin to drive oncogenesis		2
2	Candidate cancer driver mutations in superenhancers and long-range chromatin interaction networks		5
1	Metabolic adaptations underlie epigenetic vulnerabilities in chemoresistant breast cancer		2