

Purvesh Khatri

List of Publications by Year in Descending Order

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Version: 2024-04-27

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

151
papers

12,071
citations

55
h-index

109
g-index

181
ext. papers

15,603
ext. citations

13
avg, IF

6.46
L-index

#	Paper	IF	Citations
151	A molecular atlas of innate immunity to adjuvanted and live attenuated vaccines, in mice.. <i>Nature Communications</i> , 2022 , 13, 549	17.4	2
150	Disease characteristics and serological responses in patients with differing severity of COVID-19 infection: A longitudinal cohort study in Dhaka, Bangladesh.. <i>PLoS Neglected Tropical Diseases</i> , 2022 , 16, e0010102	4.8	5
149	A 6-mRNA host response classifier in whole blood predicts outcomes in COVID-19 and other acute viral infections.. <i>Scientific Reports</i> , 2022 , 12, 889	4.9	2
148	The immunoregulatory landscape of human tuberculosis granulomas.. <i>Nature Immunology</i> , 2022 ,	19.1	11
147	A robust gene expression signature for NASH in liver expression data.. <i>Scientific Reports</i> , 2022 , 12, 2571	4.9	1
146	Serum proteome analysis of systemic JIA and related lung disease identifies distinct inflammatory programs and biomarkers.. <i>Arthritis and Rheumatology</i> , 2022 ,	9.5	3
145	An 8-gene machine learning model improves clinical prediction of severe dengue progression.. <i>Genome Medicine</i> , 2022 , 14, 33	14.4	1
144	Mechanisms of innate and adaptive immunity to the Pfizer-BioNTech BNT162b2 vaccine.. <i>Nature Immunology</i> , 2022 ,	19.1	11
143	Increases in ambient air pollutants during pregnancy are linked to increases in methylation of IL4, IL10, and IFN γ <i>Clinical Epigenetics</i> , 2022 , 14, 40	7.7	1
142	A GMR-based assay for quantification of the human response to influenza.. <i>Biosensors and Bioelectronics</i> , 2022 , 205, 114086	11.8	1
141	A multi-scale integrated analysis identifies KRT8 as a pan-cancer early biomarker. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2021 , 26, 297-308	1.3	2
140	Gene Expression Analysis of CML Patients across the Age Spectrum. <i>Blood</i> , 2021 , 138, 1473-1473	2.2	
139	Signatures of immune dysfunction in HIV and HCV infection share features with chronic inflammation in aging and persist after viral reduction or elimination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	4
138	Multisystem inflammatory syndrome in children: a microcosm of challenges and opportunities for translational bioinformatics in pediatric research. <i>Current Opinion in Pediatrics</i> , 2021 , 33, 325-330	3.2	
137	Multi-cohort analysis of host immune response identifies conserved protective and detrimental modules associated with severity across viruses. <i>Immunity</i> , 2021 , 54, 753-768.e5	32.3	17
136	Gene Expression-Based Diagnosis of Infections in Critically Ill Patients-Prospective Validation of the SepsisMetaScore in a Longitudinal Severe Trauma Cohort. <i>Critical Care Medicine</i> , 2021 , 49, e751-e760	1.4	3
135	Repression of CTSG, ELANE and PRTN3-mediated histone H3 proteolytic cleavage promotes monocyte-to-macrophage differentiation. <i>Nature Immunology</i> , 2021 , 22, 711-722	19.1	5

