

# Heather J Lee

## List of Publications by Year in descending order

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Version: 2024-02-01

33  
papers

5,261  
citations

331670

21  
h-index

395702

33  
g-index

43  
all docs

43  
docs citations

43  
times ranked

8064  
citing authors

#	ARTICLE	IF	CITATIONS
1	Single-cell genome-wide bisulfite sequencing for assessing epigenetic heterogeneity. <i>Nature Methods</i> , 2014, 11, 817-820.	19.0	954
2	Parallel single-cell sequencing links transcriptional and epigenetic heterogeneity. <i>Nature Methods</i> , 2016, 13, 229-232.	19.0	602
3	scNMT-seq enables joint profiling of chromatin accessibility DNA methylation and transcription in single cells. <i>Nature Communications</i> , 2018, 9, 781.	12.8	513
4	Osteoclast differentiation factor RANKL controls development of progesterin-driven mammary cancer. <i>Nature</i> , 2010, 468, 98-102.	27.8	507
5	FGF Signaling Inhibition in ESCs Drives Rapid Genome-wide Demethylation to the Epigenetic Ground State of Pluripotency. <i>Cell Stem Cell</i> , 2013, 13, 351-359.	11.1	371
6	DeepCpG: accurate prediction of single-cell DNA methylation states using deep learning. <i>Genome Biology</i> , 2017, 18, 67.	8.8	361
7	Reprogramming the Methylome: Erasing Memory and Creating Diversity. <i>Cell Stem Cell</i> , 2014, 14, 710-719.	11.1	301
8	Single-cell epigenomics: powerful new methods for understanding gene regulation and cell identity. <i>Genome Biology</i> , 2016, 17, 72.	8.8	253
9	A Menin-MLL Inhibitor Induces Specific Chromatin Changes and Eradicates Disease in Models of MLL-Rearranged Leukemia. <i>Cancer Cell</i> , 2019, 36, 660-673.e11.	16.8	231
10	Tracking the embryonic stem cell transition from ground state pluripotency. <i>Development (Cambridge)</i> , 2017, 144, 1221-1234.	2.5	226
11	Genome-wide base-resolution mapping of DNA methylation in single cells using single-cell bisulfite sequencing (scBS-seq). <i>Nature Protocols</i> , 2017, 12, 534-547.	12.0	199
12	Progesterone drives mammary secretory differentiation via RankL-mediated induction of Elf5 in luminal progenitor cells. <i>Development (Cambridge)</i> , 2013, 140, 1397-1401.	2.5	86
13	Insulin, a key regulator of hormone responsive milk protein synthesis during lactogenesis in murine mammary explants. <i>Functional and Integrative Genomics</i> , 2010, 10, 87-95.	3.5	80
14	ELF5 Suppresses Estrogen Sensitivity and Underpins the Acquisition of Antiestrogen Resistance in Luminal Breast Cancer. <i>PLoS Biology</i> , 2012, 10, e1001461.	5.6	74
15	Genome-Scale Oscillations in DNA Methylation during Exit from Pluripotency. <i>Cell Systems</i> , 2018, 7, 63-76.e12.	6.2	70
16	ELF5 Drives Lung Metastasis in Luminal Breast Cancer through Recruitment of Gr1+ CD11b+ Myeloid-Derived Suppressor Cells. <i>PLoS Biology</i> , 2015, 13, e1002330.	5.6	59
17	Allosteric activation of the extracellular Ca <sup>2+</sup> -sensing receptor by L-amino acids enhances ERK1/2 phosphorylation. <i>Biochemical Journal</i> , 2007, 404, 141-149.	3.7	56
18	Interplay between progesterone and prolactin in mammary development and implications for breast cancer. <i>Molecular and Cellular Endocrinology</i> , 2012, 357, 101-107.	3.2	48

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19	Lineage Specific Methylation of the <i>Elf5</i> Promoter in Mammary Epithelial Cells. <i>Stem Cells</i> , 2011, 29, 1611-1619.	3.2	39
20	ELF5 isoform expression is tissue-specific and significantly altered in cancer. <i>Breast Cancer Research</i> , 2016, 18, 4.	5.0	37
21	Elf5, hormones and cell fate. <i>Trends in Endocrinology and Metabolism</i> , 2012, 23, 292-298.	7.1	31
22	Smchd1 is a maternal effect gene required for genomic imprinting. <i>ELife</i> , 2020, 9, .	6.0	24
23	The Antiproliferative Effects of Progestins in T47D Breast Cancer Cells Are Tempered by Progestin Induction of the ETS Transcription Factor Elf5. <i>Molecular Endocrinology</i> , 2010, 24, 1380-1392.	3.7	16
24	Unravelling the Epigenome of Myelodysplastic Syndrome: Diagnosis, Prognosis, and Response to Therapy. <i>Cancers</i> , 2020, 12, 3128.	3.7	12
25	Genome-Wide Analysis of DNA Methylation in Single Cells Using a Post-bisulfite Adapter Tagging Approach. <i>Methods in Molecular Biology</i> , 2018, 1712, 87-95.	0.9	11
26	scTEM-seq: Single-cell analysis of transposable element methylation to link global epigenetic heterogeneity with transcriptional programs. <i>Scientific Reports</i> , 2022, 12, 5776.	3.3	10
27	Regulation of Growth Hormone Signaling by Selective Estrogen Receptor Modulators Occurs through Suppression of Protein Tyrosine Phosphatases. <i>Endocrinology</i> , 2007, 148, 2417-2423.	2.8	9
28	Single-cell epigenomics in cancer: charting a course to clinical impact. <i>Epigenomics</i> , 2020, 12, 1139-1151.	2.1	9
29	ELF5, normal mammary development and the heterogeneous phenotypes of breast cancer. <i>Breast Cancer Management</i> , 2013, 2, 489-498.	0.2	6
30	Etoposide Induces Nuclear Re-Localisation of AID. <i>PLoS ONE</i> , 2013, 8, e82110.	2.5	4
31	The Promise of Single-cell Technology in Providing New Insights Into the Molecular Heterogeneity and Management of Acute Lymphoblastic Leukemia. <i>HemaSphere</i> , 2022, 6, e734.	2.7	4
32	Maternal SMCHD1 controls both imprinted Xist expression and imprinted X chromosome inactivation. <i>Epigenetics and Chromatin</i> , 2022, 15, .	3.9	4
33	Single-Cell Genomics and Epigenomics. <i>Series in Bioengineering</i> , 2016, , 257-301.	0.6	2