

# Jason D Lieb

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

107 papers	21,576 citations	60 h-index	113 g-index
113 ext. papers	24,788 ext. citations	16.4 avg, IF	6.34 L-index

#	Paper	IF	Citations
107	Phosphorylated Lamin A/C in the Nuclear Interior Binds Active Enhancers Associated with Abnormal Transcription in Progeria. <i>Developmental Cell</i> , <b>2020</b> , 52, 699-713.e11	10.2	33
106	Tissue- and strain-specific effects of a genotoxic carcinogen 1,3-butadiene on chromatin and transcription. <i>Mammalian Genome</i> , <b>2018</b> , 29, 153-167	3.2	17
105	Variation in DNA-Damage Responses to an Inhalational Carcinogen (1,3-Butadiene) in Relation to Strain-Specific Differences in Chromatin Accessibility and Gene Transcription Profiles in C57BL/6J and CAST/EiJ Mice. <i>Environmental Health Perspectives</i> , <b>2017</b> , 125, 107006	8.4	17
104	Nucleosome fragility is associated with future transcriptional response to developmental cues and stress in <i>C. elegans</i> . <i>Genome Research</i> , <b>2017</b> , 27, 75-86	9.7	11
103	A Transcriptional Lineage of the Early <i>C. elegans</i> Embryo. <i>Developmental Cell</i> , <b>2016</b> , 38, 430-44	10.2	54
102	Chromatin profiling of <i>Drosophila</i> CNS subpopulations identifies active transcriptional enhancers. <i>Development (Cambridge)</i> , <b>2016</b> , 143, 3723-3732	6.6	12
101	Alterations to chromatin in intestinal macrophages link IL-10 deficiency to inappropriate inflammatory responses. <i>European Journal of Immunology</i> , <b>2016</b> , 46, 1912-25	6.1	24
100	Genome-wide kinetics of DNA excision repair in relation to chromatin state and mutagenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, E2124-33	11.5	100
99	The function and regulation of the GATA factor ELT-2 in the <i>C. elegans</i> endoderm. <i>Development (Cambridge)</i> , <b>2016</b> , 143, 483-91	6.6	20
98	Cisplatin DNA damage and repair maps of the human genome at single-nucleotide resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 11507-11512	11.5	96
97	Asymmetric transcript discovery by RNA-seq in <i>C. elegans</i> blastomeres identifies neg-1, a gene important for anterior morphogenesis. <i>PLoS Genetics</i> , <b>2015</b> , 11, e1005117	6	14
96	Histone modifications predispose genome regions to breakage and translocation. <i>Genes and Development</i> , <b>2015</b> , 29, 1393-402	12.6	42
95	Genome-wide analysis of human global and transcription-coupled excision repair of UV damage at single-nucleotide resolution. <i>Genes and Development</i> , <b>2015</b> , 29, 948-60	12.6	147
94	STAT3 acts through pre-existing nucleosome-depleted regions bound by FOS during an epigenetic switch linking inflammation to cancer. <i>Epigenetics and Chromatin</i> , <b>2015</b> , 8, 7	5.8	26
93	Zelda is differentially required for chromatin accessibility, transcription factor binding, and gene expression in the early <i>Drosophila</i> embryo. <i>Genome Research</i> , <b>2015</b> , 25, 1715-26	9.7	106
92	Single-cell ATAC-seq: strength in numbers. <i>Genome Biology</i> , <b>2015</b> , 16, 172	18.3	41
91	What are super-enhancers?. <i>Nature Genetics</i> , <b>2015</b> , 47, 8-12	36.3	398

