

# Guangchuang Yu

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

46  
papers

14,595  
citations

23  
h-index

57  
g-index

57  
ext. papers

26,709  
ext. citations

5.7  
avg, IF

7.3  
L-index

#	Paper	IF	Citations
46	Altered Gut Microbiota as an Auxiliary Diagnostic Indicator for Patients With Fracture-Related Infection.. <i>Frontiers in Microbiology</i> , <b>2022</b> , 13, 723791	5.7	
45	Use to Effectively Utilize Plotting Space to Deal With Large Datasets and Outliers. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 774846	4.5	9
44	nCov2019: an R package for studying the COVID-19 coronavirus pandemic. <i>PeerJ</i> , <b>2021</b> , 9, e11421	3.1	5
43	ggtreeExtra: Compact Visualization of Richly Annotated Phylogenetic Data. <i>Molecular Biology and Evolution</i> , <b>2021</b> , 38, 4039-4042	8.3	15
42	IOBR: Multi-Omics Immuno-Oncology Biological Research to Decode Tumor Microenvironment and Signatures. <i>Frontiers in Immunology</i> , <b>2021</b> , 12, 687975	8.4	42
41	Identification of Prognostic Stromal-Immune Score-Based Genes in Hepatocellular Carcinoma Microenvironment. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 625236	4.5	1
40	clusterProfiler 4.0: A universal enrichment tool for interpreting omics data. <i>Innovation(China)</i> , <b>2021</b> , 2, 100141	17.8	238
39	ggVennDiagram: An Intuitive, Easy-to-Use, and Highly Customizable R Package to Generate Venn Diagram. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 706907	4.5	13
38	Using ggtree to Visualize Data on Tree-Like Structures. <i>Current Protocols in Bioinformatics</i> , <b>2020</b> , 69, e9624.2		233
37	TreeSummarizedExperiment: a S4 class for data with hierarchical structure. <i>F1000Research</i> , <b>2020</b> , 9, 1246.6		1
36	Gut microbiota and metabolite alterations associated with reduced bone mineral density or bone metabolic indexes in postmenopausal osteoporosis. <i>Aging</i> , <b>2020</b> , 12, 8583-8604	5.6	34
35	: drawing SVG graphics to visualize and map genome-wide data on the idiograms. <i>PeerJ Computer Science</i> , <b>2020</b> , 6, e251	2.7	73
34	Treeio: An R Package for Phylogenetic Tree Input and Output with Richly Annotated and Associated Data. <i>Molecular Biology and Evolution</i> , <b>2020</b> , 37, 599-603	8.3	118
33	TreeSummarizedExperiment: a S4 class for data with hierarchical structure. <i>F1000Research</i> , <b>2020</b> , 9, 1246.6		1
32	Gene Ontology Semantic Similarity Analysis Using GOSemSim. <i>Methods in Molecular Biology</i> , <b>2020</b> , 2117, 207-215	1.4	30
31	Two Methods for Mapping and Visualizing Associated Data on Phylogeny Using Ggtree. <i>Molecular Biology and Evolution</i> , <b>2018</b> , 35, 3041-3043	8.3	223
30	Using meshes for MeSH term enrichment and semantic analyses. <i>Bioinformatics</i> , <b>2018</b> , 34, 3766-3767	7.2	26

