Steven E Jacobsen

List of Publications by Year
in descending order

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139	33,877	9234 74	14702 127
papers	citations	h-index	g-index

147	147	147	21258
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Establishing, maintaining and modifying DNA methylation patterns in plants and animals. Nature Reviews Genetics, 2010, 11, 204-220.	7.7	3,201
2	Shotgun bisulphite sequencing of the Arabidopsis genome reveals DNA methylation patterning. Nature, 2008, 452, 215-219.	13.7	2,039
3	Genetic and Functional Diversification of Small RNA Pathways in Plants. PLoS Biology, 2004, 2, e104.	2.6	1,347
4	Conservation and divergence of methylation patterning in plants and animals. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 8689-8694.	3.3	1,160
5	Control of CpNpG DNA methylation by the KRYPTONITE histone H3 methyltransferase. Nature, 2002, 416, 556-560.	13.7	1,156
6	Epigenetic Reprogramming in Plant and Animal Development. Science, 2010, 330, 622-627.	6.0	1,042
7	ARGONAUTE4 Control of Locus-Specific siRNA Accumulation and DNA and Histone Methylation. Science, 2003, 299, 716-719.	6.0	966
8	Requirement of CHROMOMETHYLASE3 for Maintenance of CpXpG Methylation. Science, 2001, 292, 2077-2080.	6.0	820
9	DNA methylation pathways and their crosstalk with histone methylation. Nature Reviews Molecular Cell Biology, 2015, 16, 519-532.	16.1	779
10	Comprehensive Analysis of Silencing Mutants Reveals Complex Regulation of the Arabidopsis Methylome. Cell, 2013, 152, 352-364.	13.5	748
11	Epigenetic inheritance in plants. Nature, 2007, 447, 418-424.	13.7	737
12	DEMETER, a DNA Glycosylase Domain Protein, Is Required for Endosperm Gene Imprinting and Seed Viability in Arabidopsis. Cell, 2002, 110, 33-42.	13.5	729
13	Non-CG methylation patterns shape the epigenetic landscape in Arabidopsis. Nature Structural and Molecular Biology, 2014, 21, 64-72.	3.6	690
14	Role of the Arabidopsis DRM Methyltransferases in De Novo DNA Methylation and Gene Silencing. Current Biology, 2002, 12, 1138-1144.	1.8	679
15	Whole-Genome Analysis of Histone H3 Lysine 27 Trimethylation in Arabidopsis. PLoS Biology, 2007, 5, e129.	2.6	667
16	Dissecting Arabidopsis thaliana DICER function in small RNA processing, gene silencing and DNA methylation patterning. Nature Genetics, 2006, 38, 721-725.	9.4	561
17	The Late Flowering Phenotype of fwa Mutants Is Caused by Gain-of-Function Epigenetic Alleles of a Homeodomain Gene. Molecular Cell, 2000, 6, 791-802.	4.5	545
18	One-Way Control of FWA Imprinting in Arabidopsis Endosperm by DNA Methylation. Science, 2004, 303, 521-523.	6.0	517

