Song Liu

List of Publications by Year
in descending order

138 papers	9,147 citations	81839 39 h-index	43868 91 g-index
141 all docs	141 docs citations	141 times ranked	14500 citing authors

#	Article	IF	Citations
1	A Draft Sequence of the Rice Genome (Oryza sativa L. ssp. indica). Science, 2002, 296, 79-92.	6.0	3,146
2	A Pilot Study of Circulating miRNAs as Potential Biomarkers of Early Stage Breast Cancer. PLoS ONE, 2010, 5, e13735.	1.1	350
3	IMA: an R package for high-throughput analysis of Illumina's 450K Infinium methylation data. Bioinformatics, 2012, 28, 729-730.	1.8	275
4	A Knowledge-Based Energy Function for Prot'einâˆ'Ligand, Proteinâˆ'Protein, and Proteinâˆ'DNA Complexes. Journal of Medicinal Chemistry, 2005, 48, 2325-2335.	2.9	264
5	Myeloid-derived suppressor cell development is regulated by a STAT/IRF-8 axis. Journal of Clinical Investigation, 2013, 123, 4464-4478.	3.9	261
6	Protein binding site prediction using an empirical scoring function. Nucleic Acids Research, 2006, 34, 3698-3707.	6.5	223
7	Tumor-Derived G-CSF Facilitates Neoplastic Growth through a Granulocytic Myeloid-Derived Suppressor Cell-Dependent Mechanism. PLoS ONE, 2011, 6, e27690.	1.1	199
8	Nrf2 Amplifies Oxidative Stress via Induction of Klf9. Molecular Cell, 2014, 53, 916-928.	4.5	186
9	A physical reference state unifies the structure-derived potential of mean force for protein folding and binding. Proteins: Structure, Function and Bioinformatics, 2004, 56, 93-101.	1.5	176
10	An accurate, residue-level, pair potential of mean force for folding and binding based on the distance-scaled, ideal-gas reference state. Protein Science, 2004, 13, 400-411.	3.1	153
11	A comparison of RNA-Seq and high-density exon array for detecting differential gene expression between closely related species. Nucleic Acids Research, 2011, 39, 578-588.	6.5	123
12	Facilitates Chromatin Transcription Complex Is an â€œAcceleratorâ€•of Tumor Transformation and Potential Marker and Target of Aggressive Cancers. Cell Reports, 2013, 4, 159-173.	2.9	116
13	Accurate and efficient loop selections by the DFIRE-based all-atom statistical potential. Protein Science, 2004, 13, 391-399.	3.1	112
14	Association of Serum Level of Vitamin D at Diagnosis With Breast Cancer Survival. JAMA Oncology, 2017, 3, 351.	3.4	111
15	Fold recognition by concurrent use of solvent accessibility and residue depth. Proteins: Structure, Function and Bioinformatics, 2007, 68, 636-645.	1.5	87
16	MUC1-C regulates lineage plasticity driving progression to neuroendocrine prostate cancer. Nature Communications, 2020, 11, 338.	5.8	87
17	Nanog Reverses the Effects of Organismal Aging on Mesenchymal Stem Cell Proliferation and Myogenic Differentiation Potential. Stem Cells, 2012, 30, 2746-2759.	1.4	81
18	Tumor Infiltrating Lymphocytes and Macrophages Improve Survival in Microsatellite Unstable Colorectal Cancer. Scientific Reports, 2019, 9, 13455.	1.6	80

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19	Computational methods for detecting copy number variations in cancer genome using next generation sequencing: principles and challenges. Oncotarget, 2013, 4, 1868-1881.	0.8	77
20	Circulating miR-148b and miR-133a as biomarkers for breast cancer detection. Oncotarget, 2014, 5, 5284-5294.	0.8	74
21	Whole-genome sequencing identifies genomic heterogeneity at a nucleotide and chromosomal level in bladder cancer. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E672-81.	3.3	72
22	SP5: Improving Protein Fold Recognition by Using Torsion Angle Profiles and Profile-Based Gap Penalty Model. PLoS ONE, 2008, 3, e2325.	1.1	68
23	Overexpression of suppressive microRNAs, miR-30a and miR-200c are associated with improved survival of breast cancer patients. Scientific Reports, 2017, 7, 15945.	1.6	62