90	Interrogating the function of metazoan histones using engineered gene clusters. <i>Developmental Cell</i> , <b>2015</b> , 32, 373-86	10.2	86
89	Ancient transposable elements transformed the uterine regulatory landscape and transcriptome during the evolution of mammalian pregnancy. <i>Cell Reports</i> , <b>2015</b> , 10, 551-61	10.6	158
88	Genome-wide analysis links emerin to neuromuscular junction activity in <i>Caenorhabditis elegans</i> . <i>Genome Biology</i> , <b>2014</b> , 15, R21	18.3	37
87	Variation in chromatin accessibility in human kidney cancer links H3K36 methyltransferase loss with widespread RNA processing defects. <i>Genome Research</i> , <b>2014</b> , 24, 241-50	9.7	124
86	Comparative analysis of metazoan chromatin organization. <i>Nature</i> , <b>2014</b> , 512, 449-52	50.4	265
85	Reply to Brunet and Doolittle: Both selected effect and causal role elements can influence human biology and disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, E3366	11.5	22
84	Regulation of the X chromosomes in <i>Caenorhabditis elegans</i> . <i>Cold Spring Harbor Perspectives in Biology</i> , <b>2014</b> , 6,	10.2	38
83	Defining functional DNA elements in the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 6131-8	11.5	490
82	Quantitative genetics of CTCF binding reveal local sequence effects and different modes of X-chromosome association. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004798	6	38
81	A split personality for nucleosomes. <i>Cell</i> , <b>2014</b> , 159, 1249-51	56.2	1
80	A common set of DNA regulatory elements shapes <i>Drosophila</i> appendages. <i>Developmental Cell</i> , <b>2013</b> , 27, 306-18	10.2	93
79	The open chromatin landscape of Kaposi's sarcoma-associated herpesvirus. <i>Journal of Virology</i> , <b>2013</b> , 87, 11831-42	6.6	32
78	Integral nuclear pore proteins bind to Pol III-transcribed genes and are required for Pol III transcript processing in <i>C. elegans</i> . <i>Molecular Cell</i> , <b>2013</b> , 51, 840-9	17.6	44
77	Promoter- and RNA polymerase II-dependent hsp-16 gene association with nuclear pores in <i>Caenorhabditis elegans</i> . <i>Journal of Cell Biology</i> , <b>2013</b> , 200, 589-604	7.3	50
76	Genome-wide measurement of protein-DNA binding dynamics using competition ChIP. <i>Nature Protocols</i> , <b>2013</b> , 8, 1337-53	18.8	11
75	A detailed protocol for formaldehyde-assisted isolation of regulatory elements (FAIRE). <i>Current Protocols in Molecular Biology</i> , <b>2013</b> , Chapter 21, Unit21.26	2.9	27
74	TRA-1 ChIP-seq reveals regulators of sexual differentiation and multilevel feedback in nematode sex determination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 16033-8	11.5	39
73	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. <i>Genome Research</i> , <b>2012</b> , 22, 1813-31	9.7	1211

