

Gong Zhang

List of Publications by Year in descending order

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79
papers

3,636
citations

159585

30
h-index

149698

56
g-index

87
all docs

87
docs citations

87
times ranked

5549
citing authors

#	ARTICLE	IF	CITATIONS
1	Highly Robust <i>de Novo</i> Full-Length Protein Sequencing. <i>Analytical Chemistry</i> , 2022, 94, 3467-3475.	6.5	7
2	Efficient Detection of the Alternative Spliced Human Proteome Using Translatome Sequencing. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, .	3.5	2
3	Increased photosystem II translation efficiency as an important photoprotective mechanism in an <i>Arabidopsis thaliana</i> ecotype (Tibet-0) adapted to high light environments. <i>Environmental and Experimental Botany</i> , 2021, 183, 104350.	4.2	7
4	Temperature dependence of the SARS-CoV-2 affinity to human ACE2 determines COVID-19 progression and clinical outcome. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 161-167.	4.1	33
5	The Ultrafast and Accurate Mapping Algorithm FANSe3: Mapping a Human Whole-Genome Sequencing Dataset Within 30 Minutes. <i>Phenomics</i> , 2021, 1, 22-30.	2.9	13
6	Autoactivation of Translation Causes the Bloom of <i>Prorocentrum donghaiense</i> in Harmful Algal Blooms. <i>Journal of Proteome Research</i> , 2021, 20, 3179-3187.	3.7	1
7	V367F Mutation in SARS-CoV-2 Spike RBD Emerging during the Early Transmission Phase Enhances Viral Infectivity through Increased Human ACE2 Receptor Binding Affinity. <i>Journal of Virology</i> , 2021, 95, e0061721.	3.4	90
8	Robust Glycogene-Based Prognostic Signature for Proficient Mismatch Repair Colorectal Adenocarcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 727752.	2.8	2
9	Genome Recombination-Mediated tRNA Up-Regulation Conducts General Antibiotic Resistance of Bacteria at Early Stage. <i>Frontiers in Microbiology</i> , 2021, 12, 793923.	3.5	0
10	A tumor suppressor enhancing module orchestrated by GATA4 denotes a therapeutic opportunity for GATA4 deficient HCC patients. <i>Theranostics</i> , 2020, 10, 484-497.	10.0	17
11	Germline variation networks in the PI3K/AKT pathway corresponding to familial high-incidence lung cancer pedigrees. <i>BMC Cancer</i> , 2020, 20, 1209.	2.6	4
12	Induction of immunogenic cell death in radiation-resistant breast cancer stem cells by repurposing anti-alcoholism drug disulfiram. <i>Cell Communication and Signaling</i> , 2020, 18, 36.	6.5	47
13	XY-Meta: A High-Efficiency Search Engine for Large-Scale Metabolome Annotation with Accurate FDR Estimation. <i>Analytical Chemistry</i> , 2020, 92, 5701-5707.	6.5	12
14	A fast, simple, and cost-effective method of expanding patient-derived xenograft mouse models of pancreatic ductal adenocarcinoma. <i>Journal of Translational Medicine</i> , 2020, 18, 255.	4.4	8
15	Understanding the proteome encoded by non-coding RNAs: new insights into human genome. <i>Science China Life Sciences</i> , 2020, 63, 986-995.	4.9	17
16	De novo transcriptome analysis of the mussel <i>Perna viridis</i> after exposure to the toxic dinoflagellate <i>Prorocentrum lima</i> . <i>Ecotoxicology and Environmental Safety</i> , 2020, 192, 110265.	6.0	25
17	A hidden human proteome encoded by non-coding genes. <i>Nucleic Acids Research</i> , 2019, 47, 8111-8125.	14.5	110
18	Translatomics: The Global View of Translation. <i>International Journal of Molecular Sciences</i> , 2019, 20, 212.	4.1	62