24	A simple reference state makes a significant improvement in near‑native selections from structurally refined docking decoys. Proteins: Structure, Function and Bioinformatics, 2007, 69, 244-253.	1.5	59
25	Genome-wide methylation patterns provide insight into differences in breast tumor biology between American women of African and European ancestry. Oncotarget, 2014, 5, 237-248.	0.8	57
26	Elevated NCOR1 disrupts PPARÎ±/Î³ signaling in prostate cancer and forms a targetable epigenetic lesion. Carcinogenesis, 2010, 31, 1650-1660.	1.3	56
27	KLF9 is a novel transcriptional regulator of bortezomib- and LBH589-induced apoptosis in multiple myeloma cells. Blood, 2012, 119, 1450-1458.	0.6	56
28	Targeting FACT Complex Suppresses Mammary Tumorigenesis in <i>Her2</i>/<i>neu</i> Transgenic Mice. Cancer Prevention Research, 2012, 5, 1025-1035.	0.7	52
29	Serum microRNA expression patterns that predict early treatment failure in prostate cancer patients. Oncotarget, 2014, 5, 824-840.	0.8	52
30	What is a Desirable Statistical Energy Function for Proteins and How Can It Be Obtained?. Cell Biochemistry and Biophysics, 2006, 46, 165-174.	0.9	50
31	Pleomorphic lobular carcinoma <i>inÂsitu</i> of the breast: clinicopathological review of 47 cases. Histopathology, 2014, 64, 981-993.	1.6	50
32	A comprehensive analysis of coregulator recruitment, androgen receptor function and gene expression in prostate cancer. ELife, 2017, 6, .	2.8	49
33	MUC1-C Activates the BAF (mSWI/SNF) Complex in Prostate Cancer Stem Cells. Cancer Research, 2021, 81, 1111-1122.	0.4	46
34	OSAT: a tool for sample-to-batch allocations in genomics experiments. BMC Genomics, 2012, 13, 689.	1.2	45
35	Characterization of TAZ domains important for the induction of breast cancer stem cell properties and tumorigenesis. Cell Cycle, 2015, 14, 146-156.	1.3	45
36	Replication and validation of genetic polymorphisms associated with survival after allogeneic blood or marrow transplant. Blood, 2017, 130, 1585-1596.	0.6	45

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37	MUC1-C Activates the NuRD Complex to Drive Dedifferentiation of Triple-Negative Breast Cancer Cells. Cancer Research, 2019, 79, 5711-5722.	0.4	45
38	ER$^+$/PR$^+$/TFF3$^+$/IMP3$^-$ immunoprofile distinguishes endometrioid from serous and clear cell carcinomas of the endometrium: a study of 401 cases. Histopathology, 2013, 62, 976-985.	1.6	44
39	Pathway-guided analysis identifies Myc-dependent alternative pre-mRNA splicing in aggressive prostate cancers. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 5269-5279.	3.3	44
40	The Dependence of All-Atom Statistical Potentials on Structural Training Database. Biophysical Journal, 2004, 86, 3349-3358.	0.2	41
41	NANOG reprograms prostate cancer cells to castration resistance via dynamically repressing and engaging the AR/FOXA1 signaling axis. Cell Discovery, 2016, 2, 16041.	3.1	41
42	MUC1-C integrates activation of the IFN-Î³ pathway with suppression of the tumor immune microenvironment in triple-negative breast cancer. , 2021, 9, e002115.		41
43	MUC1-C activates the PBAF chromatin remodeling complex in integrating redox balance with progression of human prostate cancer stem cells. Oncogene, 2021, 40, 4930-4940.	2.6	41
44	XBP1-KLF9 Axis Acts as a Molecular Rheostat to Control the Transition from Adaptive to Cytotoxic Unfolded Protein Response. Cell Reports, 2018, 25, 212-223.e4.	2.9	40
45	IDO1 Expression in Ovarian Cancer Induces PD-1 in T Cells via Aryl Hydrocarbon Receptor Activation. Frontiers in Immunology, 2021, 12, 678999.	2.2	40
46	RNA Dysregulation: An Expanding Source of Cancer Immunotherapy Targets. Trends in Pharmacological Sciences, 2021, 42, 268-282.	4.0	39
47	Identification of a Clinically Relevant Androgen-Dependent Gene Signature in Prostate Cancer. Cancer Research, 2011, 71, 1978-1988.	0.4	38
