

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	Trans-omics analysis of insulin action reveals a cell growth subnetwork which co-regulates anabolic processes. <i>IScience</i> , 2022, 25, 104231.	4.1	6
2	FlyPhoneDB: an integrated web-based resource for cell-cell communication prediction in <i>Drosophila</i> . <i>Genetics</i> , 2022, 220, .	2.9	25
3	The Quest for Orthologs orthology benchmark service in 2022. <i>Nucleic Acids Research</i> , 2022, 50, W623-W632.	14.5	29
4	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
5	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
6	DRscDB: A single-cell RNA-seq resource for data mining and data comparison across species. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2018-2026.	4.1	17
7	Cross-species identification of PIP5K1-, splicing- and ubiquitin-related pathways as potential targets for RB1-deficient cells. <i>PLoS Genetics</i> , 2021, 17, e1009354.	3.5	5
8	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
9	Methods and tools for spatial mapping of single-cell RNAseq clusters in <i>Drosophila</i> . <i>Genetics</i> , 2021, 217, .	2.9	10
10	Proteomics of protein trafficking by in vivo tissue-specific labeling. <i>Nature Communications</i> , 2021, 12, 2382.	12.8	51
11	TIMEOR: a web-based tool to uncover temporal regulatory mechanisms from multi-omics data. <i>Nucleic Acids Research</i> , 2021, 49, W641-W653.	14.5	9
12	Coordination of tumor growth and host wasting by tumor-derived Upd3. <i>Cell Reports</i> , 2021, 36, 109553.	6.4	35
13	Systematic discovery of signaling pathways linking immune activation to schizophrenia. <i>IScience</i> , 2021, 24, 103209.	4.1	2
14	Bioinformatic and cell-based tools for pooled CRISPR knockout screening in mosquitos. <i>Nature Communications</i> , 2021, 12, 6825.	12.8	3
15	SNP-CRISPR: A Web Tool for SNP-Specific Genome Editing. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 489-494.	1.8	35
16	A cell atlas of the adult <i>Drosophila</i> midgut. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 1514-1523.	7.1	175
17	Use of the CRISPR-Cas9 System in <i>Drosophila</i> Cultured Cells to Introduce Fluorescent Tags into Endogenous Genes. <i>Current Protocols in Molecular Biology</i> , 2020, 130, e112.	2.9	6
18	An in vivo RNAi screen uncovers the role of AdoR signaling and adenosine deaminase in controlling intestinal stem cell activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 464-471.	7.1	14

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19	BioLitMine: Advanced Mining of Biomedical and Biological Literature About Human Genes and Genes from Major Model Organisms. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 4531-4539.	1.8	9
20	Single-cell transcriptome maps of myeloid blood cell lineages in <i>Drosophila</i> . <i>Nature Communications</i> , 2020, 11, 4483.	12.8	100
21	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
22	A single-cell survey of <i>Drosophila</i> blood. <i>ELife</i> , 2020, 9, .	6.0	134
23	<i>Drosophila</i> PDGF/VEGF signaling from muscles to hepatocyte-like cells protects against obesity. <i>ELife</i> , 2020, 9, .	6.0	26
24	Interspecies analysis of MYC targets identifies tRNA synthetases as mediators of growth and survival in MYC-overexpressing cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 14614-14619.	7.1	14
25	Pooled CRISPR Screens in <i>Drosophila</i> Cells. <i>Current Protocols in Molecular Biology</i> , 2019, 129, e111.	2.9	13
26	iProteinDB: An Integrative Database of <i>Drosophila</i> Post-translational Modifications. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1-11.	1.8	24
27	Genetic architecture of subcortical brain structures in 38,851 individuals. <i>Nature Genetics</i> , 2019, 51, 1624-1636.	21.4	192
28	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
29	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
30	An efficient CRISPR-based strategy to insert small and large fragments of DNA using short homology arms. <i>ELife</i> , 2019, 8, .	6.0	105
31	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
32	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
33	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
34	A gene-specific T2A-GAL4 library for <i>Drosophila</i> . <i>ELife</i> , 2018, 7, .	6.0	203
35	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
36	<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