72	Using formaldehyde-assisted isolation of regulatory elements (FAIRE) to isolate active regulatory DNA. <i>Nature Protocols</i> , <b>2012</b> , 7, 256-67	18.8	230
71	The accessible chromatin landscape of the human genome. <i>Nature</i> , <b>2012</b> , 489, 75-82	50.4	1900
70	Systematic evaluation of factors influencing ChIP-seq fidelity. <i>Nature Methods</i> , <b>2012</b> , 9, 609-14	21.6	112
69	Isolation of Active Regulatory Elements from Eukaryotic Chromatin Using FAIRE (Formaldehyde-Assisted Isolation of Regulatory Elements) <b>2012</b> , 243-255		
68	An inverse relationship to germline transcription defines centromeric chromatin in <i>C. elegans</i> . <i>Nature</i> , <b>2012</b> , 484, 534-7	50.4	119
67	Genome-wide protein-DNA binding dynamics suggest a molecular clutch for transcription factor function. <i>Nature</i> , <b>2012</b> , 484, 251-5	50.4	175
66	H4K20me1 contributes to downregulation of X-linked genes for <i>C. elegans</i> dosage compensation. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1002933	6	60
65	In vivo effects of histone H3 depletion on nucleosome occupancy and position in <i>Saccharomyces cerevisiae</i> . <i>PLoS Genetics</i> , <b>2012</b> , 8, e1002771	6	62
64	Tumor-specific retargeting of an oncogenic transcription factor chimera results in dysregulation of chromatin and transcription. <i>Genome Research</i> , <b>2012</b> , 22, 259-70	9.7	77
63	Cell-type specific and combinatorial usage of diverse transcription factors revealed by genome-wide binding studies in multiple human cells. <i>Genome Research</i> , <b>2012</b> , 22, 9-24	9.7	86
62	ZINBA integrates local covariates with DNA-seq data to identify broad and narrow regions of enrichment, even within amplified genomic regions. <i>Genome Biology</i> , <b>2011</b> , 12, R67	18.3	139
61	The stress response factors Yap6, Cin5, Phd1, and Skn7 direct targeting of the conserved co-repressor Tup1-Ssn6 in <i>S. cerevisiae</i> . <i>PLoS ONE</i> , <b>2011</b> , 6, e19060	3.7	58
60	An assessment of histone-modification antibody quality. <i>Nature Structural and Molecular Biology</i> , <b>2011</b> , 18, 91-3	17.6	306
59	Broad chromosomal domains of histone modification patterns in <i>C. elegans</i> . <i>Genome Research</i> , <b>2011</b> , 21, 227-36	9.7	208
58	High nucleosome occupancy is encoded at X-linked gene promoters in <i>C. elegans</i> . <i>Genome Research</i> , <b>2011</b> , 21, 237-44	9.7	29
57	Evidence for compensatory upregulation of expressed X-linked genes in mammals, <i>Caenorhabditis elegans</i> and <i>Drosophila melanogaster</i> . <i>Nature Genetics</i> , <b>2011</b> , 43, 1179-85	36.3	206
56	Open chromatin defined by DNaseI and FAIRE identifies regulatory elements that shape cell-type identity. <i>Genome Research</i> , <b>2011</b> , 21, 1757-67	9.7	391
55	A conserved PHD finger protein and endogenous RNAi modulate insulin signaling in <i>Caenorhabditis elegans</i> . <i>PLoS Genetics</i> , <b>2011</b> , 7, e1002299	6	20

54	Nucleosome sequence preferences influence in vivo nucleosome organization. <i>Nature Structural and Molecular Biology</i> , <b>2010</b> , 17, 918-20	17.6	87
53	A map of open chromatin in human pancreatic islets. <i>Nature Genetics</i> , <b>2010</b> , 42, 255-9	36.3	435
52	Nucleosome dynamics define transcriptional enhancers. <i>Nature Genetics</i> , <b>2010</b> , 42, 343-7	36.3	382
51	The histone H3K36 methyltransferase MES-4 acts epigenetically to transmit the memory of germline gene expression to progeny. <i>PLoS Genetics</i> , <b>2010</b> , 6, e1001091	6	137
50	High nucleosome occupancy is encoded at human regulatory sequences. <i>PLoS ONE</i> , <b>2010</b> , 5, e9129	3.7	140
49	Allele-specific and heritable chromatin signatures in humans. <i>Human Molecular Genetics</i> , <b>2010</b> , 19, R204-9	3.6	24
48	Integrative analysis of the <i>Caenorhabditis elegans</i> genome by the modENCODE project. <i>Science</i> , <b>2010</b> , 330, 1775-87	33.3	744
47	<i>Caenorhabditis elegans</i> chromosome arms are anchored to the nuclear membrane via discontinuous association with LEM-2. <i>Genome Biology</i> , <b>2010</b> , 11, R120	18.3	142
46	Contribution of histone sequence preferences to nucleosome organization: proposed definitions and methodology. <i>Genome Biology</i> , <b>2010</b> , 11, 140	18.3	46
45	Heritable individual-specific and allele-specific chromatin signatures in humans. <i>Science</i> , <b>2010</b> , 328, 235-9	33.3	260
44	DNA-binding specificity and in vivo targets of <i>Caenorhabditis elegans</i> nuclear factor I. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 12049-54	11.5	23
43	A positive but complex association between meiotic double-strand break hotspots and open chromatin in <i>Saccharomyces cerevisiae</i> . <i>Genome Research</i> , <b>2009</b> , 19, 2245-57	9.7	51
42	Systematic identification of balanced transposition polymorphisms in <i>Saccharomyces cerevisiae</i> . <i>PLoS Genetics</i> , <b>2009</b> , 5, e1000502	6	5
41	The <i>C. elegans</i> dosage compensation complex propagates dynamically and independently of X chromosome sequence. <i>Current Biology</i> , <b>2009</b> , 19, 1777-87	6.3	38
40	<i>C. elegans</i> dosage compensation: a window into mechanisms of domain-scale gene regulation. <i>Chromosome Research</i> , <b>2009</b> , 17, 215-27	4.4	31
39	The DNA-encoded nucleosome organization of a eukaryotic genome. <i>Nature</i> , <b>2009</b> , 458, 362-6	50.4	926
38	Unlocking the secrets of the genome. <i>Nature</i> , <b>2009</b> , 459, 927-30	50.4	620
37	Gene expression divergence in yeast is coupled to evolution of DNA-encoded nucleosome organization. <i>Nature Genetics</i> , <b>2009</b> , 41, 438-45	36.3	121