48	Tamoxifen sensitivity-related microRNA-342 is a useful biomarker for breast cancer survival. Oncotarget, 2017, 8, 99978-99989.	0.8	38
49	1,25-Dihydroxyvitamin D3 (1,25(OH)2D3) Signaling Capacity and the Epithelial-Mesenchymal Transition in Non-Small Cell Lung Cancer (NSCLC): Implications for Use of 1,25(OH)2D3 in NSCLC Treatment. Cancers, 2013, 5, 1504-1521.	1.7	37
50	Nomogram to predict the likelihood of upgrade of atypical ductal hyperplasia diagnosed on a core needle biopsy in mammographically detected lesions. Histopathology, 2015, 67, 106-120.	1.6	37
51	Establishment of Definitions and Review Process for Consistent Adjudication of Cause-specific Mortality after Allogeneic Unrelated-donor Hematopoietic Cell Transplantation. Biology of Blood and Marrow Transplantation, 2015, 21, 1679-1686.	2.0	37
52	Impact of chemotherapy for breast cancer on leukocyte DNA methylation landscape and cognitive function: a prospective study. Clinical Epigenetics, 2019, 11, 45.	1.8	36
53	MUC1-C drives stemness in progression of colitis to colorectal cancer. JCI Insight, 2020, 5, .	2.3	36
54	FAK inhibition with small molecule inhibitor Y15 decreases viability, clonogenicity, and cell attachment in thyroid cancer cell lines and synergizes with targeted therapeutics. Oncotarget, 2014, 5, 7945-7959.	0.8	36

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55	A draft sequence of the rice (Oryza sativa ssp.indica) genome. Science Bulletin, 2001, 46, 1937-1942.	1.7	35
56	Docking prediction using biological information, ZDOCK sampling technique, and clustering guided by the DFIRE statistical energy function. Proteins: Structure, Function and Bioinformatics, 2005, 60, 314-318.	1.5	34
57	Novel MicroRNA-Based Risk Score Identified by Integrated Analyses to Predict Metastasis and Poor Prognosis in Breast Cancer. Annals of Surgical Oncology, 2018, 25, 4037-4046.	0.7	34
58	Genetic variants in microRNAs and breast cancer risk in African American and European American women. Breast Cancer Research and Treatment, 2013, 141, 447-459.	1.1	33
59	Structural variation discovery in the cancer genome using next generation sequencing: Computational solutions and perspectives. Oncotarget, 2015, 6, 5477-5489.	0.8	33
60	SCNVSim: somatic copy number variation and structure variation simulator. BMC Bioinformatics, 2015, 16, 66.	1.2	32
61	Replication of associations between genetic polymorphisms and chronic graft-versus-host disease. Blood, 2016, 128, 2450-2456.	0.6	32
62	Genomic profiling is predictive of response to cisplatin treatment but not to PI3K inhibition in bladder cancer patient-derived xenografts. Oncotarget, 2016, 7, 76374-76389.	0.8	32
63	MAC: identifying and correcting annotation for multi-nucleotide variations. BMC Genomics, 2015, 16, 569.	1.2	31
64	NANOG Reverses the Myogenic Differentiation Potential of Senescent Stem Cells by Restoring ACTIN Filamentous Organization and SRF-Dependent Gene Expression. Stem Cells, 2017, 35, 207-221.	1.4	30
65	Ultradeep sequencing differentiates patterns of skin clonal mutations associated with sun-exposure status and skin cancer burden. Science Advances, 2021, 7, .	4.7	29
66	Gene Expression Profiles in Stage I Uterine Serous Carcinoma in Comparison to Grade 3 and Grade 1 Stage I Endometrioid Adenocarcinoma. PLoS ONE, 2011, 6, e18066.	1.1	28
67	Metabolic adaptation of ovarian tumors in patients treated with an IDO1 inhibitor constrains antitumor immune responses. Science Translational Medicine, 2022, 14, eabg8402.	5.8	28
68	Genome-Wide Scan for Copy Number Variation Association with Age at Onset of Alzheimer's Disease. Journal of Alzheimer's Disease, 2012, 33, 517-523.	1.2	27
69	Sox4 Expression Confers Bladder Cancer Stem Cell Properties and Predicts for Poor Patient Outcome. International Journal of Biological Sciences, 2015, 11, 1363-1375.	2.6	27
