

Heather J Lee

List of Publications by Year in descending order

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33
papers

5,261
citations

331670

21
h-index

395702

33
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43
all docs

43
docs citations

43
times ranked

8064
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	Maternal SMCHD1 controls both imprinted Xist expression and imprinted X chromosome inactivation. <i>Epigenetics and Chromatin</i> , 2022, 15, .	3.9	4
4	Single-cell epigenomics in cancer: charting a course to clinical impact. <i>Epigenomics</i> , 2020, 12, 1139-1151.	2.1	9
5	Unravelling the Epigenome of Myelodysplastic Syndrome: Diagnosis, Prognosis, and Response to Therapy. <i>Cancers</i> , 2020, 12, 3128.	3.7	12
6	Smchd1 is a maternal effect gene required for genomic imprinting. <i>ELife</i> , 2020, 9, .	6.0	24
7	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
8	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
9	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
10	Genome-Scale Oscillations in DNA Methylation during Exit from Pluripotency. <i>Cell Systems</i> , 2018, 7, 63-76.e12.	6.2	70
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	Tracking the embryonic stem cell transition from ground state pluripotency. <i>Development (Cambridge)</i> , 2017, 144, 1221-1234.	2.5	226
13	DeepCpG: accurate prediction of single-cell DNA methylation states using deep learning. <i>Genome Biology</i> , 2017, 18, 67.	8.8	361
14	ELF5 isoform expression is tissue-specific and significantly altered in cancer. <i>Breast Cancer Research</i> , 2016, 18, 4.	5.0	37
15	Single-cell epigenomics: powerful new methods for understanding gene regulation and cell identity. <i>Genome Biology</i> , 2016, 17, 72.	8.8	253
16	Single-Cell Genomics and Epigenomics. <i>Series in Bioengineering</i> , 2016, , 257-301.	0.6	2
17	Parallel single-cell sequencing links transcriptional and epigenetic heterogeneity. <i>Nature Methods</i> , 2016, 13, 229-232.	19.0	602
18	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

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19	Single-cell genome-wide bisulfite sequencing for assessing epigenetic heterogeneity. <i>Nature Methods</i> , 2014, 11, 817-820.	19.0	954
20	Reprogramming the Methylome: Erasing Memory and Creating Diversity. <i>Cell Stem Cell</i> , 2014, 14, 710-719.	11.1	301
21	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
22	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
23	ELF5, normal mammary development and the heterogeneous phenotypes of breast cancer. <i>Breast Cancer Management</i> , 2013, 2, 489-498.	0.2	6
24	Etoposide Induces Nuclear Re-Localisation of AID. <i>PLoS ONE</i> , 2013, 8, e82110.	2.5	4
25	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
26	Elf5, hormones and cell fate. <i>Trends in Endocrinology and Metabolism</i> , 2012, 23, 292-298.	7.1	31
27	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
28	Lineage Specific Methylation of the <i>Elf5</i> Promoter in Mammary Epithelial Cells. <i>Stem Cells</i> , 2011, 29, 1611-1619.	3.2	39
29	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
30	Osteoclast differentiation factor RANKL controls development of progestin-driven mammary cancer. <i>Nature</i> , 2010, 468, 98-102.	27.8	507
31	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
32	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
33	Allosteric activation of the extracellular Ca ²⁺ -sensing receptor by L-amino acids enhances ERK1/2 phosphorylation. <i>Biochemical Journal</i> , 2007, 404, 141-149.	3.7	56