

Quanhu Sheng

List of Publications by Citations

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125
papers

3,438
citations

36
h-index

53
g-index

141
ext. papers

4,367
ext. citations

7
avg, IF

5.22
L-index

#	Paper	IF	Citations
125	Advanced heat map and clustering analysis using heatmap3. <i>BioMed Research International</i> , 2014 , 2014, 986048	3	150
124	Large scale comparison of gene expression levels by microarrays and RNAseq using TCGA data. <i>PLoS ONE</i> , 2013 , 8, e71462	3.7	149
123	Protein phosphorylation and expression profiling by Yin-yang multidimensional liquid chromatography (Yin-yang MDLC) mass spectrometry. <i>Journal of Proteome Research</i> , 2007 , 6, 250-62	5.6	116
122	Clinical and Biological Insights Into Combined Post- and Pre-Capillary Pulmonary Hypertension. <i>Journal of the American College of Cardiology</i> , 2016 , 68, 2525-2536	15.1	111
121	Three-stage quality control strategies for DNA re-sequencing data. <i>Briefings in Bioinformatics</i> , 2014 , 15, 879-89	13.4	106
120	Finding the lost treasures in exome sequencing data. <i>Trends in Genetics</i> , 2013 , 29, 593-9	8.5	105
119	Illumina human exome genotyping array clustering and quality control. <i>Nature Protocols</i> , 2014 , 9, 2643-628.8	28.8	101
118	In vivo base editing rescues Hutchinson-Gilford progeria syndrome in mice. <i>Nature</i> , 2021 , 589, 608-614	50.4	92
117	A Randomized Phase II Neoadjuvant Study of Cisplatin, Paclitaxel With or Without Everolimus in Patients with Stage II/III Triple-Negative Breast Cancer (TNBC): Responses and Long-term Outcome Correlated with Increased Frequency of DNA Damage Response Gene Mutations, TNBC Subtype, <i>Journal of Clinical Oncology</i> , 2017 , 35, 1005-1015	12.9	79
116	Proteomic analysis with integrated multiple dimensional liquid chromatography/mass spectrometry based on elution of ion exchange column using pH steps. <i>Analytical Chemistry</i> , 2005 , 77, 5793-9	7.8	68
115	A high-throughput approach for subcellular proteome: identification of rat liver proteins using subcellular fractionation coupled with two-dimensional liquid chromatography tandem mass spectrometry and bioinformatic analysis. <i>Molecular and Cellular Proteomics</i> , 2004 , 3, 441-55	7.6	66
114	The human plasma proteome: analysis of Chinese serum using shotgun strategy. <i>Proteomics</i> , 2005 , 5, 3442-53	4.8	65
113	Heatmap3: an improved heatmap package with more powerful and convenient features. <i>BMC Bioinformatics</i> , 2014 , 15, P16	3.6	64
112	A comparative proteomic strategy for subcellular proteome research: ICAT approach coupled with bioinformatics prediction to ascertain rat liver mitochondrial proteins and indication of mitochondrial localization for catalase. <i>Molecular and Cellular Proteomics</i> , 2005 , 4, 12-34	7.6	62
111	Multi-perspective quality control of Illumina exome sequencing data using QC3. <i>Genomics</i> , 2014 , 103, 323-8	4.3	61
110	Fully automatic separation and identification of phosphopeptides by continuous pH-gradient anion exchange online coupled with reversed-phase liquid chromatography mass spectrometry. <i>Journal of Proteome Research</i> , 2009 , 8, 133-41	5.6	56
109	A bayesian approach to protein inference problem in shotgun proteomics. <i>Journal of Computational Biology</i> , 2009 , 16, 1183-93	1.7	55

