

Quanhu Sheng

List of Publications by Year in descending order

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Version: 2024-02-01

131
papers

5,065
citations

76294

40
h-index

114418

63
g-index

141
all docs

141
docs citations

141
times ranked

9838
citing authors

#	ARTICLE	IF	CITATIONS
1	In vivo base editing rescues Hutchinsonâ€“Gilford progeria syndrome in mice. <i>Nature</i> , 2021, 589, 608-614.	13.7	275
2	Advanced Heat Map and Clustering Analysis Using Heatmap3. <i>BioMed Research International</i> , 2014, 2014, 1-6.	0.9	252
3	Large Scale Comparison of Gene Expression Levels by Microarrays and RNAseq Using TCGA Data. <i>PLoS ONE</i> , 2013, 8, e71462.	1.1	189
4	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.	1.2	160
5	Illumina human exome genotyping array clustering and quality control. <i>Nature Protocols</i> , 2014, 9, 2643-2662.	5.5	153
6	Three-stage quality control strategies for DNA re-sequencing data. <i>Briefings in Bioinformatics</i> , 2014, 15, 879-889.	3.2	141
7	Differential pre-malignant programs and microenvironment chart distinct paths to malignancy in human colorectal polyps. <i>Cell</i> , 2021, 184, 6262-6280.e26.	13.5	125
8	Finding the lost treasures in exome sequencing data. <i>Trends in Genetics</i> , 2013, 29, 593-599.	2.9	124
9	Protein Phosphorylation and Expression Profiling by Yin-Yang Multidimensional Liquid Chromatography (Yin-Yang MDLC) Mass Spectrometry. <i>Journal of Proteome Research</i> , 2007, 6, 250-262.	1.8	123
10	Heatmap3: an improved heatmap package with more powerful and convenient features. <i>BMC Bioinformatics</i> , 2014, 15, .	1.2	122
11	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, AR Status, and Ki67. <i>Clinical Cancer Research</i> , 2017, 23, 4035-4045.	3.2	104
12	Multi-perspective quality control of Illumina exome sequencing data using QC3. <i>Genomics</i> , 2014, 103, 323-328.	1.3	79
13	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, 5793-5799.	3.2	75
14	A micro-RNA expression signature for human NAFLD progression. <i>Journal of Gastroenterology</i> , 2016, 51, 1022-1030.	2.3	74
15	A Bayesian Approach to Protein Inference Problem in Shotgun Proteomics. <i>Journal of Computational Biology</i> , 2009, 16, 1183-1193.	0.8	72
16	A High-throughput Approach for Subcellular Proteome. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 441-455.	2.5	71
17	A Comparative Proteomic Strategy for Subcellular Proteome Research. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 12-34.	2.5	71
18	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, 2003-2016.	2.9	69

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19	Human PAH is characterized by a pattern of lipid-related insulin resistance. JCI Insight, 2019, 4, .	2.3	69
20	Multi-perspective quality control of Illumina RNA sequencing data analysis. Briefings in Functional Genomics, 2017, 16, elw035.	1.3	68
21	The human plasma proteome: Analysis of Chinese serum using shotgun strategy. Proteomics, 2005, 5, 3442-3453.	1.3	66
22	BET bromodomain proteins regulate enhancer function during adipogenesis. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 2144-2149.	3.3	65
23	Very Low-Level Heteroplasmy mtDNA Variations Are Inherited in Humans. Journal of Genetics and Genomics, 2013, 40, 607-615.	1.7	63
24	High-coverage proteome analysis reveals the first insight of protein modification systems in the pathogenic spirochete Leptospira interrogans. Cell Research, 2010, 20, 197-210.	5.7	60
25	Bioinformatic analysis of endogenous and exogenous small RNAs on lipoproteins. Journal of Extracellular Vesicles, 2018, 7, 1506198.	5.5	60
26	Fully Automatic Separation and Identification of Phosphopeptides by Continuous pH-Gradient Anion Exchange Online Coupled with Reversed-Phase Liquid Chromatography Mass Spectrometry. Journal of Proteome Research, 2009, 8, 133-141.	1.8	59
27	RnaSeqSampleSize: real data based sample size estimation for RNA sequencing. BMC Bioinformatics, 2018, 19, 191.	1.2	59
28	Quantitative Phosphoproteome Profiling of Wnt3a-mediated Signaling Network. Molecular and Cellular Proteomics, 2007, 6, 1952-1967.	2.5	57
29	Dual inhibition of endothelial miR-92a-3p and miR-489-3p reduces renal injury-associated atherosclerosis. Atherosclerosis, 2019, 282, 121-131.	0.4	55
30	Chronic rhinosinusitis in elderly patients is associated with an exaggerated neutrophilic proinflammatory response to pathogenic bacteria. Journal of Allergy and Clinical Immunology, 2019, 143, 990-1002.e6.	1.5	54
31	ProteinQuant Suite: a bundle of automated software tools for label-free quantitative proteomics. Rapid Communications in Mass Spectrometry, 2008, 22, 3823-3834.	0.7	52
32	BuildSummary: Using a Group-Based Approach To Improve the Sensitivity of Peptide/Protein Identification in Shotgun Proteomics. Journal of Proteome Research, 2012, 11, 1494-1502.	1.8	52
33	Hyperoxia Injury in the Developing Lung Is Mediated by Mesenchymal Expression of Wnt5A. American Journal of Respiratory and Critical Care Medicine, 2020, 201, 1249-1262.	2.5	52
34	MultiRankSeq: Multiperspective Approach for RNAseq Differential Expression Analysis and Quality Control. BioMed Research International, 2014, 2014, 1-8.	0.9	50
35	A fully automated 2D LC-MS method utilizing online continuous pH and RP gradients for global proteome analysis. Electrophoresis, 2007, 28, 4311-4319.	1.3	47
36	Fast and accurate identification of semi-tryptic peptides in shotgun proteomics. Bioinformatics, 2008, 24, 102-109.	1.8	47

