## Jasper Rine

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Distinguishing between recruitment and spread of silent chromatin structures in Saccharomyces cerevisiae. ELife, 2022, 11, .	6.0	18
2	A novel allele of <i>SIR2</i> reveals a heritable intermediate state of gene silencing. Genetics, 2021, 218,	2.9	1
3	Nucleosome Positioning Regulates the Establishment, Stability, and Inheritance of Heterochromatin in <i>Saccharomyces cerevisiae</i> . Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 27493-27501.	7.1	19
4	S-phase-independent silencing establishment in Saccharomyces cerevisiae. ELife, 2020, 9, .	6.0	17
5	Assessing computational predictions of the phenotypic effect of cystathionineâ€betaâ€synthase variants. Human Mutation, 2019, 40, 1530-1545.	2.5	5
6	The nucleosome core particle remembers its position through DNA replication and RNA transcription. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 20605-20611.	7.1	53
7	Mutations in the PCNA DNA Polymerase Clamp of <i>Saccharomyces cerevisiae</i> Reveal Complexities of the Cell Cycle and Ploidy on Heterochromatin Assembly. Genetics, 2019, 213, 449-463.	2.9	23
8	Epigenetic memory independent of symmetric histone inheritance. ELife, 2019, 8, .	6.0	30
9	Impact of Homologous Recombination on Silent Chromatin in <i>Saccharomyces cerevisiae</i> . Genetics, 2018, 208, 1099-1113.	2.9	1
10	Pivotal roles of PCNA loading and unloading in heterochromatin function. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E2030-E2039.	7.1	38
11	Nutritional Control of Chronological Aging and Heterochromatin in <i>Saccharomyces cerevisiae</i> . Genetics, 2017, 205, 1179-1193.	2.9	8
12	Aggregation of the Whi3 protein, not loss of heterochromatin, causes sterility in old yeast cells. Science, 2017, 355, 1184-1187.	12.6	51
13	Oncometabolite D-2-Hydroxyglutarate enhances gene silencing through inhibition of specific H3K36 histone demethylases. ELife, 2017, 6, .	6.0	25
14	Riches of phenotype computationally extracted from microbial colonies. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E2822-E2831.	7.1	7
15	Sir protein–independent repair of dicentric chromosomes in Saccharomyces cerevisiae. Molecular Biology of the Cell, 2016, 27, 2879-2883.	2.1	0
16	Histone Deacetylases with Antagonistic Roles in <i>Saccharomyces cerevisiae</i> Heterochromatin Formation. Genetics, 2016, 204, 177-190.	2.9	18
17	Donor Preference Meets Heterochromatin: Moonlighting Activities of a Recombinational Enhancer in <i>Saccharomyces cerevisiae</i> . Genetics, 2016, 204, 1065-1074.	2.9	4
18	Evolution and Functional Trajectory of Sir1 in Gene Silencing. Molecular and Cellular Biology, 2016, 36, 1164-1179.	2.3	11

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19	On the Mechanism of Gene Silencing in <i>Saccharomyces cerevisiae</i> . G3: Genes, Genomes, Genetics, 2015, 5, 1751-1763.	1.8	13
20	Maintenance of Nucleosomal Balance in <i>cis</i> by Conserved AAA-ATPase Yta7. Genetics, 2015, 199, 105-116.	2.9	18
21	The Chromatin and Transcriptional Landscape of Native <i>Saccharomyces cerevisiae</i> Telomeres and Subtelomeric Domains. Genetics, 2015, 200, 505-521.	2.9	92
22	The State of Federal Research Funding in Genetics as Reflected by Members of the Genetics Society of America. Genetics, 2015, 200, 1015-1019.	2.9	0
23	Metabolism and Epigenetics. Annual Review of Cell and Developmental Biology, 2015, 31, 473-496.	9.4	147
24	Heritable capture of heterochromatin dynamics in Saccharomyces cerevisiae. ELife, 2015, 4, e05007.	6.0	76
25	Multiple inputs control sulfur-containing amino acid synthesis in <i>Saccharomyces cerevisiae</i> . Molecular Biology of the Cell, 2014, 25, 1653-1665.	2.1	39
26	A future of the model organism model. Molecular Biology of the Cell, 2014, 25, 549-553.	2.1	23
27	The molecular topography of silenced chromatin in Saccharomyces cerevisiae. Genes and Development, 2014, 28, 245-258.	5.9	66
28	Highly expressed loci are vulnerable to misleading ChIP localization of multiple unrelated proteins. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 18602-18607.	7.1	373
29	Mono and Dual Cofactor Dependence of Human Cystathionine β-Synthase Enzyme Variants <i>In Vivo</i> and <i>In Vitro</i> . G3: Genes, Genomes, Genetics, 2013, 3, 1619-1628.	1.8	7
30	Surrogate Genetics and Metabolic Profiling for Characterization of Human Disease Alleles. Genetics, 2012, 190, 1309-1323.	2.9	46
31	Two surfaces on the histone chaperone Rtt106 mediate histone binding, replication, and silencing. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E144-53.	7.1	43
32	The establishment of gene silencing at single-cell resolution. Nature Genetics, 2009, 41, 800-806.	21.4	71
33	Cell Cycle Requirements in Assembling Silent Chromatin in Saccharomyces cerevisiae. Molecular and Cellular Biology, 2006, 26, 852-862.	2.3	45
34	Telomeric heterochromatin boundaries require NuA4-dependent acetylation of histone variant H2A.Z in Saccharomy cescerevisiae. Genes and Development, 2006, 20, 700-710.	5.9	176
35	CELL BIOLOGY: Twists in the Tale of the Aging Yeast. Science, 2005, 310, 1124-1125.	12.6	16
36	The Establishment, Inheritance, and Function of Silenced Chromatin inSaccharomyces cerevisiae. Annual Review of Biochemistry, 2003, 72, 481-516.	11.1	678