108	Quantitative phosphoproteome profiling of Wnt3a-mediated signaling network: indicating the involvement of ribonucleoside-diphosphate reductase M2 subunit phosphorylation at residue serine 20 in canonical Wnt signal transduction. <i>Molecular and Cellular Proteomics</i> , 2007 , 6, 1952-67	7.6	54
107	A micro-RNA expression signature for human NAFLD progression. <i>Journal of Gastroenterology</i> , 2016 , 51, 1022-30	6.9	53
106	High-coverage proteome analysis reveals the first insight of protein modification systems in the pathogenic spirochete <i>Leptospira interrogans</i> . <i>Cell Research</i> , 2010 , 20, 197-210	24.7	52
105	ProteinQuant Suite: a bundle of automated software tools for label-free quantitative proteomics. <i>Rapid Communications in Mass Spectrometry</i> , 2008 , 22, 3823-34	2.2	49
104	High-Resolution Mapping of RNA Polymerases Identifies Mechanisms of Sensitivity and Resistance to BET Inhibitors in t(8;21) AML. <i>Cell Reports</i> , 2016 , 16, 2003-16	10.6	48
103	BET bromodomain proteins regulate enhancer function during adipogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 2144-2149	11.5	45
102	Very low-level heteroplasmy mtDNA variations are inherited in humans. <i>Journal of Genetics and Genomics</i> , 2013 , 40, 607-15	4	45
101	MultiRankSeq: multiperspective approach for RNAseq differential expression analysis and quality control. <i>BioMed Research International</i> , 2014 , 2014, 248090	3	44
100	A fully automated 2-D LC-MS method utilizing online continuous pH and RP gradients for global proteome analysis. <i>Electrophoresis</i> , 2007 , 28, 4311-9	3.6	43
99	BuildSummary: using a group-based approach to improve the sensitivity of peptide/protein identification in shotgun proteomics. <i>Journal of Proteome Research</i> , 2012 , 11, 1494-502	5.6	42
98	RnaSeqSampleSize: real data based sample size estimation for RNA sequencing. <i>BMC Bioinformatics</i> , 2018 , 19, 191	3.6	41
97	Multi-perspective quality control of Illumina RNA sequencing data analysis. <i>Briefings in Functional Genomics</i> , 2017 , 16, 194-204	4.9	41
96	Fast and accurate identification of semi-tryptic peptides in shotgun proteomics. <i>Bioinformatics</i> , 2008 , 24, 102-9	7.2	40
95	Quantitative comparison of sarcomeric phosphoproteomes of neonatal and adult rat hearts. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2008 , 295, H647-56	5.2	39
94	Systematic assessment of survey scan and MS2-based abundance strategies for label-free quantitative proteomics using high-resolution MS data. <i>Journal of Proteome Research</i> , 2014 , 13, 2069-79	5.6	38
93	Transfer RNA detection by small RNA deep sequencing and disease association with myelodysplastic syndromes. <i>BMC Genomics</i> , 2015 , 16, 727	4.5	37
92	Comprehensive profiling of phosphopeptides based on anion exchange followed by flow-through enrichment with titanium dioxide (AFET). <i>Journal of Proteome Research</i> , 2010 , 9, 4585-94	5.6	37
91	Proteomic analysis of SARS associated coronavirus using two-dimensional liquid chromatography mass spectrometry and one-dimensional sodium dodecyl sulfate-polyacrylamide gel electrophoresis followed by mass spectroemtric analysis. <i>Journal of Proteome Research</i> , 2004 , 3, 549-55	5.6	37

