

Felix Krueger

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5035297/publications.pdf>

Version: 2024-02-01

61
papers

14,819
citations

87888

38
h-index

155660

55
g-index

78
all docs

78
docs citations

78
times ranked

20498
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Bismark: a flexible aligner and methylation caller for Bisulfite-Seq applications. <i>Bioinformatics</i> , 2011, 27, 1571-1572. | 4.1 | 4,080 |
| 2 | Dynamic regulation of 5-hydroxymethylcytosine in mouse ES cells and during differentiation. <i>Nature</i> , 2011, 473, 398-402. | 27.8 | 1,035 |
| 3 | Single-cell genome-wide bisulfite sequencing for assessing epigenetic heterogeneity. <i>Nature Methods</i> , 2014, 11, 817-820. | 19.0 | 954 |
| 4 | Quantitative Sequencing of 5-Methylcytosine and 5-Hydroxymethylcytosine at Single-Base Resolution. <i>Science</i> , 2012, 336, 934-937. | 12.6 | 850 |
| 5 | The Dynamics of Genome-wide DNA Methylation Reprogramming in Mouse Primordial Germ Cells. <i>Molecular Cell</i> , 2012, 48, 849-862. | 9.7 | 837 |
| 6 | Resetting Transcription Factor Control Circuitry toward Ground-State Pluripotency in Human. <i>Cell</i> , 2014, 158, 1254-1269. | 28.9 | 784 |
| 7 | Parallel single-cell sequencing links transcriptional and epigenetic heterogeneity. <i>Nature Methods</i> , 2016, 13, 229-232. | 19.0 | 602 |
| 8 | Dynamic CpG island methylation landscape in oocytes and preimplantation embryos. <i>Nature Genetics</i> , 2011, 43, 811-814. | 21.4 | 579 |
| 9 | 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 |
| 10 | 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 |
| 11 | Multi-tissue DNA methylation age predictor in mouse. <i>Genome Biology</i> , 2017, 18, 68. | 8.8 | 341 |
| 12 | DNA methylome analysis using short bisulfite sequencing data. <i>Nature Methods</i> , 2012, 9, 145-151. | 19.0 | 313 |
| 13 | Multi-omics profiling of mouse gastrulation at single-cell resolution. <i>Nature</i> , 2019, 576, 487-491. | 27.8 | 307 |
| 14 | Efficient targeted DNA methylation with chimeric dCas9-Dnmt3a-Dnmt3L methyltransferase. <i>Nucleic Acids Research</i> , 2017, 45, 1703-1713. | 14.5 | 224 |
| 15 | Comparison of whole-genome bisulfite sequencing library preparation strategies identifies sources of biases affecting DNA methylation data. <i>Genome Biology</i> , 2018, 19, 33. | 8.8 | 201 |
| 16 | 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 |
| 17 | Molecular signatures of plastic phenotypes in two eusocial insect species with simple societies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13970-13975. | 7.1 | 192 |
| 18 | MERVL/Zscan4 Network Activation Results in Transient Genome-wide DNA Demethylation of mESCs. <i>Cell Reports</i> , 2016, 17, 179-192. | 6.4 | 174 |

