Kathrin Plath

List of Publications by Year in Descending Order

113 papers	20,843 citations	52 h-index	124 g-index
124 ext. papers	23,712 ext. citations	17.7 avg, IF	6.44 L-index

#	Paper	IF	Citations
113	Genome-wide screening identifies Polycomb repressive complex 1.3 as an essential regulator of human na�ve pluripotent cell reprogramming.. *Science Advances*, **2022**, 8, eabk0013	14.3	0
112	RNA promotes the formation of spatial compartments in the nucleus. *Cell*, **2021**, 184, 5775-5790.e30	56.2	36
111	Xist nucleates local protein gradients to propagate silencing across the X chromosome. *Cell*, **2021**, 184, 6174-6192.e32	56.2	12
110	Single-cell analysis of the developing human testis reveals somatic niche cell specification and fetal germline stem cell establishment. *Cell Stem Cell*, **2021**, 28, 764-778.e4	18	21
109	Transcriptional analysis of cystic fibrosis airways at single-cell resolution reveals altered epithelial cell states and composition. *Nature Medicine*, **2021**, 27, 806-814	50.5	29
108	Carboxylate-Modified Magnetic Bead (CMMB)-Based Isopropanol Gradient Peptide Fractionation (CIF) Enables Rapid and Robust Off-Line Peptide Mixture Fractionation in Bottom-Up Proteomics. *Molecular and Cellular Proteomics*, **2021**, 20, 100039	7.6	2
107	SARS-CoV-2 infection rewires host cell metabolism and is potentially susceptible to mTORC1 inhibition. *Nature Communications*, **2021**, 12, 1876	17.4	31
106	Identification of neural oscillations and epileptiform changes in human brain organoids. *Nature Neuroscience*, **2021**, 24, 1488-1500	25.5	20
105	Defining the nature of human pluripotent stem cell-derived interneurons via single-cell analysis. *Stem Cell Reports*, **2021**, 16, 2548-2564	8	1
104	The transcription factor code in iPSC reprogramming. *Current Opinion in Genetics and Development*, **2021**, 70, 89-96	4.9	1
103	A Human Skeletal Muscle Atlas Identifies the Trajectories of Stem and Progenitor Cells across Development and from Human Pluripotent Stem Cells. *Cell Stem Cell*, **2020**, 27, 158-176.e10	18	32
102	Chromatin and Nuclear Architecture in Stem Cells. *Stem Cell Reports*, **2020**, 15, 1155-1157	8	0
101	Pressure-Driven Mitochondrial Transfer Pipeline Generates Mammalian Cells of Desired Genetic Combinations and Fates. *Cell Reports*, **2020**, 33, 108562	10.6	12
100	Defining Transcriptional Signatures of Human Hair Follicle Cell States. *Journal of Investigative Dermatology*, **2020**, 140, 764-773.e4	4.3	12
99	Direct Exposure to SARS-CoV-2 and Cigarette Smoke Increases Infection Severity and Alters the Stem Cell-Derived Airway Repair Response. *Cell Stem Cell*, **2020**, 27, 869-875.e4	18	32
98	Female human primordial germ cells display X-chromosome dosage compensation despite the absence of X-inactivation. *Nature Cell Biology*, **2020**, 22, 1436-1446	23.4	19
97	A protein assembly mediates Xist localization and gene silencing. *Nature*, **2020**, 587, 145-151	50.4	52