90	Chronic rhinosinusitis in elderly patients is associated with an exaggerated neutrophilic proinflammatory response to pathogenic bacteria. <i>Journal of Allergy and Clinical Immunology</i> , 2019 , 143, 990-1002.e6	11.5	37
89	Comparative study of exome copy number variation estimation tools using array comparative genomic hybridization as control. <i>BioMed Research International</i> , 2013 , 2013, 915636	3	36
88	Large-scale identification of human biliary proteins from a cholesterol stone patient using a proteomic approach. <i>Rapid Communications in Mass Spectrometry</i> , 2005 , 19, 3569-78	2.2	36
87	Human PAH is characterized by a pattern of lipid-related insulin resistance. <i>JCI Insight</i> , 2019 , 4,	9.9	36
86	First insight into the human liver proteome from PROTEOME(SKY)-LIVER(Hu) 1.0, a publicly available database. <i>Journal of Proteome Research</i> , 2010 , 9, 79-94	5.6	35
85	High-sensitivity analysis of human plasma proteome by immobilized isoelectric focusing fractionation coupled to mass spectrometry identification. <i>Journal of Proteome Research</i> , 2005 , 4, 1265-73	5.6	34
84	Dual inhibition of endothelial miR-92a-3p and miR-489-3p reduces renal injury-associated atherosclerosis. <i>Atherosclerosis</i> , 2019 , 282, 121-131	3.1	33
83	Quantitative detection of single amino acid polymorphisms by targeted proteomics. <i>Journal of Molecular Cell Biology</i> , 2011 , 3, 309-15	6.3	32
82	Bioinformatic analysis of endogenous and exogenous small RNAs on lipoproteins. <i>Journal of Extracellular Vesicles</i> , 2018 , 7, 1506198	16.4	30
81	Quantitative proteomics reveal up-regulated protein expression of the SET complex associated with hepatocellular carcinoma. <i>Journal of Proteome Research</i> , 2012 , 11, 871-85	5.6	30
80	Concurrent quantification of proteome and phosphoproteome to reveal system-wide association of protein phosphorylation and gene expression. <i>Molecular and Cellular Proteomics</i> , 2009 , 8, 2809-26	7.6	28
79	RNAseq by Total RNA Library Identifies Additional RNAs Compared to Poly(A) RNA Library. <i>BioMed Research International</i> , 2015 , 2015, 862130	3	26
78	Comprehensive evaluation of extracellular small RNA isolation methods from serum in high throughput sequencing. <i>BMC Genomics</i> , 2017 , 18, 50	4.5	25
77	RNAseqPS: A Web Tool for Estimating Sample Size and Power for RNAseq Experiment. <i>Cancer Informatics</i> , 2014 , 13, 1-5	2.4	25
76	Large scale phosphoproteome profiles comprehensive features of mouse embryonic stem cells. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M110.001750	7.6	25
75	Patterns of olfactory dysfunction in chronic rhinosinusitis identified by hierarchical cluster analysis and machine learning algorithms. <i>International Forum of Allergy and Rhinology</i> , 2019 , 9, 255-264	6.3	24
74	Beta cell secretion of miR-375 to HDL is inversely associated with insulin secretion. <i>Scientific Reports</i> , 2019 , 9, 3803	4.9	23
73	Optimization of Search Engines and Postprocessing Approaches to Maximize Peptide and Protein Identification for High-Resolution Mass Data. <i>Journal of Proteome Research</i> , 2015 , 14, 4662-73	5.6	23