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37	Comparative Study of Exome Copy Number Variation Estimation Tools Using Array Comparative Genomic Hybridization as Control. <i>BioMed Research International</i> , 2013, 2013, 1-7.	0.9	47
38	Targeting MYCN-expressing triple-negative breast cancer with BET and MEK inhibitors. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	46
39	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.	1.5	43
40	Quantitative comparison of sarcomeric phosphoproteomes of neonatal and adult rat hearts. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2008, 295, H647-H656.	1.5	42
41	Transfer RNA detection by small RNA deep sequencing and disease association with myelodysplastic syndromes. <i>BMC Genomics</i> , 2015, 16, 727.	1.2	42
42	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, 2069-2079.	1.8	41
43	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, 549-555.	1.8	40
44	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.	1.8	40
45	Quantitative assessment of cell population diversity in single-cell landscapes. <i>PLoS Biology</i> , 2018, 16, e2006687.	2.6	40
46	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, 1265-1273.	1.8	39
47	Quantitative detection of single amino acid polymorphisms by targeted proteomics. <i>Journal of Molecular Cell Biology</i> , 2011, 3, 309-315.	1.5	39
48	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, 27, 5299-5306.	3.2	39
49	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, 3569-3578.	0.7	38
50	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, 4585-4594.	1.8	37
51	Inflammatory heterogeneity in aspirin-exacerbated respiratory disease. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 147, 1318-1328.e5.	1.5	37
52	Beta cell secretion of miR-375 to HDL is inversely associated with insulin secretion. <i>Scientific Reports</i> , 2019, 9, 3803.	1.6	35
53	beRBP: binding estimation for human RNA-binding proteins. <i>Nucleic Acids Research</i> , 2019, 47, e26-e26.	6.5	35
54	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, 2809-2826.	2.5	34

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55	RNAseq by Total RNA Library Identifies Additional RNAs Compared to Poly(A) RNA Library. <i>BioMed Research International</i> , 2015, 2015, 1-9.	0.9	34
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.	1.2	33
57	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.	1.0	33
58	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.	1.5	32
59	DC ENaC-Dependent Inflammasome Activation Contributes to Salt-Sensitive Hypertension. <i>Circulation Research</i> , 2022, 131, 328-344.	2.0	31
60	Quantitative Proteomics Reveal up-regulated Protein Expression of the SET Complex Associated with Hepatocellular Carcinoma. <i>Journal of Proteome Research</i> , 2012, 11, 871-885.	1.8	30
61	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, 4662-4673.	1.8	30
62	Practicability of detecting somatic point mutation from RNA high throughput sequencing data. <i>Genomics</i> , 2016, 107, 163-169.	1.3	30
63	The discrepancy among single nucleotide variants detected by DNA and RNA high throughput sequencing data. <i>BMC Genomics</i> , 2017, 18, 690.	1.2	30
64	Acquisition of aneuploidy drives mutant p53-associated gain-of-function phenotypes. <i>Nature Communications</i> , 2021, 12, 5184.	5.8	30
65	Large Scale Phosphoproteome Profiles Comprehensive Features of Mouse Embryonic Stem Cells. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.001750.	2.5	29
66	RNAseqPS: A Web Tool for Estimating Sample Size and Power for RNAseq Experiment. <i>Cancer Informatics</i> , 2014, 13s6, CIN.S17688.	0.9	28
67	Isolation of High-density Lipoproteins for Non-coding Small RNA Quantification. <i>Journal of Visualized Experiments</i> , 2016, , .	0.2	28
68	Comprehensive evaluation of extracellular small RNA isolation methods from serum in high throughput sequencing. <i>BMC Genomics</i> , 2017, 18, 50.	1.2	28
69	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, 405-417.	2.5	27
70	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.	1.1	27
71	MicroRNAs and tRNA-derived fragments predict the transformation of myelodysplastic syndromes to acute myeloid leukemia. <i>Leukemia and Lymphoma</i> , 2017, 58, 2144-2155.	0.6	26
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, 1256-1264.	1.8	24