29	ggtree: an r package for visualization and annotation of phylogenetic trees with their covariates and other associated data. <i>Methods in Ecology and Evolution</i> , <b>2017</b> , 8, 28-36	7.7	1399
28	ReactomePA: an R/Bioconductor package for reactome pathway analysis and visualization. <i>Molecular BioSystems</i> , <b>2016</b> , 12, 477-9		576
27	Genetic characterization of highly pathogenic H5 influenza viruses from poultry in Taiwan, 2015. <i>Infection, Genetics and Evolution</i> , <b>2016</b> , 38, 96-100	4.5	12
26	Integrated Translatomics with Proteomics to Identify Novel Iron-Transporting Proteins in <i>Streptococcus pneumoniae</i> . <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 78	5.7	28
25	Proteomic analysis of the copper resistance of <i>Streptococcus pneumoniae</i> . <i>Metallomics</i> , <b>2015</b> , 7, 448-54	4.5	14
24	ACK1 promotes gastric cancer epithelial-mesenchymal transition and metastasis through AKT-POU2F1-ECD signalling. <i>Journal of Pathology</i> , <b>2015</b> , 236, 175-85	9.4	57
23	ChIPseeker: an R/Bioconductor package for ChIP peak annotation, comparison and visualization. <i>Bioinformatics</i> , <b>2015</b> , 31, 2382-3	7.2	1036
22	DOSE: an R/Bioconductor package for disease ontology semantic and enrichment analysis. <i>Bioinformatics</i> , <b>2015</b> , 31, 608-9	7.2	360
21	Proteomic analysis on the antibacterial activity of a Ru(II) complex against <i>Streptococcus pneumoniae</i> . <i>Journal of Proteomics</i> , <b>2015</b> , 115, 107-16	3.9	12
20	Proteomic analysis of putative heme-binding proteins in <i>Streptococcus pyogenes</i> . <i>Metallomics</i> , <b>2014</b> , 6, 1451-9	4.5	0
19	Putative cobalt- and nickel-binding proteins and motifs in <i>Streptococcus pneumoniae</i> . <i>Metallomics</i> , <b>2013</b> , 5, 928-35	4.5	28
18	Proteomic investigation of the interactome of FMNL1 in hematopoietic cells unveils a role in calcium-dependent membrane plasticity. <i>Journal of Proteomics</i> , <b>2013</b> , 78, 72-82	3.9	24
17	A novel andrographolide derivative AL-1 exerts its cytotoxicity on K562 cells through a ROS-dependent mechanism. <i>Proteomics</i> , <b>2013</b> , 13, 169-78	4.8	21
16	Quantitative proteomics characterization on the antitumor effects of isodeoxyelephantopin against nasopharyngeal carcinoma. <i>Proteomics</i> , <b>2013</b> , 13, 3222-32	4.8	19
15	A DNA-based semantic fusion model for remote sensing data. <i>PLoS ONE</i> , <b>2013</b> , 8, e77090	3.7	1
14	Design, SAR, angiogenic activities evaluation and pro-angiogenic mechanism of new marine cyclopeptide analogs. <i>Current Medicinal Chemistry</i> , <b>2013</b> , 20, 1183-94	4.3	3
13	Genistein-induced mitotic arrest of gastric cancer cells by downregulating KIF20A, a proteomics study. <i>Proteomics</i> , <b>2012</b> , 12, 2391-9	4.8	61
12	LXtoo: an integrated live Linux distribution for the bioinformatics community. <i>BMC Research Notes</i> , <b>2012</b> , 5, 360	2.3	3

11	Cellular microRNA let-7c inhibits M1 protein expression of the H1N1 influenza A virus in infected human lung epithelial cells. <i>Journal of Cellular and Molecular Medicine</i> , <b>2012</b> , 16, 2539-46	5.6	90
10	clusterProfiler: an R package for comparing biological themes among gene clusters. <i>OMICS A Journal of Integrative Biology</i> , <b>2012</b> , 16, 284-7	3.8	9093
9	Phosphoproteome profile of human lung cancer cell line A549. <i>Molecular BioSystems</i> , <b>2011</b> , 7, 472-9		12
8	A new method for measuring functional similarity of microRNAs. <i>Journal of Integrated OMICS</i> , <b>2011</b> , 1,	0.5	3
7	Functional similarity analysis of human virus-encoded miRNAs. <i>Journal of Clinical Bioinformatics</i> , <b>2011</b> , 1, 15		12
6	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> , <b>2011</b> , 15, 683-94	3.8	14
5	GOSemSim: an R package for measuring semantic similarity among GO terms and gene products. <i>Bioinformatics</i> , <b>2010</b> , 26, 976-8	7.2	595
4	Design of 16 S rRNA-based Oligonucleotide Array Using Group-specific Non-unique Probes in Large Scale Bacteria Detection*. <i>Progress in Biochemistry and Biophysics</i> , <b>2009</b> , 36, 1025-1034		
3	Rideogram: drawing SVG graphics to visualize and map genome-wide data on the idiograms		2
2	Open-source analytics tools for studying the COVID-19 coronavirus outbreak		24
1	clusterProfiler: An universal enrichment tool for functional and comparative study		25