72	Prefractionation of proteome by liquid isoelectric focusing prior to two-dimensional liquid chromatography mass spectrometric identification. <i>Journal of Proteome Research</i> , 2005 , 4, 1256-64	5.6	23
71	Practicability of detecting somatic point mutation from RNA high throughput sequencing data. <i>Genomics</i> , 2016 , 107, 163-9	4.3	23
70	Targeting MYCN-expressing triple-negative breast cancer with BET and MEK inhibitors. <i>Science Translational Medicine</i> , 2020 , 12,	17.5	22
69	beRBP: binding estimation for human RNA-binding proteins. <i>Nucleic Acids Research</i> , 2019 , 47, e26	20.1	22
68	Quantitative assessment of cell population diversity in single-cell landscapes. <i>PLoS Biology</i> , 2018 , 16, e2006687	9.7	22
67	ICan: an optimized ion-current-based quantification procedure with enhanced quantitative accuracy and sensitivity in biomarker discovery. <i>Journal of Proteome Research</i> , 2014 , 13, 5888-97	5.6	21
66	Comparison of triple-negative breast cancer molecular subtyping using RNA from matched fresh-frozen versus formalin-fixed paraffin-embedded tissue. <i>BMC Cancer</i> , 2017 , 17, 241	4.8	20
65	Hyperoxia Injury in the Developing Lung Is Mediated by Mesenchymal Expression of Wnt5A. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020 , 201, 1249-1262	10.2	20
64	Monitoring newly synthesized proteins over the adult life span of <i>Caenorhabditis elegans</i> . <i>Journal of Proteome Research</i> , 2015 , 14, 1483-94	5.6	19
63	MicroRNAs and tRNA-derived fragments predict the transformation of myelodysplastic syndromes to acute myeloid leukemia. <i>Leukemia and Lymphoma</i> , 2017 , 58, 1-15	1.9	18
62	The discrepancy among single nucleotide variants detected by DNA and RNA high throughput sequencing data. <i>BMC Genomics</i> , 2017 , 18, 690	4.5	18
61	Isolation of High-density Lipoproteins for Non-coding Small RNA Quantification. <i>Journal of Visualized Experiments</i> , 2016 ,	1.6	18
60	Preprocessing significantly improves the peptide/protein identification sensitivity of high-resolution isobarically labeled tandem mass spectrometry data. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 405-17	7.6	18
59	Interim analysis of an open-label randomized controlled trial evaluating nasal irrigations in non-hospitalized patients with coronavirus disease 2019. <i>International Forum of Allergy and Rhinology</i> , 2020 , 10, 1325-1328	6.3	18
58	Proteomic changes in the photoreceptor outer segment upon intense light exposure. <i>Journal of Proteome Research</i> , 2010 , 9, 1173-81	5.6	17
57	Performance Investigation of Proteomic Identification by HCD/CID Fragmentations in Combination with High/Low-Resolution Detectors on a Tribid, High-Field Orbitrap Instrument. <i>PLoS ONE</i> , 2016 , 11, e0160160	3.7	17
56	Heterozygosity Ratio, a Robust Global Genomic Measure of Autozygosity and Its Association with Height and Disease Risk. <i>Genetics</i> , 2016 , 204, 893-904	4	16
55	lncRNA expression in the auditory forebrain during postnatal development. <i>Gene</i> , 2016 , 593, 201-216	3.8	16