36	Isolation of active regulatory elements from eukaryotic chromatin using FAIRE (Formaldehyde Assisted Isolation of Regulatory Elements). <i>Methods</i> , <b>2009</b> , 48, 233-9	4.6	156
35	Highly transcribed RNA polymerase II genes are impediments to replication fork progression in <i>Saccharomyces cerevisiae</i> . <i>Molecular Cell</i> , <b>2009</b> , 34, 722-34	17.6	229
34	The Set2/Rpd3S pathway suppresses cryptic transcription without regard to gene length or transcription frequency. <i>PLoS ONE</i> , <b>2009</b> , 4, e4886	3.7	44
33	A library of yeast transcription factor motifs reveals a widespread function for Rsc3 in targeting nucleosome exclusion at promoters. <i>Molecular Cell</i> , <b>2008</b> , 32, 878-87	17.6	346
32	Chromatin proteins do double duty. <i>Cell</i> , <b>2008</b> , 133, 763-5	56.2	
31	DNA Immunoprecipitation (DIP) for the Determination of DNA-Binding Specificity. <i>Cold Spring Harbor Protocols</i> , <b>2008</b> , 2008, pdb.prot4972	1.2	8
30	The genomic distribution and function of histone variant HTZ-1 during <i>C. elegans</i> embryogenesis. <i>PLoS Genetics</i> , <b>2008</b> , 4, e1000187	6	81
29	Systematic evaluation of variability in ChIP-chip experiments using predefined DNA targets. <i>Genome Research</i> , <b>2008</b> , 18, 393-403	9.7	111
28	FAIRE (Formaldehyde-Assisted Isolation of Regulatory Elements) isolates active regulatory elements from human chromatin. <i>Genome Research</i> , <b>2007</b> , 17, 877-85	9.7	674
27	X chromosome repression by localization of the <i>C. elegans</i> dosage compensation machinery to sites of transcription initiation. <i>Nature Genetics</i> , <b>2007</b> , 39, 403-8	36.3	98
26	Forkhead proteins control the outcome of transcription factor binding by antiactivation. <i>EMBO Journal</i> , <b>2007</b> , 26, 4324-34	13	54
25	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , <b>2007</b> , 447, 799-816	50.4	4121
24	Identification of histone H3 lysine 36 acetylation as a highly conserved histone modification. <i>Journal of Biological Chemistry</i> , <b>2007</b> , 282, 7632-40	5.4	103
23	Loss of a histone deacetylase dramatically alters the genomic distribution of Spo11p-catalyzed DNA breaks in <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2007</b> , 104, 3955-60	11.5	64
22	The RNA polymerase II kinase Ctk1 regulates positioning of a 5Rhistone methylation boundary along genes. <i>Molecular and Cellular Biology</i> , <b>2007</b> , 27, 721-31	4.8	48
21	The <i>Saccharomyces cerevisiae</i> histone demethylase Jhd1 fine-tunes the distribution of H3K36me2. <i>Molecular and Cellular Biology</i> , <b>2007</b> , 27, 5055-65	4.8	25
20	Global analysis of the relationship between the binding of the Bas1p transcription factor and meiosis-specific double-strand DNA breaks in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , <b>2006</b> , 26, 1014-27	4.8	56
19	Cell cycle-specified fluctuation of nucleosome occupancy at gene promoters. <i>PLoS Genetics</i> , <b>2006</b> , 2, e158	6	95