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|----|--|------|-----------|
| 19 | Deep sequencing and de novo assembly of the mouse oocyte transcriptome define the contribution of transcription to the DNA methylation landscape. <i>Genome Biology</i> , 2015, 16, 209. | 8.8 | 164 |
| 20 | Dietary restriction protects from age-associated DNA methylation and induces epigenetic reprogramming of lipid metabolism. <i>Genome Biology</i> , 2017, 18, 56. | 8.8 | 164 |
| 21 | Allele-specific binding of ZFP57 in the epigenetic regulation of imprinted and non-imprinted monoallelic expression. <i>Genome Biology</i> , 2015, 16, 112. | 8.8 | 150 |
| 22 | SNPsplit: Allele-specific splitting of alignments between genomes with known SNP genotypes. <i>F1000Research</i> , 2016, 5, 1479. | 1.6 | 149 |
| 23 | Genome-wide Bisulfite Sequencing in Zygotes Identifies Demethylation Targets and Maps the Contribution of TET3 Oxidation. <i>Cell Reports</i> , 2014, 9, 1990-2000. | 6.4 | 116 |
| 24 | SNPsplit: Allele-specific splitting of alignments between genomes with known SNP genotypes. <i>F1000Research</i> , 2016, 5, 1479. | 1.6 | 109 |
| 25 | Comparative Principles of DNA Methylation Reprogramming during Human and Mouse In Vitro Primordial Germ Cell Specification. <i>Developmental Cell</i> , 2016, 39, 104-115. | 7.0 | 102 |
| 26 | Large Scale Loss of Data in Low-Diversity Illumina Sequencing Libraries Can Be Recovered by Deferred Cluster Calling. <i>PLoS ONE</i> , 2011, 6, e16607. | 2.5 | 88 |
| 27 | The non-canonical SMC protein SmcHD1 antagonises TAD formation and compartmentalisation on the inactive X chromosome. <i>Nature Communications</i> , 2019, 10, 30. | 12.8 | 87 |
| 28 | Two Mutually Exclusive Local Chromatin States Drive Efficient V(D)J Recombination. <i>Cell Reports</i> , 2016, 15, 2475-2487. | 6.4 | 78 |
| 29 | DNA Methylation Profiles Define Stem Cell Identity and Reveal a Tight Embryonic–Extraembryonic Lineage Boundary. <i>Stem Cells</i> , 2012, 30, 2732-2745. | 3.2 | 77 |
| 30 | Genome-Scale Oscillations in DNA Methylation during Exit from Pluripotency. <i>Cell Systems</i> , 2018, 7, 63-76.e12. | 6.2 | 70 |
| 31 | Transcription-induced formation of extrachromosomal DNA during yeast ageing. <i>PLoS Biology</i> , 2019, 17, e3000471. | 5.6 | 69 |
| 32 | Epigenetic memory of the first cell fate decision prevents complete ES cell reprogramming into trophoblast. <i>Nature Communications</i> , 2014, 5, 5538. | 12.8 | 68 |
| 33 | Endogenous retroviral insertions drive non-canonical imprinting in extra-embryonic tissues. <i>Genome Biology</i> , 2019, 20, 225. | 8.8 | 67 |
| 34 | Low rates of mutation in clinical grade human pluripotent stem cells under different culture conditions. <i>Nature Communications</i> , 2020, 11, 1528. | 12.8 | 67 |
| 35 | 8C-like cells capture the human zygotic genome activation program in vitro. <i>Cell Stem Cell</i> , 2022, 29, 449-459.e6. | 11.1 | 62 |
| 36 | 5-hydroxymethylcytosine marks promoters in colon that resist DNA hypermethylation in cancer. <i>Genome Biology</i> , 2015, 16, 69. | 8.8 | 60 |

