Felix Krueger

List of Publications by Year
in descending order

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Version: 2024-02-01

61 papers	14,819 citations	100601 38 h-index	175968 55 g-index
78 all docs	78 docs citations	78 times ranked	22722 citing authors

#	ARTICLE	IF	CITATIONS
1	Stimulation of adaptive gene amplification by origin firing under replication fork constraint. Nucleic Acids Research, 2022, 50, 915-936.	6.5	10
2	8C-like cells capture the human zygotic genome activation program inÂvitro. Cell Stem Cell, 2022, 29, 449-459.e6.	5.2	62
3	Single-cell Atlas of common variable immunodeficiency shows germinal center-associated epigenetic dysregulation in B-cell responses. Nature Communications, 2022, 13, 1779.	5.8	25
4	Genome-wide analysis of DNA replication and DNA double-strand breaks using TrAEL-seq. PLoS Biology, 2021, 19, e3000886.	2.6	19
5	DNA methylation changes during preimplantation development reveal inter-species differences and reprogramming events at imprinted genes. Clinical Epigenetics, 2020, 12, 64.	1.8	46
6	IMPLICON: an ultra-deep sequencing method to uncover DNA methylation at imprinted regions. Nucleic Acids Research, 2020, 48, e92-e92.	6.5	15
7	Low rates of mutation in clinical grade human pluripotent stem cells under different culture conditions. Nature Communications, 2020, 11, 1528.	5.8	67
8	Endogenous retroviral insertions drive non-canonical imprinting in extra-embryonic tissues. Genome Biology, 2019, 20, 225.	3.8	67
9	Transcription-induced formation of extrachromosomal DNA during yeast ageing. PLoS Biology, 2019, 17, e3000471.	2.6	69
10	Multi-omics profiling of mouse gastrulation at single-cell resolution. Nature, 2019, 576, 487-491.	13.7	307
11	The non-canonical SMC protein SmcHD1 antagonises TAD formation and compartmentalisation on the inactive X chromosome. Nature Communications, 2019, 10, 30.	5.8	87
12	Transcription-induced formation of extrachromosomal DNA during yeast ageing. , 2019, 17, e3000471.		0
13	Transcription-induced formation of extrachromosomal DNA during yeast ageing. , 2019, 17, e3000471.		0
14	Transcription-induced formation of extrachromosomal DNA during yeast ageing. , 2019, 17, e3000471.		0
15	Transcription-induced formation of extrachromosomal DNA during yeast ageing. , 2019, 17, e3000471.		0
16	Transcription-induced formation of extrachromosomal DNA during yeast ageing. , 2019, 17, e3000471.		0
17	Transcription-induced formation of extrachromosomal DNA during yeast ageing. , 2019, 17, e3000471.		0
18	scNMT-seq enables joint profiling of chromatin accessibility DNA methylation and transcription in single cells. Nature Communications, 2018, 9, 781.	5.8	513

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19	Unbiased quantification of immunoglobulin diversity at the DNA level with VDJ-seq. Nature Protocols, 2018, 13, 1232-1252.	5.5	21
20	Comparison of whole-genome bisulfite sequencing library preparation strategies identifies sources of biases affecting DNA methylation data. Genome Biology, 2018, 19, 33.	3.8	201
21	Multiplexing for Oxidative Bisulfite Sequencing (oxBS-seq). Methods in Molecular Biology, 2018, 1708, 665-678.	0.4	5
22	Genome-Scale Oscillations in DNA Methylation during Exit from Pluripotency. Cell Systems, 2018, 7, 63-76.e12.	2.9	70
23	Gender Differences in Global but Not Targeted Demethylation in iPSC Reprogramming. Cell Reports, 2017, 18, 1079-1089.	2.9	54
24	Genome-wide base-resolution mapping of DNA methylation in single cells using single-cell bisulfite sequencing (scBS-seq). Nature Protocols, 2017, 12, 534-547.	5.5	199
25	Multi-tissue DNA methylation age predictor in mouse. Genome Biology, 2017, 18, 68.	3.8	341
26	Dietary restriction protects from age-associated DNA methylation and induces epigenetic reprogramming of lipid metabolism. Genome Biology, 2017, 18, 56.	3.8	164
27	cuRRBS: simple and robust evaluation of enzyme combinations for reduced representation approaches. Nucleic Acids Research, 2017, 45, 11559-11569.	6.5	14
28	Efficient targeted DNA methylation with chimeric dCas9â€“Dnmt3aâ€“Dnmt3L methyltransferase. Nucleic Acids Research, 2017, 45, 1703-1713.	6.5	224
29	Local Chromatin Features Including PU.1 and IKAROS Binding and H3K4 Methylation Shape the Repertoire of Immunoglobulin Kappa Genes Chosen for V(D)J Recombination. Frontiers in Immunology, 2017, 8, 1550.	2.2	40
30	Comparative Principles of DNA Methylation Reprogramming during Human and Mouse InÂVitro Primordial Germ Cell Specification. Developmental Cell, 2016, 39, 104-115.	3.1	102
31	Two Mutually Exclusive Local Chromatin States Drive Efficient V(D)J Recombination. Cell Reports, 2016, 15, 2475-2487.	2.9	78
32	MERVL/Zscan4 Network Activation Results in Transient Genome-wide DNA Demethylation of mESCs. Cell Reports, 2016, 17, 179-192.	2.9	174
33	Paternal chronic colitis causes epigenetic inheritance of susceptibility to colitis. Scientific Reports, 2016, 6, 31640.	1.6	15
34	Parallel single-cell sequencing links transcriptional and epigenetic heterogeneity. Nature Methods, 2016, 13, 229-232.	9.0	602
35	Cluster Flow: A user-friendly bioinformatics workflow tool. F1000Research, 2016, 5, 2824.	0.8	18
36	SNPsplit: Allele-specific splitting of alignments between genomes with known SNP genotypes. F1000Research, 2016, 5, 1479.	0.8	149