134	Multicohort Analysis Identifies Monocyte Gene Signatures to Accurately Monitor Subset-Specific Changes in Human Diseases. <i>Frontiers in Immunology</i> , 2021 , 12, 659255	8.4	2
133	Diversity in immunogenomics: the value and the challenge. <i>Nature Methods</i> , 2021 , 18, 588-591	21.6	11
132	iPSC-endothelial cell phenotypic drug screening and in silico analyses identify tyrphostin-AG1296 for pulmonary arterial hypertension. <i>Science Translational Medicine</i> , 2021 , 13,	17.5	4
131	A novel blood-based assay for treatment monitoring of tuberculosis. <i>BMC Research Notes</i> , 2021 , 14, 2472.3	2.3	3
130	Prospective validation of an 11-gene mRNA host response score for mortality risk stratification in the intensive care unit. <i>Scientific Reports</i> , 2021 , 11, 13062	4.9	1
129	The single-cell epigenomic and transcriptional landscape of immunity to influenza vaccination. <i>Cell</i> , 2021 , 184, 3915-3935.e21	56.2	23
128	Systems vaccinology of the BNT162b2 mRNA vaccine in humans. <i>Nature</i> , 2021 , 596, 410-416	50.4	67
127	Transcriptomic similarities and differences in host response between SARS-CoV-2 and other viral infections. <i>iScience</i> , 2021 , 24, 101947	6.1	23
126	Diagnostic Accuracy Study of a Novel Blood-Based Assay for Identification of Tuberculosis in People Living with HIV. <i>Journal of Clinical Microbiology</i> , 2021 , 59,	9.7	12
125	Blood-based host biomarker diagnostics in active case finding for pulmonary tuberculosis: A diagnostic case-control study. <i>EClinicalMedicine</i> , 2021 , 33, 100776	11.3	6
124	Macrophage-derived IL-6 trans-signaling as a novel target in the pathogenesis of bronchopulmonary dysplasia. <i>European Respiratory Journal</i> , 2021 ,	13.6	5
123	Evolution of Cytomegalovirus-Responsive T Cell Clonality following Solid Organ Transplantation. <i>Journal of Immunology</i> , 2021 , 207, 2077-2085	5.3	2
122	Functional Consequences of Memory Inflation after Solid Organ Transplantation. <i>Journal of Immunology</i> , 2021 , 207, 2086-2095	5.3	2
121	Computational drug repositioning of atorvastatin for ulcerative colitis. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2021 , 28, 2325-2335	8.6	2
120	SIMON: Open-Source Knowledge Discovery Platform. <i>Patterns</i> , 2021 , 2, 100178	5.1	6
119	T cell-inducing vaccine durably prevents mucosal SHIV infection even with lower neutralizing antibody titers. <i>Nature Medicine</i> , 2020 , 26, 932-940	50.5	60
118	High-throughput quantitative histology in systemic sclerosis skin disease using computer vision. <i>Arthritis Research and Therapy</i> , 2020 , 22, 48	5.7	4
117	A generalizable 29-mRNA neural-network classifier for acute bacterial and viral infections. <i>Nature Communications</i> , 2020 , 11, 1177	17.4	46

116	Response to: Effectiveness and safety of ruxolitinib for the treatment of refractory systemic idiopathic juvenile arthritis like associated with interstitial lung disease: case report Tby Bader-Meunier. <i>Annals of the Rheumatic Diseases</i> , 2020 ,	2.4	3
115	Response to: Successful treatment of plasma exchange for refractory systemic juvenile idiopathic arthritis complicated with macrophage activation syndrome and severe lung disease Tby Sato. <i>Annals of the Rheumatic Diseases</i> , 2020 ,	2.4	1
114	Comparison of the Transcriptomic Signatures in Pediatric and Adult CML. <i>Blood</i> , 2020 , 136, 39-40	2.2	1
113	Integrated, multicohort analysis reveals unified signature of systemic lupus erythematosus. <i>JCI Insight</i> , 2020 , 5,	9.9	20
112	Data Heterogeneity: The Enzyme to Catalyze Translational Bioinformatics?. <i>Journal of Medical Internet Research</i> , 2020 , 22, e18044	7.6	1
111	Cellular senescence impairs the reversibility of pulmonary arterial hypertension. <i>Science Translational Medicine</i> , 2020 , 12,	17.5	24
110	Systems biological assessment of immunity to mild versus severe COVID-19 infection in humans. <i>Science</i> , 2020 , 369, 1210-1220	33.3	485
109	Emergent high fatality lung disease in systemic juvenile arthritis. <i>Annals of the Rheumatic Diseases</i> , 2019 , 78, 1722-1731	2.4	61
108	A 20-Gene Set Predictive of Progression to Severe Dengue. <i>Cell Reports</i> , 2019 , 26, 1104-1111.e4	10.6	26
107	Discovery of Distinct Immune Phenotypes Using Machine Learning in Pulmonary Arterial Hypertension. <i>Circulation Research</i> , 2019 , 124, 904-919	15.7	81
106	Single-cell technologies - studying rheumatic diseases one cell at a time. <i>Nature Reviews Rheumatology</i> , 2019 , 15, 340-354	8.1	19
105	Host-response-based gene signatures for tuberculosis diagnosis: A systematic comparison of 16 signatures. <i>PLoS Medicine</i> , 2019 , 16, e1002786	11.6	77
104	A clinically meaningful metric of immune age derived from high-dimensional longitudinal monitoring. <i>Nature Medicine</i> , 2019 , 25, 487-495	50.5	162
103	Increased monocyte count as a cellular biomarker for poor outcomes in fibrotic diseases: a retrospective, multicentre cohort study. <i>Lancet Respiratory Medicine</i> , 2019 , 7, 497-508	35.1	72
102	CD22 blockade restores homeostatic microglial phagocytosis in ageing brains. <i>Nature</i> , 2019 , 568, 187-193	30.4	156
101	FHIT, a Novel Modifier Gene in Pulmonary Arterial Hypertension. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2019 , 199, 83-98	10.2	26
100	Computational and Systems Immunology: A Student's Perspective. <i>Trends in Immunology</i> , 2019 , 40, 665-668	6.4	1
99	Pregnancy-Induced Alterations in NK Cell Phenotype and Function. <i>Frontiers in Immunology</i> , 2019 , 10, 2469	8.4	23

