Purvesh Khatri

List of Publications by Year
in descending order

146 papers	17,496 citations	22132 59 h-index	16636 123 g-index
181 all docs	181 docs citations	181 times ranked	27168 citing authors

#	Article	IF	Citations
1	Ten Years of Pathway Analysis: Current Approaches and Outstanding Challenges. PLoS Computational Biology, 2012, 8, e1002375.	1.5	1,267
2	A systems biology approach for pathway level analysis. Genome Research, 2007, 17, 1537-1545.	2.4	1,036
3	A novel signaling pathway impact analysis. Bioinformatics, 2009, 25, 75-82.	1.8	950
4	Systems biological assessment of immunity to mild versus severe COVID-19 infection in humans. Science, 2020, 369, 1210-1220.	6.0	947
5	Ontological analysis of gene expression data: current tools, limitations, and open problems. Bioinformatics, 2005, 21, 3587-3595.	1.8	766
6	Global functional profiling of gene expressionâ˜†â˜†This work was funded in part by a Sun Microsystems grant awarded to S.D., NIH Grant HD36512 to S.A.K., a Wayne State University SOM Deanâ€™s Post-Doctoral Fellowship, and an NICHD Contraception and Infertility Loan to G.C.O. Support from the WSU MCBI mode is gratefully appreciated.. Genomics, 2003, 81, 98-104.	1.3	544
7	Reliability and reproducibility issues in DNA microarray measurements. Trends in Genetics, 2006, 22, 101-109.	2.9	516
8	Spermatozoal RNA profiles of normal fertile men. Lancet, The, 2002, 360, 772-777.	6.3	483
9	Cell typeâ€"specific gene expression differences in complex tissues. Nature Methods, 2010, 7, 287-289.	9.0	460
10	Profiling Gene Expression Using Onto-Express. Genomics, 2002, 79, 266-270.	1.3	429
11	A Drug Repositioning Approach Identifies Tricyclic Antidepressants as Inhibitors of Small Cell Lung Cancer and Other Neuroendocrine Tumors. Cancer Discovery, 2013, 3, 1364-1377.	7.7	366
12	Genome-wide expression for diagnosis of pulmonary tuberculosis: a multicohort analysis. Lancet Respiratory Medicine,the, 2016, 4, 213-224.	5.2	361
13	Combined inhibition of BET family proteins and histone deacetylases as a potential epigenetics-based therapy for pancreatic ductal adenocarcinoma. Nature Medicine, 2015, 21, 1163-1171.	15.2	349
14	SMYD3 links lysine methylation of MAP3K2 to Ras-driven cancer. Nature, 2014, 510, 283-287.	13.7	331
15	Onto-Tools, the toolkit of the modern biologist: Onto-Express, Onto-Compare, Onto-Design and Onto-Translate. Nucleic Acids Research, 2003, 31, 3775-3781.	6.5	319
16	A clinically meaningful metric of immune age derived from high-dimensional longitudinal monitoring. Nature Medicine, 2019, 25, 487-495.	15.2	317
17	Systems vaccinology of the BNT162b2 mRNA vaccine in humans. Nature, 2021, 596, 410-416.	13.7	313
18	Robust classification of bacterial and viral infections via integrated host gene expression diagnostics. Science Translational Medicine, 2016, 8, 346ra91.	5.8	299

