

Steven E Jacobsen

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.

137
papers

26,373
citations

69
h-index

147
g-index

147
ext. papers

31,007
ext. citations

18.1
avg, IF

7.1
L-index

#	Paper	IF	Citations
137	CRISPR-CAS mediated transcriptional control and epi-mutagenesis.. <i>Plant Physiology</i> , 2022 ,	6.6	1
136	A SYBR Gold-based Label-free Dicing Assay.. <i>Bio-protocol</i> , 2022 , 12, e4382	0.9	
135	Mechanism of siRNA production by a plant Dicer-RNA complex in dicing-competent conformation. <i>Science</i> , 2021 , 374, 1152-1157	33.3	7
134	MORC3, a novel MIWI2 association partner, as an epigenetic regulator of piRNA dependent transposon silencing in male germ cells. <i>Scientific Reports</i> , 2021 , 11, 20472	4.9	1
133	The role of MORC3 in silencing transposable elements in mouse embryonic stem cells. <i>Epigenetics and Chromatin</i> , 2021 , 14, 49	5.8	1
132	The histone variant H2A.W and linker histone H1 co-regulate heterochromatin accessibility and DNA methylation. <i>Nature Communications</i> , 2021 , 12, 2683	17.4	12
131	Ectopic targeting of CG DNA methylation in Arabidopsis with the bacterial Sssl methyltransferase. <i>Nature Communications</i> , 2021 , 12, 3130	17.4	6
130	CRISPR-based targeting of DNA methylation in by a bacterial CG-specific DNA methyltransferase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	14
129	MBD5 and MBD6 couple DNA methylation to gene silencing through the J-domain protein SILENZIO. <i>Science</i> , 2021 , 372,	33.3	8
128	SNPC-1.3 is a sex-specific transcription factor that drives male piRNA expression in. <i>ELife</i> , 2021 , 10,	8.9	2
127	Whole-genome characterization of chronological age-associated changes in methylome and circular RNAs in moso bamboo (<i>Phyllostachys edulis</i>) from vegetative to floral growth. <i>Plant Journal</i> , 2021 , 106, 435-453	6.9	3
126	Arabidopsis MORC proteins function in the efficient establishment of RNA directed DNA methylation. <i>Nature Communications</i> , 2021 , 12, 4292	17.4	4
125	DNA methylation-linked chromatin accessibility affects genomic architecture in. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	12
124	The characterization of Mediator 12 and 13 as conditional positive gene regulators in Arabidopsis. <i>Nature Communications</i> , 2020 , 11, 2798	17.4	6
123	NAP1-RELATED PROTEIN1 and 2 negatively regulate H2A.Z abundance in chromatin in Arabidopsis. <i>Nature Communications</i> , 2020 , 11, 2887	17.4	8
122	A kinesin Klp10A mediates cell cycle-dependent shuttling of Piwi between nucleus and nuage. <i>PLoS Genetics</i> , 2020 , 16, e1008648	6	1
121	Promoter and Terminator Optimization for DNA Methylation Targeting in .. <i>Epigenomes</i> , 2020 , 4,	2.3	1

120	A viral guide RNA delivery system for CRISPR-based transcriptional activation and heritable targeted DNA demethylation in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2020 , 16, e1008983	6	10
119	Efficient and accurate determination of genome-wide DNA methylation patterns in <i>Arabidopsis thaliana</i> with enzymatic methyl sequencing. <i>Epigenetics and Chromatin</i> , 2020 , 13, 42	5.8	16
118	CRISPR-Cas1 from huge phages is a hypercompact genome editor. <i>Science</i> , 2020 , 369, 333-337	33.3	158
117	DNA polymerase epsilon is required for heterochromatin maintenance in <i>Arabidopsis</i> . <i>Genome Biology</i> , 2020 , 21, 283	18.3	3
116	The plant mobile domain proteins MAIN and MAIL1 interact with the phosphatase PP7L to regulate gene expression and silence transposable elements in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2020 , 16, e1008324 ⁴	6	16
115	The plant mobile domain proteins MAIN and MAIL1 interact with the phosphatase PP7L to regulate gene expression and silence transposable elements in <i>Arabidopsis thaliana</i> 2020 , 16, e1008324		
114	The plant mobile domain proteins MAIN and MAIL1 interact with the phosphatase PP7L to regulate gene expression and silence transposable elements in <i>Arabidopsis thaliana</i> 2020 , 16, e1008324		
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110	The plant mobile domain proteins MAIN and MAIL1 interact with the phosphatase PP7L to regulate gene expression and silence transposable elements in <i>Arabidopsis thaliana</i> 2020 , 16, e1008324		
109	The plant mobile domain proteins MAIN and MAIL1 interact with the phosphatase PP7L to regulate gene expression and silence transposable elements in <i>Arabidopsis thaliana</i> 2020 , 16, e1008324		
108	The plant mobile domain proteins MAIN and MAIL1 interact with the phosphatase PP7L to regulate gene expression and silence transposable elements in <i>Arabidopsis thaliana</i> 2020 , 16, e1008324		
107	A kinesin Klp10A mediates cell cycle-dependent shuttling of Piwi between nucleus and nuage 2020 , 16, e1008648		
106	A kinesin Klp10A mediates cell cycle-dependent shuttling of Piwi between nucleus and nuage 2020 , 16, e1008648		
105	A kinesin Klp10A mediates cell cycle-dependent shuttling of Piwi between nucleus and nuage 2020 , 16, e1008648		
104	A kinesin Klp10A mediates cell cycle-dependent shuttling of Piwi between nucleus and nuage 2020 , 16, e1008648		
103	CryoEM structures of <i>Arabidopsis</i> DDR complexes involved in RNA-directed DNA methylation. <i>Nature Communications</i> , 2019 , 10, 3916	17.4	12