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19	Misassembly of long reads undermines de novo-assembled ethnicity-specific genomes: validation in a Chinese Han population. <i>Human Genetics</i> , 2019, 138, 757-769.	3.8	6
20	Multifaceted Stoichiometry Control of Bacterial Operons Revealed by Deep Proteome Quantification. <i>Frontiers in Genetics</i> , 2019, 10, 473.	2.3	9
21	Photocatalytic Protein Damage by Silver Nanoparticles Circumvents Bacterial Stress Response and Multidrug Resistance. <i>MSphere</i> , 2019, 4, .	2.9	23
22	The long noncoding RNA lnc-ob1 facilitates bone formation by upregulating Osterix in osteoblasts. <i>Nature Metabolism</i> , 2019, 1, 485-496.	11.9	41
23	Lung cancer deficient in the tumor suppressor GATA4 is sensitive to TGFBR1 inhibition. <i>Nature Communications</i> , 2019, 10, 1665.	12.8	45
24	Enhancing co-translational folding of heterologous protein by deleting non-essential ribosomal proteins in <i>Pichia pastoris</i> . <i>Biotechnology for Biofuels</i> , 2019, 12, 38.	6.2	7
25	Two zinc-binding domains in the transporter AdcA from facilitate high-affinity binding and fast transport of zinc. <i>Journal of Biological Chemistry</i> , 2018, 293, 6075-6089.	3.4	28
26	In vivo CRISPR screening unveils histone demethylase UTX as an important epigenetic regulator in lung tumorigenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3978-E3986.	7.1	78
27	Capturing the interactome of newly transcribed RNA. <i>Nature Methods</i> , 2018, 15, 213-220.	19.0	170
28	Steady-state structural fluctuation is a predictor of the necessity of pausing-mediated co-translational folding for small proteins. <i>Biochemical and Biophysical Research Communications</i> , 2018, 498, 186-192.	2.1	2
29	TranslatomeDB: a comprehensive database and cloud-based analysis platform for translatome sequencing data. <i>Nucleic Acids Research</i> , 2018, 46, D206-D212.	14.5	36
30	Optimal Settings of Mass Spectrometry Open Search Strategy for Higher Confidence. <i>Journal of Proteome Research</i> , 2018, 17, 3719-3729.	3.7	7
31	A peptide encoded by circular form of LINC-PINT suppresses oncogenic transcriptional elongation in glioblastoma. <i>Nature Communications</i> , 2018, 9, 4475.	12.8	519
32	Low-cost, Low-bias and Low-input RNA-seq with High Experimental Verifiability based on Semiconductor Sequencing. <i>Scientific Reports</i> , 2017, 7, 1053.	3.3	8
33	Sets of serum exosomal microRNAs as candidate diagnostic biomarkers for Kawasaki disease. <i>Scientific Reports</i> , 2017, 7, 44706.	3.3	34
34	Protein-Level Integration Strategy of Multiengine MS Spectra Search Results for Higher Confidence and Sequence Coverage. <i>Journal of Proteome Research</i> , 2017, 16, 4446-4454.	3.7	14
35	The flightless I protein interacts with RNA-binding proteins and is involved in the genome-wide mRNA post-transcriptional regulation in lung carcinoma cells. <i>International Journal of Oncology</i> , 2017, 51, 347-361.	3.3	5
36	Application of the hyper-accurate mapping algorithm FANSe for next-generation sequencing in non-model organisms. <i>Scientia Sinica Vitae</i> , 2017, 47, 702-707.	0.3	2

