David John Tremethick

List of Publications by Year
in descending order

61	5,943	94433 37	118850 62
papers	citations	h-index	g-index

67	67	67	5228
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	New insights into nucleosome and chromatin structure: an ordered state or a disordered affair?. Nature Reviews Molecular Cell Biology, 2012, 13, 436-447.	37.0	573
2	Crystal structure of a nucleosome core particle containing the variant histone H2A.Z. Nature Structural Biology, 2000, 7, 1121-1124.	9.7	459
3	Histone variant H2A.Z is required for early mammalian development. Current Biology, 2001, 11, 1183-1187.	3.9	338
4	Higher-Order Structures of Chromatin: The Elusive 30 nm Fiber. Cell, 2007, 128, 651-654.	28.9	285
5	H2A.Z Alters the Nucleosome Surface to Promote HP1Î±-Mediated Chromatin Fiber Folding. Molecular Cell, 2004, 16, 655-661.	9.7	270
6	A unified phylogeny-based nomenclature for histone variants. Epigenetics and Chromatin, 2012, 5, 7.	3.9	265
7	RNA interference demonstrates a novel role for H2A.Z in chromosome segregation. Nature Structural and Molecular Biology, 2004, 11, 650-655.	8.2	205
8	Pericentric heterochromatin becomes enriched with H2A.Z during early mammalian development. EMBO Journal, 2003, 22, 1599-1607.	7.8	202
9	A New Fluorescence Resonance Energy Transfer Approach Demonstrates That the Histone Variant H2AZ Stabilizes the Histone Octamer within the Nucleosome. Journal of Biological Chemistry, 2004, 279, 24274-24282.	3.4	193
10	Regions of variant histone His2AvD required for Drosophila development. Nature, 1999, 399, 694-697.	27.8	187
11	Nucleosomes containing the histone variant H2A.Bbd organize only 118 base pairs of DNA. EMBO Journal, 2004, 23, 3314-3324.	7.8	181
12	The nucleosome surface regulates chromatin compaction and couples it with transcriptional repression. Nature Structural and Molecular Biology, 2007, 14, 1070-1076.	8.2	174
13	Acetylation of H2A.Z is a key epigenetic modification associated with gene deregulation and epigenetic remodeling in cancer. Genome Research, 2012, 22, 307-321.	5.5	155
14	H2A.Z contributes to the unique 3D structure of the centromere. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 525-530.	7.1	153
15	The replacement histone H2A.Z in a hyperacetylated form is a feature of active genes in the chicken. Nucleic Acids Research, 2005, 33, 5633-5639.	14.5	150
16	The essential histone variant H2A.Z regulates the equilibrium between different chromatin conformational states. Nature Structural Biology, 2002, 9, 172-6.	9.7	137
17	Long-range interactions between topologically associating domains shape the four-dimensional genome during differentiation. Nature Genetics, 2019, 51, 835-843.	21.4	114
18	The X and Y Chromosomes Assemble into H2A.Z, Containing Facultative Heterochromatin, following Meiosis. Molecular and Cellular Biology, 2006, 26, 5394-5405.	2.3	111

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19	POWERDRESS-mediated histone deacetylation is essential for thermomorphogenesis in Arabidopsis thaliana. PLoS Genetics, 2018, 14, e1007280.	3.5	99
20	Histone H2A.Z inheritance during the cell cycle and its impact on promoter organization and dynamics. Nature Structural and Molecular Biology, 2012, 19, 1076-1083.	8.2	97
21	Inhibition of Arginase I Activity by RNA Interference Attenuates IL-13-Induced Airways Hyperresponsiveness. Journal of Immunology, 2006, 177, 5595-5603.	0.8	94
22	A unique H2A histone variant occupies the transcriptional start site of active genes. Nature Structural and Molecular Biology, 2012, 19, 25-30.	8.2	91
23	Recruitment of SWI/SNF to the Human Immunodeficiency Virus Type 1 Promoter. Molecular and Cellular Biology, 2004, 24, 389-397.	2.3	79
24	The binding of a Fos/Jun heterodimer can completely disrupt the structure of a nucleosome. EMBO Journal, 1997, 16, 2072-2085.	7.8	78
25	Unique Residues on the H2A.Z Containing Nucleosome Surface Are Important for Xenopus laevis Development. Journal of Biological Chemistry, 2004, 279, 43815-43820.	3.4	77
26	Effects of high mobility group proteins 1 and 2 on initiation and elongation of specific transcription by RNA polymerase IIin vitro. Nucleic Acids Research, 1988, 16, 11107-11123.	14.5	71
27	Multiple ISWI ATPase Complexes from Xenopus laevis. Journal of Biological Chemistry, 2000, 275, 35248-35255.	3.4	67
28	Dynamic Histone Variant Exchange Accompanies Gene Induction in T Cells. Molecular and Cellular Biology, 2009, 29, 1972-1986.	2.3	67
29	Histone-mediated Transduction as an Efficient Means for Gene Delivery. Molecular Therapy, 2007, 15, 721-731.	8.2	62
30	Structural Characterization of Histone H2A Variants. Cold Spring Harbor Symposia on Quantitative Biology, 2004, 69, 227-234.	1.1	56
31	Histone variants at the transcription start-site. Trends in Genetics, 2014, 30, 199-209.	6.7	55
32	The Human IL-2 Gene Promoter Can Assemble a Positioned Nucleosome That Becomes Remodeled Upon T Cell Activation. Journal of Immunology, 2002, 169, 2466-2476.	0.8	52
33	Specific patterns of histone marks accompany X chromosome inactivation in a marsupial. Chromosome Research, 2009, 17, 115-26.	2.2	48
34	The Histone Variant H2A.Z Is a Master Regulator of the Epithelial-Mesenchymal Transition. Cell Reports, 2017, 21, 943-952.	6.4	45
35	A new link between transcriptional initiation and pre-mRNA splicing: The RNA binding histone variant H2A.B. PLoS Genetics, 2017, 13, e1006633.	3.5	42
36	Cathepsin L Stabilizes the Histone Modification Landscape on the Y Chromosome and Pericentromeric Heterochromatin. Molecular and Cellular Biology, 2006, 26, 4172-4184.	2.3	41