102	Multi-level Modulation of Light Signaling by GIGANTEA Regulates Both the Output and Pace of the Circadian Clock. <i>Developmental Cell</i> , 2019 , 49, 840-851.e8	10.2	34
101	Genome mining and biosynthesis of a polyketide from a biofertilizer fungus that can facilitate reductive iron assimilation in plant. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 5499-5504	11.5	27
100	Co-targeting RNA Polymerases IV and V Promotes Efficient De Novo DNA Methylation in Arabidopsis. <i>Cell</i> , 2019 , 176, 1068-1082.e19	56.2	68
99	Arabidopsis SWR1-associated protein methyl-CpG-binding domain 9 is required for histone H2A.Z deposition. <i>Nature Communications</i> , 2019 , 10, 3352	17.4	31
98	Site-specific manipulation of Arabidopsis loci using CRISPR-Cas9 SunTag systems. <i>Nature Communications</i> , 2019 , 10, 729	17.4	114
97	A Nucleosome Bridging Mechanism for Activation of a Maintenance DNA Methyltransferase. <i>Molecular Cell</i> , 2019 , 73, 73-83.e6	17.6	23
96	ADCP1: a novel plant H3K9me2 reader. <i>Cell Research</i> , 2019 , 29, 6-7	24.7	0
95	TFAP2C regulates transcription in human naive pluripotency by opening enhancers. <i>Nature Cell Biology</i> , 2018 , 20, 553-564	23.4	73
94	Targeted DNA demethylation of the genome using the human TET1 catalytic domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E2125-E2134	11.5	128
93	RNA-directed DNA methylation involves co-transcriptional small-RNA-guided slicing of polymerase V transcripts in Arabidopsis. <i>Nature Plants</i> , 2018 , 4, 181-188	11.5	51
92	Large-scale comparative epigenomics reveals hierarchical regulation of non-CG methylation in. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E1069-E1074	11.5	34
91	Resistance-gene-directed discovery of a natural-product herbicide with a new mode of action. <i>Nature</i> , 2018 , 559, 415-418	50.4	108
90	Mechanistic insights into plant SUVH family H3K9 methyltransferases and their binding to context-biased non-CG DNA methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E8793-E8802	11.5	53
89	The TFAP2C-Regulated OCT4 Naive Enhancer Is Involved in Human Germline Formation. <i>Cell Reports</i> , 2018 , 25, 3591-3602.e5	10.6	29
88	A DNA methylation reader complex that enhances gene transcription. <i>Science</i> , 2018 , 362, 1182-1186	33.3	103
87	The impact and prospect of natural product discovery in agriculture: New technologies to explore the diversity of secondary metabolites in plants and microorganisms for applications in agriculture. <i>EMBO Reports</i> , 2018 , 19,	6.5	18
86	MORC-1 Integrates Nuclear RNAi and Transgenerational Chromatin Architecture to Promote Germline Immortality. <i>Developmental Cell</i> , 2017 , 41, 408-423.e7	10.2	36
85	Large-scale heterochromatin remodeling linked to overreplication-associated DNA damage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 406-411	11.5	17

