

# Guoqing Zhang

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1834091/publications.pdf>

Version: 2024-02-01

34  
papers

1,912  
citations

623734

14  
h-index

414414

32  
g-index

37  
all docs

37  
docs citations

37  
times ranked

3265  
citing authors

| #  | ARTICLE                                                                                                                                                                                                    | IF   | CITATIONS |
|----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----------|
| 1  | iProX: an integrated proteome resource. <i>Nucleic Acids Research</i> , 2019, 47, D1211-D1217.                                                                                                             | 14.5 | 1,001     |
| 2  | Database Resources of the National Genomics Data Center, China National Center for Bioinformatics in 2021. <i>Nucleic Acids Research</i> , 2021, 49, D18-D28.                                              | 14.5 | 168       |
| 3  | Database Resources of the National Genomics Data Center in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D24-D33.                                                                                        | 14.5 | 165       |
| 4  | Multi-kingdom microbiota analyses identify bacterial–fungal interactions and biomarkers of colorectal cancer across cohorts. <i>Nature Microbiology</i> , 2022, 7, 238-250.                                | 13.3 | 99        |
| 5  | TransCirc: an interactive database for translatable circular RNAs based on multi-omics evidence. <i>Nucleic Acids Research</i> , 2021, 49, D236-D242.                                                      | 14.5 | 65        |
| 6  | SysPTM 2.0: an updated systematic resource for post-translational modification. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau025-bau025.                             | 3.0  | 58        |
| 7  | PGC.Han: the Han Chinese genome database and analysis platform. <i>Nucleic Acids Research</i> , 2020, 48, D971-D976.                                                                                       | 14.5 | 51        |
| 8  | EpiDISH web server: Epigenetic Dissection of Intra-Sample-Heterogeneity with online GUI. <i>Bioinformatics</i> , 2020, 36, 1950-1951.                                                                      | 4.1  | 40        |
| 9  | Operon prediction based on SVM. <i>Computational Biology and Chemistry</i> , 2006, 30, 233-240.                                                                                                            | 2.3  | 25        |
| 10 | Detection of human novel influenza A (H1N1) viruses using multi-fluorescent real-time RT-PCR. <i>Virus Research</i> , 2010, 147, 85-90.                                                                    | 2.2  | 25        |
| 11 | Web Resources for Pharmacogenomics. <i>Genomics, Proteomics and Bioinformatics</i> , 2015, 13, 51-54.                                                                                                      | 6.9  | 23        |
| 12 | The HuaBiao project: whole-exome sequencing of 5000 Han Chinese individuals. <i>Journal of Genetics and Genomics</i> , 2021, 48, 1032-1035.                                                                | 3.9  | 22        |
| 13 | dbDEPC 2.0: updated database of differentially expressed proteins in human cancers. <i>Nucleic Acids Research</i> , 2012, 40, D964-D971.                                                                   | 14.5 | 19        |
| 14 | SySAP: a system-level predictor of deleterious single amino acid polymorphisms. <i>Protein and Cell</i> , 2012, 3, 38-43.                                                                                  | 11.0 | 18        |
| 15 | Prediction of functional phosphorylation sites by incorporating evolutionary information. <i>Protein and Cell</i> , 2012, 3, 675-690.                                                                      | 11.0 | 14        |
| 16 | SyStemCell: A Database Populated with Multiple Levels of Experimental Data from Stem Cell Differentiation Research. <i>PLoS ONE</i> , 2012, 7, e35230.                                                     | 2.5  | 13        |
| 17 | Construction and Deciphering of Human Phosphorylation-Mediated Signaling Transduction Networks. <i>Journal of Proteome Research</i> , 2015, 14, 2745-2757.                                                 | 3.7  | 12        |
| 18 | Differential proteomic analysis of fetal and geriatric lumbar nucleus pulposus: immunoinflammation and age-related intervertebral disc degeneration. <i>BMC Musculoskeletal Disorders</i> , 2020, 21, 339. | 1.9  | 12        |

| #  | ARTICLE                                                                                                                                                                                       | IF   | CITATIONS |
|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----------|
| 19 | GORouter: an RDF model for providing semantic query and inference services for Gene Ontology and its associations. BMC Bioinformatics, 2008, 9, S6.                                           | 2.6  | 11        |
| 20 | PhenoModifier: a genetic modifier database for elucidating the genetic basis of human phenotypic variation. Nucleic Acids Research, 2019, 48, D977-D982.                                      | 14.5 | 10        |
| 21 | GTDB: an integrated resource for glycosyltransferase sequences and annotations. Database: the Journal of Biological Databases and Curation, 2020, 2020, .                                     | 3.0  | 9         |
| 22 | Convergent alteration of lung tissue microbiota and tumor cells in lung cancer. IScience, 2022, 25, 103638.                                                                                   | 4.1  | 9         |
| 23 | An interactive viral genome evolution network analysis system enabling rapid large-scale molecular tracing of SARS-CoV-2. Science Bulletin, 2022, 67, 665-669.                                | 9.0  | 9         |
| 24 | Dynamic alterations of genome and transcriptome in KRAS G13D mutant CRC PDX model treated with cetuximab. BMC Cancer, 2020, 20, 416.                                                          | 2.6  | 5         |
| 25 | Dr <i>AFC</i>: drug repositioning through anti-fibrosis characteristic. Briefings in Bioinformatics, 2021, 22, .                                                                              | 6.5  | 5         |
| 26 | Bioinformatics Research on the SARS Coronavirus (SARS_CoV) in China. Current Pharmaceutical Design, 2006, 12, 4565-4572.                                                                      | 1.9  | 4         |
| 27 | Subtyping of type A influenza by sequencing the variable regions of HA gene specifically amplified with RT-PCR. Science Bulletin, 2009, 54, 2164-2167.                                        | 1.7  | 3         |
| 28 | A Novel Mutation of the KLK6 Gene in a Family With Knee Osteoarthritis. Frontiers in Genetics, 2021, 12, 784176.                                                                              | 2.3  | 3         |
| 29 | Linking genomic and epidemiologic information to advance the study of COVID-19. Scientific Data, 2022, 9, 121.                                                                                | 5.3  | 3         |
| 30 | The optimization of running time for a maximum common substructure-based algorithm and its application in drug design. Computational Biology and Chemistry, 2014, 48, 14-20.                  | 2.3  | 2         |
| 31 | SAS: A Platform of Spike Antigenicity for SARS-CoV-2. Frontiers in Cell and Developmental Biology, 2021, 9, 713188.                                                                           | 3.7  | 1         |
| 32 | SysFinder: A customized platform for search, comparison and assisted design of appropriate animal models based on systematic similarity. Journal of Genetics and Genomics, 2017, 44, 251-258. | 3.9  | 0         |
| 33 | Putative Familial Transmissible Bacteria of Various Body Niches Link with Home Environment and Children's Immune Health. Microbiology Spectrum, 2021, 9, e0087221.                            | 3.0  | 0         |
| 34 | Quantitative Data Integration Analysis Method for Cross-Studies: Obstructive Sleep Apnea as an Example. Computational and Mathematical Methods in Medicine, 2022, 2022, 1-10.                 | 1.3  | 0         |