98	Sex Differences in the Blood Transcriptome Identify Robust Changes in Immune Cell Proportions with Aging and Influenza Infection. <i>Cell Reports</i> , 2019 , 29, 1961-1973.e4	10.6	35
97	Pilot study of a novel serum mRNA gene panel for diagnosis of acute septic arthritis. <i>World Journal of Orthopedics</i> , 2019 , 10, 424-433	2.2	1
96	Diverse nephron cell type-specific adaptation to furosemide by morphometry and single cell RNA sequencing. <i>FASEB Journal</i> , 2019 , 33, 862.29	0.9	
95	Single cell immune profiling in transplantation research. <i>American Journal of Transplantation</i> , 2019 , 19, 1278-1287	8.7	5
94	Data analytics for precision medicine 2019 , 25-33		
93	Cell-centred meta-analysis reveals baseline predictors of anti-TNF α non-response in biopsy and blood of patients with IBD. <i>Gut</i> , 2019 , 68, 604-614	19.2	97
92	Single-Cell Chromatin Modification Profiling Reveals Increased Epigenetic Variations with Aging. <i>Cell</i> , 2018 , 173, 1385-1397.e14	56.2	156
91	A community approach to mortality prediction in sepsis via gene expression analysis. <i>Nature Communications</i> , 2018 , 9, 694	17.4	106
90	Gene annotation bias impedes biomedical research. <i>Scientific Reports</i> , 2018 , 8, 1362	4.9	71
89	A Human Genome-Wide RNAi Screen Reveals Diverse Modulators that Mediate IRE1 α BP1 Activation. <i>Molecular Cancer Research</i> , 2018 , 16, 745-753	6.6	3
88	Multicohort Analysis of Whole-Blood Gene Expression Data Does Not Form a Robust Diagnostic for Acute Respiratory Distress Syndrome. <i>Critical Care Medicine</i> , 2018 , 46, 244-251	1.4	19
87	Antigen Identification for Orphan T Cell Receptors Expressed on Tumor-Infiltrating Lymphocytes. <i>Cell</i> , 2018 , 172, 549-563.e16	56.2	160
86	Unsupervised Analysis of Transcriptomics in Bacterial Sepsis Across Multiple Datasets Reveals Three Robust Clusters. <i>Critical Care Medicine</i> , 2018 , 46, 915-925	1.4	115
85	Future Research Directions in Pneumonia. NHLBI Working Group Report. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2018 , 198, 256-263	10.2	33
84	Validation of the Sepsis MetaScore for Diagnosis of Neonatal Sepsis. <i>Journal of the Pediatric Infectious Diseases Society</i> , 2018 , 7, 129-135	4.8	23
83	Single-cell epigenetics - Chromatin modification atlas unveiled by mass cytometry. <i>Clinical Immunology</i> , 2018 , 196, 40-48	9	13
82	KLRD1-expressing natural killer cells predict influenza susceptibility. <i>Genome Medicine</i> , 2018 , 10, 45	14.4	30
81	Interpretation of biological experiments changes with evolution of the Gene Ontology and its annotations. <i>Scientific Reports</i> , 2018 , 8, 5115	4.9	41