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37	SNPsplit: Allele-specific splitting of alignments between genomes with known SNP genotypes. F1000Research, 2016, 5, 1479.	0.8	109
38	Transcriptional Activation of Pericentromeric Satellite Repeats and Disruption of Centromeric Clustering upon Proteasome Inhibition. PLoS ONE, 2016, 11, e0165873.	1.1	6
39	Allele-specific binding of ZFP57 in the epigenetic regulation of imprinted and non-imprinted monoallelic expression. Genome Biology, 2015, 16, 112.	3.8	150
40	5-hydroxymethylcytosine marks promoters in colon that resist DNA hypermethylation in cancer. Genome Biology, 2015, 16, 69.	3.8	60
41	Molecular signatures of plastic phenotypes in two eusocial insect species with simple societies. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 13970-13975.	3.3	192
42	Deep sequencing and de novo assembly of the mouse oocyte transcriptome define the contribution of transcription to the DNA methylation landscape. Genome Biology, 2015, 16, 209.	3.8	164
43	Epigenetic memory of the first cell fate decision prevents complete ES cell reprogramming into trophoblast. Nature Communications, 2014, 5, 5538.	5.8	68
44	Genome-wide Bisulfite Sequencing in Zygotes Identifies Demethylation Targets and Maps the Contribution of TET3 Oxidation. Cell Reports, 2014, 9, 1990-2000.	2.9	116
45	Resetting Transcription Factor Control Circuitry toward Ground-State Pluripotency in Human. Cell, 2014, 158, 1254-1269.	13.5	784
46	Single-cell genome-wide bisulfite sequencing for assessing epigenetic heterogeneity. Nature Methods, 2014, 11, 817-820.	9.0	954
47	FGF Signaling Inhibition in ESCs Drives Rapid Genome-wide Demethylation to the Epigenetic Ground State of Pluripotency. Cell Stem Cell, 2013, 13, 351-359.	5.2	371
48	FGF signalling inhibition in ESCs drives rapid genome-wide demethylation to the epigenetic ground state of pluripotency. Clinical Epigenetics, 2013, 5, .	1.8	2
49	Base-pair resolution DNA methylome of the EBV-positive Endemic Burkitt lymphoma cell line DAUDI determined by SOLiD bisulfite-sequencing. Leukemia, 2013, 27, 1751-1753.	3.3	31
50	SWI/SNF-Like Chromatin Remodeling Factor Fun30 Supports Point Centromere Function in S. cerevisiae. PLoS Genetics, 2012, 8, e1002974.	1.5	38
51	B-SOLANA: an approach for the analysis of two-base encoding bisulfite sequencing data. Bioinformatics, 2012, 28, 428-429.	1.8	37
52	DNA methylome analysis using short bisulfite sequencing data. Nature Methods, 2012, 9, 145-151.	9.0	313
53	The Dynamics of Genome-wide DNA Methylation Reprogramming in Mouse Primordial Germ Cells. Molecular Cell, 2012, 48, 849-862.	4.5	837
54	DNA Methylation Profiles Define Stem Cell Identity and Reveal a Tight Embryonicâ€“Extraembryonic Lineage Boundary. Stem Cells, 2012, 30, 2732-2745.	1.4	77

#	Article	IF	Citations
55	Pairing of Homologous Regions in the Mouse Genome Is Associated with Transcription but Not Imprinting Status. PLoS ONE, 2012, 7, e38983.	1.1	24
56	Quantitative Sequencing of 5-Methylcytosine and 5-Hydroxymethylcytosine at Single-Base Resolution. Science, 2012, 336, 934-937.	6.0	850
57	Dynamic CpG island methylation landscape in oocytes and preimplantation embryos. Nature Genetics, 2011, 43, 811-814.	9.4	579
58	Dynamic regulation of 5-hydroxymethylcytosine in mouse ES cells and during differentiation. Nature, 2011, 473, 398-402.	13.7	1,035
59	Bismark: a flexible aligner and methylation caller for Bisulfite-Seq applications. Bioinformatics, 2011, 27, 1571-1572.	1.8	4,080
60	Large Scale Loss of Data in Low-Diversity Illumina Sequencing Libraries Can Be Recovered by Deferred Cluster Calling. PLoS ONE, 2011, 6, e16607.	1.1	88
61	Down-regulation of Cdx2 in colorectal carcinoma cells by the Rafâ€“MEKâ€“ERK 1/2 pathway. Cellular Signalling, 2009, 21, 1846-1856.	1.7	23