

# Guangchuang Yu

## List of Publications by Year in descending order

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Version: 2024-02-01

47  
papers

36,378  
citations

236612

25  
h-index

223531

46  
g-index

57  
all docs

57  
docs citations

57  
times ranked

50966  
citing authors

#	ARTICLE	IF	CITATIONS
1	clusterProfiler: an R Package for Comparing Biological Themes Among Gene Clusters. OMICS A Journal of Integrative Biology, 2012, 16, 284-287.	1.0	21,237
2	<scp>ggtree</scp>: an <scp>r</scp> package for visualization and annotation of phylogenetic trees with their covariates and other associated data. Methods in Ecology and Evolution, 2017, 8, 28-36.	2.2	2,998
3	clusterProfiler 4.0: A universal enrichment tool for interpreting omics data. Innovation(China), 2021, 2, 100141.	5.2	2,743
4	ChIPseeker: an R/Bioconductor package for ChIP peak annotation, comparison and visualization. Bioinformatics, 2015, 31, 2382-2383.	1.8	2,603
5	ReactomePA: an R/Bioconductor package for reactome pathway analysis and visualization. Molecular BioSystems, 2016, 12, 477-479.	2.9	1,237
6	GOSemSim: an R package for measuring semantic similarity among GO terms and gene products. Bioinformatics, 2010, 26, 976-978.	1.8	978
7	Using ggtree to Visualize Data on Tree-Like Structures. Current Protocols in Bioinformatics, 2020, 69, e96.	25.8	810
8	DOSE: an R/Bioconductor package for disease ontology semantic and enrichment analysis. Bioinformatics, 2015, 31, 608-609.	1.8	762
9	Two Methods for Mapping and Visualizing Associated Data on Phylogeny Using <i>Ggtree</i>. Molecular Biology and Evolution, 2018, 35, 3041-3043.	3.5	535
10	IOBR: Multi-Omics Immuno-Oncology Biological Research to Decode Tumor Microenvironment and Signatures. Frontiers in Immunology, 2021, 12, 687975.	2.2	361
11	Treeio: An R Package for Phylogenetic Tree Input and Output with Richly Annotated and Associated Data. Molecular Biology and Evolution, 2020, 37, 599-603.	3.5	348
12	<i>Rldeogram</i>: drawing SVG graphics to visualize and map genome-wide data on the idiograms. PeerJ Computer Science, 2020, 6, e251.	2.7	265
13	Gene Ontology Semantic Similarity Analysis Using GOSemSim. Methods in Molecular Biology, 2020, 2117, 207-215.	0.4	143
14	ggtreeExtra: Compact Visualization of Richly Annotated Phylogenetic Data. Molecular Biology and Evolution, 2021, 38, 4039-4042.	3.5	134
15	ggVennDiagram: An Intuitive, Easy-to-Use, and Highly Customizable R Package to Generate Venn Diagram. Frontiers in Genetics, 2021, 12, 706907.	1.1	134
16	Gut microbiota and metabolite alterations associated with reduced bone mineral density or bone metabolic indexes in postmenopausal osteoporosis. Aging, 2020, 12, 8583-8604.	1.4	130
17	Use ggbreak to Effectively Utilize Plotting Space to Deal With Large Datasets and Outliers. Frontiers in Genetics, 2021, 12, 774846.	1.1	116
18	Cellular microRNA letâ€c7c inhibits M1 protein expression of the H1N1 influenza A virus in infected human lung epithelial cells. Journal of Cellular and Molecular Medicine, 2012, 16, 2539-2546.	1.6	110