96	DNA methylation estimation using methylation-sensitive restriction enzyme bisulfite sequencing (MREBS). *PLoS ONE*, **2019**, 14, e0214368	3.7	10
95	A Single-Cell Transcriptomic Atlas of Human Neocortical Development during Mid-gestation. *Neuron*, **2019**, 103, 785-801.e8	13.9	148
94	The BAF and PRC2 Complex Subunits Dpf2 and Eed Antagonistically Converge on Tbx3 to Control ESC Differentiation. *Cell Stem Cell*, **2019**, 24, 138-152.e8	18	15
93	Promoter-Enhancer Communication Occurs Primarily within Insulated Neighborhoods. *Molecular Cell*, **2019**, 73, 250-263.e5	17.6	44
92	Analysis of cardiomyocyte clonal expansion during mouse heart development and injury. *Nature Communications*, **2018**, 9, 754	17.4	65
91	High-Throughput Screening of a Luciferase Reporter of Gene Silencing on the Inactive X Chromosome. *Methods in Molecular Biology*, **2018**, 1755, 75-87	1.4	
90	X Chromosome Dosage Influences DNA Methylation Dynamics during Reprogramming to Mouse iPSCs. *Stem Cell Reports*, **2018**, 10, 1537-1550	8	24
89	Mapping Metabolism: Monitoring Lactate Dehydrogenase Activity Directly in Tissue. *Journal of Visualized Experiments*, **2018**,	1.6	5
88	Loss of MECP2 Leads to Activation of P53 and Neuronal Senescence. *Stem Cell Reports*, **2018**, 10, 1453-1463	8	28
87	Reduced MEK inhibition preserves genomic stability in naive human embryonic stem cells. *Nature Methods*, **2018**, 15, 732-740	21.6	44
86	The Role of Xist in X-Chromosome Dosage Compensation. *Trends in Cell Biology*, **2018**, 28, 999-1013	18.3	71
85	Comparison of reprogramming factor targets reveals both species-specific and conserved mechanisms in early iPSC reprogramming. *BMC Genomics*, **2018**, 19, 956	4.5	8
84	Identification and Single-Cell Functional Characterization of an Endodermally Biased Pluripotent Substate in Human Embryonic Stem Cells. *Stem Cell Reports*, **2018**, 10, 1895-1907	8	18
83	Cooperative Binding of Transcription Factors Orchestrates Reprogramming. *Cell*, **2017**, 168, 442-459.e20	56.2	274
82	Cbx3 maintains lineage specificity during neural differentiation. *Genes and Development*, **2017**, 31, 241-246	12.6	26
81	Human Embryonic Stem Cells Do Not Change Their X Inactivation Status during Differentiation. *Cell Reports*, **2017**, 18, 54-67	10.6	72
80	Human Naive Pluripotent Stem Cells Model X Chromosome Dampening and X Inactivation. *Cell Stem Cell*, **2017**, 20, 87-101	18	136
79	Regulation of X-chromosome dosage compensation in human: mechanisms and model systems. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2017**, 372,	5.8	20

78	Epigenetic resetting of human pluripotency. *Development (Cambridge)*, **2017**, 144, 2748-2763	6.6	135
77	Naive Human Pluripotent Cells Feature a Methylation Landscape Devoid of Blastocyst or Germline Memory. *Cell Stem Cell*, **2016**, 18, 323-329	18	161
76	The "lnc" between 3D chromatin structure and X chromosome inactivation. *Seminars in Cell and Developmental Biology*, **2016**, 56, 35-47	7.5	13
75	Transcriptome Encyclopedia of Early Human Development. *Cell*, **2016**, 165, 777-9	56.2	5
74	Glycolytic Metabolism Plays a Functional Role in Regulating Human Pluripotent Stem Cell State. *Cell Stem Cell*, **2016**, 19, 476-490	18	153
73	The Xist lncRNA interacts directly with SHARP to silence transcription through HDAC3. *Nature*, **2015**, 521, 232-6	50.4	730
72	A high-throughput screen of inactive X chromosome reactivation identifies the enhancement of DNA demethylation by 5-aza-2ɄdC upon inhibition of ribonucleotide reductase. *Epigenetics and Chromatin*, **2015**, 8, 42	5.8	29
71	X chromosome reactivation in reprogramming and in development. *Current Opinion in Cell Biology*, **2015**, 37, 75-83	9	48
70	The Mbd1-Atf7ip-Setdb1 pathway contributes to the maintenance of X chromosome inactivation. *Epigenetics and Chromatin*, **2014**, 7, 12	5.8	50
69	A mechanistic link between gene regulation and genome architecture in mammalian development. *Current Opinion in Genetics and Development*, **2014**, 27, 92-101	4.9	34
68	X chromosome reactivation dynamics reveal stages of reprogramming to pluripotency. *Cell*, **2014**, 159, 1681-97	56.2	77
67	A new route to human embryonic stem cells. *Nature Medicine*, **2013**, 19, 820-1	50.5	5
66	Long-range chromatin contacts in embryonic stem cells reveal a role for pluripotency factors and polycomb proteins in genome organization. *Cell Stem Cell*, **2013**, 13, 602-16	18	197
65	Initial characterization of histone H3 serine 10 O-acetylation. *Epigenetics*, **2013**, 8, 1101-13	5.7	17
64	Stage-specific regulation of reprogramming to induced pluripotent stem cells by Wnt signaling and T cell factor proteins. *Cell Reports*, **2013**, 3, 2113-26	10.6	70
63	The pluripotency factor-bound intron 1 of Xist is dispensable for X chromosome inactivation and reactivation in vitro and in vivo. *Cell Reports*, **2013**, 3, 905-18	10.6	37
62	Epigenetics of reprogramming to induced pluripotency. *Cell*, **2013**, 152, 1324-43	56.2	231
61	Proteomic and genomic approaches reveal critical functions of H3K9 methylation and heterochromatin protein-1 in reprogramming to pluripotency. *Nature Cell Biology*, **2013**, 15, 872-82	23.4	164

