Guanming Wu

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1531085/publications.pdf

Version: 2024-02-01

44	16,717	186265	276875
papers	citations	28 h-index	41 g-index

46	46	46	30637
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The reactome pathway knowledgebase 2022. Nucleic Acids Research, 2022, 50, D687-D692.	14.5	924
2	Using Reactome to build an autophagy mechanism knowledgebase. Autophagy, 2021, 17, 1543-1554.	9.1	5
3	VaximmutorDB: A Web-Based Vaccine Immune Factor Database and Its Application for Understanding Vaccine-Induced Immune Mechanisms. Frontiers in Immunology, 2021, 12, 639491.	4.8	6
4	CIDO ontology updates and secondary analysis of host responses to COVID-19 infection based on ImmPort reports and literature. Journal of Biomedical Semantics, 2021, 12, 18.	1.6	9
5	COVID19 Disease Map, a computational knowledge repository of virusâ€“host interaction mechanisms. Molecular Systems Biology, 2021, 17, e10387.	7.2	53
6	The reactome pathway knowledgebase. Nucleic Acids Research, 2020, 48, D498-D503.	14.5	1,570
7	Perform Pathway Enrichment Analysis Using ReactomeFIViz. Methods in Molecular Biology, 2020, 2074, 165-179.	0.9	10
8	Acute myeloid leukemiaâ€“induced T-cell suppression can be reversed by inhibition of the MAPK pathway. Blood Advances, 2019, 3, 3038-3051.	5.2	14
9	Reactome and ORCIDâ€”fine-grained credit attribution for community curation. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	12
10	Visualization of drug target interactions in the contexts of pathways and networks with ReactomeFIViz. F1000Research, 2019, 8, 908.	1.6	20
11	The Reactome Pathway Knowledgebase. Nucleic Acids Research, 2018, 46, D649-D655.	14.5	2,388
12	Network-Based Predictors of Progression in Head and Neck Squamous Cell Carcinoma. Frontiers in Genetics, 2018, 9, 183.	2.3	34
13	Reactome graph database: Efficient access to complex pathway data. PLoS Computational Biology, 2018, 14, e1005968.	3.2	202
14	Automation of ReactomeFIViz via CyREST API. F1000Research, 2018, 7, 531.	1.6	0
15	Automation of ReactomeFIViz via CyREST API. F1000Research, 2018, 7, 531.	1.6	1
16	Evidence-Based Precision Oncology with the Cancer Targetome. Trends in Pharmacological Sciences, 2017, 38, 1085-1099.	8.7	25
17	The Reactome pathway Knowledgebase. Nucleic Acids Research, 2016, 44, D481-D487.	14.5	3,319
18	Reactome from a WikiPathways Perspective. PLoS Computational Biology, 2016, 12, e1004941.	3.2	35

#	Article	IF	Citations
19	Pathway and network analysis of cancer genomes. Nature Methods, 2015, 12, 615-621.	19.0	297
20	Manic Fringe Promotes a Claudin-Low Breast Cancer Phenotype through Notch-Mediated PIK3CG Induction. Cancer Research, 2015, 75, 1936-1943.	0.9	64
21	Between Pathways and Networks Lies Context: Implications for Precision Medicine. Science Progress, 2015, 98, 253-263.	1.9	0
22	ReactomeFIViz: a Cytoscape app for pathway and network-based data analysis. F1000Research, 2014, 3, 146.	1.6	155
23	The Reactome pathway knowledgebase. Nucleic Acids Research, 2014, 42, D472-D477.	14.5	1,448
24	A controlled vocabulary for pathway entities and events. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau060-bau060.	3.0	11
25	Gramene 2013: comparative plant genomics resources. Nucleic Acids Research, 2014, 42, D1193-D1199.	14.5	163
26	Leveraging Cross-Species Transcription Factor Binding Site Patterns: From Diabetes Risk Loci to Disease Mechanisms. Cell, 2014, 156, 343-358.	28.9	113
27	Tumor-Suppressive Activity of Lunatic Fringe in Prostate through Differential Modulation of Notch Receptor Activation. Neoplasia, 2014, 16, 158-167.	5.3	34
28	ReactomeFIViz: the Reactome FI Cytoscape app for pathway and network-based data analysis. F1000Research, 2014, 3, 146.	1.6	129
29	Systematic MicroRNA Analysis Identifies ATP6V0C as an Essential Host Factor for Human Cytomegalovirus Replication. PLoS Pathogens, 2013, 9, e1003820.	4.7	44
30	Annotating Cancer Variants and Anti-Cancer Therapeutics in Reactome. Cancers, 2012, 4, 1180-1211.	3.7	270
31	A network module-based method for identifying cancer prognostic signatures. Genome Biology, 2012, 13, R112.	9.6	141
32	PSICQUIC and PSISCORE: accessing and scoring molecular interactions. Nature Methods, 2011, 8, 528-529.	19.0	274
33	Identification of a Therapeutic Strategy Targeting Amplified FGF19 in Liver Cancer by Oncogenomic Screening. Cancer Cell, 2011, 19, 347-358.	16.8	379
34	The BioPAX community standard for pathway data sharing. Nature Biotechnology, 2010, 28, 935-942.	17.5	613
35	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	21.4	1,631
36	A Viral microRNA Down-Regulates Multiple Cell Cycle Genes through mRNA 5â€²UTRs. PLoS Pathogens, 2010, 6, e1000967.	4.7	191

#	Article	IF	Citations
37	A human functional protein interaction network and its application to cancer data analysis. Genome Biology, 2010, 11, R53.	9.6	591
38	The Systems Biology Graphical Notation. Nature Biotechnology, 2009, 27, 735-741.	17.5	828
39	Arabidopsis Reactome: A Foundation Knowledgebase for Plant Systems Biology. Plant Cell, 2008, 20, 1426-1436.	6.6	52
40	Reactome: An integrated expert model of human molecular processes and access toolkit. Journal of Integrative Bioinformatics, 2007, 4, 286-296.	1.5	0
41	Reactome: a knowledge base of biologic pathways and processes. Genome Biology, 2007, 8, R39.	9.6	539
42	Myosin V attachment to cargo requires the tight association of two functional subdomains. Journal of Cell Biology, 2005, 168, 359-364.	5.2	37
43	Two distinct myosin light chain structures are induced by specific variations within the bound IQ motifs--functional implications. EMBO Journal, 2003, 22, 362-371.	7.8	71
44	Leveraging biochemical reactions to unravel functional impacts of cancer somatic variants affecting protein interaction interfaces. F1000Research, 0, 10, 1111.	1.6	1