## CITATION REPORT List of articles citing

A distinct influenza infection signature in the blood transcriptome of patients with severe community-acquired pneumonia

DOI: 10.1186/cc11477 Critical Care, 2012, 16, R157.

Source: https://exaly.com/paper-pdf/53183176/citation-report.pdf

Version: 2024-04-28

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

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

#	Paper	IF	Citations
95	The host response to infection: advancing a novel diagnostic paradigm. <i>Critical Care</i> , <b>2012</b> , 16, 168	10.8	6
94	Transcriptomic profiling in childhood H1N1/09 influenza reveals reduced expression of protein synthesis genes. <i>Journal of Infectious Diseases</i> , <b>2013</b> , 208, 1664-8	7	51
93	Identifying key regulatory genes in the whole blood of septic patients to monitor underlying immune dysfunctions. <i>Shock</i> , <b>2013</b> , 40, 166-74	3.4	59
92	Identification of host cell factors involved in influenza A virus infection. Future Virology, 2013, 8, 195-20	0&.4	3
91	Digital cell quantification identifies global immune cell dynamics during influenza infection. <i>Molecular Systems Biology</i> , <b>2014</b> , 10, 720	12.2	63
90	Detecting specific infections in children through host responses: a paradigm shift. <i>Current Opinion in Infectious Diseases</i> , <b>2014</b> , 27, 228-35	5.4	21
89	Systems biology and systems genetics - novel innovative approaches to study host-pathogen interactions during influenza infection. <i>Current Opinion in Virology</i> , <b>2014</b> , 6, 47-54	7.5	18
88	Comprehensive Validation of the FAIM3:PLAC8 Ratio in Time-matched Public Gene Expression Data. <i>American Journal of Respiratory and Critical Care Medicine</i> , <b>2015</b> , 192, 1260-1	10.2	20
87	Reply: Comprehensive Validation of the FAIM3:PLAC8 Ratio in Time-matched Public Gene Expression Data. <i>American Journal of Respiratory and Critical Care Medicine</i> , <b>2015</b> , 192, 1261-2	10.2	1
86	Integrated, Multi-cohort Analysis Identifies Conserved Transcriptional Signatures across Multiple Respiratory Viruses. <i>Immunity</i> , <b>2015</b> , 43, 1199-211	32.3	118
85	What was old is new again: using the host response to diagnose infectious disease. <i>Expert Review of Molecular Diagnostics</i> , <b>2015</b> , 15, 1143-58	3.8	20
84	Transcriptomic profiling facilitates classification of response to influenza challenge. <i>Journal of Molecular Medicine</i> , <b>2015</b> , 93, 105-14	5.5	26
83	A comprehensive time-course-based multicohort analysis of sepsis and sterile inflammation reveals a robust diagnostic gene set. <i>Science Translational Medicine</i> , <b>2015</b> , 7, 287ra71	17.5	197
82	Influenza Virus. <b>2016</b> , 1009-1058		0
81	Late regulation of immune genes and microRNAs in circulating leukocytes in a pig model of influenza A (H1N2) infection. <i>Scientific Reports</i> , <b>2016</b> , 6, 21812	4.9	17
80	Current and future molecular diagnostics for ocular infectious diseases. <i>Current Opinion in Ophthalmology</i> , <b>2016</b> , 27, 561-567	5.1	19
79	Robust classification of bacterial and viral infections via integrated host gene expression diagnostics. <i>Science Translational Medicine</i> , <b>2016</b> , 8, 346ra91	17.5	180