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37	Interplay between Chromatin Remodeling and Epigenetic Changes during Lineage-Specific Commitment to Granzyme B Expression. Journal of Immunology, 2009, 183, 7063-7072.	0.8	40
38	The interplay between H2A.Z and H3K9 methylation in regulating HP1Î± binding to linker histone-containing chromatin. Nucleic Acids Research, 2018, 46, 9353-9366.	14.5	40
39	SLY regulates genes involved in chromatin remodeling and interacts with TBL1XR1 during sperm differentiation. Cell Death and Differentiation, 2017, 24, 1029-1044.	11.2	39
40	Distinct importin recognition properties of histones and chromatin assembly factors. FEBS Letters, 2000, 467, 169-174.	2.8	34
41	High-Mobility-Group Protein I Can Modulate Binding of Transcription Factors to the U5 Region of the Human Immunodeficiency Virus Type 1 Proviral Promoter. Journal of Virology, 2000, 74, 10523-10534.	3.4	33
42	Efficient gene delivery using reconstituted chromatin enhanced for nuclear targeting. FASEB Journal, 2008, 22, 2232-2242.	0.5	31
43	Gene editing of the multi-copy H2A.B gene and its importance for fertility. Genome Biology, 2019, 20, 23.	8.8	29
44	High Mobility Group Proteins 14 and 17 Can Prevent the Close Packing of Nucleosomes by Increasing the Strength of Protein Contacts in the Linker DNA. Journal of Biological Chemistry, 1996, 271, 12009-12016.	3.4	24
45	Histone variant selectivity at the transcription start site: H2A.Z or H2A.Lap1. Nucleus, 2013, 4, 431-437.	2.2	24
46	Gene knockdown by ecdysone-based inducible RNAi in stable mammalian cell lines. Nature Protocols, 2008, 3, 79-88.	12.0	22
47	Multiple roles of H2A.Z in regulating promoter chromatin architecture in human cells. Nature Communications, 2021, 12, 2524.	12.8	22
48	Short Histone H2A Variants: Small in Stature but not in Function. Cells, 2020, 9, 867.	4.1	18
49	Stimulation of transcription from different RNA polymerase II promoters by high mobility group proteins 1 and 2. FEBS Letters, 1989, 242, 346-350.	2.8	11
50	H2A.B is a cancer/testis factor involved in the activation of ribosome biogenesis in Hodgkin lymphoma. EMBO Reports, 2021, 22, e52462.	4.5	8
51	A dual affinity-tag strategy for the expression and purification of human linker histone H1.4 in Escherichia coli. Protein Expression and Purification, 2016, 120, 160-168.	1.3	7
52	Site-specific modification and segmental isotope labelling of HMGN1 reveals long-range conformational perturbations caused by posttranslational modifications. RSC Chemical Biology, 2021, 2, 537-550.	4.1	7
53	The Role of the Histone Variant H2A.Z in Metazoan Development. Journal of Developmental Biology, 2022, 10, 28.	1.7	7
54	Quantitative analysis of HP1Î± binding to nucleosomal arrays. Methods, 2007, 41, 286-290.	3.8	5

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55	Analysis of Histone Variant H2A.Z Localization and Expression during Early Development. Methods in Enzymology, 2003, 375, 239-252.	1.0	4
56	Chromatin assembly in Xenopus extracts. Methods in Enzymology, 1999, 304, 50-63.	1.0	2
57	Evidence That the Coactivator CBP/p300 Is Important for Phenobarbital-Induced but Not Basal Expression of theCYP2H1Gene. Molecular Pharmacology, 2003, 63, 73-80.	2.3	2
58	Chromatin: the dynamic link between structure and function. Chromosome Research, 2006, 14, 1-4.	2.2	1
59	RChIP-Seq: Chromatin-Associated RNA Sequencing in Developmentally Staged Mouse Testes. Methods in Molecular Biology, 2018, 1832, 169-184.	0.9	1
60	Sequential Chromatin Immunoprecipitation to Identify Heterotypic Nucleosomes. Methods in Molecular Biology, 2021, 2351, 147-161.	0.9	1
61	Interplay between chromatin remodeling and epigenetic changes during lineage-specific commitment to granzyme B expression. Journal of Immunology, 2010, 184, 1653-1653.	0.8	0