## Michael P Meers

List of Publications by Year in descending order

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933447 1281871 11 801 10 11 citations h-index g-index papers 16 16 16 1271 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Peak calling by Sparse Enrichment Analysis for CUT&RUN chromatin profiling. Epigenetics and Chromatin, 2019, 12, 42.	3.9	267
2	Interrogating the Function of Metazoan Histones using Engineered Gene Clusters. Developmental Cell, 2015, 32, 373-386.	7.0	139
3	Old cogs, new tricks: the evolution of gene expression in a chromatin context. Nature Reviews Genetics, 2019, 20, 283-297.	16.3	86
4	Automated in situ chromatin profiling efficiently resolves cell types and gene regulatory programs. Epigenetics and Chromatin, 2018, 11, 74.	3.9	53
5	Developmental arrest of Drosophila survival motor neuron (Smn) mutants accounts for differences in expression of minor intron-containing genes. Rna, 2013, 19, 1510-1516.	3.5	51
6	Histone gene replacement reveals a post-transcriptional role for H3K36 in maintaining metazoan transcriptome fidelity. ELife, 2017, 6, .	6.0	42
7	Histone deposition pathways determine the chromatin landscapes of H3.1 and H3.3 K27M oncohistones. ELife, 2020, 9, .	6.0	42
8	Automated CUT& Tag profiling of chromatin heterogeneity in mixed-lineage leukemia. Nature Genetics, 2021, 53, 1586-1596.	21.4	42
9	Transcription start site profiling uncovers divergent transcription and enhancer-associated RNAs in Drosophila melanogaster. BMC Genomics, 2018, 19, 157.	2.8	34
10	CUT& Tag2for1: a modified method for simultaneous profiling of the accessible and silenced regulome in singleÂcells. Genome Biology, 2022, 23, 81.	8.8	30
11	An Animal Model for Genetic Analysis of Multi-Gene Families: Cloning and Transgenesis of Large Tandemly Repeated Histone Gene Clusters. Methods in Molecular Biology, 2018, 1832, 309-325.	0.9	8