#	Article	IF	Citations
19	CD22 blockade restores homeostatic microglial phagocytosis in ageing brains. Nature, 2019, 568, 187-192.	13.7	283
20	A comprehensive time-course–based multicohort analysis of sepsis and sterile inflammation reveals a robust diagnostic gene set. Science Translational Medicine, 2015, 7, 287ra71.	5.8	271
21	Single-Cell Chromatin Modification Profiling Reveals Increased Epigenetic Variations with Aging. Cell, 2018, 173, 1385-1397.e14.	13.5	250
22	Antigen Identification for Orphan T Cell Receptors Expressed on Tumor-Infiltrating Lymphocytes. Cell, 2018, 172, 549-563.e16.	13.5	226
23	Unsupervised Analysis of Transcriptomics in Bacterial Sepsis Across Multiple Datasets Reveals Three Robust Clusters. Critical Care Medicine, 2018, 46, 915-925.	0.4	219
24	A common rejection module (CRM) for acute rejection across multiple organs identifies novel therapeutics for organ transplantation. Journal of Experimental Medicine, 2013, 210, 2205-2221.	4.2	201
25	Integrated, Multi-cohort Analysis Identifies Conserved Transcriptional Signatures across Multiple Respiratory Viruses. Immunity, 2015, 43, 1199-1211.	6.6	197
26	Mechanisms of innate and adaptive immunity to the Pfizer-BioNTech BNT162b2 vaccine. Nature Immunology, 2022, 23, 543-555.	7.0	185
27	A multi-cohort study of the immune factors associated with M. tuberculosis infection outcomes. Nature, 2018, 560, 644-648.	13.7	184
28	A community approach to mortality prediction in sepsis via gene expression analysis. Nature Communications, 2018, 9, 694.	5.8	178
29	Increased monocyte count as a cellular biomarker for poor outcomes in fibrotic diseases: a retrospective, multicentre cohort study. Lancet Respiratory Medicine,the, 2019, 7, 497-508.	5.2	168
30	Cell-centred meta-analysis reveals baseline predictors of anti-TNFα non-response in biopsy and blood of patients with IBD. Gut, 2019, 68, 604-614.	6.1	153
31	Discovery of Distinct Immune Phenotypes Using Machine Learning in Pulmonary Arterial Hypertension. Circulation Research, 2019, 124, 904-919.	2.0	141
32	Onto-Tools: an ensemble of web-accessible, ontology-based tools for the functional design and interpretation of high-throughput gene expression experiments. Nucleic Acids Research, 2004, 32, W449-W456.	6.5	139
33	Methods to increase reproducibility in differential gene expression via meta-analysis. Nucleic Acids Research, 2017, 45, e1-e1.	6.5	137
34	Host-response-based gene signatures for tuberculosis diagnosis: A systematic comparison of 16 signatures. PLoS Medicine, 2019, 16, e1002786.	3.9	137
35	The single-cell epigenomic and transcriptional landscape of immunity to influenza vaccination. Cell, 2021, 184, 3915-3935.e21.	13.5	133
36	A Meta-analysis of Lung Cancer Gene Expression Identifies *PTK7* as a Survival Gene in Lung Adenocarcinoma. Cancer Research, 2014, 74, 2892-2902.	0.4	131

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37	Leveraging heterogeneity across multiple datasets increases cell-mixture deconvolution accuracy and reduces biological and technical biases. Nature Communications, 2018, 9, 4735.	5.8	128
38	Gene annotation bias impedes biomedical research. Scientific Reports, 2018, 8, 1362.	1.6	125
39	A Peripheral Blood Diagnostic Test for Acute Rejection in Renal Transplantation. American Journal of Transplantation, 2012, 12, 2710-2718.	2.6	124
40	T cell-inducing vaccine durably prevents mucosal SHIV infection even with lower neutralizing antibody titers. Nature Medicine, 2020, 26, 932-940.	15.2	124
41	Multicohort analysis reveals baseline transcriptional predictors of influenza vaccination responses. Science Immunology, 2017, 2, .	5.6	122
42	Emergent high fatality lung disease in systemic juvenile arthritis. Annals of the Rheumatic Diseases, 2019, 78, 1722-1731.	0.5	122
43	Complement pathway amplifies caspase-11â€"dependent cell death and endotoxin-induced sepsis severity. Journal of Experimental Medicine, 2016, 213, 2365-2382.	4.2	120
44	An integrative approach unveils FOSL1 as an oncogene vulnerability in KRAS-driven lung and pancreatic cancer. Nature Communications, 2017, 8, 14294.	5.8	119
45	Interpretation of biological experiments changes with evolution of the Gene Ontology and its annotations. Scientific Reports, 2018, 8, 5115.	1.6	110
46	The immunoregulatory landscape of human tuberculosis granulomas. Nature Immunology, 2022, 23, 318-329.	7.0	110
47	Recent additions and improvements to the Onto-Tools. Nucleic Acids Research, 2005, 33, W762-W765.	6.5	106
48	Progressive histological damage in renal allografts is associated with expression of innate and adaptive immunity genes. Kidney International, 2011, 80, 1364-1376.	2.6	96
49	Cross-Species Functional Analysis of Cancer-Associated Fibroblasts Identifies a Critical Role for CLCF1 and IL-6 in Nonâ€"Small Cell Lung Cancer <i>In Vivo</i>. Cancer Research, 2012, 72, 5744-5756.	0.4	96
50	Benchmarking Sepsis Gene Expression Diagnostics Using Public Data*. Critical Care Medicine, 2017, 45, 1-10.	0.4	96
51	Assessment of Validity of a Blood-Based 3-Gene Signature Score for Progression and Diagnosis of Tuberculosis, Disease Severity, and Treatment Response. JAMA Network Open, 2018, 1, e183779.	2.8	96
52	Integrated multi-cohort transcriptional meta-analysis of neurodegenerative diseases. Acta Neuropathologica Communications, 2014, 2, 93.	2.4	94
53	Onto-Tools: new additions and improvements in 2006. Nucleic Acids Research, 2007, 35, W206-W211.	6.5	87
54	Non-HLA Antibodies to Immunogenic Epitopes Predict the Evolution of Chronic Renal Allograft Injury. Journal of the American Society of Nephrology: JASN, 2012, 23, 750-763.	3.0	87