70	Comparative survival analysis of breast cancer microarray studies identifies important prognostic genetic pathways. BMC Cancer, 2010, 10, 573.	1.1	26
71	Trefoil factor family 3 (TFF3) expression and its interaction with estrogen receptor (ER) in endometrial adenocarcinoma. Gynecologic Oncology, 2013, 130, 174-180.	0.6	26
72	Differential response to 1α,25-dihydroxyvitamin D3 (1α,25(OH)2D3) in non-small cell lung cancer cells with distinct oncogene mutations. Journal of Steroid Biochemistry and Molecular Biology, 2013, 136, 264-270.	1.2	26

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73	The Impact of DNA Input Amount and DNA Source on the Performance of Whole-Exome Sequencing in Cancer Epidemiology. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1207-1213.	1.1	26
74	The risk of upgrade for atypical ductal hyperplasia detected on magnetic resonance imaging‐guided biopsy: a study of 100 cases from four academic institutions. Histopathology, 2016, 68, 713-721.	1.6	26
75	Lobular neoplasia detected in MRI-guided core biopsy carries a high risk for upgrade: a study of 63 cases from four different institutions. Modern Pathology, 2016, 29, 25-33.	2.9	26
76	FOXA1 hypermethylation: link between parity and ER-negative breast cancer in African American women?. Breast Cancer Research and Treatment, 2017, 166, 559-568.	1.1	24
77	Synuclein-Î³ (SNCG) protein expression is associated with poor outcome in endometrial adenocarcinoma. Gynecologic Oncology, 2012, 124, 148-152.	0.6	23
78	Whole-genome sequencing of a malignant granular cell tumor with metabolic response to pazopanib. Journal of Physical Education and Sports Management, 2015, 1, a000380.	0.5	23
79	Molecular Analysis of Mixed Endometrioid and Serous Adenocarcinoma of the Endometrium. PLoS ONE, 2015, 10, e0130909.	1.1	23
80	Reprogramming Postnatal Human Epidermal Keratinocytes Toward Functional Neural Crest Fates. Stem Cells, 2017, 35, 1402-1415.	1.4	23
81	Homogeneity Test for Correlated Binary Data. PLoS ONE, 2015, 10, e0124337.	1.1	22
82	6p22.3 amplification as a biomarker and potential therapeutic target of advanced stage bladder cancer. Oncotarget, 2013, 4, 2124-2134.	0.8	21
83	Down-regulation of ALDH1A3, CD44 or MDR1 sensitizes resistant cancer cells to FAK autophosphorylation inhibitor Y15. Journal of Cancer Research and Clinical Oncology, 2015, 141, 1613-1631.	1.2	21
84	Genetic variations in vitamin D-related pathways and breast cancer risk in African American women in the AMBER consortium. International Journal of Cancer, 2016, 138, 2118-2126.	2.3	21
85	Exome chip analyses identify genes affecting mortality after HLA-matched unrelated-donor blood and marrow transplantation. Blood, 2018, 131, 2490-2499.	0.6	21
86	Differences in microRNA expression in breast cancer between women of African and European ancestry. Carcinogenesis, 2019, 40, 61-69.	1.3	21
87	Genetic variations in the Hippo signaling pathway and breast cancer risk in African American women in the AMBER Consortium. Carcinogenesis, 2016, 37, 951-956.	1.3	20
88	Ordered Subset Analysis of Copy Number Variation Association with Age at Onset of Alzheimer's Disease. Journal of Alzheimer's Disease, 2014, 41, 1063-1071.	1.2	19
89	QBES: Predicting real values of solvent accessibility from sequences by efficient, constrained energy optimization. Proteins: Structure, Function and Bioinformatics, 2006, 63, 961-966.	1.5	18
90	Microarray Analysis Reveals Distinct Gene Expression Profiles Among Different Tumor Histology, Stage and Disease Outcomes in Endometrial Adenocarcinoma. PLoS ONE, 2010, 5, e15415.	1.1	18

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91	Pair Box 8 (PAX8) protein expression in high grade, late stage (stages III and IV) ovarian serous carcinoma. Gynecologic Oncology, 2012, 127, 198-201.	0.6	18
