Peter J Rugg-Gunn

List of Publications by Year
in descending order

#	Article	IF	Citations
1	Derivation of pluripotent epiblast stem cells from mammalian embryos. Nature, 2007, 448, 191-195.	27.8	1,842
2	Characterization of human embryonic stem cell lines by the International Stem Cell Initiative. Nature Biotechnology, 2007, 25, 803-816.	17.5	983
3	Gata3 regulates trophoblast development downstream of Tead4 and in parallel to Cdx2. Development (Cambridge), 2010, 137, 395-403.	2.5	389
4	Activin/Nodal signalling maintains pluripotency by controlling Nanog expression. Development (Cambridge), 2009, 136, 1339-1349.	2.5	379
5	Multi-omics profiling of mouse gastrulation at single-cell resolution. Nature, 2019, 576, 487-491.	27.8	307
6	Global Chromatin Architecture Reflects Pluripotency and Lineage Commitment in the Early Mouse Embryo. PLoS ONE, 2010, 5, e10531.	2.5	233
7	Early Cell Fate Decisions of Human Embryonic Stem Cells and Mouse Epiblast Stem Cells Are Controlled by the Same Signalling Pathways. PLoS ONE, 2009, 4, e6082.	2.5	232
8	Distinct histone modifications in stem cell lines and tissue lineages from the early mouse embryo. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 10783-10790.	7.1	212
9	XACT Noncoding RNA Competes with XIST in the Control of X Chromosome Activity during Human Early Development. Cell Stem Cell, 2017, 20, 102-111.	11.1	181
10	Epigenetic status of human embryonic stem cells. Nature Genetics, 2005, 37, 585-587.	21.4	169
11	Comprehensive Cell Surface Protein Profiling Identifies Specific Markers of Human Naive and Primed Pluripotent States. Cell Stem Cell, 2017, 20, 874-890.e7.	11.1	150
12	Recombination Signatures Distinguish Embryonic Stem Cells Derived by Parthenogenesis and Somatic Cell Nuclear Transfer. Cell Stem Cell, 2007, 1, 346-352.	11.1	137
13	Cell-Surface Proteomics Identifies Lineage-Specific Markers of Embryo-Derived Stem Cells. Developmental Cell, 2012, 22, 887-901.	7.0	134
14	Global reorganisation of cis-regulatory units upon lineage commitment of human embryonic stem cells. ELife, 2017, 6, .	6.0	130
15	Status of genomic imprinting in human embryonic stem cells as revealed by a large cohort of independently derived and maintained lines. Human Molecular Genetics, 2007, 16, R243-R251.	2.9	121
16	Enhancing and Diminishing Gene Function in Human Embryonic Stem Cells. Stem Cells, 2004, 22, 2-11.	3.2	119
17	Deletion of the Polycomb-Group Protein EZH2 Leads to Compromised Self-Renewal and Differentiation Defects in Human Embryonic Stem Cells. Cell Reports, 2016, 17, 2700-2714.	6.4	110
18	Comparative Principles of DNA Methylation Reprogramming during Human and Mouse InÂVitro Primordial Germ Cell Specification. Developmental Cell, 2016, 39, 104-115.	7.0	102

