Guangchuang Yu

List of Publications by Year
in descending order

47	36,378	236925	223800
papers	citations	25	46
		h-index	g-index

57	57	57	50966
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	*CBNplot*: Bayesian network plots for enrichment analysis. Bioinformatics, 2022, 38, 2959-2960.	4.1	19
2	Altered Gut Microbiota as an Auxiliary Diagnostic Indicator for Patients With Fracture-Related Infection. Frontiers in Microbiology, 2022, 13, 723791.	3.5	2
3	ggmsa: a visual exploration tool for multiple sequence alignment and associated data. Briefings in Bioinformatics, 2022, 23, .	6.5	71
4	Editorial: Biomedical Data Visualization: Methods and Applications. Frontiers in Genetics, 2022, 13, 890775.	2.3	2
5	Identification of Prognostic Stromal-Immune Score–Based Genes in Hepatocellular Carcinoma Microenvironment. Frontiers in Genetics, 2021, 12, 625236.	2.3	5
6	nCov2019: an R package for studying the COVID-19 coronavirus pandemic. PeerJ, 2021, 9, e11421.	2.0	10
7	ggtreeExtra: Compact Visualization of Richly Annotated Phylogenetic Data. Molecular Biology and Evolution, 2021, 38, 4039-4042.	8.9	134
8	IOBR: Multi-Omics Immuno-Oncology Biological Research to Decode Tumor Microenvironment and Signatures. Frontiers in Immunology, 2021, 12, 687975.	4.8	361
9	clusterProfiler 4.0: A universal enrichment tool for interpreting omics data. Innovation(China), 2021, 2, 100141.	9.1	2,743
10	ggVennDiagram: An Intuitive, Easy-to-Use, and Highly Customizable R Package to Generate Venn Diagram. Frontiers in Genetics, 2021, 12, 706907.	2.3	134
11	Use ggbreak to Effectively Utilize Plotting Space to Deal With Large Datasets and Outliers. Frontiers in Genetics, 2021, 12, 774846.	2.3	116
12	Treeio: An R Package for Phylogenetic Tree Input and Output with Richly Annotated and Associated Data. Molecular Biology and Evolution, 2020, 37, 599-603.	8.9	348
13	Using ggtree to Visualize Data on Tree–Like Structures. Current Protocols in Bioinformatics, 2020, 69, e96.	25.8	810
14	TreeSummarizedExperiment: a S4 class for data with hierarchical structure. F1000Research, 2020, 9, 1246.	1.6	16
15	Gene Ontology Semantic Similarity Analysis Using GOSemSim. Methods in Molecular Biology, 2020, 2117, 207-215.	0.9	143
16	TreeSummarizedExperiment: a S4 class for data with hierarchical structure. F1000Research, 2020, 9, 1246.	1.6	11
17	Gut microbiota and metabolite alterations associated with reduced bone mineral density or bone metabolic indexes in postmenopausal osteoporosis. Aging, 2020, 12, 8583-8604.	3.1	130
18	*RIdeogram*: drawing SVG graphics to visualize and map genome-wide data on the idiograms. PeerJ Computer Science, 2020, 6, e251.	4.5	265