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37	Expression status of folate receptor alpha is a predictor of survival in pancreatic ductal adenocarcinoma. <i>Oncotarget</i> , 2017, 8, 37646-37656.	1.8	23
38	Integrated Translatomics with Proteomics to Identify Novel Iron-Transporting Proteins in <i>Streptococcus pneumoniae</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 78.	3.5	37
39	Cytoskeleton-centric protein transportation by exosomes transforms tumor-favorable macrophages. <i>Oncotarget</i> , 2016, 7, 67387-67402.	1.8	56
40	Phosphoproteome Characterization of Human Colorectal Cancer SW620 Cell-Derived Exosomes and New Phosphosite Discovery for C-HPP. <i>Journal of Proteome Research</i> , 2016, 15, 4060-4072.	3.7	31
41	Cytoplasmic hnRNPK interacts with GSK3 β and is essential for the osteoclast differentiation. <i>Scientific Reports</i> , 2016, 5, 17732.	3.3	35
42	Heterogeneity of CD34 and CD38 expression in acute B lymphoblastic leukemia cells is reversible and not hierarchically organized. <i>Journal of Hematology and Oncology</i> , 2016, 9, 94.	17.0	15
43	Bacteria differently regulate mRNA abundance to specifically respond to various stresses. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2016, 374, 20150069.	3.4	82
44	Genome-Wide and Experimental Resolution of Relative Translation Elongation Speed at Individual Gene Level in Human Cells. <i>PLoS Genetics</i> , 2016, 12, e1005901.	3.5	36
45	Revealing crosstalk of plant and fungi in the symbiotic roots of sewage-cleaning <i>Eichhornia crassipes</i> using direct de novo metatranscriptomic analysis. <i>Scientific Reports</i> , 2015, 5, 15407.	3.3	15
46	Transfer RNAs Mediate the Rapid Adaptation of <i>Escherichia coli</i> to Oxidative Stress. <i>PLoS Genetics</i> , 2015, 11, e1005302.	3.5	93
47	Finding Missing Proteins from the Epigenetically Manipulated Human Cell with Stringent Quality Criteria. <i>Journal of Proteome Research</i> , 2015, 14, 3645-3657.	3.7	22
48	Identification of Missing Proteins Defined by Chromosome-Centric Proteome Project in the Cytoplasmic Detergent-Insoluble Proteins. <i>Journal of Proteome Research</i> , 2015, 14, 3693-3709.	3.7	29
49	Length-dependent translation initiation benefits the functional proteome of human cells. <i>Molecular BioSystems</i> , 2015, 11, 370-378.	2.9	23
50	FANSe2: A Robust and Cost-Efficient Alignment Tool for Quantitative Next-Generation Sequencing Applications. <i>PLoS ONE</i> , 2014, 9, e94250.	2.5	42
51	Systematic identification of tRNA ^{ome} and its dynamics in <i>actococcus lactis</i> . <i>Molecular Microbiology</i> , 2014, 93, 944-956.	2.5	52
52	How to discover new proteins—translatome profiling. <i>Science China Life Sciences</i> , 2014, 57, 358-360.	4.9	18
53	Omics Evidence: Single Nucleotide Variants Transmissions on Chromosome 20 in Liver Cancer Cell Lines. <i>Journal of Proteome Research</i> , 2014, 13, 200-211.	3.7	14
54	Systematic Analyses of the Transcriptome, Translatome, and Proteome Provide a Global View and Potential Strategy for the C-HPP. <i>Journal of Proteome Research</i> , 2014, 13, 38-49.	3.7	60