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19	Locus-specific control of asymmetric and CpNpG methylation by the DRM and CMT3 methyltransferase genes. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16491-16498.	3.3	511
20	Genome-wide analysis of mono-, di- and trimethylation of histone H3 lysine 4 in Arabidopsis thaliana. Genome Biology, 2009, 10, R62.	13.9	504
21	RNA Silencing Genes Control de Novo DNA Methylation. Science, 2004, 303, 1336-1336.	6.0	484
22	Role of the DRM and CMT3 Methyltransferases in RNA-Directed DNA Methylation. Current Biology, 2003, 13, 2212-2217.	1.8	462
23	Isolation and characterization of abscisic acid-deficient Arabidopsis mutants at two new loci. Plant Journal, 1996, 10, 655-661.	2.8	456
24	Dual Binding of Chromomethylase Domains to H3K9me2-Containing Nucleosomes Directs DNA Methylation in Plants. Cell, 2012, 151, 167-180.	13.5	446
25	DNA methylation controls histone H3 lysine 9 methylation and heterochromatin assembly in Arabidopsis. EMBO Journal, 2002, 21, 6549-6559.	3.5	439
26	HypermethylatedSUPERMANEpigenetic Alleles inArabidopsis. Science, 1997, 277, 1100-1103.	6.0	422
27	The SRA Methyl-Cytosine-Binding Domain Links DNA and Histone Methylation. Current Biology, 2007, 17, 379-384.	1.8	357
28	CRISPR-Casî¦ from huge phages is a hypercompact genome editor. Science, 2020, 369, 333-337.	6.0	352
29	An ARGONAUTE4-Containing Nuclear Processing Center Colocalized with Cajal Bodies in Arabidopsis thaliana. Cell, 2006, 126, 93-106.	13.5	350
30	The Arabidopsis LHP1 protein colocalizes with histone H3 Lys27 trimethylation. Nature Structural and Molecular Biology, 2007, 14, 869-871.	3.6	328
31	Polymerase IV occupancy at RNA-directed DNA methylation sites requires SHH1. Nature, 2013, 498, 385-389.	13.7	310
32	Genome-Wide Association of Histone H3 Lysine Nine Methylation with CHG DNA Methylation in Arabidopsis thaliana. PLoS ONE, 2008, 3, e3156.	1.1	293
33	Genome-wide Hi-C Analyses in Wild-Type and Mutants Reveal High-Resolution Chromatin Interactions in Arabidopsis. Molecular Cell, 2014, 55, 694-707.	4.5	283
34	The Functional Topography of the Arabidopsis Genome Is Organized in a Reduced Number of Linear Motifs of Chromatin States Â. Plant Cell, 2014, 26, 2351-2366.	3.1	281
35	Reiterated WG/GW motifs form functionally and evolutionarily conserved ARGONAUTE-binding platforms in RNAi-related components. Genes and Development, 2007, 21, 2539-2544.	2.7	280
36	MORC Family ATPases Required for Heterochromatin Condensation and Gene Silencing. Science, 2012, 336, 1448-1451.	6.0	279

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37	ATXR5 and ATXR6 are H3K27 monomethyltransferases required for chromatin structure and gene silencing. Nature Structural and Molecular Biology, 2009, 16, 763-768.	3.6	278
38	SRA- and SET-domain-containing proteins link RNA polymerase V occupancy to DNA methylation. Nature, 2014, 507, 124-128.	13.7	271
39	A One Precursor One siRNA Model for Pol IV-Dependent siRNA Biogenesis. Cell, 2015, 163, 445-455.	13.5	260
40	On the origin and evolutionary consequences of gene body DNA methylation. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 9111-9116.	3.3	260
41	The Histone Variant H2A.W Defines Heterochromatin and Promotes Chromatin Condensation in Arabidopsis. Cell, 2014, 158, 98-109.	13.5	257
42	Role of RNA polymerase IV in plant small RNA metabolism. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 4536-4541.	3.3	256
43	Molecular Mechanism of Action of Plant DRM De Novo DNA Methyltransferases. Cell, 2014, 157, 1050-1060.	13.5	245
44	Naive Human Pluripotent Cells Feature a Methylation Landscape Devoid of Blastocyst or Germline Memory. Cell Stem Cell, 2016, 18, 323-329.	5.2	242
45	Ectopic hypermethylation of flower-specific genes in Arabidopsis. Current Biology, 2000, 10, 179-186.	1.8	240
46	Rare allele of a previously unidentified histone H4 acetyltransferase enhances grain weight, yield, and plant biomass in rice. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 76-81.	3.3	236
47	Site-specific manipulation of Arabidopsis loci using CRISPR-Cas9 SunTag systems. Nature Communications, 2019, 10, 729.	5.8	215
48	DNA Methylation Profiling Identifies CG Methylation Clusters in Arabidopsis Genes. Current Biology, 2005, 15, 154-159.	1.8	212
49	RNAi, DRD1, and Histone Methylation Actively Target Developmentally Important Non-CG DNA Methylation in Arabidopsis. PLoS Genetics, 2006, 2, e83.	1.5	204
50	Tandem repeats upstream of the Arabidopsis endogene SDC recruit non-CG DNA methylation and initiate siRNA spreading. Genes and Development, 2008, 22, 1597-1606.	2.7	196
51	A Protein Complex Required for Polymerase V Transcripts and RNA- Directed DNA Methylation in Arabidopsis. Current Biology, 2010, 20, 951-956.	1.8	195
52	DOMAINS REARRANGED METHYLTRANSFERASE3 controls DNA methylation and regulates RNA polymerase V transcript abundance in Arabidopsis. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 911-916.	3.3	192
53	Targeted DNA demethylation of the Arabidopsis genome using the human TET1 catalytic domain. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E2125-E2134.	3.3	190
54	Mechanism of DNA Methylation-Directed Histone Methylation by KRYPTONITE. Molecular Cell, 2014, 55, 495-504.	4.5	186