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19	<scp>ACK1</scp> promotes gastric cancer epithelialâ€“mesenchymal transition and metastasis through <scp>AKTâ€“POU2F1â€“ECD</scp> signalling. <i>Journal of Pathology</i> , 2015, 236, 175-185.	2.1	84
20	Genisteinâ€“induced mitotic arrest of gastric cancer cells by downregulating <scp>KIF</scp>20<scp>A</scp>, a proteomics study. <i>Proteomics</i> , 2012, 12, 2391-2399.	1.3	80
21	ggmsa: a visual exploration tool for multiple sequence alignment and associated data. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	71
22	Using <i>meshes</i> for MeSH term enrichment and semantic analyses. <i>Bioinformatics</i> , 2018, 34, 3766-3767.	1.8	55
23	Putative cobalt- and nickel-binding proteins and motifs in <i>Streptococcus pneumoniae</i> . <i>Metallomics</i> , 2013, 5, 928.	1.0	37
24	Integrated Translatomics with Proteomics to Identify Novel Ironâ€“Transporting Proteins in <i>Streptococcus pneumoniae</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 78.	1.5	37
25	Proteomic investigation of the interactome of FMNL1 in hematopoietic cells unveils a role in calcium-dependent membrane plasticity. <i>Journal of Proteomics</i> , 2013, 78, 72-82.	1.2	35
26	Quantitative proteomics characterization on the antitumor effects of isodeoxyelephantopin against nasopharyngeal carcinoma. <i>Proteomics</i> , 2013, 13, 3222-3232.	1.3	24
27	A novel andrographolide derivative <scp>AL</scp>â€“1 exerts its cytotoxicity on <scp>K</scp>562 cells through a <scp>ROS</scp>-dependent mechanism. <i>Proteomics</i> , 2013, 13, 169-178.	1.3	23
28	<i>CBNplot</i>: Bayesian network plots for enrichment analysis. <i>Bioinformatics</i> , 2022, 38, 2959-2960.	1.8	19
29	Proteomic Analysis of Membrane Proteins from <i>Streptococcus pneumoniae</i> with Multiple Separation Methods Plus High Accuracy Mass Spectrometry. <i>OMICS A Journal of Integrative Biology</i> , 2011, 15, 683-694.	1.0	16
30	TreeSummarizedExperiment: a S4 class for data with hierarchical structure. <i>F1000Research</i> , 2020, 9, 1246.	0.8	16
31	Proteomic analysis on the antibacterial activity of a Ru(II) complex against <i>Streptococcus pneumoniae</i> . <i>Journal of Proteomics</i> , 2015, 115, 107-116.	1.2	15
32	Proteomic analysis of the copper resistance of <i>Streptococcus pneumoniae</i> . <i>Metallomics</i> , 2015, 7, 448-454.	1.0	15
33	Genetic characterization of highly pathogenic H5 influenza viruses from poultry in Taiwan, 2015. <i>Infection, Genetics and Evolution</i> , 2016, 38, 96-100.	1.0	15
34	Phosphoproteome profile of human lung cancer cell line A549. <i>Molecular BioSystems</i> , 2011, 7, 472-479.	2.9	13
35	Functional similarity analysis of human virus-encoded miRNAs. <i>Journal of Clinical Bioinformatics</i> , 2011, 1, 15.	1.2	13
36	TreeSummarizedExperiment: a S4 class for data with hierarchical structure. <i>F1000Research</i> , 2020, 9, 1246.	0.8	11

#	ARTICLE	IF	CITATIONS
37	nCov2019: an R package for studying the COVID-19 coronavirus pandemic. PeerJ, 2021, 9, e11421.	0.9	10
38	A new method for measuring functional similarity of microRNAs. Journal of Integrated OMICS, 2011, 1, .	0.5	8
39	Identification of Prognostic Stromal-Immune Score-Based Genes in Hepatocellular Carcinoma Microenvironment. Frontiers in Genetics, 2021, 12, 625236.	1.1	5
40	Proteomic analysis of putative heme-binding proteins in Streptococcus pyogenes. Metallomics, 2014, 6, 1451.	1.0	4
41	Design, SAR, Angiogenic Activities Evaluation and Pro-Angiogenic Mechanism of New Marine Cyclopeptide Analogs. Current Medicinal Chemistry, 2013, 20, 1183-1194.	1.2	4
42	LXtoo: an integrated live Linux distribution for the bioinformatics community. BMC Research Notes, 2012, 5, 360.	0.6	3
43	A DNA-Based Semantic Fusion Model for Remote Sensing Data. PLoS ONE, 2013, 8, e77090.	1.1	2
44	Altered Gut Microbiota as an Auxiliary Diagnostic Indicator for Patients With Fracture-Related Infection. Frontiers in Microbiology, 2022, 13, 723791.	1.5	2
45	Editorial: Biomedical Data Visualization: Methods and Applications. Frontiers in Genetics, 2022, 13, 890775.	1.1	2
46	Towards a Comprehensive HBV-Human Interaction Map. , 2009, , .		0
47	Design of 16 S rRNA-based Oligonucleotide Array Using Group-specific Non-unique Probes in Large Scale Bacteria Detection*. Progress in Biochemistry and Biophysics, 2009, 36, 1025-1034.	0.3	0