

Kevin M Brick

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

2,145
citations

516710

16
h-index

580821

25
g-index

30
all docs

30
docs citations

30
times ranked

2429
citing authors

#	ARTICLE	IF	CITATIONS
1	Rat PRDM9 shapes recombination landscapes, duration of meiosis, gametogenesis, and age of fertility. <i>BMC Biology</i> , 2021, 19, 86.	3.8	12
2	Meiotic recombination mirrors patterns of germline replication in mice and humans. <i>Cell</i> , 2021, 184, 4251-4267.e20.	28.9	31
3	Cataloging Human PRDM9 Allelic Variation Using Long-Read Sequencing Reveals PRDM9 Population Specificity and Two Distinct Groupings of Related Alleles. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 675286.	3.7	13
4	After the break: DSB end processing in mouse meiosis. <i>Genes and Development</i> , 2020, 34, 731-732.	5.9	5
5	Ensuring meiotic DNA break formation in the mouse pseudoautosomal region. <i>Nature</i> , 2020, 582, 426-431.	27.8	73
6	Cell-type-specific genomics reveals histone modification dynamics in mammalian meiosis. <i>Nature Communications</i> , 2019, 10, 3821.	12.8	33
7	Histone methyltransferase PRDM9 is not essential for meiosis in male mice. <i>Genome Research</i> , 2019, 29, 1078-1086.	5.5	34
8	REC114 Partner ANKRD31 Controls Number, Timing, and Location of Meiotic DNA Breaks. <i>Molecular Cell</i> , 2019, 74, 1053-1068.e8.	9.7	89
9	Interrogating the Functions of PRDM9 Domains in Meiosis. <i>Genetics</i> , 2018, 209, 475-487.	2.9	23
10	Extensive sex differences at the initiation of genetic recombination. <i>Nature</i> , 2018, 561, 338-342.	27.8	76
11	Analysis of Meiotic Double-Strand Break Initiation in Mammals. <i>Methods in Enzymology</i> , 2018, 601, 391-418.	1.0	19
12	Re-engineering the zinc fingers of PRDM9 reverses hybrid sterility in mice. <i>Nature</i> , 2016, 530, 171-176.	27.8	194
13	The evolutionary turnover of recombination hot spots contributes to speciation in mice. <i>Genes and Development</i> , 2016, 30, 266-280.	5.9	130
14	Recombination initiation maps of individual human genomes. <i>Science</i> , 2014, 346, 1256442.	12.6	254
15	Suppression of genetic recombination in the pseudoautosomal region and at subtelomeres in mice with a hypomorphic Spo11 allele. <i>BMC Genomics</i> , 2013, 14, 493.	2.8	17
16	Vezf1 protein binding sites genome-wide are associated with pausing of elongating RNA polymerase II. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 2370-2375.	7.1	35
17	Sensitive mapping of recombination hotspots using sequencing-based detection of ssDNA. <i>Genome Research</i> , 2012, 22, 957-965.	5.5	103
18	Genetic recombination is directed away from functional genomic elements in mice. <i>Nature</i> , 2012, 485, 642-645.	27.8	372

#	ARTICLE	IF	CITATIONS
19	Genome-wide analysis reveals novel molecular features of mouse recombination hotspots. <i>Nature</i> , 2011, 472, 375-378.	27.8	325
20	Genome-wide Analysis Reveals Novel Molecular Features of Mouse Recombination. <i>FASEB Journal</i> , 2011, 25, 882.2.	0.5	1
21	Mediation of CTCF transcriptional insulation by DEAD-box RNA-binding protein p68 and steroid receptor RNA activator SRA. <i>Genes and Development</i> , 2010, 24, 2543-2555.	5.9	231
22	Revisiting the <i>Plasmodium falciparum</i> RIFIN family: from comparative genomics to 3D-model prediction. <i>BMC Genomics</i> , 2009, 10, 445.	2.8	20
23	A novel series of compositionally biased substitution matrices for comparing <i>Plasmodium</i> proteins. <i>BMC Bioinformatics</i> , 2008, 9, 236.	2.6	18
24	Core promoters are predicted by their distinct physicochemical properties in the genome of <i>Plasmodium falciparum</i> . <i>Genome Biology</i> , 2008, 9, R178.	9.6	26