#	ARTICLE	IF	CITATIONS
19	Two Methods for Mapping and Visualizing Associated Data on Phylogeny Using *Ggtree*. Molecular Biology and Evolution, 2018, 35, 3041-3043.	8.9	535
20	Using *meshes* for MeSH term enrichment and semantic analyses. Bioinformatics, 2018, 34, 3766-3767.	4.1	55
21	ggtree: an r package for visualization and annotation of phylogenetic trees with their covariates and other associated data. Methods in Ecology and Evolution, 2017, 8, 28-36.	5.2	2,998
22	Integrated Translatomics with Proteomics to Identify Novel Iron–Transporting Proteins in Streptococcus pneumoniae. Frontiers in Microbiology, 2016, 7, 78.	3.5	37
23	ReactomePA: an R/Bioconductor package for reactome pathway analysis and visualization. Molecular BioSystems, 2016, 12, 477-479.	2.9	1,237
24	Genetic characterization of highly pathogenic H5 influenza viruses from poultry in Taiwan, 2015. Infection, Genetics and Evolution, 2016, 38, 96-100.	2.3	15
25	Proteomic analysis on the antibacterial activity of a Ru(II) complex against Streptococcus pneumoniae. Journal of Proteomics, 2015, 115, 107-116.	2.4	15
26	Proteomic analysis of the copper resistance of Streptococcus pneumoniae. Metallomics, 2015, 7, 448-454.	2.4	15
27	ACK1 promotes gastric cancer epithelial–mesenchymal transition and metastasis through AKT–POU2F1–ECD signalling. Journal of Pathology, 2015, 236, 175-185.	4.5	84
28	ChIPseeker: an R/Bioconductor package for ChIP peak annotation, comparison and visualization. Bioinformatics, 2015, 31, 2382-2383.	4.1	2,603
29	DOSE: an R/Bioconductor package for disease ontology semantic and enrichment analysis. Bioinformatics, 2015, 31, 608-609.	4.1	762
30	Proteomic analysis of putative heme-binding proteins in Streptococcus pyogenes. Metallomics, 2014, 6, 1451.	2.4	4
31	Putative cobalt- and nickel-binding proteins and motifs in Streptococcus pneumoniae. Metallomics, 2013, 5, 928.	2.4	37
32	Proteomic investigation of the interactome of FMNL1 in hematopoietic cells unveils a role in calcium-dependent membrane plasticity. Journal of Proteomics, 2013, 78, 72-82.	2.4	35
33	A novel andrographolide derivative AL–1 exerts its cytotoxicity on K562 cells through a ROS–dependent mechanism. Proteomics, 2013, 13, 169-178.	2.2	23
34	Quantitative proteomics characterization on the antitumor effects of isodeoxyelephantopin against nasopharyngeal carcinoma. Proteomics, 2013, 13, 3222-3232.	2.2	24
35	A DNA-Based Semantic Fusion Model for Remote Sensing Data. PLoS ONE, 2013, 8, e77090.	2.5	2
36	Design, SAR, Angiogenic Activities Evaluation and Pro-Angiogenic Mechanism of New Marine Cyclopeptide Analogs. Current Medicinal Chemistry, 2013, 20, 1183-1194.	2.4	4

#	Article	IF	Citations
37	Genistein‐induced mitotic arrest of gastric cancer cells by downregulating <scp>KIF</scp>20<scp>A</scp>, a proteomics study. Proteomics, 2012, 12, 2391-2399.	2.2	80
38	LXtoo: an integrated live Linux distribution for the bioinformatics community. BMC Research Notes, 2012, 5, 360.	1.4	3
39	Cellular micro<scp>RNA</scp> let‐7c inhibits M1 protein expression of the H1N1 influenza <scp>A</scp> virus in infected human lung epithelial cells. Journal of Cellular and Molecular Medicine, 2012, 16, 2539-2546.	3.6	110
40	clusterProfiler: an R Package for Comparing Biological Themes Among Gene Clusters. OMICS A Journal of Integrative Biology, 2012, 16, 284-287.	2.0	21,237
41	Proteomic Analysis of Membrane Proteins from *Streptococcus pneumoniae* with Multiple Separation Methods Plus High Accuracy Mass Spectrometry. OMICS A Journal of Integrative Biology, 2011, 15, 683-694.	2.0	16
42	Phosphoproteome profile of human lung cancer cell line A549. Molecular BioSystems, 2011, 7, 472-479.	2.9	13
43	A new method for measuring functional similarity of microRNAs. Journal of Integrated OMICS, 2011, 1, .	0.5	8
44	Functional similarity analysis of human virus-encoded miRNAs. Journal of Clinical Bioinformatics, 2011, 1, 15.	1.2	13
45	GOSemSim: an R package for measuring semantic similarity among GO terms and gene products. Bioinformatics, 2010, 26, 976-978.	4.1	978
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