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73	Plasma miRNAs improve the prediction of coronary atherosclerosis in patients with rheumatoid arthritis. <i>Clinical Rheumatology</i> , 2021, 40, 2211-2219.	1.0	24
74	Monitoring Newly Synthesized Proteins over the Adult Life Span of <i>Caenorhabditis elegans</i> . <i>Journal of Proteome Research</i> , 2015, 14, 1483-1494.	1.8	23
75	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, 5888-5897.	1.8	22
76	Proteomic Changes in the Photoreceptor Outer Segment upon Intense Light Exposure. <i>Journal of Proteome Research</i> , 2010, 9, 1173-1181.	1.8	21
77	Performance Investigation of Proteomic Identification by HCD/CID Fragmentations in Combination with High/Low-Resolution Detectors on a Tribrid, High-Field Orbitrap Instrument. <i>PLoS ONE</i> , 2016, 11, e0160160.	1.1	21
78	The Landscape of Small Non-Coding RNAs in Triple-Negative Breast Cancer. <i>Genes</i> , 2018, 9, 29.	1.0	21
79	Genomic Positional Dissection of RNA Editomes in Tumor and Normal Samples. <i>Frontiers in Genetics</i> , 2019, 10, 211.	1.1	19
80	lncRNA expression in the auditory forebrain during postnatal development. <i>Gene</i> , 2016, 593, 201-216.	1.0	18
81	Dynamics of Zebrafish Heart Regeneration Using an HPLC-ESI-MS/MS Approach. <i>Journal of Proteome Research</i> , 2018, 17, 1300-1308.	1.8	17
82	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.	1.9	17
83	scRNABatchQC: multi-samples quality control for single cell RNA-seq data. <i>Bioinformatics</i> , 2019, 35, 5306-5308.	1.8	16
84	The Endogenous Plasma Small RNAome of Rheumatoid Arthritis. <i>ACR Open Rheumatology</i> , 2020, 2, 97-105.	0.9	16
85	scMRMA: single cell multiresolution marker-based annotation. <i>Nucleic Acids Research</i> , 2022, 50, e7-e7.	6.5	16
86	RNA Sequencing of Formalin-Fixed, Paraffin-Embedded Specimens for Gene Expression Quantification and Data Mining. <i>International Journal of Genomics</i> , 2016, 2016, 1-10.	0.8	15
87	Longitudinal stability of chronic rhinosinusitis endotypes. <i>Clinical and Experimental Allergy</i> , 2019, 49, 1637-1640.	1.4	14
88	Pharmacological blockade of the EP3 prostaglandin E2 receptor in the setting of type 2 diabetes enhances β -cell proliferation and identity and relieves oxidative damage. <i>Molecular Metabolism</i> , 2021, 54, 101347.	3.0	14
89	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.	1.3	13
90	Delicate Analysis of Post-Translational Modifications on Dishevelled 3. <i>Journal of Proteome Research</i> , 2012, 11, 3829-3837.	1.8	12

