

Eric M Mendenhall

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

21
papers

5,724
citations

16
h-index

25
g-index

25
ext. papers

6,812
ext. citations

18.3
avg, IF

4.54
L-index

#	Paper	IF	Citations
21	A small molecule that induces translational readthrough of CFTR nonsense mutations by eRF1 depletion. <i>Nature Communications</i> , 2021 , 12, 4358	17.4	12
20	Occupancy maps of 208 chromatin-associated proteins in one human cell type. <i>Nature</i> , 2020 , 583, 720-728	50.4	28
19	Perspectives on ENCODE. <i>Nature</i> , 2020 , 583, 693-698	50.4	61
18	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020 , 583, 699-710	50.4	360
17	Identification and function of enhancers in the human genome. <i>Human Molecular Genetics</i> , 2016 , 25, R190-R197	5.6	18
16	Every transcription factor deserves its map: Scaling up epitope tagging of proteins to bypass antibody problems. <i>BioEssays</i> , 2016 , 38, 801-11	4.1	11
15	CETCh-seq: CRISPR epitope tagging ChIP-seq of DNA-binding proteins. <i>Genome Research</i> , 2015 , 25, 1581-97	9.7	84
14	Htt CAG repeat expansion confers pleiotropic gains of mutant huntingtin function in chromatin regulation. <i>Human Molecular Genetics</i> , 2015 , 24, 2442-57	5.6	38
13	Tissue-specific SMARCA4 binding at active and repressed regulatory elements during embryogenesis. <i>Genome Research</i> , 2014 , 24, 920-9	9.7	47
12	Locus-specific editing of histone modifications at endogenous enhancers. <i>Nature Biotechnology</i> , 2013 , 31, 1133-6	44.5	295
11	DNA-protein interactions in high definition. <i>Genome Biology</i> , 2012 , 13, 139	18.3	1
10	GC-rich sequence elements recruit PRC2 in mammalian ES cells. <i>PLoS Genetics</i> , 2010 , 6, e1001244	6	314
9	Chromatin state maps: new technologies, new insights. <i>Current Opinion in Genetics and Development</i> , 2008 , 18, 109-15	4.9	63
8	Genomewide analysis of PRC1 and PRC2 occupancy identifies two classes of bivalent domains. <i>PLoS Genetics</i> , 2008 , 4, e1000242	6	746
7	Genome-wide maps of chromatin state in pluripotent and lineage-committed cells. <i>Nature</i> , 2007 , 448, 553-60	50.4	3296
6	Genome-wide reverse genetics framework to identify novel functions of the vertebrate secretome. <i>PLoS ONE</i> , 2006 , 1, e104	3.7	63
5	The molecular repertoire of the balmighty stem cell. <i>Nature Reviews Molecular Cell Biology</i> , 2005 , 6, 726-37	38.7	160

4	Characterization of expanded intermediate cell mass in zebrafish chordin morphant embryos. <i>Developmental Biology</i> , 2005 , 277, 235-54	3.1	40
3	Functional analysis of human hematopoietic stem cell gene expression using zebrafish. <i>PLoS Biology</i> , 2005 , 3, e254	9.7	86
2	SPRY1 Is a Negative Regulator of Long-Term In Vivo Engraftment and Ex Vivo Expansion of Primitive Human Umbilical Cord Blood Cells.. <i>Blood</i> , 2005 , 106, 1715-1715	2.2	
1	Functional Analysis of the Differential Gene Expression Profile of Human HSC Using a Functional Genomics Screen in the Zebrafish.. <i>Blood</i> , 2004 , 104, 136-136	2.2	1