Stephanie E Mohr

List of Publications by Year
in descending order

55 papers	4,878 citations	159585 30 h-index	175258 52 g-index
67 all docs	67 docs citations	67 times ranked	7895 citing authors

#	Article	IF	Citations
1	Protein visualization and manipulation in Drosophila through the use of epitope tags recognized by nanobodies. ELife, 2022, 11, .	6.0	22
2	State-of-the-art CRISPR for in vivo and cell-based studies in Drosophila. Trends in Genetics, 2022, 38, 437-453.	6.7	26
3	FlyRNAi.org€"the database of the Drosophila RNAi screening center and transgenic RNAi project: 2021 update. Nucleic Acids Research, 2021, 49, D908-D915.	14.5	36
4	DRscDB: A single-cell RNA-seq resource for data mining and data comparison across species. Computational and Structural Biotechnology Journal, 2021, 19, 2018-2026.	4.1	17
5	Methods and tools for spatial mapping of single-cell RNAseq clusters in *Drosophila*. Genetics, 2021, 217, .	2.9	10
6	Coordination of tumor growth and host wasting by tumor-derived Upd3. Cell Reports, 2021, 36, 109553.	6.4	35
7	Bioinformatic and cell-based tools for pooled CRISPR knockout screening in mosquitos. Nature Communications, 2021, 12, 6825.	12.8	3
8	SNP-CRISPR: A Web Tool for SNP-Specific Genome Editing. G3: Genes, Genomes, Genetics, 2020, 10, 489-494.	1.8	35
9	Intestinal response to dietary manganese depletion in *Drosophila*. Metallomics, 2020, 12, 218-240.	2.4	16
10	Use of the CRISPR€Cas9 System in Drosophila Cultured Cells to Introduce Fluorescent Tags into Endogenous Genes. Current Protocols in Molecular Biology, 2020, 130, e112.	2.9	6
11	Targeting metabolic pathways for extension of lifespan and healthspan across multiple species. Ageing Research Reviews, 2020, 64, 101188.	10.9	30
12	BioLitMine: Advanced Mining of Biomedical and Biological Literature About Human Genes and Genes from Major Model Organisms. G3: Genes, Genomes, Genetics, 2020, 10, 4531-4539.	1.8	9
13	CRISPR-based engineering of gene knockout cells by homology-directed insertion in polyploid Drosophila S2R+ cells. Nature Protocols, 2020, 15, 3478-3498.	12.0	5
14	Large-Scale Transgenic *Drosophila* Resource Collections for Loss- and Gain-of-Function Studies. Genetics, 2020, 214, 755-767.	2.9	81
15	Pooled CRISPR Screens in Drosophila Cells. Current Protocols in Molecular Biology, 2019, 129, e111.	2.9	13
16	Methionine metabolism and methyltransferases in the regulation of aging and lifespan extension across species. Aging Cell, 2019, 18, e13034.	6.7	151
17	*Drosophila melanogaster*: a simple system for understanding complexity. DMM Disease Models and Mechanisms, 2019, 12, .	2.4	15
18	An efficient CRISPR-based strategy to insert small and large fragments of DNA using short homology arms. ELife, 2019, 8, .	6.0	105