80	A multi-cohort study of the immune factors associated with M. tuberculosis infection outcomes. <i>Nature</i> , 2018 , 560, 644-648	50.4	117
79	Inflammatory macrophage-associated 3-gene signature predicts subclinical allograft injury and graft survival. <i>JCI Insight</i> , 2018 , 3,	9.9	17
78	Comparison of the Transcriptomic Signature of Pediatric Vs. Adult CML and Normal Bone Marrow Stem Cells. <i>Blood</i> , 2018 , 132, 4246-4246	2.2	3
77	2016. TaqMan Multiplex PCR of a Seven-Gene Host Biomarker to Discriminate Bacterial from Viral Infections. <i>Open Forum Infectious Diseases</i> , 2018 , 5, S587-S587	1	78
76	119. Prospective Validation of a 3-Gene Signature for Tuberculosis Diagnosis, Predicting Progression and Evaluating Treatment Response. <i>Open Forum Infectious Diseases</i> , 2018 , 5, S5-S5	1	78
75	Leveraging heterogeneity across multiple datasets increases cell-mixture deconvolution accuracy and reduces biological and technical biases. <i>Nature Communications</i> , 2018 , 9, 4735	17.4	77
74	Early life immunity in the era of systems biology: understanding development and disease. <i>Genome Medicine</i> , 2018 , 10, 88	14.4	5
73	Assessment of Validity of a Blood-Based 3-Gene Signature Score for Progression and Diagnosis of Tuberculosis, Disease Severity, and Treatment Response. <i>JAMA Network Open</i> , 2018 , 1, e183779	10.4	59
72	META-ANALYSIS OF CONTINUOUS PHENOTYPES IDENTIFIES A GENE SIGNATURE THAT CORRELATES WITH COPD DISEASE STATUS. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2017 , 22, 266-275	1.3	3
71	An integrative approach unveils FOSL1 as an oncogene vulnerability in KRAS-driven lung and pancreatic cancer. <i>Nature Communications</i> , 2017 , 8, 14294	17.4	73
70	Chemical Space Mimicry for Drug Discovery. <i>Journal of Chemical Information and Modeling</i> , 2017 , 57, 875-882	6.1	40
69	Benchmarking Sepsis Gene Expression Diagnostics Using Public Data. <i>Critical Care Medicine</i> , 2017 , 45, 1-10	1.4	70
68	Generalizable Biomarkers in Critical Care: Toward Precision Medicine. <i>Critical Care Medicine</i> , 2017 , 45, 934-939	1.4	36
67	A B-Cell Gene Signature Correlates With the Extent of Gluten-Induced Intestinal Injury in Celiac Disease. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2017 , 4, 1-17	7.9	7
66	Gene Expression Analysis to Assess the Relevance of Rodent Models to Human Lung Injury. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2017 , 57, 184-192	5.7	14
65	The authors reply. <i>Critical Care Medicine</i> , 2017 , 45, e457-e458	1.4	1
64	Pediatric Sepsis Endotypes Among Adults With Sepsis. <i>Critical Care Medicine</i> , 2017 , 45, e1289-e1291	1.4	22
63	Unique transcriptomic response to sepsis is observed among patients of different age groups. <i>PLoS ONE</i> , 2017 , 12, e0184159	3.7	33