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37	Ordered Nucleation and Spreading of Silenced Chromatin inSaccharomyces cerevisiae. Molecular Biology of the Cell, 2002, 13, 2207-2222.	2.1	235
38	DNA Replication-Independent Silencing in S. cerevisiae. Science, 2001, 291, 646-650.	12.6	119
39	The <i>rye</i> Mutants Identify a Role for Ssn/Srb Proteins of the RNA Polymerase II Holoenzyme During Stationary Phase Entry in <i>Saccharomyces cerevisiae</i> . Genetics, 2001, 157, 17-26.	2.9	47
40	Overlapping Functions of the Yeast Oxysterol-Binding Protein Homologues. Genetics, 2001, 157, 1117-1140.	2.9	233
41	<i>Kluyveromyces lactis</i> Sir2p Regulates Cation Sensitivity and Maintains a Specialized Chromatin Structure at the Cryptic α-Locus. Genetics, 2000, 156, 81-91.	2.9	35
42	Yeast cell-type regulation of DNA repair. Nature, 1999, 397, 310-310.	27.8	113
43	A Region of the Sir1 Protein Dedicated to Recognition of a Silencer and Required for Interaction with the Orc1 Protein in Saccharomyces cerevisiae. Genetics, 1999, 151, 31-44.	2.9	91
44	HMR-I Is an Origin of Replication and a Silencer in Saccharomyces cerevisiae. Genetics, 1999, 151, 521-529.	2.9	53
45	A Second-Generation Genetic Linkage Map of the Domestic Dog, Canis familiaris. Genetics, 1999, 151, 803-820.	2.9	186
46	A Role for the Replication Proteins PCNA, RF-C, Polymerase Îμ and Cdc45 in Transcriptional Silencing in Saccharomyces cerevisiae. Genetics, 1999, 153, 1171-1182.	2.9	83
47	Location of mouse and human genes corresponding to conserved canine olfactory receptor gene subfamilies. Mammalian Genome, 1998, 9, 349-354.	2.2	19
48	Theme and Variation Among Silencing Proteins in Saccharomyces cerevisiae and Kluyveromyces lactis. Genetics, 1998, 148, 1021-1029.	2.9	37
49	Sir- and Silencer-Independent Disruption of Silencing in Saccharomyces by Sas10p. Genetics, 1998, 149, 903-914.	2.9	35
50	Roles of Prenyl Protein Proteases in Maturation of Saccharomyces cerevisiae a-Factor. Genetics, 1998, 150, 95-101.	2.9	49
51	The Origin Recognition Complex, SIR1, and the S Phase Requirement for Silencing. Science, 1997, 276, 1547-1551.	12.6	160
52	The Role of Sas2, an Acetyltransferase Homologue of <i>Saccharomyces cerevisiae</i> , in Silencing and ORC Function. Genetics, 1997, 145, 923-934.	2.9	126
53	lsolation and DNA sequence of the STE14 gene encoding farnesyl cysteine: Carboxyl methyltransferase. Yeast, 1993, 9, 907-913.	1.7	35
54	Epigenetic inheritance of transcriptional states in S. cerevisiae. Cell, 1989, 59, 637-647.	28.9	349

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55	Four Genes Responsible for a Position Effect on Expression From <i>HML</i> and <i>HMR</i> in <i>Saccharomyces cerevisiae</i> . Genetics, 1987, 116, 9-22.	2.9	685
56	The trans action of HMRa in mating type interconversion. Molecular Genetics and Genomics, 1980, 180, 99-105.	2.4	6