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55	DDR complex facilitates global association of RNA polymerase V to promoters and evolutionarily young transposons. Nature Structural and Molecular Biology, 2012, 19, 870-875.	3.6	182
56	Resistance-gene-directed discovery of a natural-product herbicide with a new mode of action. Nature, 2018, 559, 415-418.	13.7	182
57	A DNA methylation reader complex that enhances gene transcription. Science, 2018, 362, 1182-1186.	6.0	181
58	Regulation of heterochromatic DNA replication by histone H3 lysine 27 methyltransferases. Nature, 2010, 466, 987-991.	13.7	171
59	Two-Step Recruitment of RNA-Directed DNA Methylation to Tandem Repeats. PLoS Biology, 2006, 4, e363.	2.6	159
60	In vivo targeting of de novo DNA methylation by histone modifications in yeast and mouse. ELife, 2015, 4, e06205.	2.8	146
61	SRA-Domain Proteins Required for DRM2-Mediated De Novo DNA Methylation. PLoS Genetics, 2008, 4, e1000280.	1.5	141
62	Dissecting the dynamic changes of 5-hydroxymethylcytosine in T-cell development and differentiation. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E3306-15.	3.3	139
63	TFAP2C regulates transcription in human naive pluripotency by opening enhancers. Nature Cell Biology, 2018, 20, 553-564.	4.6	134
64	CG gene body DNA methylation changes and evolution of duplicated genes in cassava. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 13729-13734.	3.3	129
65	Co-targeting RNA Polymerases IV and V Promotes Efficient De Novo DNA Methylation in Arabidopsis. Cell, 2019, 176, 1068-1082.e19.	13.5	124
66	The histone H3 variant H3.3 regulates gene body DNA methylation in Arabidopsis thaliana. Genome Biology, 2017, 18, 94.	3.8	116
67	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. Genes and Development, 2011, 25, 137-152.	2.7	108
68	MORC1 represses transposable elements in the mouse male germline. Nature Communications, 2014, 5, 5795.	5.8	108
69	RNA-directed DNA methylation involves co-transcriptional small-RNA-guided slicing of polymerase V transcripts in Arabidopsis. Nature Plants, 2018, 4, 181-188.	4.7	106
70	Regulation of SUP Expression Identifies Multiple Regulators Involved in Arabidopsis Floral Meristem Development. Plant Cell, 2000, 12, 1607-1618.	3.1	99
71	IDN1 and IDN2 are required for de novo DNA methylation in Arabidopsis thaliana. Nature Structural and Molecular Biology, 2009, 16, 1325-1327.	3.6	98
72	Mechanistic insights into plant SUVH family H3K9 methyltransferases and their binding to context-biased non-CG DNA methylation. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E8793-E8802.	3.3	89

