

# Jason H Brickner

## List of Publications by Year in descending order

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48  
papers

3,494  
citations

218677

26  
h-index

206112

48  
g-index

56  
all docs

56  
docs citations

56  
times ranked

3397  
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene Recruitment of the Activated INO1 Locus to the Nuclear Membrane. <i>PLoS Biology</i> , 2004, 2, e342.	5.6	357
2	H2A.Z-Mediated Localization of Genes at the Nuclear Periphery Confers Epigenetic Memory of Previous Transcriptional State. <i>PLoS Biology</i> , 2007, 5, e81.	5.6	351
3	Eisosomes mark static sites of endocytosis. <i>Nature</i> , 2006, 439, 998-1003.	27.8	304
4	Structural Basis of FFAT Motif-Mediated ER Targeting. <i>Structure</i> , 2005, 13, 1035-1045.	3.3	218
5	Mechanisms of epigenetic memory. <i>Trends in Genetics</i> , 2014, 30, 230-236.	6.7	207
6	Interaction of a DNA Zip Code with the Nuclear Pore Complex Promotes H2A.Z Incorporation and INO1 Transcriptional Memory. <i>Molecular Cell</i> , 2010, 40, 112-125.	9.7	175
7	DNA zip codes control an ancient mechanism for gene targeting to the nuclear periphery. <i>Nature Cell Biology</i> , 2010, 12, 111-118.	10.3	170
8	SOI1 Encodes a Novel, Conserved Protein That Promotes TGN-Endosomal Cycling of Kex2p and Other Membrane Proteins by Modulating the Function of Two TGN Localization Signals. <i>Journal of Cell Biology</i> , 1997, 139, 23-36.	5.2	168
9	A Conserved Role for Human Nup98 in Altering Chromatin Structure and Promoting Epigenetic Transcriptional Memory. <i>PLoS Biology</i> , 2013, 11, e1001524.	5.6	160
10	Epigenetic transcriptional memory. <i>Current Genetics</i> , 2017, 63, 435-439.	1.7	113
11	Set1/COMPASS and Mediator are repurposed to promote epigenetic transcriptional memory. <i>ELife</i> , 2016, 5, .	6.0	107
12	Transcription Factor Binding to a DNA Zip Code Controls Interchromosomal Clustering at the Nuclear Periphery. <i>Developmental Cell</i> , 2012, 22, 1234-1246.	7.0	90
13	Compartmentalization of the nucleus. <i>Trends in Cell Biology</i> , 2011, 21, 701-708.	7.9	84
14	Cohesinopathy mutations disrupt the subnuclear organization of chromatin. <i>Journal of Cell Biology</i> , 2009, 187, 455-462.	5.2	83
15	Gene positioning and expression. <i>Current Opinion in Cell Biology</i> , 2011, 23, 338-345.	5.4	82
16	Transcriptional memory at the nuclear periphery. <i>Current Opinion in Cell Biology</i> , 2009, 21, 127-133.	5.4	63
17	Strategies to regulate transcription factor-mediated gene positioning and interchromosomal clustering at the nuclear periphery. <i>Journal of Cell Biology</i> , 2016, 212, 633-646.	5.2	59
18	The dynamic three-dimensional organization of the diploid yeast genome. <i>ELife</i> , 2017, 6, .	6.0	57