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37	Histone H1 defect in escort cells triggers germline tumor in <i>Drosophila</i> ovary. <i>Developmental Biology</i> , 2017, 424, 40-49.	2.0	14
38	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
39	MARRVEL: Integration of Human and Model Organism Genetic Resources to Facilitate Functional Annotation of the Human Genome. <i>American Journal of Human Genetics</i> , 2017, 100, 843-853.	6.2	181
40	FlyBase at 25: looking to the future. <i>Nucleic Acids Research</i> , 2017, 45, D663-D671.	14.5	563
41	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
42	Accessing the Phenotype Gap: Enabling Systematic Investigation of Paralog Functional Complexity with CRISPR. <i>Developmental Cell</i> , 2017, 43, 6-9.	7.0	35
43	Proteomic and Metabolomic Characterization of a Mammalian Cellular Transition from Quiescence to Proliferation. <i>Cell Reports</i> , 2017, 20, 721-736.	6.4	41
44	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
45	The <i>Drosophila</i> Gene Expression Tool (DGET) for expression analyses. <i>BMC Bioinformatics</i> , 2017, 18, 98.	2.6	49
46	Improved detection of synthetic lethal interactions in <i>Drosophila</i> cells using variable dose analysis (VDA). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E10755-E10762.	7.1	8
47	Gene2Function: An Integrated Online Resource for Gene Function Discovery. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2855-2858.	1.8	27
48	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
49	CRISPR guide RNA design for research applications. <i>FEBS Journal</i> , 2016, 283, 3232-3238.	4.7	74
50	Controllability analysis of the directed human protein interaction network identifies disease genes and drug targets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 4976-4981.	7.1	249
51	Design and Generation of <i>Drosophila</i> Single Guide RNA Expression Constructs. <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.prot090779.	0.3	12
52	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
53	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
54	GLAD: an Online Database of Gene Lists Annotation for <i>Drosophila</i> . <i>Journal of Genomics</i> , 2015, 3, 75-81.	0.9	79

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55	The Transgenic RNAi Project at Harvard Medical School: Resources and Validation. <i>Genetics</i> , 2015, 201, 843-852.	2.9	502
56	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
57	Systemic Organ Wasting Induced by Localized Expression of the Secreted Insulin/IGF Antagonist ImpL2. <i>Developmental Cell</i> , 2015, 33, 36-46.	7.0	209
58	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
59	Identification of potential drug targets for tuberous sclerosis complex by synthetic screens combining CRISPR-based knockouts with RNAi. <i>Science Signaling</i> , 2015, 8, rs9.	3.6	113
60	Proteomic mapping in live <i>Drosophila</i> tissues using an engineered ascorbate peroxidase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 12093-12098.	7.1	143
61	Reagent and Data Resources for Investigation of RNA Binding Protein Functions in <i>Drosophila melanogaster</i> Cultured Cells. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1919-1924.	1.8	7
62	Enhanced Specificity and Efficiency of the CRISPR/Cas9 System with Optimized sgRNA Parameters in <i>Drosophila</i> . <i>Cell Reports</i> , 2014, 9, 1151-1162.	6.4	284
63	A Regulatory Network of <i>Drosophila</i> Germline Stem Cell Self-Renewal. <i>Developmental Cell</i> , 2014, 28, 459-473.	7.0	128
64	Integrating protein-protein interaction networks with phenotypes reveals signs of interactions. <i>Nature Methods</i> , 2014, 11, 94-99.	19.0	130
65	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
66	UP-TORR: Online Tool for Accurate and Up-to-Date Annotation of RNAi Reagents. <i>Genetics</i> , 2013, 195, 37-45.	2.9	47
67	FlyPrimerBank: An Online Database for <i>Drosophila melanogaster</i> Gene Expression Analysis and Knockdown Evaluation of RNAi Reagents. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1607-1616.	1.8	129
68	An integrative approach to ortholog prediction for disease-focused and other functional studies. <i>BMC Bioinformatics</i> , 2011, 12, 357.	2.6	629
69	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
70	Tracking gene-disease relationships for high-throughput functional studies. <i>Surgery</i> , 2004, 136, 504-510.	1.9	1
71	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