#	ARTICLE	IF	CITATIONS
19	Molecular Interaction Search Tool (MIST): an integrated resource for mining gene and protein interaction data. Nucleic Acids Research, 2018, 46, D567-D574.	14.5	66
20	Zinc Detoxification: A Functional Genomics and Transcriptomics Analysis in *Drosophila melanogaster* Cultured Cells. G3: Genes, Genomes, Genetics, 2018, 8, 631-641.	1.8	19
21	A gene-specific T2A-GAL4 library for Drosophila. ELife, 2018, 7, .	6.0	203
22	Functional Genomics Screens in Drosophila Cells. , 2018, , 165-191.		0
23	CRISPR-Based Perturbation of Gene Function in Drosophila Cells. , 2018, , 193-206.		0
24	Editorial: Metal Biology Takes Flight: The Study of Metal Homeostasis and Detoxification in Insects. Frontiers in Genetics, 2018, 9, 221.	2.3	4
25	MARRVEL: Integration of Human and Model Organism Genetic Resources to Facilitate Functional Annotation of the Human Genome. American Journal of Human Genetics, 2017, 100, 843-853.	6.2	181
26	FlyRNAi.org—the database of the *Drosophila* RNAi screening center and transgenic RNAi project: 2017 update. Nucleic Acids Research, 2017, 45, D672-D678.	14.5	51
27	Accessing the Phenotype Gap: Enabling Systematic Investigation of Paralog Functional Complexity with CRISPR. Developmental Cell, 2017, 43, 6-9.	7.0	35
28	Optimized strategy for in vivo Cas9-activation in *Drosophila*. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 9409-9414.	7.1	75
29	The Drosophila Gene Expression Tool (DGET) for expression analyses. BMC Bioinformatics, 2017, 18, 98.	2.6	49
30	Loss-of-function genetic tools for animal models: cross-species and cross-platform differences. Nature Reviews Genetics, 2017, 18, 24-40.	16.3	159
31	Gene2Function: An Integrated Online Resource for Gene Function Discovery. G3: Genes, Genomes, Genetics, 2017, 7, 2855-2858.	1.8	27
32	CRISPR guide RNA design for research applications. FEBS Journal, 2016, 283, 3232-3238.	4.7	74
33	An Integrative Analysis of the InR/PI3K/Akt Network Identifies the Dynamic Response to Insulin Signaling. Cell Reports, 2016, 16, 3062-3074.	6.4	78
34	GLAD: an Online Database of Gene List Annotation for *Drosophila*. Journal of Genomics, 2015, 3, 75-81.	0.9	79
35	The Transgenic RNAi Project at Harvard Medical School: Resources and Validation. Genetics, 2015, 201, 843-852.	2.9	502
36	Identification of potential drug targets for tuberous sclerosis complex by synthetic screens combining CRISPR-based knockouts with RNAi. Science Signaling, 2015, 8, rs9.	3.6	113

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37	Reagent and Data Resources for Investigation of RNA Binding Protein Functions in Drosophila melanogaster Cultured Cells. G3: Genes, Genomes, Genetics, 2015, 5, 1919-1924.	1.8	7
38	Integrating protein-protein interaction networks with phenotypes reveals signs of interactions. Nature Methods, 2014, 11, 94-99.	19.0	130
39	Resources for Functional Genomics Studies in *Drosophila melanogaster*. Genetics, 2014, 197, 1-18.	2.9	61
40	RNAi screening comes of age: improved techniques and complementary approaches. Nature Reviews Molecular Cell Biology, 2014, 15, 591-600.	37.0	289
41	Online GESS: prediction of miRNA-like off-target effects in large-scale RNAi screen data by seed region analysis. BMC Bioinformatics, 2014, 15, 192.	2.6	32
42	RNAi screening in Drosophila cells and in vivo. Methods, 2014, 68, 82-88.	3.8	32
43	UP-TORR: Online Tool for Accurate and Up-to-Date Annotation of RNAi Reagents. Genetics, 2013, 195, 37-45.	2.9	47
44	Optimized gene editing technology for *Drosophila melanogaster* using germ line-specific Cas9. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 19012-19017.	7.1	365
45	Protein Complex–Based Analysis Framework for High-Throughput Data Sets. Science Signaling, 2013, 6, rs5.	3.6	110
46	FlyPrimerBank: An Online Database for *Drosophila melanogaster* Gene Expression Analysis and Knockdown Evaluation of RNAi Reagents. G3: Genes, Genomes, Genetics, 2013, 3, 1607-1616.	1.8	129
47	FlyRNAi.org--the database of the Drosophila RNAi screening center: 2012 update. Nucleic Acids Research, 2012, 40, D715-D719.	14.5	48
48	Stringent Analysis of Gene Function and Protein–Protein Interactions Using Fluorescently Tagged Genes. Genetics, 2012, 190, 931-940.	2.9	92
49	RNAi screening: new approaches, understandings, and organisms. Wiley Interdisciplinary Reviews RNA, 2012, 3, 145-158.	6.4	120
50	An integrative approach to ortholog prediction for disease-focused and other functional studies. BMC Bioinformatics, 2011, 12, 357.	2.6	629
51	False negative rates in Drosophila cell-based RNAi screens: a case study. BMC Genomics, 2011, 12, 50.	2.8	43
52	Genomic Screening with RNAi: Results and Challenges. Annual Review of Biochemistry, 2010, 79, 37-64.	11.1	260
53	Approaching a complete repository of sequence-verified protein-encoding clones for Saccharomyces cerevisiae. Genome Research, 2007, 17, 536-543.	5.5	99
54	PlasmID: a centralized repository for plasmid clone information and distribution. Nucleic Acids Research, 2007, 35, D680-D684.	14.5	32

#	Article	IF	Citations
55	Inferring genetic architecture from systems genetics studies. , 0, , 139-160.		0