62	Multicohort analysis reveals baseline transcriptional predictors of influenza vaccination responses. <i>Science Immunology</i> , 2017 , 2,	28	66
61	The authors reply. <i>Critical Care Medicine</i> , 2017 , 45, e341	1.4	
60	Methods to increase reproducibility in differential gene expression via meta-analysis. <i>Nucleic Acids Research</i> , 2017 , 45, e1	20.1	75
59	EMPOWERING MULTI-COHORT GENE EXPRESSION ANALYSIS TO INCREASE REPRODUCIBILITY. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2017 , 22, 144-153	1.3	40
58	Integration of Next-Generation Sequencing, Viral Sequencing, and Host-Response Profiling for the Diagnosis of Acute Infections. <i>Open Forum Infectious Diseases</i> , 2017 , 4, S71-S71	1	78
57	Complementing single-cell RNA-seq using bulk transcriptional profiles 2017 ,		1
56	Robust classification of bacterial and viral infections via integrated host gene expression diagnostics. <i>Science Translational Medicine</i> , 2016 , 8, 346ra91	17.5	180
55	Coordination of stress signals by the lysine methyltransferase SMYD2 promotes pancreatic cancer. <i>Genes and Development</i> , 2016 , 30, 772-85	12.6	54
54	Genome-wide expression for diagnosis of pulmonary tuberculosis: a multicohort analysis. <i>Lancet Respiratory Medicine</i> , 2016 , 4, 213-24	35.1	225
53	Integrated, multicohort analysis of systemic sclerosis identifies robust transcriptional signature of disease severity. <i>JCI Insight</i> , 2016 , 1, e89073	9.9	41
52	Hospital-acquired Pneumonia: A Host of Factors. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2016 , 194, 1309-1311	10.2	1
51	Blood transcriptional signatures for tuberculosis diagnosis: a glass half-empty perspective - AuthorsReply. <i>Lancet Respiratory Medicine</i> , 2016 , 4, e29	35.1	6
50	Complement pathway amplifies caspase-11-dependent cell death and endotoxin-induced sepsis severity. <i>Journal of Experimental Medicine</i> , 2016 , 213, 2365-2382	16.6	78
49	The center for expanded data annotation and retrieval. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2015 , 22, 1148-52	8.6	56
48	A comprehensive time-course-based multicohort analysis of sepsis and sterile inflammation reveals a robust diagnostic gene set. <i>Science Translational Medicine</i> , 2015 , 7, 287ra71	17.5	197
47	Combined inhibition of BET family proteins and histone deacetylases as a potential epigenetics-based therapy for pancreatic ductal adenocarcinoma. <i>Nature Medicine</i> , 2015 , 21, 1163-71	50.5	275
46	Comprehensive Validation of the FAIM3:PLAC8 Ratio in Time-matched Public Gene Expression Data. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2015 , 192, 1260-1	10.2	20
45	Integrated, Multi-cohort Analysis Identifies Conserved Transcriptional Signatures across Multiple Respiratory Viruses. <i>Immunity</i> , 2015 , 43, 1199-211	32.3	118

44	A meta-analysis of lung cancer gene expression identifies PTK7 as a survival gene in lung adenocarcinoma. <i>Cancer Research</i> , 2014 , 74, 2892-902	10.1	108
43	SMYD3 links lysine methylation of MAP3K2 to Ras-driven cancer. <i>Nature</i> , 2014 , 510, 283-7	50.4	259
42	Integrated multi-cohort transcriptional meta-analysis of neurodegenerative diseases. <i>Acta Neuropathologica Communications</i> , 2014 , 2, 93	7.3	67
41	A drug repositioning approach identifies tricyclic antidepressants as inhibitors of small cell lung cancer and other neuroendocrine tumors. <i>Cancer Discovery</i> , 2013 , 3, 1364-77	24.4	272
40	A common rejection module (CRM) for acute rejection across multiple organs identifies novel therapeutics for organ transplantation. <i>Journal of Experimental Medicine</i> , 2013 , 210, 2205-21	16.6	166
39	A peripheral blood diagnostic test for acute rejection in renal transplantation. <i>American Journal of Transplantation</i> , 2012 , 12, 2710-8	8.7	105
38	Ten years of pathway analysis: current approaches and outstanding challenges. <i>PLoS Computational Biology</i> , 2012 , 8, e1002375	5	974
37	Cross-species functional analysis of cancer-associated fibroblasts identifies a critical role for CLCF1 and IL-6 in non-small cell lung cancer in vivo. <i>Cancer Research</i> , 2012 , 72, 5744-56	10.1	75
36	Non-HLA antibodies to immunogenic epitopes predict the evolution of chronic renal allograft injury. <i>Journal of the American Society of Nephrology: JASN</i> , 2012 , 23, 750-63	12.7	68
35	Biomarkers in solid organ transplantation: establishing personalized transplantation medicine. <i>Genome Medicine</i> , 2011 , 3, 37	14.4	65
34	Profiling of autoantibodies in IgA nephropathy, an integrative antiomics approach. <i>Clinical Journal of the American Society of Nephrology: CJASN</i> , 2011 , 6, 2775-84	6.9	9
33	Progressive histological damage in renal allografts is associated with expression of innate and adaptive immunity genes. <i>Kidney International</i> , 2011 , 80, 1364-76	9.9	76
32	Applications of translational bioinformatics in transplantation. <i>Clinical Pharmacology and Therapeutics</i> , 2011 , 90, 323-7	6.1	7
31	Cell type-specific gene expression differences in complex tissues. <i>Nature Methods</i> , 2010 , 7, 287-9	21.6	356
30	A microarray analysis of the effects of moderate hypothermia and rewarming on gene expression by human hepatocytes (HepG2). <i>Cell Stress and Chaperones</i> , 2010 , 15, 687-702	4	15
29	A novel signaling pathway impact analysis. <i>Bioinformatics</i> , 2009 , 25, 75-82	7.2	715
28	Using gene arrays in diagnosis of rejection. <i>Current Opinion in Organ Transplantation</i> , 2009 , 14, 34-9	2.5	28
27	A systems biology approach for pathway level analysis. <i>Genome Research</i> , 2007 , 17, 1537-45	9.7	796

