Sebastian Bultman

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5115283/publications.pdf

Version: 2024-02-01

218381 301761 2,720 39 26 39 citations g-index h-index papers 45 45 45 4771 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Sensitive enzymatic quantification of 5-hydroxymethylcytosine in genomic DNA. Nucleic Acids Research, 2010, 38, e181-e181.	6.5	385
2	<scp>TREM2 deficiency impairs chemotaxis and microglial responses to neuronal injury. EMBO Reports, 2017, 18, 1186-1198.</scp>	2.0	240
3	Targeted transcriptional activation of silent oct4 pluripotency gene by combining designer TALEs and inhibition of epigenetic modifiers. Nucleic Acids Research, 2012, 40, 5368-5377.	6.5	178
4	Np95 interacts with <i>de novo</i> DNA methyltransferases, Dnmt3a and Dnmt3b, and mediates epigenetic silencing of the viral CMV promoter in embryonic stem cells. EMBO Reports, 2009, 10, 1259-1264.	2.0	167
5	Recognition of 5-Hydroxymethylcytosine by the Uhrf1 SRA Domain. PLoS ONE, 2011, 6, e21306.	1.1	159
6	Visualization of specific DNA sequences in living mouse embryonic stem cells with a programmable fluorescent CRISPR/Cas system. Nucleus, 2014, 5, 163-172.	0.6	146
7	The poly(ADP-ribose)-dependent chromatin remodeler Alc1 induces local chromatin relaxation upon DNA damage. Molecular Biology of the Cell, 2016, 27, 3791-3799.	0.9	104
8	The rRNA m ⁶ A methyltransferase METTL5 is involved in pluripotency and developmental programs. Genes and Development, 2020, 34, 715-729.	2.7	93
9	Opposite microglial activation stages upon loss of <scp>PGRN</scp> or <scp>TREM</scp> 2 result in reduced cerebral glucose metabolism. EMBO Molecular Medicine, 2019, 11, .	3.3	87
10	Different Binding Properties and Function of CXXC Zinc Finger Domains in Dnmt1 and Tet1. PLoS ONE, 2011, 6, e16627.	1.1	87
11	Two distinct modes of DNMT1 recruitment ensure stable maintenance DNA methylation. Nature Communications, 2020, 11, 1222.	5.8	82
12	Growth hormone receptor-deficient pigs resemble the pathophysiology of human Laron syndrome and reveal altered activation of signaling cascades in the liver. Molecular Metabolism, 2018, 11, 113-128.	3.0	79
13	Targeting and tracing of specific DNA sequences with dTALEs in living cells. Nucleic Acids Research, 2014, 42, e38-e38.	6.5	66
14	Critical Role of the UBL Domain in Stimulating the E3ÂUbiquitin Ligase Activity of UHRF1 toward Chromatin. Molecular Cell, 2018, 72, 739-752.e9.	4.5	63
15	Staying true to yourself: mechanisms of DNA methylation maintenance in mammals. Nucleic Acids Research, 2021, 49, 3020-3032.	6.5	62
16	Genomic 5-hydroxymethylcytosine levels correlate with TET2 mutations and a distinct global gene expression pattern in secondary acute myeloid leukemia. Leukemia, 2011, 25, 1649-1652.	3.3	57
17	Loss of KDM6A confers drug resistance in acute myeloid leukemia. Leukemia, 2020, 34, 50-62.	3.3	56
18	Spatial organization of transcribed eukaryotic genes. Nature Cell Biology, 2022, 24, 327-339.	4.6	55

#	Article	IF	CITATIONS
19	Characterization of PvuRts1I endonuclease as a tool to investigate genomic 5–hydroxymethylcytosine. Nucleic Acids Research, 2011, 39, 5149-5156.	6.5	51
20	METTL6 is a tRNA m ³ C methyltransferase that regulates pluripotency and tumor cell growth. Science Advances, 2020, 6, eaaz4551.	4.7	51
21	Cathepsin S Alterations Induce a Tumor-Promoting Immune Microenvironment in Follicular Lymphoma. Cell Reports, 2020, 31, 107522.	2.9	50
22	Live cell PNA labelling enables erasable fluorescence imaging of membrane proteins. Nature Chemistry, 2021, 13, 15-23.	6.6	48
23	Ubiquitome Analysis Reveals PCNA-Associated Factor 15 (PAF15) as a Specific Ubiquitination Target of UHRF1 in Embryonic Stem Cells. Journal of Molecular Biology, 2017, 429, 3814-3824.	2.0	43
24	A modular open platform for systematic functional studies under physiological conditions. Nucleic Acids Research, 2015, 43, e112-e112.	6.5	39
25	Recent evolution of a TET-controlled and DPPA3/STELLA-driven pathway of passive DNA demethylation in mammals. Nature Communications, 2020, 11, 5972.	5.8	38
26	Global DNA Hypomethylation Prevents Consolidation of Differentiation Programs and Allows Reversion to the Embryonic Stem Cell State. PLoS ONE, 2012, 7, e52629.	1.1	34
27	Identification of permissive amber suppression sites for efficient non-canonical amino acid incorporation in mammalian cells. Nucleic Acids Research, 2021, 49, e62-e62.	6.5	30
28	Quick and reliable method for retina dissociation and separation of rod photoreceptor perikarya from adult mice. MethodsX, 2015, 2, 39-46.	0.7	29
29	Loss-of-function mutations in the histone methyltransferase EZH2 promote chemotherapy resistance in AML. Scientific Reports, 2021, 11, 5838.	1.6	22
30	Applications of the CRISPR/Cas system beyond gene editing. Biology Methods and Protocols, 2018, 3, bpy002.	1.0	21
31	Site-specific recruitment of epigenetic factors with a modular CRISPR/Cas system. Nucleus, 2017, 8, 279-286.	0.6	20
32	Azacitidine combined with the selective FLT3 kinase inhibitor crenolanib disrupts stromal protection and inhibits expansion of residual leukemia-initiating cells in <i>FLT3</i> -ITD AML with concurrent epigenetic mutations. Oncotarget, 2017, 8, 108738-108759.	0.8	14
33	Distinct and stage-specific contributions of TET1 and TET2 to stepwise cytosine oxidation in the transition from naive to primed pluripotency. Scientific Reports, 2020, 10, 12066.	1.6	13
34	<scp>CRISPR</scp> â€essisted receptor deletion reveals distinct roles for <scp>ERBB</scp> 2 and <scp>ERBB</scp> 3 in skin keratinocytes. FEBS Journal, 2017, 284, 3339-3349.	2.2	10
35	Phosphorylation of the HP1 \hat{i}^2 hinge region sequesters KAP1 in heterochromatin and promotes the exit from na \hat{A} ve pluripotency. Nucleic Acids Research, 2021, 49, 7406-7423.	6.5	9
36	Entering the post-epigenomic age: back to epigenetics. Open Biology, 2018, 8, 180013.	1.5	5

#	Article	IF	CITATIONS
37	Orthogonal coiled coils enable rapid covalent labelling of two distinct membrane proteins with peptide nucleic acid barcodes. RSC Chemical Biology, 2021, 2, 1291-1295.	2.0	4
38	Fluorescence Microscopy-Based High-Throughput Screening for Factors Involved in Gene Silencing. Methods in Molecular Biology, 2013, 1042, 237-244.	0.4	1
39	ARID1A Controls a Novel Transcriptional Network Regulating FAS in Follicular Lymphoma. Blood, 2021, 138, 3492-3492.	0.6	0