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73	DDM1 Binds Arabidopsis Methyl-CpG Binding Domain Proteins and Affects Their Subnuclear Localization. Plant Cell, 2005, 17, 1549-1558.	3.1	86
74	INVOLVED IN DE NOVO 2-containing complex involved in RNA-directed DNA methylation in Arabidopsis. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 8374-8381.	3.3	85
75	DNA methylome of the 20-gigabase Norway spruce genome. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E8106-E8113.	3.3	85
76	Germline competency of human embryonic stem cells depends on eomesodermin†. Biology of Reproduction, 2017, 97, 850-861.	1.2	84
77	Evidence for ARGONAUTE4â€“DNA interactions in RNA-directed DNA methylation in plants. Genes and Development, 2016, 30, 2565-2570.	2.7	75
78	Interplay between Active Chromatin Marks and RNA-Directed DNA Methylation in Arabidopsis thaliana. PLoS Genetics, 2013, 9, e1003946.	1.5	70
79	DNA methylation-linked chromatin accessibility affects genomic architecture in Arabidopsis. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	70
80	MORC-1 Integrates Nuclear RNAi and Transgenerational Chromatin Architecture to Promote Germline Immortality. Developmental Cell, 2017, 41, 408-423.e7.	3.1	69
81	Site specificity of the Arabidopsis METI DNA methyltransferase demonstrated through hypermethylation of the superman locus. Plant Molecular Biology, 2001, 46, 171-183.	2.0	67
82	Identification of genes required for de novo DNA methylation in Arabidopsis. Epigenetics, 2011, 6, 344-354.	1.3	64
83	Transcriptional gene silencing by Arabidopsis microrchidia homologues involves the formation of heteromers. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 7474-7479.	3.3	61
84	MTHFD1 controls DNA methylation in Arabidopsis. Nature Communications, 2016, 7, 11640.	5.8	61
85	The TFAP2C-Regulated OCT4 Naive Enhancer Is Involved in Human Germline Formation. Cell Reports, 2018, 25, 3591-3602.e5.	2.9	60
86	Arabidopsis SWR1-associated protein methyl-CpG-binding domain 9 is required for histone H2A.Z deposition. Nature Communications, 2019, 10, 3352.	5.8	60
87	Efficient and accurate determination of genome-wide DNA methylation patterns in Arabidopsis thaliana with enzymatic methyl sequencing. Epigenetics and Chromatin, 2020, 13, 42.	1.8	60
88	Mechanism of siRNA production by a plant Dicer-RNA complex in dicing-competent conformation. Science, 2021, 374, 1152-1157.	6.0	58
89	The histone variant H2A.W and linker histone H1 co-regulate heterochromatin accessibility and DNA methylation. Nature Communications, 2021, 12, 2683.	5.8	56
90	Epigenetic differences between shoots and roots inArabidopsisreveals tissue-specific regulation. Epigenetics, 2014, 9, 236-242.	1.3	54

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91	Multi-level Modulation of Light Signaling by GIGANTEA Regulates Both the Output and Pace of the Circadian Clock. Developmental Cell, 2019, 49, 840-851.e8.	3.1	53
92	Large-scale comparative epigenomics reveals hierarchical regulation of non-CG methylation in Arabidopsis. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E1069-E1074.	3.3	51
93	C-terminal domains of histone demethylase JMJ14 interact with a pair of NAC transcription factors to mediate specific chromatin association. Cell Discovery, 2015, 1, .	3.1	47
94	Arabidopsis AtMORC4 and AtMORC7 Form Nuclear Bodies and Repress a Large Number of Protein-Coding Genes. PLoS Genetics, 2016, 12, e1005998.	1.5	42
95	Mouse MORC3 is a GHKL ATPase that localizes to H3K4me3 marked chromatin. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E5108-16.	3.3	41
96	Genome mining and biosynthesis of a polyketide from a biofertilizer fungus that can facilitate reductive iron assimilation in plant. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 5499-5504.	3.3	39
97	MBD5 and MBD6 couple DNA methylation to gene silencing through the J-domain protein SILENZIO. Science, 2021, 372, 1434-1439.	6.0	38
98	CRISPR-based targeting of DNA methylation in Arabidopsis thaliana by a bacterial CG-specific DNA methyltransferase. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	35
99	The impact and prospect of natural product discovery in agriculture. EMBO Reports, 2018, 19, .	2.0	34
100	Large-scale heterochromatin remodeling linked to overreplication-associated DNA damage. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 406-411.	3.3	33
101	A Nucleosome Bridging Mechanism for Activation of a Maintenance DNA Methyltransferase. Molecular Cell, 2019, 73, 73-83.e6.	4.5	33
102	CryoEM structures of Arabidopsis DDR complexes involved in RNA-directed DNA methylation. Nature Communications, 2019, 10, 3916.	5.8	31
103	A viral guide RNA delivery system for CRISPR-based transcriptional activation and heritable targeted DNA demethylation in Arabidopsis thaliana. PLoS Genetics, 2020, 16, e1008983.	1.5	31
104	Identification of Multiple Proteins Coupling Transcriptional Gene Silencing to Genome Stability in Arabidopsis thaliana. PLoS Genetics, 2016, 12, e1006092.	1.5	30
105	Increasing Nucleosome Occupancy Is Correlated with an Increasing Mutation Rate so Long as DNA Repair Machinery Is Intact. PLoS ONE, 2015, 10, e0136574.	1.1	29
106	Arabidopsis MORC proteins function in the efficient establishment of RNA directed DNA methylation. Nature Communications, 2021, 12, 4292.	5.8	28
107	SNF2 chromatin remodeler-family proteins FRG1 and -2 are required for RNA-directed DNA methylation. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17666-17671.	3.3	27
108	Wholeâ€genome characterization of chronological ageâ€associated changes in methylome and circular RNAs in moso bamboo (Phyllostachys edulis) from vegetative to floral growth. Plant Journal, 2021, 106, 435-453.	2.8	27