26	Onto-Tools: new additions and improvements in 2006. <i>Nucleic Acids Research</i> , 2007 , 35, W206-11	20.1	84
25	Semantic Analysis of Genome Annotations using Weighting Schemes 2007 ,		8
24	Reliability and reproducibility issues in DNA microarray measurements. <i>Trends in Genetics</i> , 2006 , 22, 101-9.5		459
23	New Onto-Tools: Promoter-Express, nsSNPCounter and Onto-Translate. <i>Nucleic Acids Research</i> , 2006 , 34, W626-31	20.1	17
22	Babel Tower revisited: a universal resource for cross-referencing across annotation databases. <i>Bioinformatics</i> , 2006 , 22, 2934-9	7.2	33
21	Ontological analysis of gene expression data: current tools, limitations, and open problems. <i>Bioinformatics</i> , 2005 , 21, 3587-95	7.2	669
20	A semantic analysis of the annotations of the human genome. <i>Bioinformatics</i> , 2005 , 21, 3416-21	7.2	55
19	Recent additions and improvements to the Onto-Tools. <i>Nucleic Acids Research</i> , 2005 , 33, W762-5	20.1	101
18	Onto-Tools: an ensemble of web-accessible, ontology-based tools for the functional design and interpretation of high-throughput gene expression experiments. <i>Nucleic Acids Research</i> , 2004 , 32, W449-56	20.1	120
17	Onto-Tools, the toolkit of the modern biologist: Onto-Express, Onto-Compare, Onto-Design and Onto-Translate. <i>Nucleic Acids Research</i> , 2003 , 31, 3775-81	20.1	280
16	Global functional profiling of gene expression. <i>Genomics</i> , 2003 , 81, 98-104	4.3	479
15	Assessing the Functional Bias of Commercial Microarrays Using the Onto-Compare Database. <i>BioTechniques</i> , 2003 , 34, S55-S61	2.5	8
14	Profiling gene expression using onto-express. <i>Genomics</i> , 2002 , 79, 266-70	4.3	398
13	Spermatozoal RNA profiles of normal fertile men. <i>Lancet, The</i> , 2002 , 360, 772-7	4.0	410
12	Empowering Multi-Cohort Gene Expression Analysis to Increase Reproducibility		6
11	Mortality prediction in sepsis via gene expression analysis: a community approach		1
10	Gene annotation bias impedes biomedical research		4
9	Multiplexed imaging of human tuberculosis granulomas uncovers immunoregulatory features conserved across tissue and blood		8

8	Diagnostic accuracy study of a novel blood-based assay# for identification of TB in people living with HIV	2
7	Transcriptomic Similarities and Differences in Host Response between SARS-CoV-2 and Other Viral Infections	2
6	Multi-cohort analysis of host immune response identifies conserved protective and detrimental modules associated with severity irrespective of virus	5
5	A 6-mRNA host response whole-blood classifier trained on pre-pandemic data accurately predicts severity in COVID-19 and other acute viral infections	2
4	Leveraging heterogeneity across multiple data sets increases accuracy of cell-mixture deconvolution and reduces biological and technical biases	3
3	Integrated molecular, clinical, and ontological analysis identifies overlooked disease relationships	4
2	CD38 contributes to human natural killer cell responses through a role in immune synapse formation	7
1	Combined use of metagenomic sequencing and host response profiling for the diagnosis of suspected sepsis	2