Shaun Webb

List of Publications by Year in descending order

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SHALIN WER

#	Article	IF	CITATIONS
1	Genomic loci mispositioning in Tmem120a knockout mice yields latent lipodystrophy. Nature Communications, 2022, 13, 321.	12.8	24
2	Neuronal non-CG methylation is an essential target for MeCP2 function. Molecular Cell, 2021, 81, 1260-1275.e12.	9.7	24
3	Activity of Lymphostatin, A Lymphocyte Inhibitory Virulence Factor of Pathogenic Escherichia coli, is Dependent on a Cysteine Protease Motif. Journal of Molecular Biology, 2021, 433, 167200.	4.2	1
4	Absence of MeCP2 binding to non-methylated GT-rich sequences in vivo. Nucleic Acids Research, 2020, 48, 3542-3552.	14.5	10
5	Quantitative modelling predicts the impact of DNA methylation on RNA polymerase II traffic. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 14995-15000.	7.1	42
6	An Orphan CpG Island Drives Expression of a let-7 miRNA Precursor with an Important Role in Mouse Development. Epigenomes, 2019, 3, 7.	1.8	2
7	RNA-binding activity of TRIM25 is mediated by its PRY/SPRY domain and is required for ubiquitination. BMC Biology, 2017, 15, 105.	3.8	125
8	MeCP2 recognizes cytosine methylated tri-nucleotide and di-nucleotide sequences to tune transcription in the mammalian brain. PLoS Genetics, 2017, 13, e1006793.	3.5	117
9	Loss of Tet1-Associated 5-Hydroxymethylcytosine Is Concomitant with Aberrant Promoter Hypermethylation in Liver Cancer. Cancer Research, 2016, 76, 3097-3108.	0.9	71
10	The molecular basis of variable phenotypic severity among common missense mutations causing Rett syndrome. Human Molecular Genetics, 2016, 25, 558-570.	2.9	76
11	Tissue-Specific Gene Repositioning by Muscle Nuclear Membrane Proteins Enhances Repression of Critical Developmental Genes during Myogenesis. Molecular Cell, 2016, 62, 834-847.	9.7	165
12	Global regulation of heterochromatin spreading by Leo1. Open Biology, 2015, 5, 150045.	3.6	43
13	Inter-individual variability contrasts with regional homogeneity in the human brain DNA methylome. Nucleic Acids Research, 2015, 43, 732-744.	14.5	42
14	Genome-Wide Distribution of RNA-DNA Hybrids Identifies RNase H Targets in tRNA Genes, Retrotransposons and Mitochondria. PLoS Genetics, 2014, 10, e1004716.	3.5	179
15	A Splicing-Dependent Transcriptional Checkpoint Associated with Prespliceosome Formation. Molecular Cell, 2014, 53, 779-790.	9.7	87
16	Synthetic CpG islands reveal DNA sequence determinants of chromatin structure. ELife, 2014, 3, e03397.	6.0	95
17	Orphan CpG Islands Identify Numerous Conserved Promoters in the Mammalian Genome. PLoS Genetics, 2010, 6, e1001134.	3.5	445
18	Neuronal MeCP2 Is Expressed at Near Histone-Octamer Levels and Globally Alters the Chromatin State. Molecular Cell, 2010, 37, 457-468.	9.7	609