84	The histone H3 variant H3.3 regulates gene body DNA methylation in <i>Arabidopsis thaliana</i> . <i>Genome Biology</i> , 2017 , 18, 94	18.3	66
83	Germline competency of human embryonic stem cells depends on eomesodermin. <i>Biology of Reproduction</i> , 2017 , 97, 850-861	3.9	49
82	Mouse MORC3 is a GHKL ATPase that localizes to H3K4me3 marked chromatin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E5108-16	11.5	28
81	On the origin and evolutionary consequences of gene body DNA methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 9111-6	11.5	189
80	MTHFD1 controls DNA methylation in <i>Arabidopsis</i> . <i>Nature Communications</i> , 2016 , 7, 11640	17.4	39
79	Structural Basis for the Unique Multivalent Readout of Unmodified H3 Tail by <i>Arabidopsis</i> ORC1b BAH-PHD Cassette. <i>Structure</i> , 2016 , 24, 486-94	5.2	15
78	Naive Human Pluripotent Cells Feature a Methylation Landscape Devoid of Blastocyst or Germline Memory. <i>Cell Stem Cell</i> , 2016 , 18, 323-329	18	161
77	<i>Arabidopsis</i> AtMORC4 and AtMORC7 Form Nuclear Bodies and Repress a Large Number of Protein-Coding Genes. <i>PLoS Genetics</i> , 2016 , 12, e1005998	6	27
76	Identification of Multiple Proteins Coupling Transcriptional Gene Silencing to Genome Stability in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2016 , 12, e1006092	6	18
75	DNA methylome of the 20-gigabase Norway spruce genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E8106-E8113	11.5	56
74	Evidence for ARGONAUTE4-DNA interactions in RNA-directed DNA methylation in plants. <i>Genes and Development</i> , 2016 , 30, 2565-2570	12.6	39
73	Rare allele of a previously unidentified histone H4 acetyltransferase enhances grain weight, yield, and plant biomass in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 76-81	11.5	156
72	C-terminal domains of a histone demethylase interact with a pair of transcription factors and mediate specific chromatin association. <i>Cell Discovery</i> , 2015 , 1,	22.3	33
71	CG gene body DNA methylation changes and evolution of duplicated genes in cassava. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 13729-34	11.5	91
70	A One Precursor One siRNA Model for Pol IV-Dependent siRNA Biogenesis. <i>Cell</i> , 2015 , 163, 445-55	56.2	166
69	Nucleosome Organization in Human Embryonic Stem Cells. <i>PLoS ONE</i> , 2015 , 10, e0136314	3.7	15
68	DNA methylation pathways and their crosstalk with histone methylation. <i>Nature Reviews Molecular Cell Biology</i> , 2015 , 16, 519-32	48.7	558
67	Domains rearranged methyltransferase3 controls DNA methylation and regulates RNA polymerase V transcript abundance in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 911-6	11.5	110

66	Increasing Nucleosome Occupancy Is Correlated with an Increasing Mutation Rate so Long as DNA Repair Machinery Is Intact. <i>PLoS ONE</i> , 2015 , 10, e0136574	3.7	23
65	In vivo targeting of de novo DNA methylation by histone modifications in yeast and mouse. <i>ELife</i> , 2015 , 4, e06205	8.9	107
64	SRA- and SET-domain-containing proteins link RNA polymerase V occupancy to DNA methylation. <i>Nature</i> , 2014 , 507, 124-128	50.4	199
63	Transcriptional gene silencing by Arabidopsis microRNA homologues involves the formation of heteromers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 7474-9	11.5	48
62	Non-CG methylation patterns shape the epigenetic landscape in Arabidopsis. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 64-72	17.6	488
61	The Functional Topography of the Arabidopsis Genome Is Organized in a Reduced Number of Linear Motifs of Chromatin States. <i>Plant Cell</i> , 2014 , 26, 2351-2366	11.6	167
60	Dissecting the dynamic changes of 5-hydroxymethylcytosine in T-cell development and differentiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E3306-15	11.5	110
59	Genome-wide Hi-C analyses in wild-type and mutants reveal high-resolution chromatin interactions in Arabidopsis. <i>Molecular Cell</i> , 2014 , 55, 694-707	17.6	216
58	Mechanism of DNA methylation-directed histone methylation by KRYPTONITE. <i>Molecular Cell</i> , 2014 , 55, 495-504	17.6	120
57	The histone variant H2A.W defines heterochromatin and promotes chromatin condensation in Arabidopsis. <i>Cell</i> , 2014 , 158, 98-109	56.2	160
56	Molecular mechanism of action of plant DRM de novo DNA methyltransferases. <i>Cell</i> , 2014 , 157, 1050-60	56.2	179
55	Epigenetic differences between shoots and roots in Arabidopsis reveals tissue-specific regulation. <i>Epigenetics</i> , 2014 , 9, 236-42	5.7	44
54	MORC1 represses transposable elements in the mouse male germline. <i>Nature Communications</i> , 2014 , 5, 5795	17.4	71
53	SNF2 chromatin remodeler-family proteins FRG1 and -2 are required for RNA-directed DNA methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 17666-71	11.5	19
52	Comprehensive analysis of silencing mutants reveals complex regulation of the Arabidopsis methylome. <i>Cell</i> , 2013 , 152, 352-64	56.2	572
51	Polymerase IV occupancy at RNA-directed DNA methylation sites requires SHH1. <i>Nature</i> , 2013 , 498, 385-90	50.4	234
50	Interplay between active chromatin marks and RNA-directed DNA methylation in Arabidopsis thaliana. <i>PLoS Genetics</i> , 2013 , 9, e1003946	6	53
49	INVOLVED IN DE NOVO 2-containing complex involved in RNA-directed DNA methylation in Arabidopsis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 8374-81	11.5	61