60	The Xist lncRNA exploits three-dimensional genome architecture to spread across the X chromosome. *Science*, **2013**, 341, 1237973	33.3	695
59	Pluripotency in 3D: genome organization in pluripotent cells. *Current Opinion in Cell Biology*, **2012**, 24, 793-801	9	15
58	The roles of the reprogramming factors Oct4, Sox2 and Klf4 in resetting the somatic cell epigenome during induced pluripotent stem cell generation. *Genome Biology*, **2012**, 13, 251	18.3	75
57	Mediator and SAGA have distinct roles in Pol II preinitiation complex assembly and function. *Cell Reports*, **2012**, 2, 1061-7	10.6	24
56	Concise review: Pluripotency and the transcriptional inactivation of the female Mammalian X chromosome. *Stem Cells*, **2012**, 30, 48-54	5.8	46
55	Derivation of new human embryonic stem cell lines reveals rapid epigenetic progression in vitro that can be prevented by chemical modification of chromatin. *Human Molecular Genetics*, **2012**, 21, 751-64	5.6	37
54	Pluripotency re-centered around Esrrb. *EMBO Journal*, **2012**, 31, 4255-7	13	18
53	From skin biopsy to neurons through a pluripotent intermediate under Good Manufacturing Practice protocols. *Stem Cells Translational Medicine*, **2012**, 1, 36-43	6.9	41
52	Characterization and therapeutic potential of induced pluripotent stem cell-derived cardiovascular progenitor cells. *PLoS ONE*, **2012**, 7, e45603	3.7	28
51	Reprogramming to pluripotency: stepwise resetting of the epigenetic landscape. *Cell Research*, **2011**, 21, 486-501	24.7	137
50	Small RNAs loom large during reprogramming. *Cell Stem Cell*, **2011**, 8, 599-601	18	14
49	Progress in understanding reprogramming to the induced pluripotent state. *Nature Reviews Genetics*, **2011**, 12, 253-65	30.1	220
48	Highly efficient large-scale lentiviral vector concentration by tandem tangential flow filtration. *Journal of Virological Methods*, **2011**, 177, 1-9	2.6	51
47	Mechanistic insights into reprogramming to induced pluripotency. *Journal of Cellular Physiology*, **2011**, 226, 868-78	7	38
46	Mediator coordinates PIC assembly with recruitment of CHD1. *Genes and Development*, **2011**, 25, 2198-209	12.6	71
45	Molecular analyses of human induced pluripotent stem cells and embryonic stem cells. *Cell Stem Cell*, **2010**, 7, 263-9	18	133
44	Female human iPSCs retain an inactive X chromosome. *Cell Stem Cell*, **2010**, 7, 329-42	18	223
43	Identification and classification of chromosomal aberrations in human induced pluripotent stem cells. *Cell Stem Cell*, **2010**, 7, 521-31	18	595

42	Identification of context-dependent motifs by contrasting ChIP binding data. *Bioinformatics*, **2010**, 26, 2826-32	7.2	34
41	Genome-wide dynamics of replication timing revealed by in vitro models of mouse embryogenesis. *Genome Research*, **2010**, 20, 155-69	9.7	241
40	X chromosome inactivation in the absence of Dicer. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 1122-7	11.5	48
39	Transcriptional competence and the active marking of tissue-specific enhancers by defined transcription factors in embryonic and induced pluripotent stem cells. *Genes and Development*, **2009**, 23, 2824-38	12.6	145
38	Signed weighted gene co-expression network analysis of transcriptional regulation in murine embryonic stem cells. *BMC Genomics*, **2009**, 10, 327	4.5	155
37	Derivation of primordial germ cells from human embryonic and induced pluripotent stem cells is significantly improved by coculture with human fetal gonadal cells. *Stem Cells*, **2009**, 27, 783-95	5.8	202
36	Directed differentiation of human-induced pluripotent stem cells generates active motor neurons. *Stem Cells*, **2009**, 27, 806-11	5.8	288
35	Chd1 regulates open chromatin and pluripotency of embryonic stem cells. *Nature*, **2009**, 460, 863-8	50.4	406
34	Role of the murine reprogramming factors in the induction of pluripotency. *Cell*, **2009**, 136, 364-77	56.2	517
33	Broader implications of defining standards for the pluripotency of iPSCs. *Cell Stem Cell*, **2009**, 4, 200-1; author reply 202	18	101
32	Induced pluripotent stem cells and embryonic stem cells are distinguished by gene expression signatures. *Cell Stem Cell*, **2009**, 5, 111-23	18	816
31	Histone h3 lysine 56 acetylation is linked to the core transcriptional network in human embryonic stem cells. *Molecular Cell*, **2009**, 33, 417-27	17.6	160
30	Epigenetic reprogramming and induced pluripotency. *Development (Cambridge)*, **2009**, 136, 509-23	6.6	435
29	Post-translational regulation of Oct4 transcriptional activity. *PLoS ONE*, **2009**, 4, e4467	3.7	101
28	Reprogrammed mouse fibroblasts differentiate into cells of the cardiovascular and hematopoietic lineages. *Stem Cells*, **2008**, 26, 1537-46	5.8	204
27	Directly reprogrammed fibroblasts show global epigenetic remodeling and widespread tissue contribution. *Cell Stem Cell*, **2007**, 1, 55-70	18	1406
26	The histone domain of macroH2A1 contains several dispersed elements that are each sufficient to direct enrichment on the inactive X chromosome. *Journal of Molecular Biology*, **2007**, 371, 11-8	6.5	23
25	Efficient method to generate single-copy transgenic mice by site-specific integration in embryonic stem cells. *Genesis*, **2006**, 44, 23-8	1.9	351