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|----|--|------|-----------|
| 37 | Gender Differences in Global but Not Targeted Demethylation in iPSC Reprogramming. <i>Cell Reports</i> , 2017, 18, 1079-1089. | 6.4 | 54 |
| 38 | DNA methylation changes during preimplantation development reveal inter-species differences and reprogramming events at imprinted genes. <i>Clinical Epigenetics</i> , 2020, 12, 64. | 4.1 | 46 |
| 39 | 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. <i>Frontiers in Immunology</i> , 2017, 8, 1550. | 4.8 | 40 |
| 40 | SWI/SNF-Like Chromatin Remodeling Factor Fun30 Supports Point Centromere Function in <i>S. cerevisiae</i> . <i>PLoS Genetics</i> , 2012, 8, e1002974. | 3.5 | 38 |
| 41 | B-SOLANA: an approach for the analysis of two-base encoding bisulfite sequencing data. <i>Bioinformatics</i> , 2012, 28, 428-429. | 4.1 | 37 |
| 42 | Base-pair resolution DNA methylome of the EBV-positive Endemic Burkitt lymphoma cell line DAUDI determined by SOLiD bisulfite-sequencing. <i>Leukemia</i> , 2013, 27, 1751-1753. | 7.2 | 31 |
| 43 | Single-cell Atlas of common variable immunodeficiency shows germinal center-associated epigenetic dysregulation in B-cell responses. <i>Nature Communications</i> , 2022, 13, 1779. | 12.8 | 25 |
| 44 | Pairing of Homologous Regions in the Mouse Genome Is Associated with Transcription but Not Imprinting Status. <i>PLoS ONE</i> , 2012, 7, e38983. | 2.5 | 24 |
| 45 | Down-regulation of Cdx2 in colorectal carcinoma cells by the Raf→MEK→ERK 1/2 pathway. <i>Cellular Signalling</i> , 2009, 21, 1846-1856. | 3.6 | 23 |
| 46 | Unbiased quantification of immunoglobulin diversity at the DNA level with VDJ-seq. <i>Nature Protocols</i> , 2018, 13, 1232-1252. | 12.0 | 21 |
| 47 | Genome-wide analysis of DNA replication and DNA double-strand breaks using TrAEL-seq. <i>PLoS Biology</i> , 2021, 19, e3000886. | 5.6 | 19 |
| 48 | Cluster Flow: A user-friendly bioinformatics workflow tool. <i>F1000Research</i> , 2016, 5, 2824. | 1.6 | 18 |
| 49 | Paternal chronic colitis causes epigenetic inheritance of susceptibility to colitis. <i>Scientific Reports</i> , 2016, 6, 31640. | 3.3 | 15 |
| 50 | IMPLICON: an ultra-deep sequencing method to uncover DNA methylation at imprinted regions. <i>Nucleic Acids Research</i> , 2020, 48, e92-e92. | 14.5 | 15 |
| 51 | cuRRBS: simple and robust evaluation of enzyme combinations for reduced representation approaches. <i>Nucleic Acids Research</i> , 2017, 45, 11559-11569. | 14.5 | 14 |
| 52 | Stimulation of adaptive gene amplification by origin firing under replication fork constraint. <i>Nucleic Acids Research</i> , 2022, 50, 915-936. | 14.5 | 10 |
| 53 | Transcriptional Activation of Pericentromeric Satellite Repeats and Disruption of Centromeric Clustering upon Proteasome Inhibition. <i>PLoS ONE</i> , 2016, 11, e0165873. | 2.5 | 6 |
| 54 | Multiplexing for Oxidative Bisulfite Sequencing (oxBS-seq). <i>Methods in Molecular Biology</i> , 2018, 1708, 665-678. | 0.9 | 5 |

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|----|---|-----|-----------|
| 55 | FGF signalling inhibition in ESCs drives rapid genome-wide demethylation to the epigenetic ground state of pluripotency. <i>Clinical Epigenetics</i> , 2013, 5, . | 4.1 | 2 |
| 56 | Transcription-induced formation of extrachromosomal DNA during yeast ageing. , 2019, 17, e3000471. | | 0 |
| 57 | Transcription-induced formation of extrachromosomal DNA during yeast ageing. , 2019, 17, e3000471. | | 0 |
| 58 | Transcription-induced formation of extrachromosomal DNA during yeast ageing. , 2019, 17, e3000471. | | 0 |
| 59 | Transcription-induced formation of extrachromosomal DNA during yeast ageing. , 2019, 17, e3000471. | | 0 |
| 60 | Transcription-induced formation of extrachromosomal DNA during yeast ageing. , 2019, 17, e3000471. | | 0 |
| 61 | Transcription-induced formation of extrachromosomal DNA during yeast ageing. , 2019, 17, e3000471. | | 0 |