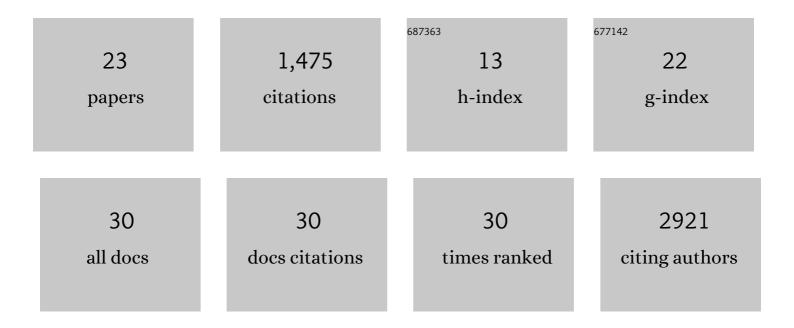
## Mary Ann Allen

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1192184/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Protocol variations in run-on transcription dataset preparation produce detectable signatures in sequencing libraries. BMC Genomics, 2022, 23, 187.	2.8	5
2	Nuclear mechanosensing drives chromatin remodelling in persistently activated fibroblasts. Nature Biomedical Engineering, 2021, 5, 1485-1499.	22.5	71
3	Characterization of Global Gene Expression, Regulation of Metal Ions, and Infection Outcomes in Immune-Competent 129S6 Mouse Macrophages. Infection and Immunity, 2021, 89, e0027321.	2.2	2
4	Lessons from eRNAs: understanding transcriptional regulation through the lens of nascent RNAs. Transcription, 2020, 11, 3-18.	3.1	13
5	Train students to navigate ethical swamps. Nature, 2019, 568, 145-145.	27.8	0
6	Nascent transcript analysis of glucocorticoid crosstalk with TNF defines primary and cooperative inflammatory repression. Genome Research, 2019, 29, 1753-1765.	5.5	36
7	Identification and characterization of a novel anti-inflammatory lipid isolated from Mycobacterium vaccae, a soil-derived bacterium with immunoregulatory and stress resilience properties. Psychopharmacology, 2019, 236, 1653-1670.	3.1	28
8	Heat shock in C. elegans induces downstream of gene transcription and accumulation of double-stranded RNA. PLoS ONE, 2019, 14, e0206715.	2.5	14
9	Two-stage ML Classifier for Identifying Host Protein Targets of the Dengue Protease. , 2019, , .		2
10	Enhancer RNA profiling predicts transcription factor activity. Genome Research, 2018, 28, 334-344.	5.5	88
11	Detecting Differential Transcription Factor Activity from ATAC-Seq Data. Molecules, 2018, 23, 1136.	3.8	33
12	An Annotation Agnostic Algorithm for Detecting Nascent RNA Transcripts in GRO-Seq. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1070-1081.	3.0	19
13	RNA Pol II transcription model and interpretation of GRO-seq data. Journal of Mathematical Biology, 2017, 74, 77-97.	1.9	9
14	Human TFIIH Kinase CDK7 Regulates Transcription-Associated Chromatin Modifications. Cell Reports, 2017, 20, 1173-1186.	6.4	123
15	FStitch. , 2014, , .		8
16	Global analysis of p53-regulated transcription identifies its direct targets and unexpected regulatory mechanisms. ELife, 2014, 3, e02200.	6.0	205
17	Retrospective Reflections of a Whistleblower: Opinions on Misconduct Responses. Accountability in Research, 2013, 20, 339-348.	2.4	8
18	HIF1A Employs CDK8-Mediator to Stimulate RNAPII Elongation in Response to Hypoxia. Cell, 2013, 153, 1327-1339.	28.9	300

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#	Article	IF	CITATIONS
19	A global analysis of <i>C. elegans trans</i> -splicing. Genome Research, 2011, 21, 255-264.	5.5	152
20	Basal cell carcinomas in mice arise from hair follicle stem cells and multiple epithelial progenitor populations. Journal of Clinical Investigation, 2011, 121, 1768-1781.	8.2	160
21	Polycistronic pre-mRNA processing in vitro: snRNP and pre-mRNA role reversal in trans-splicing. Genes and Development, 2010, 24, 1645-1658.	5.9	13
22	Genes involved in pre-mRNA 3′-end formation and transcription termination revealed by a <i>lin-15</i> operon Muv suppressor screen. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 16665-16670.	7.1	50
23	Hedgehog Signaling Regulates Sebaceous Gland Development. American Journal of Pathology, 2003, 163, 2173-2178.	3.8	118