24	Mapping post-translational modifications of the histone variant MacroH2A1 using tandem mass spectrometry. *Molecular and Cellular Proteomics*, **2006**, 5, 194-203	7.6	62
23	A bivalent chromatin structure marks key developmental genes in embryonic stem cells. *Cell*, **2006**, 125, 315-26	56.2	4097
22	Polycomb complexes repress developmental regulators in murine embryonic stem cells. *Nature*, **2006**, 441, 349-53	50.4	2008
21	Developmental regulation of Suz 12 localization. *Chromosoma*, **2005**, 114, 183-92	2.8	27
20	Developmentally regulated alterations in Polycomb repressive complex 1 proteins on the inactive X chromosome. *Journal of Cell Biology*, **2004**, 167, 1025-35	7.3	120
19	Interactions between Sec complex and prepro-alpha-factor during posttranslational protein transport into the endoplasmic reticulum. *Molecular Biology of the Cell*, **2004**, 15, 1-10	3.5	45
18	Role of histone H3 lysine 27 methylation in X inactivation. *Science*, **2003**, 300, 131-5	33.3	978
17	Xist RNA and the mechanism of X chromosome inactivation. *Annual Review of Genetics*, **2002**, 36, 233-78	14.5	373
16	Spontaneous release of cytosolic proteins from posttranslational substrates before their transport into the endoplasmic reticulum. *Journal of Cell Biology*, **2000**, 151, 167-78	7.3	75
15	The structure of ribosome-channel complexes engaged in protein translocation. *Molecular Cell*, **2000**, 6, 1219-32	17.6	192
14	Posttranslational protein translocation across the membrane of the endoplasmic reticulum. *Biological Chemistry*, **1999**, 380, 1143-50	4.5	63
13	BiP acts as a molecular ratchet during posttranslational transport of prepro-alpha factor across the ER membrane. *Cell*, **1999**, 97, 553-64	56.2	343
12	Signal sequence recognition in posttranslational protein transport across the yeast ER membrane. *Cell*, **1998**, 94, 795-807	56.2	285
11	Protein transport by purified yeast Sec complex and Kar2p without membranes. *Science*, **1997**, 277, 938-41	33.3	73
10	Oligomeric rings of the Sec61p complex induced by ligands required for protein translocation. *Cell*, **1996**, 87, 721-32	56.2	303
9	Constitutive activation of mitogen-activated protein kinase-activated protein kinase 2 by mutation of phosphorylation sites and an A-helix motif. *Journal of Biological Chemistry*, **1995**, 270, 27213-21	5.4	85
8	The MAP kinase-activated protein kinase 2 contains a proline-rich SH3-binding domain. *FEBS Letters*, **1993**, 336, 143-7	3.8	34
7	AnXist-dependent protein assembly mediatesXistlocalization and gene silencing		1

6	Epigenetic resetting of human pluripotency	1
5	TGFβ superfamily signaling regulates the state of human stem cell pluripotency and competency to create telencephalic organoids	3
4	RNA promotes the formation of spatial compartments in the nucleus	12
3	Xist-seeded nucleation sites form local concentration gradients of silencing proteins to inactivate the X-chromosome	7
2	DNA methylation estimation using methylation-sensitive restriction enzyme bisulfite sequencing (MREBS)	1
1	Identification of neural oscillations and epileptiform changes in human brain organoids	6