92	FAK and HAS Inhibition Synergistically Decrease Colon Cancer Cell Viability and Affect Expression of Critical Genes. Anti-Cancer Agents in Medicinal Chemistry, 2013, 13, 584-594.	0.9	18
93	Web-based toolkits for topology prediction of transmembrane helical proteins, fold recognition, structure and binding scoring, folding-kinetics analysis and comparative analysis of domain combinations. Nucleic Acids Research, 2005, 33, W193-W197.	6.5	17
94	Using high-density exon arrays to profile gene expression in closely related species. Nucleic Acids Research, 2009, 37, e90-e90.	6.5	17
95	Error control variability in pathway-based microarray analysis. Bioinformatics, 2009, 25, 2216-2221.	1.8	17
96	MUC1-C represses the RASSF1A tumor suppressor in human carcinoma cells. Oncogene, 2019, 38, 7266-7277.	2.6	17
97	MUC1-C Dictates JUN and BAF-Mediated Chromatin Remodeling at Enhancer Signatures in Cancer Stem Cells. Molecular Cancer Research, 2022, 20, 556-567.	1.5	17
98	MUC1-C integrates type II interferon and chromatin remodeling pathways in immunosuppression of prostate cancer. OncoImmunology, 2022, 11, 2029298.	2.1	17
99	Evaluation of microRNA expression profiles and their associations with risk alleles in lymphoblastoid cell lines of familial ovarian cancer. Carcinogenesis, 2012, 33, 604-612.	1.3	16
100	Pax€8 is a reliable marker in making the diagnosis in advanced stage epithelial ovarian carcinoma and primary peritoneal carcinoma for neoadjuvant chemotherapy on cell block and biopsy specimens. Histopathology, 2012, 60, 1019-1020.	1.6	16
101	Ameliorating the hallmarks of cellular senescence in skeletal muscle myogenic progenitors in vitro and in vivo. Science Advances, 2021, 7, eabe5671.	4.7	16
102	VDR regulation of microRNA differs across prostate cell models suggesting extremely flexible control of transcription. Epigenetics, 2015, 10, 40-49.	1.3	15
103	Testing equality of proportions for correlated binary data in ophthalmologic studies. Journal of Biopharmaceutical Statistics, 2017, 27, 611-619.	0.4	15
104	Genetic association with B-cell acute lymphoblastic leukemia in allogeneic transplant patients differs by age and sex. Blood Advances, 2017, 1, 1717-1728.	2.5	15
105	Pitfalls of improperly procured adjacent non-neoplastic tissue for somatic mutation analysis using next-generation sequencing. BMC Medical Genomics, 2016, 9, 64.	0.7	14
106	Targeting MUC1-C Suppresses Chronic Activation of Cytosolic Nucleotide Receptors and STING in Triple-Negative Breast Cancer. Cancers, 2022, 14, 2580.	1.7	14
107	Analysis of mutations in primary and metastatic synovial sarcoma. Oncotarget, 2018, 9, 36878-36888.	0.8	12
108	Template€based structure prediction and classification of transcription factors in <i>Arabidopsis thaliana</i>. Protein Science, 2012, 21, 828-838.	3.1	11

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109	Domain Graph ofArabidopsisProteome by Comparative Analysis. Journal of Proteome Research, 2005, 4, 435-444.	1.8	10
110	Genetic variants in the mTOR pathway and breast cancer risk in African American women. Carcinogenesis, 2016, 37, 49-55.	1.3	10
111	Restoring extracellular matrix synthesis in senescent stem cells. FASEB Journal, 2019, 33, 10954-10965.	0.2	10
112	Body fatness and mTOR pathway activation of breast cancer in the Women's Circle of Health Study. Npj Breast Cancer, 2020, 6, 45.	2.3	10
113	Claudin7 and moesin in endometrial Adenocarcinoma; a retrospective study of 265 patients. BMC Research Notes, 2012, 5, 65.	0.6	9
114	Trans-ethnic follow-up of breast cancer GWAS hits using the preferential linkage disequilibrium approach. Oncotarget, 2016, 7, 83160-83176.	0.8	9
115	A methodological study of genome-wide DNA methylation analyses using matched archival formalin-fixed paraffin embedded and fresh frozen breast tumors. Oncotarget, 2017, 8, 14821-14829.	0.8	8
