

Yanhui Hu

List of Publications by Year in descending order

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Version: 2024-02-01

71
papers

6,143
citations

101543

36
h-index

95266

68
g-index

85
all docs

85
docs citations

85
times ranked

9537
citing authors

#	ARTICLE	IF	CITATIONS
1	An integrative approach to ortholog prediction for disease-focused and other functional studies. BMC Bioinformatics, 2011, 12, 357.	2.6	629
2	FlyBase at 25: looking to the future. Nucleic Acids Research, 2017, 45, D663-D671.	14.5	563
3	The Transgenic RNAi Project at Harvard Medical School: Resources and Validation. Genetics, 2015, 201, 843-852.	2.9	502
4	Enhanced Specificity and Efficiency of the CRISPR/Cas9 System with Optimized sgRNA Parameters in Drosophila. Cell Reports, 2014, 9, 1151-1162.	6.4	284
5	Controllability analysis of the directed human protein interaction network identifies disease genes and drug targets. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 4976-4981.	7.1	249
6	Systemic Organ Wasting Induced by Localized Expression of the Secreted Insulin/IGF Antagonist ImpL2. Developmental Cell, 2015, 33, 36-46.	7.0	209
7	A gene-specific T2A-GAL4 library for Drosophila. ELife, 2018, 7, .	6.0	203
8	Genetic architecture of subcortical brain structures in 38,851 individuals. Nature Genetics, 2019, 51, 1624-1636.	21.4	192
9	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
10	A cell atlas of the adult <i>Drosophila</i> midgut. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 1514-1523.	7.1	175
11	Proteomic mapping in live <i>Drosophila</i> tissues using an engineered ascorbate peroxidase. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 12093-12098.	7.1	143
12	A single-cell survey of Drosophila blood. ELife, 2020, 9, .	6.0	134
13	Integrating protein-protein interaction networks with phenotypes reveals signs of interactions. Nature Methods, 2014, 11, 94-99.	19.0	130
14	FlyPrimerBank: An Online Database for <i>Drosophila melanogaster</i> Gene Expression Analysis and Knockdown Evaluation of RNAi Reagents. G3: Genes, Genomes, Genetics, 2013, 3, 1607-1616.	1.8	129
15	A Regulatory Network of Drosophila Germline Stem Cell Self-Renewal. Developmental Cell, 2014, 28, 459-473.	7.0	128
16	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
17	An efficient CRISPR-based strategy to insert small and large fragments of DNA using short homology arms. ELife, 2019, 8, .	6.0	105
18	Single-cell transcriptome maps of myeloid blood cell lineages in Drosophila. Nature Communications, 2020, 11, 4483.	12.8	100

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19	Approaching a complete repository of sequence-verified protein-encoding clones for <i>Saccharomyces cerevisiae</i> . <i>Genome Research</i> , 2007, 17, 536-543.	5.5	99
20	Midgut-Derived Activin Regulates Glucagon-like Action in the Fat Body and Glycemic Control. <i>Cell Metabolism</i> , 2017, 25, 386-399.	16.2	93
21	Genome-wide RNAi Screen Identifies Networks Involved in Intestinal Stem Cell Regulation in <i>Drosophila</i> . <i>Cell Reports</i> , 2015, 10, 1226-1238.	6.4	88
22	Large-Scale Transgenic <i>Drosophila</i> Resource Collections for Loss- and Gain-of-Function Studies. <i>Genetics</i> , 2020, 214, 755-767.	2.9	81
23	GLAD: an Online Database of Gene Lists Annotation for <i>Drosophila</i> . <i>Journal of Genomics</i> , 2015, 3, 75-81.	0.9	79
24	An Integrative Analysis of the InR/PI3K/Akt Network Identifies the Dynamic Response to Insulin Signaling. <i>Cell Reports</i> , 2016, 16, 3062-3074.	6.4	78
25	Optimized strategy for in vivo Cas9-activation in <i>Drosophila</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 9409-9414.	7.1	75
26	CRISPR guide RNA design for research applications. <i>FEBS Journal</i> , 2016, 283, 3232-3238.	4.7	74
27	Molecular Interaction Search Tool (MIST): an integrated resource for mining gene and protein interaction data. <i>Nucleic Acids Research</i> , 2018, 46, D567-D574.	14.5	66
28	Combining Genetic Perturbations and Proteomics to Examine Kinase-Phosphatase Networks in <i>Drosophila</i> Embryos. <i>Developmental Cell</i> , 2014, 31, 114-127.	7.0	64
29	Pooled genome-wide CRISPR screening for basal and context-specific fitness gene essentiality in <i>Drosophila</i> cells. <i>ELife</i> , 2018, 7, .	6.0	64
30	Tumor-Derived Ligands Trigger Tumor Growth and Host Wasting via Differential MEK Activation. <i>Developmental Cell</i> , 2019, 48, 277-286.e6.	7.0	59
31	The TORC1-Regulated CPA Complex Rewires an RNA Processing Network to Drive Autophagy and Metabolic Reprogramming. <i>Cell Metabolism</i> , 2018, 27, 1040-1054.e8.	16.2	54
32	FlyRNAi.org—the database of the <i>Drosophila</i> RNAi screening center and transgenic RNAi project: 2017 update. <i>Nucleic Acids Research</i> , 2017, 45, D672-D678.	14.5	51
33	Proteomics of protein trafficking by in vivo tissue-specific labeling. <i>Nature Communications</i> , 2021, 12, 2382.	12.8	51
34	The <i>Drosophila</i> Gene Expression Tool (DGET) for expression analyses. <i>BMC Bioinformatics</i> , 2017, 18, 98.	2.6	49
35	mTORC1-chaperonin CCT signaling regulates m ⁶ A RNA methylation to suppress autophagy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	49
36	UP-TORR: Online Tool for Accurate and Up-to-Date Annotation of RNAi Reagents. <i>Genetics</i> , 2013, 195, 37-45.	2.9	47