48	Dual binding of chromomethylase domains to H3K9me2-containing nucleosomes directs DNA methylation in plants. <i>Cell</i> , 2012 , 151, 167-80	56.2	323
47	DDR complex facilitates global association of RNA polymerase V to promoters and evolutionarily young transposons. <i>Nature Structural and Molecular Biology</i> , 2012 , 19, 870-5	17.6	144
46	MORC family ATPases required for heterochromatin condensation and gene silencing. <i>Science</i> , 2012 , 336, 1448-51	33.3	220
45	A dual flip-out mechanism for 5mC recognition by the Arabidopsis SUVH5 SRA domain and its impact on DNA methylation and H3K9 dimethylation in vivo. <i>Genes and Development</i> , 2011 , 25, 137-52	12.6	83
44	Identification of genes required for de novo DNA methylation in Arabidopsis. <i>Epigenetics</i> , 2011 , 6, 344-54	5.7	54
43	Regulation of heterochromatic DNA replication by histone H3 lysine 27 methyltransferases. <i>Nature</i> , 2010 , 466, 987-91	50.4	142
42	Establishing, maintaining and modifying DNA methylation patterns in plants and animals. <i>Nature Reviews Genetics</i> , 2010 , 11, 204-20	30.1	2480
41	Conservation and divergence of methylation patterning in plants and animals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 8689-94	11.5	884
40	Epigenetic reprogramming in plant and animal development. <i>Science</i> , 2010 , 330, 622-7	33.3	873
39	A protein complex required for polymerase V transcripts and RNA- directed DNA methylation in Arabidopsis. <i>Current Biology</i> , 2010 , 20, 951-6	6.3	167
38	ATXR5 and ATXR6 are H3K27 monomethyltransferases required for chromatin structure and gene silencing. <i>Nature Structural and Molecular Biology</i> , 2009 , 16, 763-8	17.6	217
37	IDN1 and IDN2 are required for de novo DNA methylation in Arabidopsis thaliana. <i>Nature Structural and Molecular Biology</i> , 2009 , 16, 1325-7	17.6	85
36	Genome-wide analysis of mono-, di- and trimethylation of histone H3 lysine 4 in Arabidopsis thaliana. <i>Genome Biology</i> , 2009 , 10, R62	18.3	381
35	Shotgun bisulphite sequencing of the Arabidopsis genome reveals DNA methylation patterning. <i>Nature</i> , 2008 , 452, 215-9	50.4	1704
34	Genome-wide association of histone H3 lysine nine methylation with CHG DNA methylation in Arabidopsis thaliana. <i>PLoS ONE</i> , 2008 , 3, e3156	3.7	242
33	Tandem repeats upstream of the Arabidopsis endogene SDC recruit non-CG DNA methylation and initiate siRNA spreading. <i>Genes and Development</i> , 2008 , 22, 1597-606	12.6	169
32	SRA-domain proteins required for DRM2-mediated de novo DNA methylation. <i>PLoS Genetics</i> , 2008 , 4, e1000280	6	120
31	Whole-genome analysis of histone H3 lysine 27 trimethylation in Arabidopsis. <i>PLoS Biology</i> , 2007 , 5, e129	9.7	528