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55	A generalizable 29-mRNA neural-network classifier for acute bacterial and viral infections. Nature Communications, 2020, 11, 1177.	5.8	77
56	EMPOWERING MULTI-COHORT GENE EXPRESSION ANALYSIS TO INCREASE REPRODUCIBILITY. , 2017, 22, 144-153.		75
57	The center for expanded data annotation and retrieval. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 1148-1152.	2.2	74
58	Cellular senescence impairs the reversibility of pulmonary arterial hypertension. Science Translational Medicine, 2020, 12, .	5.8	74
59	Biomarkers in solid organ transplantation: establishing personalized transplantation medicine. Genome Medicine, 2011, 3, 37.	3.6	71
60	Sex Differences in the Blood Transcriptome Identify Robust Changes in Immune Cell Proportions with Aging and Influenza Infection. Cell Reports, 2019, 29, 1961-1973.e4.	2.9	70
61	Transcriptomic similarities and differences in host response between SARS-CoV-2 and other viral infections. IScience, 2021, 24, 101947.	1.9	70
62	Coordination of stress signals by the lysine methyltransferase SMYD2 promotes pancreatic cancer. Genes and Development, 2016, 30, 772-785.	2.7	68
63	Chemical Space Mimicry for Drug Discovery. Journal of Chemical Information and Modeling, 2017, 57, 875-882.	2.5	63
64	A semantic analysis of the annotations of the human genome. Bioinformatics, 2005, 21, 3416-3421.	1.8	61
65	A 20-Gene Set Predictive of Progression to Severe Dengue. Cell Reports, 2019, 26, 1104-1111.e4.	2.9	60
66	Integrated, multicohort analysis of systemic sclerosis identifies robust transcriptional signature of disease severity. JCI Insight, 2016, 1, e89073.	2.3	57
67	Future Research Directions in Pneumonia. NHLBI Working Group Report. American Journal of Respiratory and Critical Care Medicine, 2018, 198, 256-263.	2.5	54
68	KLRD1-expressing natural killer cells predict influenza susceptibility. Genome Medicine, 2018, 10, 45.	3.6	51
69	Generalizable Biomarkers in Critical Care. Critical Care Medicine, 2017, 45, 934-939.	0.4	43
70	Multi-cohort analysis of host immune response identifies conserved protective and detrimental modules associated with severity across viruses. Immunity, 2021, 54, 753-768.e5.	6.6	42
71	Unique transcriptomic response to sepsis is observed among patients of different age groups. PLoS ONE, 2017, 12, e0184159.	1.1	40
72	Diversity in immunogenomics: the value and the challenge. Nature Methods, 2021, 18, 588-591.	9.0	40