54	Development and Validation of a MicroRNA Panel to Differentiate Between Patients with Rheumatoid Arthritis or Systemic Lupus Erythematosus and Controls. <i>Journal of Rheumatology</i> , 2020 , 47, 188-196	4.1	15
53	The Landscape of Small Non-Coding RNAs in Triple-Negative Breast Cancer. <i>Genes</i> , 2018 , 9,	4.2	14
52	RNA Sequencing of Formalin-Fixed, Paraffin-Embedded Specimens for Gene Expression Quantification and Data Mining. <i>International Journal of Genomics</i> , 2016 , 2016, 9837310	2.5	14
51	Dynamics of Zebrafish Heart Regeneration Using an HPLC-ESI-MS/MS Approach. <i>Journal of Proteome Research</i> , 2018 , 17, 1300-1308	5.6	12
50	Delicate analysis of post-translational modifications on Dishevelled 3. <i>Journal of Proteome Research</i> , 2012 , 11, 3829-37	5.6	11
49	Inflammatory heterogeneity in aspirin-exacerbated respiratory disease. <i>Journal of Allergy and Clinical Immunology</i> , 2021 , 147, 1318-1328.e5	11.5	11
48	p73 Is Required for Ovarian Follicle Development and Regulates a Gene Network Involved in Cell-to-Cell Adhesion. <i>IScience</i> , 2018 , 8, 236-249	6.1	11
47	Genomic Positional Dissection of RNA Editomes in Tumor and Normal Samples. <i>Frontiers in Genetics</i> , 2019 , 10, 211	4.5	10
46	Detection of internal exon deletion with exon Del. <i>BMC Bioinformatics</i> , 2014 , 15, 332	3.6	10
45	Differential pre-malignant programs and microenvironment chart distinct paths to malignancy in human colorectal polyps.. <i>Cell</i> , 2021 , 184, 6262-6280.e26	56.2	10
44	A Bayesian Approach to Protein Inference Problem in Shotgun Proteomics 2008 , 167-180		10
43	State-Based Liver Distribution: Broad Sharing With Less Harm to Vulnerable and Underserved Communities Compared With Concentric Circles. <i>Liver Transplantation</i> , 2019 , 25, 588-597	4.5	9
42	De novo identification and quantification of single amino-acid variants in human brain. <i>Journal of Molecular Cell Biology</i> , 2014 , 6, 421-33	6.3	9
41	On the estimation of false positives in peptide identifications using decoy search strategy. <i>Proteomics</i> , 2009 , 9, 194-204	4.8	9
40	Plasma miRNAs improve the prediction of coronary atherosclerosis in patients with rheumatoid arthritis. <i>Clinical Rheumatology</i> , 2021 , 40, 2211-2219	3.9	9
39	Tumor-Specific Major Histocompatibility-II Expression Predicts Benefit to Anti-PD-1/L1 Therapy in Patients With HER2-Negative Primary Breast Cancer. <i>Clinical Cancer Research</i> , 2021 ,	12.9	8
38	O18Quant: a semiautomatic strategy for quantitative analysis of high-resolution 16O/18O labeled data. <i>BioMed Research International</i> , 2014 , 2014, 971857	3	7
37	The Endogenous Plasma Small RNAome of Rheumatoid Arthritis. <i>ACR Open Rheumatology</i> , 2020 , 2, 97-105		7

36	scRNABatchQC: multi-samples quality control for single cell RNA-seq data. <i>Bioinformatics</i> , 2019 , 35, 5306-53086		
35	A platform to standardize, store, and visualize proteomics experimental data. <i>Acta Biochimica Et Biophysica Sinica</i> , 2009 , 41, 273-9	2.8	6
34	Comparative Transcriptomics of , Patient-Derived Endothelial Cells Reveals Novel Pathways Associated With Type2 Diabetes Mellitus. <i>JACC Basic To Translational Science</i> , 2019 , 4, 567-574	8.7	5
33	Directed solutions to address differences in access to liver transplantation. <i>American Journal of Transplantation</i> , 2018 , 18, 2670-2678	8.7	5
32	Longitudinal stability of chronic rhinosinusitis endotypes. <i>Clinical and Experimental Allergy</i> , 2019 , 49, 1637-1640	4.1	5
31	Acquisition of aneuploidy drives mutant p53-associated gain-of-function phenotypes. <i>Nature Communications</i> , 2021 , 12, 5184	17.4	5
30	SWATH-MS in proteomics: current status. <i>International Journal of Computational Biology and Drug Design</i> , 2015 , 8, 192	0.4	3
29	SRMBuilder: a user-friendly tool for selected reaction monitoring data analysis. <i>Journal of Bioinformatics and Computational Biology</i> , 2011 , 9 Suppl 1, 51-62	1	3
28	A computational approach to characterizing bond linkages of glycan isomers using matrix-assisted laser desorption/ionization tandem time-of-flight mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2008 , 22, 3561-9	2.2	3
27	Comparison of a proteomic approach with a microarray-based approach to detect exons in the mouse genome. <i>Nature Genetics</i> , 2006 , 38, 1223-4	36.3	3
26	Circulating microbial small RNAs are altered in patients with rheumatoid arthritis. <i>Annals of the Rheumatic Diseases</i> , 2020 , 79, 1557-1564	2.4	3
25	Clinical and genetic associations with prostacyclin response in pulmonary arterial hypertension. <i>Pulmonary Circulation</i> , 2018 , 8, 2045894018800544	2.7	3
24	A peptide-retrieval strategy enables significant improvement of quantitative performance without compromising confidence of identification. <i>Journal of Proteomics</i> , 2017 , 152, 276-282	3.9	2
23	Pervasive Small RNAs in Cardiometabolic Research: Great Potential Accompanied by Biological and Technical Barriers. <i>Diabetes</i> , 2020 , 69, 813-822	0.9	2
22	AnnoGen: annotating genome-wide pragmatic features. <i>Bioinformatics</i> , 2020 , 36, 2899-2901	7.2	2
21	DupChecker: a bioconductor package for checking high-throughput genomic data redundancy in meta-analysis. <i>BMC Bioinformatics</i> , 2014 , 15, 323	3.6	2
20	Pharmacological blockade of the EP3 prostaglandin E receptor in the setting of type 2 diabetes enhances cell proliferation and identity and relieves oxidative damage. <i>Molecular Metabolism</i> , 2021 , 54, 101347	8.8	2
19	Cancer-specific expression quantitative loci are affected by expression dysregulation. <i>Briefings in Bioinformatics</i> , 2018 ,	13.4	2