30	The Arabidopsis LHP1 protein colocalizes with histone H3 Lys27 trimethylation. <i>Nature Structural and Molecular Biology</i> , 2007 , 14, 869-71	17.6	288
29	Epigenetic inheritance in plants. <i>Nature</i> , 2007 , 447, 418-24	50.4	622
28	The SRA methyl-cytosine-binding domain links DNA and histone methylation. <i>Current Biology</i> , 2007 , 17, 379-84	6.3	313
27	Role of RNA polymerase IV in plant small RNA metabolism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 4536-41	11.5	234
26	Reiterated WG/GW motifs form functionally and evolutionarily conserved ARGONAUTE-binding platforms in RNAi-related components. <i>Genes and Development</i> , 2007 , 21, 2539-44	12.6	247
25	RNAi, DRD1, and histone methylation actively target developmentally important non-CG DNA methylation in arabidopsis. <i>PLoS Genetics</i> , 2006 , 2, e83	6	170
24	Two-step recruitment of RNA-directed DNA methylation to tandem repeats. <i>PLoS Biology</i> , 2006 , 4, e3639.7	14.5	
23	An ARGONAUTE4-containing nuclear processing center colocalized with Cajal bodies in Arabidopsis thaliana. <i>Cell</i> , 2006 , 126, 93-106	56.2	310
22	Dissecting Arabidopsis thaliana DICER function in small RNA processing, gene silencing and DNA methylation patterning. <i>Nature Genetics</i> , 2006 , 38, 721-5	36.3	470
21	DNA methylation profiling identifies CG methylation clusters in Arabidopsis genes. <i>Current Biology</i> , 2005 , 15, 154-9	6.3	170
20	DDM1 binds Arabidopsis methyl-CpG binding domain proteins and affects their subnuclear localization. <i>Plant Cell</i> , 2005 , 17, 1549-58	11.6	75
19	One-way control of FWA imprinting in Arabidopsis endosperm by DNA methylation. <i>Science</i> , 2004 , 303, 521-3	33.3	458
18	RNA silencing genes control de novo DNA methylation. <i>Science</i> , 2004 , 303, 1336	33.3	424
17	Genetic and functional diversification of small RNA pathways in plants. <i>PLoS Biology</i> , 2004 , 2, E104	9.7	1160
16	Role of the DRM and CMT3 methyltransferases in RNA-directed DNA methylation. <i>Current Biology</i> , 2003 , 13, 2212-7	6.3	411
15	ARGONAUTE4 control of locus-specific siRNA accumulation and DNA and histone methylation. <i>Science</i> , 2003 , 299, 716-9	33.3	860
14	Role of the arabidopsis DRM methyltransferases in de novo DNA methylation and gene silencing. <i>Current Biology</i> , 2002 , 12, 1138-44	6.3	597
13	Control of CpNpG DNA methylation by the KRYPTONITE histone H3 methyltransferase. <i>Nature</i> , 2002 , 416, 556-60	50.4	1012

12	DNA methylation controls histone H3 lysine 9 methylation and heterochromatin assembly in Arabidopsis. <i>EMBO Journal</i> , 2002 , 21, 6549-59	13	370
11	Locus-specific control of asymmetric and CpNpG methylation by the DRM and CMT3 methyltransferase genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99 Suppl 4, 16491-8	11.5	454
10	DEMETER, a DNA glycosylase domain protein, is required for endosperm gene imprinting and seed viability in Arabidopsis. <i>Cell</i> , 2002 , 110, 33-42	56.2	590
9	Site specificity of the Arabidopsis MET1 DNA methyltransferase demonstrated through hypermethylation of the superman locus. <i>Plant Molecular Biology</i> , 2001 , 46, 171-83	4.6	63
8	Requirement of CHROMOMETHYLASE3 for maintenance of CpXpG methylation. <i>Science</i> , 2001 , 292, 2077-80	33.3	678
7	Ectopic hypermethylation of flower-specific genes in Arabidopsis. <i>Current Biology</i> , 2000 , 10, 179-86	6.3	209
6	Regulation of SUP expression identifies multiple regulators involved in Arabidopsis floral meristem development. <i>Plant Cell</i> , 2000 , 12, 1607-18	11.6	79
5	The late flowering phenotype of <i>fwa</i> mutants is caused by gain-of-function epigenetic alleles of a homeodomain gene. <i>Molecular Cell</i> , 2000 , 6, 791-802	17.6	460
4	Hypermethylated SUPERMAN epigenetic alleles in Arabidopsis. <i>Science</i> , 1997 , 277, 1100-3	33.3	365
3	Isolation and characterization of abscisic acid-deficient Arabidopsis mutants at two new loci. <i>Plant Journal</i> , 1996 , 10, 655-61	6.9	393
2	SNPC-1.3 is a sex-specific transcription factor that drives male piRNA expression in <i>C. elegans</i>		1
1	The histone variant H2A.W and linker histone H1 co-regulate heterochromatin accessibility and DNA methylation		2