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55	Rational design of translational pausing without altering the amino acid sequence dramatically promotes soluble protein expression: A strategic demonstration. <i>Journal of Biotechnology</i> , 2014, 189, 104-113.	3.8	6
56	Systematic Analysis of Missing Proteins Provides Clues to Help Define All of the Protein-Coding Genes on Human Chromosome 1. <i>Journal of Proteome Research</i> , 2014, 13, 114-125.	3.7	21
57	Direct Interaction of 14-3-3 σ with Ezrin Promotes Cell Migration by Regulating the Formation of Membrane Ruffle. <i>Journal of Molecular Biology</i> , 2014, 426, 3118-3133.	4.2	14
58	Chromosome-8-Coded Proteome of Chinese Chromosome Proteome Data Set (CCPD) 2.0 with Partial Immunohistochemical Verifications. <i>Journal of Proteome Research</i> , 2014, 13, 126-136.	3.7	11
59	Resolving Chromosome-Centric Human Proteome with Translating mRNA Analysis: A Strategic Demonstration. <i>Journal of Proteome Research</i> , 2014, 13, 50-59.	3.7	38
60	Iterative Genome Correction Largely Improves Proteomic Analysis of Nonmodel Organisms. <i>Journal of Proteome Research</i> , 2014, 13, 2724-2734.	3.7	14
61	Monitoring of the serum proteome in Kawasaki disease patients before and after immunoglobulin therapy. <i>Biochemical and Biophysical Research Communications</i> , 2014, 447, 19-25.	2.1	10
62	Binomial Probability Distribution Model-Based Protein Identification Algorithm for Tandem Mass Spectrometry Utilizing Peak Intensity Information. <i>Journal of Proteome Research</i> , 2013, 12, 328-335.	3.7	14
63	Translating mRNAs strongly correlate to proteins in a multivariate manner and their translation ratios are phenotype specific. <i>Nucleic Acids Research</i> , 2013, 41, 4743-4754.	14.5	157
64	Dispec: A Novel Peptide Scoring Algorithm Based on Peptide Matching Discriminability. <i>PLoS ONE</i> , 2013, 8, e62724.	2.5	7
65	FANSe: an accurate algorithm for quantitative mapping of large scale sequencing reads. <i>Nucleic Acids Research</i> , 2012, 40, e83-e83.	14.5	39
66	Polyglutamine Expansion Alters the Dynamics and Molecular Architecture of Aggregates in Dentatorubropallidoluysian Atrophy*. <i>Journal of Biological Chemistry</i> , 2012, 287, 2068-2078.	3.4	10
67	tRNA concentration fine tunes protein solubility. <i>FEBS Letters</i> , 2012, 586, 3336-3340.	2.8	60
68	Natural Osmolytes Remodel the Aggregation Pathway of Mutant Huntingtin Exon 1. <i>Biochemistry</i> , 2011, 50, 2048-2060.	2.5	53
69	Folding at the birth of the nascent chain: coordinating translation with co-translational folding. <i>Current Opinion in Structural Biology</i> , 2011, 21, 25-31.	5.7	162
70	Length-dependent translation of messenger RNA by ribosomes. <i>Physical Review E</i> , 2011, 83, 042903.	2.1	21
71	Different sequence signatures in the upstream regions of plant and animal tRNA genes shape distinct modes of regulation. <i>Nucleic Acids Research</i> , 2011, 39, 3331-3339.	14.5	29
72	Global and local depletion of ternary complex limits translational elongation. <i>Nucleic Acids Research</i> , 2010, 38, 4778-4787.	14.5	73

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73	Silent mutations in sight: co-variations in tRNA abundance as a key to unravel consequences of silent mutations. <i>Molecular BioSystems</i> , 2010, 6, 1767.	2.9	42
74	Generic Algorithm to Predict the Speed of Translational Elongation: Implications for Protein Biogenesis. <i>PLoS ONE</i> , 2009, 4, e5036.	2.5	78
75	Transient ribosomal attenuation coordinates protein synthesis and co-translational folding. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 274-280.	8.2	493
76	Electrocardiogram data mining based on frame classification by dynamic time warping matching. <i>Computer Methods in Biomechanics and Biomedical Engineering</i> , 2009, 12, 701-707.	1.6	13
77	Computational genes: a tool for molecular diagnosis and therapy of aberrant mutational phenotype. <i>BMC Bioinformatics</i> , 2007, 8, 365.	2.6	10
78	Biomolecular autonomous solution of the Hamiltonian path problem via hairpin formation. <i>International Journal of Bioinformatics Research and Applications</i> , 2005, 1, 389.	0.2	5
79	Hospital financial electronic reporting. , 0, , .		1