

# Matthew Slattery

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/12020212/publications.pdf>

Version: 2024-02-01

35  
papers

4,494  
citations

331670

21  
h-index

345221

36  
g-index

42  
all docs

42  
docs citations

42  
times ranked

9312  
citing authors

#	ARTICLE	IF	CITATIONS
1	Ribbon boosts ribosomal protein gene expression to coordinate organ form and function. <i>Journal of Cell Biology</i> , 2022, 221, .	5.2	3
2	New regulators of <i>Drosophila</i> eye development identified from temporal transcriptome changes. <i>Genetics</i> , 2021, 217, .	2.9	3
3	Transcriptional reprogramming by oxidative stress occurs within a predefined chromatin accessibility landscape. <i>Free Radical Biology and Medicine</i> , 2021, 171, 319-331.	2.9	6
4	Creb <sup>A</sup> increases secretory capacity through direct transcriptional regulation of the secretory machinery, a subset of secretory cargo, and other key regulators. <i>Traffic</i> , 2020, 21, 560-577.	2.7	20
5	The <i>Drosophila</i> MLR COMPASS complex is essential for programming cis-regulatory information and maintaining epigenetic memory during development. <i>Nucleic Acids Research</i> , 2020, 48, 3476-3495.	14.5	8
6	A hypermorphic antioxidant response element is associated with increased MS4A6A expression and Alzheimer's disease. <i>Redox Biology</i> , 2018, 14, 686-693.	9.0	21
7	A Role for Monomethylation of Histone H3-K27 in Gene Activity in <i>Drosophila</i> . <i>Genetics</i> , 2018, 208, 1023-1036.	2.9	11
8	Identification of a functional antioxidant response element at the HIF1A locus. <i>Redox Biology</i> , 2018, 19, 401-411.	9.0	77
9	A distinct class of antioxidant response elements is consistently activated in tumors with NRF2 mutations. <i>Redox Biology</i> , 2018, 19, 235-249.	9.0	37
10	cis-regulatory architecture of a short-range EGFR organizing center in the <i>Drosophila melanogaster</i> leg. <i>PLoS Genetics</i> , 2018, 14, e1007568.	3.5	15
11	A Polymorphic Antioxidant Response Element Links NRF2/sMAF Binding to Enhanced MAPT Expression and Reduced Risk of Parkinsonian Disorders. <i>Cell Reports</i> , 2016, 15, 830-842.	6.4	40
12	Gene regulatory effects of disease-associated variation in the NRF2 network. <i>Current Opinion in Toxicology</i> , 2016, 1, 71-79.	5.0	23
13	Ribbon regulates morphogenesis of the <i>Drosophila</i> embryonic salivary gland through transcriptional activation and repression. <i>Developmental Biology</i> , 2016, 409, 234-250.	2.0	7
14	DNA-binding sequence specificity of DUX4. <i>Skeletal Muscle</i> , 2015, 6, 8.	4.2	30
15	Establishment of a Developmental Compartment Requires Interactions between Three Synergistic Cis-regulatory Modules. <i>PLoS Genetics</i> , 2015, 11, e1005376.	3.5	29
16	Beyond antioxidant genes in the ancient Nrf2 regulatory network. <i>Free Radical Biology and Medicine</i> , 2015, 88, 452-465.	2.9	74
17	Deconvolving the Recognition of DNA Shape from Sequence. <i>Cell</i> , 2015, 161, 307-318.	28.9	174
18	Transcription Factor Networks in <i>Drosophila melanogaster</i> . <i>Cell Reports</i> , 2014, 8, 2031-2043.	6.4	83

#	ARTICLE	IF	CITATIONS
19	Evolution of H3K27me3-marked chromatin is linked to gene expression evolution and to patterns of gene duplication and diversification. <i>Genome Research</i> , 2014, 24, 1115-1124.	5.5	23
20	Diverse patterns of genomic targeting by transcriptional regulators in <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2014, 24, 1224-1235.	5.5	31
21	Comparative analysis of regulatory information and circuits across distant species. <i>Nature</i> , 2014, 512, 453-456.	27.8	184
22	Yorkie Promotes Transcription by Recruiting a Histone Methyltransferase Complex. <i>Cell Reports</i> , 2014, 8, 449-459.	6.4	66
23	Absence of a simple code: how transcription factors read the genome. <i>Trends in Biochemical Sciences</i> , 2014, 39, 381-399.	7.5	447
24	SELEX-seq: A Method for Characterizing the Complete Repertoire of Binding Site Preferences for Transcription Factor Complexes. <i>Methods in Molecular Biology</i> , 2014, 1196, 255-278.	0.9	68
25	Enhanced dissection of the regulatory genome. <i>Nature Methods</i> , 2013, 10, 710-712.	19.0	2
26	Genome-wide Association of Yorkie with Chromatin and Chromatin-Remodeling Complexes. <i>Cell Reports</i> , 2013, 3, 309-318.	6.4	126
27	Divergent Transcriptional Regulatory Logic at the Intersection of Tissue Growth and Developmental Patterning. <i>PLoS Genetics</i> , 2013, 9, e1003753.	3.5	41
28	A Survey of 6,300 Genomic Fragments for cis-Regulatory Activity in the Imaginal Discs of <i>Drosophila melanogaster</i> . <i>Cell Reports</i> , 2012, 2, 1014-1024.	6.4	115
29	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. <i>Genome Research</i> , 2012, 22, 1813-1831.	5.5	1,708
30	Control of mitochondrial structure and function by the Yorkie/YAP oncogenic pathway. <i>Genes and Development</i> , 2012, 26, 2027-2037.	5.9	84
31	Interpreting the regulatory genome: the genomics of transcription factor function in <i>Drosophila melanogaster</i> . <i>Briefings in Functional Genomics</i> , 2012, 11, 336-346.	2.7	4
32	Disentangling the Many Layers of Eukaryotic Transcriptional Regulation. <i>Annual Review of Genetics</i> , 2012, 46, 43-68.	7.6	222
33	Cofactor Binding Evokes Latent Differences in DNA Binding Specificity between Hox Proteins. <i>Cell</i> , 2011, 147, 1270-1282.	28.9	454
34	Genome-Wide Tissue-Specific Occupancy of the Hox Protein Ultrabithorax and Hox Cofactor Homothorax in <i>Drosophila</i> . <i>PLoS ONE</i> , 2011, 6, e14686.	2.5	78
35	Transcription factor choice in the Hippo signaling pathway: <i>homothorax</i> and <i>yorkie</i> regulation of the microRNA <i>bantam</i> in the progenitor domain of the <i>Drosophila</i> eye imaginal disc. <i>Genes and Development</i> , 2009, 23, 2307-2319.	5.9	179