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19	Long-Range Enhancer Interactions Are Prevalent in Mouse Embryonic Stem Cells and Are Reorganized upon Pluripotent State Transition. Cell Reports, 2018, 22, 2615-2627.	6.4	99
20	Genome-Scale Oscillations in DNA Methylation during Exit from Pluripotency. Cell Systems, 2018, 7, 63-76.e12.	6.2	70
21	The pluripotency factor <i>Nanog</i> regulates pericentromeric heterochromatin organization in mouse embryonic stem cells. Genes and Development, 2016, 30, 1101-1115.	5.9	50
22	Promoter interactome of human embryonic stem cell-derived cardiomyocytes connects GWAS regions to cardiac gene networks. Nature Communications, 2018, 9, 2526.	12.8	48
23	Amniogenesis occurs in two independent waves in primates. Cell Stem Cell, 2022, 29, 744-759.e6.	11.1	48
24	Molecular profiling of aged neural progenitors identifies <i>Dbx2</i> as a candidate regulator of ageâ€associated neurogenic decline. Aging Cell, 2018, 17, e12745.	6.7	46
25	Naive Pluripotent Stem Cells Exhibit Phenotypic Variability that Is Driven by Genetic Variation. Cell Stem Cell, 2020, 27, 470-481.e6.	11.1	38
26	Epigenetic features of the mouse trophoblast. Reproductive BioMedicine Online, 2012, 25, 21-30.	2.4	34
27	Human Embryonic Stem Cells as a Model for Studying Epigenetic Regulation During Early Development. Cell Cycle, 2005, 4, 1323-1326.	2.6	30
28	Widespread reorganisation of pluripotent factor binding and gene regulatory interactions between human pluripotent states. Nature Communications, 2021, 12, 2098.	12.8	30
29	Integrated multi-omics reveal polycomb repressive complex 2 restricts human trophoblast induction. Nature Cell Biology, 2022, 24, 858-871.	10.3	30
30	Identifying Human NaÃ¯ve Pluripotent Stem Cells â˜’ Evaluating Stateâ€Specific Reporter Lines and Cellâ€Surface Markers. BioEssays, 2018, 40, e1700239.	2.5	26
31	TGFÎ² signalling is required to maintain pluripotency of human naÃ¯ve pluripotent stem cells. ELife, 2021, 10, .	6.0	24
32	Cell-Surface Proteomics Identifies Differences in Signaling and Adhesion Protein Expression between Naive and Primed Human Pluripotent Stem Cells. Stem Cell Reports, 2020, 14, 972-988.	4.8	23
33	Genome-wide analysis of DNA replication and DNA double-strand breaks using TrAEL-seq. PLoS Biology, 2021, 19, e3000886.	5.6	19
34	DNA methylation is dispensable for changes in global chromatin architecture but required for chromocentre formation in early stem cell differentiation. Chromosoma, 2017, 126, 605-614.	2.2	17
35	Satellite repeat transcripts modulate heterochromatin condensates and safeguard chromosome stability in mouse embryonic stem cells. Nature Communications, 2022, 13, .	12.8	16
36	Locus-specific induction of gene expression from heterochromatin loci during cellular senescence. Nature Aging, 2022, 2, 31-45.	11.6	12

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37	Transcriptional response of<i>Hoxb</i>genes to retinoid signalling is regionally restricted along the neural tube rostrocaudal axis. Royal Society Open Science, 2017, 4, 160913.	2.4	11
38	The Challenge of Regulating Rapidly Changing Science: Stem Cell Legislation in Canada. Cell Stem Cell, 2009, 4, 285-288.	11.1	10
39	The application of cell surface markers to demarcate distinct human pluripotent states. Experimental Cell Research, 2020, 387, 111749.	2.6	9
40	Crosstalk between pluripotency factors and higher-order chromatin organization. Nucleus, 2016, 7, 447-452.	2.2	7
41	Genome-wide screening identifies Polycomb repressive complex 1.3 as an essential regulator of human naÃ¯ve pluripotent cell reprogramming. Science Advances, 2022, 8, eabk0013.	10.3	7
42	The Legal Status of Novel Stem Cell Technologies in Canada. Journal of International Biotechnology Law, 2008, 5, .	0.1	6
43	Chromatin organization in pluripotent cells: emerging approaches to study and disrupt function. Briefings in Functional Genomics, 2016, 15, 305-314.	2.7	4
44	Induction of Human NaÃ¯ve Pluripotency Using Chemical Resetting. Methods in Molecular Biology, 2022, 2416, 29-37.	0.9	4
45	Derivation and Culture of Extra-Embryonic Endoderm Stem Cell Lines. Cold Spring Harbor Protocols, 2017, 2017, pdb.prot093963.	0.3	3
46	Derivation and Culture of Epiblast Stem Cell (EpiSC) Lines. Cold Spring Harbor Protocols, 2017, 2017, pdb.prot093971.	0.3	2
47	Naive pluripotent stem cells as a model for studying human developmental epigenomics: opportunities and limitations. Epigenomics, 2017, 9, 1485-1488.	2.1	2
48	Transcription factors make the right contacts. Nature Cell Biology, 2019, 21, 1173-1174.	10.3	1
49	Flow Cytometry Analysis of to Identify Human NaÃ¯ve Pluripotent Stem Cells. Methods in Molecular Biology, 2022, 2416, 257-265.	0.9	1