18	Comparative analysis of myometrial and vascular smooth muscle cells to determine optimal cells for use in drug discovery. <i>Pharmacological Research</i> , 2019 , 146, 104268	10.2	1
17	Non-canonical RNA-DNA differences and other human genomic features are enriched within very short tandem repeats. <i>PLoS Computational Biology</i> , 2020 , 16, e1007968	5	1
16	NGSPERL: a semi-automated framework for large scale next generation sequencing data analysis. <i>International Journal of Computational Biology and Drug Design</i> , 2015 , 8, 203	0.4	1
15	Serum Proteome Changes in Healthy Subjects with Different Genotypes of NOS1AP in the Chinese Population. <i>Journal of Diabetes Research</i> , 2013 , 2013, 357630	3.9	1
14	A streamlined solution for processing, elucidating and quality control of cyclobutane pyrimidine dimer sequencing data. <i>Nature Protocols</i> , 2021 , 16, 2190-2212	18.8	1
13	Immu-Mela: An open resource for exploring immunotherapy-related multidimensional genomic profiles in melanoma. <i>Journal of Genetics and Genomics</i> , 2021 , 48, 361-368	4	1
12	Profile of Podocyte Translatome During Development of Type 2 and Type 1 Diabetic Nephropathy Using Podocyte-Specific TRAP mRNA RNA-seq. <i>Diabetes</i> , 2021 , 70, 2377-2390	0.9	1
11	scMRMA: single cell multiresolution marker-based annotation. <i>Nucleic Acids Research</i> , 2021 ,	20.1	1
10	A pan-cancer immunogenomic atlas for immune checkpoint blockade immunotherapy.. <i>Cancer Research</i> , 2021 ,	10.1	1
9	EditPredict: Prediction of RNA editable sites with convolutional neural network. <i>Genomics</i> , 2021 , 113, 3864-3871	4.3	0
8	Elucidation of physico-chemical principles of high-density lipoprotein-small RNA binding interactions.. <i>Journal of Biological Chemistry</i> , 2022 , 101952	5.4	0
7	Reply. <i>Liver Transplantation</i> , 2019 , 25, 971-973	4.5	
6	Non-canonical RNA-DNA differences and other human genomic features are enriched within very short tandem repeats 2020 , 16, e1007968		
5	Non-canonical RNA-DNA differences and other human genomic features are enriched within very short tandem repeats 2020 , 16, e1007968		
4	Non-canonical RNA-DNA differences and other human genomic features are enriched within very short tandem repeats 2020 , 16, e1007968		
3	Non-canonical RNA-DNA differences and other human genomic features are enriched within very short tandem repeats 2020 , 16, e1007968		
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