18	Whole-genome comparison of Leu3 binding in vitro and in vivo reveals the importance of nucleosome occupancy in target site selection. <i>Genome Research</i> , <b>2006</b> , 16, 1517-28	9.7	104
17	Regulation of nucleosome stability as a mediator of chromatin function. <i>Current Opinion in Genetics and Development</i> , <b>2006</b> , 16, 171-6	4.9	20
16	A chromatin-mediated mechanism for specification of conditional transcription factor targets. <i>Nature Genetics</i> , <b>2006</b> , 38, 1446-51	36.3	77
15	Control of transcription through intragenic patterns of nucleosome composition. <i>Cell</i> , <b>2005</b> , 123, 1187-96	36.2	59
14	CHIPOTle: a user-friendly tool for the analysis of ChIP-chip data. <i>Genome Biology</i> , <b>2005</b> , 6, R97	18.3	130
13	DIP-chip: rapid and accurate determination of DNA-binding specificity. <i>Genome Research</i> , <b>2005</b> , 15, 421-7	7.7	71
12	Dimethylation of histone H3 at lysine 36 demarcates regulatory and nonregulatory chromatin genome-wide. <i>Molecular and Cellular Biology</i> , <b>2005</b> , 25, 9447-59	4.8	152
11	Evidence for nucleosome depletion at active regulatory regions genome-wide. <i>Nature Genetics</i> , <b>2004</b> , 36, 900-5	36.3	577
10	Progress and challenges in profiling the dynamics of chromatin and transcription factor binding with DNA microarrays. <i>Current Opinion in Genetics and Development</i> , <b>2004</b> , 14, 697-705	4.9	88
9	ChIP-chip: considerations for the design, analysis, and application of genome-wide chromatin immunoprecipitation experiments. <i>Genomics</i> , <b>2004</b> , 83, 349-60	4.3	461
8	Integrating regulatory motif discovery and genome-wide expression analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2003</b> , 100, 3339-44	11.5	274
7	Genomewide demarcation of RNA polymerase II transcription units revealed by physical fractionation of chromatin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2003</b> , 100, 6364-9	11.5	95
6	Genome-wide mapping of protein-DNA interactions by chromatin immunoprecipitation and DNA microarray hybridization. <i>Methods in Molecular Biology</i> , <b>2003</b> , 224, 99-109	1.4	20
5	A molecular link between gene-specific and chromosome-wide transcriptional repression. <i>Genes and Development</i> , <b>2002</b> , 16, 796-805	12.6	61
4	Promoter-specific binding of Rap1 revealed by genome-wide maps of protein-DNA association. <i>Nature Genetics</i> , <b>2001</b> , 28, 327-34	36.3	576
3	The <i>Caenorhabditis elegans</i> dosage compensation machinery is recruited to X chromosome DNA attached to an autosome. <i>Genetics</i> , <b>2000</b> , 156, 1603-21	4	22
2	MIX-1: an essential component of the <i>C. elegans</i> mitotic machinery executes X chromosome dosage compensation. <i>Cell</i> , <b>1998</b> , 92, 265-77	56.2	151
1	A Transcriptional Lineage of the Early <i>C. elegans</i> Embryo		1