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73	Babel's tower revisited: a universal resource for cross-referencing across annotation databases. Bioinformatics, 2006, 22, 2934-2939.	1.8	39
74	*FHIT*, a Novel Modifier Gene in Pulmonary Arterial Hypertension. American Journal of Respiratory and Critical Care Medicine, 2019, 199, 83-98.	2.5	39
75	Validation of the Sepsis MetaScore for Diagnosis of Neonatal Sepsis. Journal of the Pediatric Infectious Diseases Society, 2018, 7, 129-135.	0.6	37
76	Pregnancy-Induced Alterations in NK Cell Phenotype and Function. Frontiers in Immunology, 2019, 10, 2469.	2.2	36
77	Diagnostic Accuracy Study of a Novel Blood-Based Assay for Identification of Tuberculosis in People Living with HIV. Journal of Clinical Microbiology, 2021, 59, .	1.8	36
78	Repression of CTSG, ELANE and PRTN3-mediated histone H3 proteolytic cleavage promotes monocyte-to-macrophage differentiation. Nature Immunology, 2021, 22, 711-722.	7.0	36
79	Integrated, multicohort analysis reveals unified signature of systemic lupus erythematosus. JCI Insight, 2020, 5, .	2.3	36
80	Pediatric Sepsis Endotypes Among Adults With Sepsis. Critical Care Medicine, 2017, 45, e1289-e1291.	0.4	35
81	Macrophage-derived IL-6 trans-signalling as a novel target in the pathogenesis of bronchopulmonary dysplasia. European Respiratory Journal, 2022, 59, 2002248.	3.1	35
82	Using gene arrays in diagnosis of rejection. Current Opinion in Organ Transplantation, 2009, 14, 34-39.	0.8	30
83	Single-cell technologies â€" studying rheumatic diseases one cell at a time. Nature Reviews Rheumatology, 2019, 15, 340-354.	3.5	30
84	Single-cell epigenetics â€" Chromatin modification atlas unveiled by mass cytometry. Clinical Immunology, 2018, 196, 40-48.	1.4	29
85	Inflammatory macrophageâ€"associated 3-gene signature predicts subclinical allograft injury and graft survival. JCI Insight, 2018, 3, .	2.3	27
86	Multicohort Analysis of Whole-Blood Gene Expression Data Does Not Form a Robust Diagnostic for Acute Respiratory Distress Syndrome. Critical Care Medicine, 2018, 46, 244-251.	0.4	26
87	Blood-based host biomarker diagnostics in active case finding for pulmonary tuberculosis: A diagnostic case-control study. EClinicalMedicine, 2021, 33, 100776.	3.2	26
88	Identification of Distinct Inflammatory Programs and Biomarkers in Systemic Juvenile Idiopathic Arthritis and Related Lung Disease by Serum Proteome Analysis. Arthritis and Rheumatology, 2022, 74, 1271-1283.	2.9	24
89	Gene Expression Analysis to Assess the Relevance of Rodent Models to Human Lung Injury. American Journal of Respiratory Cell and Molecular Biology, 2017, 57, 184-192.	1.4	23
90	A molecular atlas of innate immunity to adjuvanted and live attenuated vaccines, in mice. Nature Communications, 2022, 13, 549.	5.8	21

