

# Shaun Webb

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4768345/publications.pdf>

Version: 2024-02-01

18  
papers

2,161  
citations

567281

15  
h-index

888059

17  
g-index

22  
all docs

22  
docs citations

22  
times ranked

3797  
citing authors

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