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91	Detection of internal exon deletion with exon Del. BMC Bioinformatics, 2014, 15, 332.	1.2	12
92	On the estimation of false positives in peptide identifications using decoy search strategy. Proteomics, 2009, 9, 194-204.	1.3	11
93	A Bayesian Approach to Protein Inference Problem in Shotgun Proteomics. , 2008, , 167-180.		11
94	De novo identification and quantification of single amino-acid variants in human brain. Journal of Molecular Cell Biology, 2014, 6, 421-433.	1.5	9
95	Comparative Transcriptomics of Ex Vivo, Patient-Derived Endothelial Cells Reveals Novel Pathways Associated With Type 2 Diabetes Mellitus. JACC Basic To Translational Science, 2019, 4, 567-574.	1.9	9
96	Circulating microbial small RNAs are altered in patients with rheumatoid arthritis. Annals of the Rheumatic Diseases, 2020, 79, 1557-1564.	0.5	9
97	A Pan-Cancer Immunogenomic Atlas for Immune Checkpoint Blockade Immunotherapy. Cancer Research, 2022, 82, 539-542.	0.4	9
98	O18Quant: A Semiautomatic Strategy for Quantitative Analysis of High-Resolution 16O/18O Labeled Data. BioMed Research International, 2014, 2014, 1-7.	0.9	8
99	Profile of Podocyte Translatome During Development of Type 2 and Type 1 Diabetic Nephropathy Using Podocyte-Specific TRAP mRNA RNA-seq. Diabetes, 2021, 70, 2377-2390.	0.3	8
100	Directed solutions to address differences in access to liver transplantation. American Journal of Transplantation, 2018, 18, 2670-2678.	2.6	7
101	A platform to standardize, store, and visualize proteomics experimental data. Acta Biochimica Et Biophysica Sinica, 2009, 41, 273-279.	0.9	6
102	EditPredict: Prediction of RNA editable sites with convolutional neural network. Genomics, 2021, 113, 3864-3871.	1.3	6
103	Clinical and genetic associations with prostacyclin response in pulmonary arterial hypertension. Pulmonary Circulation, 2018, 8, 1-9.	0.8	5
104	Comparative analysis of myometrial and vascular smooth muscle cells to determine optimal cells for use in drug discovery. Pharmacological Research, 2019, 146, 104268.	3.1	5
105	Comparison of a proteomic approach with a microarray-based approach to detect exons in the mouse genome. Nature Genetics, 2006, 38, 1223-1224.	9.4	4
106	A computational approach to characterizing bond linkages of glycan isomers using matrix-assisted laser desorption/ionization tandem time-of-flight mass spectrometry. Rapid Communications in Mass Spectrometry, 2008, 22, 3561-3569.	0.7	4
107	SRMBUILDER: A USER-FRIENDLY TOOL FOR SELECTED REACTION MONITORING DATA ANALYSIS. Journal of Bioinformatics and Computational Biology, 2011, 09, 51-62.	0.3	4
108	SWATH-MS in proteomics: current status. International Journal of Computational Biology and Drug Design, 2015, 8, 192.	0.3	4

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109	Cancer-specific expression quantitative loci are affected by expression dysregulation. <i>Briefings in Bioinformatics</i> , 2020, 21, 338-347.	3.2	4
110	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.	1.5	4
111	AnnoGen: annotating genome-wide pragmatic features. <i>Bioinformatics</i> , 2020, 36, 2899-2901.	1.8	4
112	Pharmacokinetic-based failure of a detergent virucidal for severe acute respiratory syndrome-coronavirus (SARS-CoV-2) nasal infections: A preclinical study and randomized controlled trial. <i>International Forum of Allergy and Rhinology</i> , 2022, , .	1.5	4
113	Elucidation of physico-chemical principles of high-density lipoprotein-small RNA binding interactions. <i>Journal of Biological Chemistry</i> , 2022, 298, 101952.	1.6	4
114	DupChecker: a bioconductor package for checking high-throughput genomic data redundancy in meta-analysis. <i>BMC Bioinformatics</i> , 2014, 15, 323.	1.2	3
115	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.	0.3	3
116	A peptide-retrieval strategy enables significant improvement of quantitative performance without compromising confidence of identification. <i>Journal of Proteomics</i> , 2017, 152, 276-282.	1.2	3
117	Pervasive Small RNAs in Cardiometabolic Research: Great Potential Accompanied by Biological and Technical Barriers. <i>Diabetes</i> , 2020, 69, 813-822.	0.3	3
118	A streamlined solution for processing, elucidating and quality control of cyclobutane pyrimidine dimer sequencing data. <i>Nature Protocols</i> , 2021, 16, 2190-2212.	5.5	3
119	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.	1.7	3
120	Combined Dusp4 and p53 loss with Dbf4 amplification drives tumorigenesis via cell cycle restriction and replication stress escape in breast cancer. <i>Breast Cancer Research</i> , 2022, 24, .	2.2	2
121	Serum Proteome Changes in Healthy Subjects with Different Genotypes of <i>NOS1AP</i> in the Chinese Population. <i>Journal of Diabetes Research</i> , 2013, 2013, 1-7.	1.0	1
122	Recent Advances in High Throughput Sequencing Analysis. <i>International Journal of Genomics</i> , 2017, 2017, 1-1.	0.8	1
123	Proteome Analysis Implicates Adaptive Changes in Metabolism and Body Wall Musculature of <i>Caenorhabditis elegans</i> Dauer Larva. <i>Journal of Integrated OMICS</i> , 2018, 8, .	0.5	0
124	Reply. <i>Liver Transplantation</i> , 2019, 25, 971-973.	1.3	0
125	Maternal Hyperglycemia Induces Changes in Gene Expression and Morphology in Mouse Placentas. <i>Gynecology & Reproductive Health</i> , 2021, 5, .	0.1	0
126	Title is missing!. , 2020, 16, e1007968.		0

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127	Title is missing!. , 2020, 16, e1007968.		0
128	Title is missing!. , 2020, 16, e1007968.		0
129	Title is missing!. , 2020, 16, e1007968.		0
130	Title is missing!. , 2020, 16, e1007968.		0
131	Title is missing!. , 2020, 16, e1007968.		0