116	Protein Kinase N1 control of androgen-responsive serum response factor action provides rationale for novel prostate cancer treatment strategy. Oncogene, 2019, 38, 4496-4511.	2.6	8
117	Differential methylation and expression patterns of microRNAs in relation to breast cancer subtypes among American women of African and European ancestry. PLoS ONE, 2021, 16, e0249229.	1.1	8
118	Genome-Wide Association Analyses Identify Variants in IRF4 Associated With Acute Myeloid Leukemia and Myelodysplastic Syndrome Susceptibility. Frontiers in Genetics, 2021, 12, 554948.	1.1	8
119	Novel genetic variants associated with mortality after unrelated donor allogeneic hematopoietic cell transplantation. EClinicalMedicine, 2021, 40, 101093.	3.2	8
120	Aldolase mRNA expression in endometrial cancer and the role of clotrimazole in endometrial cancer cell viability and morphology. Histopathology, 2011, 59, 1015-1018.	1.6	7
121	Gene set analysis controlling for length bias in RNA-seq experiments. BioData Mining, 2017, 10, 5.	2.2	7
122	Multiple functional variants in the IL1RL1 region are pretransplant markers for risk of GVHD and infection deaths. Blood Advances, 2019, 3, 2512-2524.	2.5	7
123	Diversity in Androgen Receptor Action Among Treatment-naïve Prostate Cancers Is Reflected in Treatment Response Predictions and Molecular Subtypes. European Urology Open Science, 2020, 22, 34-44.	0.2	7
124	Associations between Gene Expression Variations and Ovarian Cancer Risk Alleles Identified from Genome Wide Association Studies. PLoS ONE, 2012, 7, e47962.	1.1	7
125	Comparison of SureSelect and Nextera Exome Capture Performance in Single-Cell Sequencing. Human Heredity, 2018, 83, 153-162.	0.4	5
126	Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with risk of clear cell ovarian cancer. Oncotarget, 2016, 7, 69097-69110.	0.8	5

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127	Uneven size distribution of mammalian genes in the number of tissues expressed and in the number of co-expressed genes. Human Molecular Genetics, 2006, 15, 1313-1318.	1.4	4
128	Deriving and comparing the distribution for the number of false positives in single step methods to control -FWER. Statistics and Probability Letters, 2011, 81, 1695-1705.	0.4	4
129	The role of hypoxic-inducible factor (HIF1Î±) and aldolaseC protein in endometrial carcinogenesis: a retrospective study of 279 patients. BMJ Open, 2012, 2, e001450.	0.8	4
130	Asymptotic confidence interval construction for proportion ratio based on correlated paired data. Journal of Biopharmaceutical Statistics, 2019, 29, 1137-1152.	0.4	4
131	Germline Genetic Variants in GATA3 and Breast Cancer Treatment Outcomes in SWOG S8897 Trial and the Pathways Study. Clinical Breast Cancer, 2019, 19, 225-235.e2.	1.1	4
132	cnvCurator: an interactive visualization and editing tool for somatic copy number variations. BMC Bioinformatics, 2015, 16, 331.	1.2	3
133	Testing equality of correlation coefficients for paired binary data from multiple groups. Journal of Statistical Computation and Simulation, 2016, 86, 1686-1696.	0.7	3
134	Body fatness and breast cancer risk in relation to phosphorylated mTOR expression in a sample of predominately Black women. Breast Cancer Research, 2021, 23, 77.	2.2	0
135	Meta-Analysis of High Throughput Oncology Data. Handbook of Statistics, 2012, , 67-95.	0.4	0
136	Analyzing Gene Pathways from Microarrays to Sequencing Platforms. , 2020, , 289-296.		0
137	An adaptive method of defining negative mutation status for multi-sample comparison using next-generation sequencing. BMC Medical Genomics, 2021, 14, 32.	0.7	0
138	Development of KAM score to predict metastasis and worse survival in breast cancer. American Journal of Cancer Research, 2021, 11, 5388-5401.	1.4	0