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37	The Septate Junction Protein Tsp2A Restricts Intestinal Stem Cell Activity via Endocytic Regulation of aPKC and Hippo Signaling. <i>Cell Reports</i> , 2019, 26, 670-688.e6.	6.4	43
38	Proteomic and Metabolomic Characterization of a Mammalian Cellular Transition from Quiescence to Proliferation. <i>Cell Reports</i> , 2017, 20, 721-736.	6.4	41
39	Activin signaling mediates muscle-to-adipose communication in a mitochondria dysfunction-associated obesity model. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 8596-8601.	7.1	41
40	<i>Drosophila</i> and genome-wide association studies: a review and resource for the functional dissection of human complex traits. <i>DMM Disease Models and Mechanisms</i> , 2017, 10, 77-88.	2.4	37
41	FlyRNAi.org—the database of the <i>Drosophila</i> RNAi screening center and transgenic RNAi project: 2021 update. <i>Nucleic Acids Research</i> , 2021, 49, D908-D915.	14.5	36
42	Mapping signaling pathway cross-talk in <i>Drosophila</i> cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9940-9945.	7.1	35
43	Accessing the Phenotype Gap: Enabling Systematic Investigation of Paralog Functional Complexity with CRISPR. <i>Developmental Cell</i> , 2017, 43, 6-9.	7.0	35
44	SNP-CRISPR: A Web Tool for SNP-Specific Genome Editing. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 489-494.	1.8	35
45	Coordination of tumor growth and host wasting by tumor-derived Upd3. <i>Cell Reports</i> , 2021, 36, 109553.	6.4	35
46	The Quest for Orthologs orthology benchmark service in 2022. <i>Nucleic Acids Research</i> , 2022, 50, W623-W632.	14.5	29
47	Gene2Function: An Integrated Online Resource for Gene Function Discovery. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2855-2858.	1.8	27
48	Discovery of progenitor cell signatures by time-series synexpression analysis during <i>Drosophila</i> embryonic cell immortalization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 12974-12979.	7.1	26
49	<i>Drosophila</i> PDGF/VEGF signaling from muscles to hepatocyte-like cells protects against obesity. <i>ELife</i> , 2020, 9, .	6.0	26
50	FlyPhoneDB: an integrated web-based resource for cell-cell communication prediction in <i>Drosophila</i> . <i>Genetics</i> , 2022, 220, .	2.9	25
51	An expanded toolkit for <i>Drosophila</i> gene tagging using synthesized homology donor constructs for CRISPR-mediated homologous recombination. <i>ELife</i> , 0, 11, .	6.0	25
52	iProteinDB: An Integrative Database of <i>Drosophila</i> Post-translational Modifications. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1-11.	1.8	24
53	Transcriptional and functional motifs defining renal function revealed by single-nucleus RNA sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	22
54	Zinc Detoxification: A Functional Genomics and Transcriptomics Analysis in <i>Drosophila melanogaster</i> Cultured Cells. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 631-641.	1.8	19

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55	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
56	Histone H1 defect in escort cells triggers germline tumor in <i>Drosophila</i> ovary. Developmental Biology, 2017, 424, 40-49.	2.0	14
57	Interspecies analysis of MYC targets identifies tRNA synthetases as mediators of growth and survival in MYC-overexpressing cells. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 14614-14619.	7.1	14
58	An in vivo RNAi screen uncovers the role of AdoR signaling and adenosine deaminase in controlling intestinal stem cell activity. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 464-471.	7.1	14
59	Pooled CRISPR Screens in <i>Drosophila</i> Cells. Current Protocols in Molecular Biology, 2019, 129, e111.	2.9	13
60	Design and Generation of <i>Drosophila</i> Single Guide RNA Expression Constructs. Cold Spring Harbor Protocols, 2016, 2016, pdb.prot090779.	0.3	12
61	Methods and tools for spatial mapping of single-cell RNAseq clusters in <i>Drosophila</i> . Genetics, 2021, 217, .	2.9	10
62	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
63	TIMEOR: a web-based tool to uncover temporal regulatory mechanisms from multi-omics data. Nucleic Acids Research, 2021, 49, W641-W653.	14.5	9
64	Improved detection of synthetic lethal interactions in <i>Drosophila</i> cells using variable dose analysis (VDA). Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E10755-E10762.	7.1	8
65	Reagent and Data Resources for Investigation of RNA Binding Protein Functions in <i>Drosophila melanogaster</i> Cultured Cells. G3: Genes, Genomes, Genetics, 2015, 5, 1919-1924.	1.8	7
66	Use of the CRISPR-Cas9 System in <i>Drosophila</i> Cultured Cells to Introduce Fluorescent Tags into Endogenous Genes. Current Protocols in Molecular Biology, 2020, 130, e112.	2.9	6
67	Trans-omics analysis of insulin action reveals a cell growth subnetwork which co-regulates anabolic processes. IScience, 2022, 25, 104231.	4.1	6
68	Cross-species identification of PIP5K1-, splicing- and ubiquitin-related pathways as potential targets for RB1-deficient cells. PLoS Genetics, 2021, 17, e1009354.	3.5	5
69	Bioinformatic and cell-based tools for pooled CRISPR knockout screening in mosquitos. Nature Communications, 2021, 12, 6825.	12.8	3
70	Systematic discovery of signaling pathways linking immune activation to schizophrenia. IScience, 2021, 24, 103209.	4.1	2
71	Tracking gene-disease relationships for high-throughput functional studies. Surgery, 2004, 136, 504-510.	1.9	1