#	ARTICLE	IF	CITATIONS
19	Nuclear pore interactions with the genome. <i>Current Opinion in Genetics and Development</i> , 2014, 25, 43-49.	3.3	54
20	Regulation and epigenetic control of transcription at the nuclear periphery. <i>Trends in Genetics</i> , 2007, 23, 396-402.	6.7	53
21	The Role of Transcription Factors and Nuclear Pore Proteins in Controlling the Spatial Organization of the Yeast Genome. <i>Developmental Cell</i> , 2019, 49, 936-947.e4.	7.0	44
22	Subnuclear positioning and interchromosomal clustering of the <i>GAL1-10</i> locus are controlled by separable, interdependent mechanisms. <i>Molecular Biology of the Cell</i> , 2016, 27, 2980-2993.	2.1	42
23	Cdk Phosphorylation of a Nucleoporin Controls Localization of Active Genes through the Cell Cycle. <i>Molecular Biology of the Cell</i> , 2010, 21, 3421-3432.	2.1	38
24	The Tlg SNARE complex is required for TGN homotypic fusion. <i>Journal of Cell Biology</i> , 2001, 155, 969-978.	5.2	37
25	Epigenetic Transcriptional Memory of GAL Genes Depends on Growth in Glucose and the Tup1 Transcription Factor in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2017, 206, 1895-1907.	2.9	35
26	Nuclear pore proteins regulate chromatin structure and transcriptional memory by a conserved mechanism. <i>Nucleus</i> , 2013, 4, 357-360.	2.2	33
27	INO1 transcriptional memory leads to DNA zip code-dependent interchromosomal clustering. <i>Microbial Cell</i> , 2015, 2, 481-490.	3.2	30
28	Interchromosomal clustering of active genes at the nuclear pore complex. <i>Nucleus</i> , 2012, 3, 487-492.	2.2	27
29	Transcription factors dynamically control the spatial organization of the yeast genome. <i>Nucleus</i> , 2016, 7, 369-374.	2.2	25
30	Identification, Mapping and Linkage Analysis of Randomly Amplified DNA Polymorphisms in <i>Tetrahymena thermophila</i> . <i>Genetics</i> , 1996, 143, 811-821.	2.9	25
31	The Nuclear Pore Complex as a Transcription Regulator. <i>Cold Spring Harbor Perspectives in Biology</i> , 2022, 14, a039438.	5.5	23
32	Quantitative Localization of Chromosomal Loci by Immunofluorescence. <i>Methods in Enzymology</i> , 2010, 470, 569-580.	1.0	20
33	Vps Factors Are Required for Efficient Transcription Elongation in Budding Yeast. <i>Genetics</i> , 2013, 193, 829-851.	2.9	19
34	Transcriptional Memory: Staying in the Loop. <i>Current Biology</i> , 2010, 20, R20-R21.	3.9	18
35	Genetic and Epigenetic Strategies Potentiate Gal4 Activation to Enhance Fitness in Recently Diverged Yeast Species. <i>Current Biology</i> , 2017, 27, 3591-3602.e3.	3.9	18
36	Approaches to Studying Subnuclear Organization and Gene-Nuclear Pore Interactions. <i>Methods in Cell Biology</i> , 2014, 122, 463-485.	1.1	16

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37	Genetic and epigenetic control of the spatial organization of the genome. <i>Molecular Biology of the Cell</i> , 2017, 28, 364-369.	2.1	15
38	Mitotically heritable, RNA polymerase II-independent H3K4 dimethylation stimulates INO1 transcriptional memory. <i>ELife</i> , 2022, 11, .	6.0	14
39	Histone H2B ubiquitylation and H3 lysine 4 methylation prevent ectopic silencing of euchromatic loci important for the cellular response to heat. <i>Molecular Biology of the Cell</i> , 2011, 22, 2741-2753.	2.1	13
40	Random sub-diffusion and capture of genes by the nuclear pore reduces dynamics and coordinates inter-chromosomal movement. <i>ELife</i> , 2021, 10, .	6.0	9
41	Gene positioning is regulated by phosphorylation of the nuclear pore complex by Cdk1. <i>Cell Cycle</i> , 2011, 10, 392-395.	2.6	8
42	Nup98 regulation of histone methylation promotes normal gene expression and may drive leukemogenesis. <i>Genes and Development</i> , 2017, 31, 2201-2203.	5.9	7
43	A role for DNA sequence in controlling the spatial organization of the genome. <i>Nucleus</i> , 2010, 1, 402-406.	2.2	6
44	Nuclear Architecture: The Cell Biology of a Laminopathy. <i>Current Biology</i> , 2011, 21, R807-R809.	3.9	3
45	A New Direction for Gene Looping. <i>Developmental Cell</i> , 2012, 23, 919-921.	7.0	3
46	Nuclear Pore Complex in Genome Organization and Gene Expression in Yeast. , 2018, , 87-109.		3
47	Memory Is the Treasury and Guardian of All Things. <i>Molecular Cell</i> , 2017, 66, 5-6.	9.7	2
48	Nuclear Pore Complexes: A Scaffold Regulating Developmental Transcription?. <i>Trends in Cell Biology</i> , 2017, 27, 621-622.	7.9	2