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109	NAP1-RELATED PROTEIN1 and 2 negatively regulate H2A.Z abundance in chromatin in Arabidopsis. Nature Communications, 2020, 11, 2887.	5.8	25
110	Nucleosome Organization in Human Embryonic Stem Cells. PLoS ONE, 2015, 10, e0136314.	1.1	22
111	The characterization of Mediator 12 and 13 as conditional positive gene regulators in Arabidopsis. Nature Communications, 2020, 11, 2798.	5.8	22
112	CRISPRâ€“Cas-mediated transcriptional control and epi-mutagenesis. Plant Physiology, 2022, 188, 1811-1824.	2.3	21
113	Ectopic targeting of CG DNA methylation in Arabidopsis with the bacterial SssI methyltransferase. Nature Communications, 2021, 12, 3130.	5.8	20
114	Structural Basis for the Unique Multivalent Readout of Unmodified H3 Tail by Arabidopsis ORC1b BAH-PHD Cassette. Structure, 2016, 24, 486-494.	1.6	19
115	Comprehensive identification of SWI/SNF complex subunits underpins deep eukaryotic ancestry and reveals new plant components. Communications Biology, 2022, 5, .	2.0	17
116	DNA polymerase epsilon is required for heterochromatin maintenance in Arabidopsis. Genome Biology, 2020, 21, 283.	3.8	14
117	The plant mobile domain proteins MAIN and MAIL1 interact with the phosphatase PP7L to regulate gene expression and silence transposable elements in Arabidopsis thaliana. PLoS Genetics, 2020, 16, e1008324.	1.5	13
118	The role of ATXR6 expression in modulating genome stability and transposable element repression in Arabidopsis. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	11
119	The role of MORC3 in silencing transposable elements in mouse embryonic stem cells. Epigenetics and Chromatin, 2021, 14, 49.	1.8	9
120	Mutations in DNA polymerase Î´ subunit 1 co-segregate with CMD2-type resistance to Cassava Mosaic Geminiviruses. Nature Communications, 2022, 13, .	5.8	8
121	SNPC-1.3 is a sex-specific transcription factor that drives male piRNA expression in C. elegans. ELife, 2021, 10, .	2.8	7
122	MORC3, a novel MIWI2 association partner, as an epigenetic regulator of piRNA dependent transposon silencing in male germ cells. Scientific Reports, 2021, 11, 20472.	1.6	6
123	ADCP1: a novel plant H3K9me2 reader. Cell Research, 2019, 29, 6-7.	5.7	4
124	A kinesin Klp10A mediates cell cycle-dependent shuttling of Piwi between nucleus and nuage. PLoS Genetics, 2020, 16, e1008648.	1.5	4
125	Plant genome engineering from lab to fieldâ€”a Keystone Symposia report. Annals of the New York Academy of Sciences, 2021, 1506, 35-54.	1.8	4
126	Promoter and Terminator Optimization for DNA Methylation Targeting in Arabidopsis. Epigenomes, 2020, 4, 9.	0.8	3

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127	A SYBR Gold-based Label-free in vitro Dicing Assay. Bio-protocol, 2022, 12, e4382.	0.2	1
128	Title is missing!. , 2020, 16, e1008324.		0
129	Title is missing!. , 2020, 16, e1008324.		0
130	Title is missing!. , 2020, 16, e1008324.		0
131	Title is missing!. , 2020, 16, e1008324.		0
132	Title is missing!. , 2020, 16, e1008324.		0
133	Title is missing!. , 2020, 16, e1008324.		0
134	Title is missing!. , 2020, 16, e1008324.		0
135	Title is missing!. , 2020, 16, e1008324.		0
136	A kinesin Klp10A mediates cell cycle-dependent shuttling of Piwi between nucleus and nuage. , 2020, 16, e1008648.		0
137	A kinesin Klp10A mediates cell cycle-dependent shuttling of Piwi between nucleus and nuage. , 2020, 16, e1008648.		0
138	A kinesin Klp10A mediates cell cycle-dependent shuttling of Piwi between nucleus and nuage. , 2020, 16, e1008648.		0
139	A kinesin Klp10A mediates cell cycle-dependent shuttling of Piwi between nucleus and nuage. , 2020, 16, e1008648.		0