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91	Comprehensive Validation of the <i>FAIM3</i>:<i>PLAC8</i> Ratio in Time-matched Public Gene Expression Data. American Journal of Respiratory and Critical Care Medicine, 2015, 192, 1260-1261.	2.5	20
92	Signatures of immune dysfunction in HIV and HCV infection share features with chronic inflammation in aging and persist after viral reduction or elimination. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	19
93	A microarray analysis of the effects of moderate hypothermia and rewarming on gene expression by human hepatocytes (HepG2). Cell Stress and Chaperones, 2010, 15, 687-702.	1.2	18
94	Disease characteristics and serological responses in patients with differing severity of COVID-19 infection: A longitudinal cohort study in Dhaka, Bangladesh. PLoS Neglected Tropical Diseases, 2022, 16, e0010102.	1.3	18
95	An 8-gene machine learning model improves clinical prediction of severe dengue progression. Genome Medicine, 2022, 14, 33.	3.6	18
96	New Onto-Tools: Promoter-Express, nsSNPCounter and Onto-Translate. Nucleic Acids Research, 2006, 34, W626-W631.	6.5	17
97	iPSCâ€"endothelial cell phenotypic drug screening and in silico analyses identify tyrphostin-AG1296 for pulmonary arterial hypertension. Science Translational Medicine, 2021, 13, .	5.8	17
98	SIMON: Open-Source Knowledge Discovery Platform. Patterns, 2021, 2, 100178.	3.1	15
99	A 6-mRNA host response classifier in whole blood predicts outcomes in COVID-19 and other acute viral infections. Scientific Reports, 2022, 12, 889.	1.6	15
100	A B-Cell Gene Signature Correlates With the Extent of Gluten-Induced Intestinal Injury in Celiac Disease. Cellular and Molecular Gastroenterology and Hepatology, 2017, 4, 1-17.	2.3	13
101	Assessing the Functional Bias of Commercial Microarrays Using the Onto-Compare Database. BioTechniques, 2003, 34, S55-S61.	0.8	13
102	Increases in ambient air pollutants during pregnancy are linked to increases in methylation of IL4, IL10, and IFNÎ³. Clinical Epigenetics, 2022, 14, 40.	1.8	12
103	Profiling of Autoantibodies in IgA Nephropathy, an Integrative Antibiomics Approach. Clinical Journal of the American Society of Nephrology: CJASN, 2011, 6, 2775-2784.	2.2	11
104	A robust gene expression signature for NASH in liver expression data. Scientific Reports, 2022, 12, 2571.	1.6	11
105	A GMR-based assay for quantification of the human response to influenza. Biosensors and Bioelectronics, 2022, 205, 114086.	5.3	11
106	Semantic Analysis of Genome Annotations using Weighting Schemes. , 2007, , .		10
107	Early life immunity in the era of systems biology: understanding development and disease. Genome Medicine, 2018, 10, 88.	3.6	10
108	Gene Expressionâ€"Based Diagnosis of Infections in Critically Ill Patientsâ€"Prospective Validation of the SepsisMetaScore in a Longitudinal Severe Trauma Cohort. Critical Care Medicine, 2021, 49, e751-e760.	0.4	10

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109	Computational drug repositioning of atorvastatin for ulcerative colitis. Journal of the American Medical Informatics Association: JAMIA, 2021, 28, 2325-2335.	2.2	10
110	Applications of Translational Bioinformatics in Transplantation. Clinical Pharmacology and Therapeutics, 2011, 90, 323-327.	2.3	9
111	A novel blood-based assay for treatment monitoring of tuberculosis. BMC Research Notes, 2021, 14, 247.	0.6	9
112	Host protease activity classifies pneumonia etiology. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	9
113	A Human Genome-Wide RNAi Screen Reveals Diverse Modulators that Mediate IRE1Î±â€"XBP1 Activation. Molecular Cancer Research, 2018, 16, 745-753.	1.5	8
114	Multicohort Analysis Identifies Monocyte Gene Signatures to Accurately Monitor Subset-Specific Changes in Human Diseases. Frontiers in Immunology, 2021, 12, 659255.	2.2	8
115	Blood transcriptional signatures for tuberculosis diagnosis: a glass half-empty perspective â€" Authors' reply. Lancet Respiratory Medicine,the, 2016, 4, e29.	5.2	7
116	Single cell immune profiling in transplantation research. American Journal of Transplantation, 2019, 19, 1278-1287.	2.6	7
117	High-throughput quantitative histology in systemic sclerosis skin disease using computer vision. Arthritis Research and Therapy, 2020, 22, 48.	1.6	7
118	Evolution of Cytomegalovirus-Responsive T Cell Clonality following Solid Organ Transplantation. Journal of Immunology, 2021, 207, 2077-2085.	0.4	7
119	Comparison of the Transcriptomic Signatures in Pediatric and Adult CML. Cancers, 2021, 13, 6263.	1.7	7
120	A multi-scale integrated analysis identifies KRT8 as a pan-cancer early biomarker. , 2020, , .		6
121	Comparison of the Transcriptomic Signature of Pediatric Vs. Adult CML and Normal Bone Marrow Stem Cells. Blood, 2018, 132, 4246-4246.	0.6	5
122	META-ANALYSIS OF CONTINUOUS PHENOTYPES IDENTIFIES A GENE SIGNATURE THAT CORRELATES WITH COPD DISEASE STATUS. , 2017, 22, 266-275.		4
123	Septic Cardiomyopathy. Critical Care Medicine, 2017, 45, 556-557.	0.4	4
124	Response to: â€˜Effectiveness and safety of ruxolitinib for the treatment of refractory systemic idiopathic juvenile arthritis like associated with interstitial lung disease: case reportâ€™ by Bader-Meunier <i>et al</i>. Annals of the Rheumatic Diseases, 2022, 81, e21-e21.	0.5	4
125	Prospective validation of an 11-gene mRNA host response score for mortality risk stratification in the intensive care unit. Scientific Reports, 2021, 11, 13062.	1.6	4
126	Functional Consequences of Memory Inflation after Solid Organ Transplantation. Journal of Immunology, 2021, 207, ji2100405.	0.4	3

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127	Pilot study of a novel serum mRNA gene panel for diagnosis of acute septic arthritis. World Journal of Orthopedics, 2019, 10, 424-433.	0.8	3
128	A Multi-mRNA Prognostic Signature for Anti-TNFÎ± Therapy Response in Patients with Inflammatory Bowel Disease. Diagnostics, 2021, 11, 1902.	1.3	3
129	A multi-scale integrated analysis identifies KRT8 as a pan-cancer early biomarker. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2021, 26, 297-308.	0.7	3
130	Complementing single-cell RNA-seq using bulk transcriptional profiles. , 2017, , .		2
131	Computational and Systems Immunology: A Studentâ€™s Perspective. Trends in Immunology, 2019, 40, 665-668.	2.9	2
132	Data Heterogeneity: The Enzyme to Catalyze Translational Bioinformatics?. Journal of Medical Internet Research, 2020, 22, e18044.	2.1	2
133	Hospital-acquired Pneumonia: A Host of Factors. American Journal of Respiratory and Critical Care Medicine, 2016, 194, 1309-1311.	2.5	1
134	The authors reply. Critical Care Medicine, 2017, 45, e457-e458.	0.4	1
135	Response to: â€˜Successful treatment of plasma exchange for refractory systemic juvenile idiopathic arthritis complicated with macrophage activation syndrome and severe lung diseaseâ€™ by Sato<i>et al</i>. Annals of the Rheumatic Diseases, 2022, 81, e62-e62.	0.5	1
136	Comparison of the Transcriptomic Signatures in Pediatric and Adult CML. Blood, 2020, 136, 39-40.	0.6	1
137	Increasing reproducibility, robustness, and generalizability of biomarker selection from meta-analysis using Bayesian methodology. PLoS Computational Biology, 2022, 18, e1010260.	1.5	1
138	The authors reply. Critical Care Medicine, 2017, 45, e341.	0.4	0
139	Integration of Nextâ€"Generation Sequencing, Viral Sequencing, and Host-Response Profiling for the Diagnosis of Acute Infections. Open Forum Infectious Diseases, 2017, 4, S71-S71.	0.4	0
140	2016. TaqMan Multiplex PCR of a Seven-Gene Host Biomarker to Discriminate Bacterial from Viral Infections. Open Forum Infectious Diseases, 2018, 5, S587-S587.	0.4	0
141	119. Prospective Validation of a 3-Gene Signature for Tuberculosis Diagnosis, Predicting Progression and Evaluating Treatment Response. Open Forum Infectious Diseases, 2018, 5, S5-S5.	0.4	0
142	Data analytics for precision medicine. , 2019, , 25-33.		0
143	Multisystem inflammatory syndrome in children: a microcosm of challenges and opportunities for translational bioinformatics in pediatric research. Current Opinion in Pediatrics, 2021, 33, 325-330.	1.0	0
144	Diverse nephron cell typeâ€specific adaptation to furosemide by morphometry and single cell RNA sequencing. FASEB Journal, 2019, 33, 862.29.	0.2	0

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145	Gene Expression Analysis of CML Patients across the Age Spectrum. Blood, 2021, 138, 1473-1473.	0.6	0
146	The Single Cell Transcriptomic and Epigenomic Map of the Innate Immune Response to Vaccination in Lymph Nodes. Journal of Allergy and Clinical Immunology, 2022, 149, AB316.	1.5	0