## (2019-2016)

78	Host gene expression classifiers diagnose acute respiratory illness etiology. <i>Science Translational Medicine</i> , <b>2016</b> , 8, 322ra11	17.5	150
77	Prostaglandin El£onstrains systemic inflammation through an innate lymphoid cell-IL-22 axis. <i>Science</i> , <b>2016</b> , 351, 1333-8	33.3	111
76	Enhanced understanding of the host-pathogen interaction in sepsis: new opportunities for omic approaches. <i>Lancet Respiratory Medicine,the</i> , <b>2017</b> , 5, 212-223	35.1	24
75	Benchmarking Sepsis Gene Expression Diagnostics Using Public Data. <i>Critical Care Medicine</i> , <b>2017</b> , 45, 1-10	1.4	70
74	A novel immune biomarker discriminates between influenza and bacteria in patients with suspected respiratory infection. <i>European Respiratory Journal</i> , <b>2017</b> , 49,	13.6	55
73	A Four-Biomarker Blood Signature Discriminates Systemic Inflammation Due to Viral Infection Versus Other Etiologies. <i>Scientific Reports</i> , <b>2017</b> , 7, 2914	4.9	37
72	Transcriptomic Biomarkers to Discriminate Bacterial from Nonbacterial Infection in Adults Hospitalized with Respiratory Illness. <i>Scientific Reports</i> , <b>2017</b> , 7, 6548	4.9	37
71	Increased incidence of co-infection in critically ill patients with influenza. <i>Intensive Care Medicine</i> , <b>2017</b> , 43, 48-58	14.5	109
70	Genomic Circuitry Underlying Immunological Response to Pediatric Acute Respiratory Infection. <i>Cell Reports</i> , <b>2018</b> , 22, 411-426	10.6	9
69	Unsupervised Analysis of Transcriptomics in Bacterial Sepsis Across Multiple Datasets Reveals Three Robust Clusters. <i>Critical Care Medicine</i> , <b>2018</b> , 46, 915-925	1.4	115
68	Biomarkers in Sepsis. <i>Critical Care Clinics</i> , <b>2018</b> , 34, 139-152	4.5	76
67	Immune Signatures and Microbial Load at the Nasopharyngeal Interface in Children With Acute Respiratory Infection. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 2475	5.7	5
66	Evaluating the Value of Defensins for Diagnosing Secondary Bacterial Infections in Influenza-Infected Patients. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 2762	5.7	5
65	Personalizing the Management of Pneumonia. <i>Clinics in Chest Medicine</i> , <b>2018</b> , 39, 871-900	5.3	5
64	Of mice and men: the host response to influenza virus infection. <i>Mammalian Genome</i> , <b>2018</b> , 29, 446-470	3.2	12
63	Transcriptome Analysis of Infected and Bystander Type 2 Alveolar Epithelial Cells during Influenza A Virus Infection Reveals Wnt Pathway Downregulation. <i>Journal of Virology</i> , <b>2018</b> , 92,	6.6	31
62	Characterization of cellular transcriptomic signatures induced by different respiratory viruses in human reconstituted airway epithelia. <i>Scientific Reports</i> , <b>2019</b> , 9, 11493	4.9	18
61	Neutrophils-related host factors associated with severe disease and fatality in patients with influenza infection. <i>Nature Communications</i> , <b>2019</b> , 10, 3422	17.4	66

60	Validation of a host response test to distinguish bacterial and viral respiratory infection. <i>EBioMedicine</i> , <b>2019</b> , 48, 453-461	8.8	22
59	Rapid, Sample-to-Answer Host Gene Expression Test to Diagnose Viral Infection. <i>Open Forum Infectious Diseases</i> , <b>2019</b> , 6, ofz466	1	5
58	Decreased plasma phospholipid concentrations and increased acid sphingomyelinase activity are accurate biomarkers for community-acquired pneumonia. <i>Journal of Translational Medicine</i> , <b>2019</b> , 17, 365	8.5	23
57	What can we learn about influenza infection and vaccination from transcriptomics?. <i>Human Vaccines and Immunotherapeutics</i> , <b>2019</b> , 15, 2615-2623	4.4	4
56	Respiratory viral infections. <b>2019</b> , 117-139		1
55	Host Gene Expression in Nose and Blood for the Diagnosis of Viral Respiratory Infection. <i>Journal of Infectious Diseases</i> , <b>2019</b> , 219, 1151-1161	7	22
54	Sepsis: future role of omics in diagnosis and therapy. <b>2020</b> , 281-289		0
53	A generalizable 29-mRNA neural-network classifier for acute bacterial and viral infections. <i>Nature Communications</i> , <b>2020</b> , 11, 1177	17.4	46
52	Previously Derived Host Gene Expression Classifiers Identify Bacterial and Viral Etiologies of Acute Febrile Respiratory Illness in a South Asian Population. <i>Open Forum Infectious Diseases</i> , <b>2020</b> , 7, ofaa194	.1	1
51	Immune and Metabolic Signatures of COVID-19 Revealed by Transcriptomics Data Reuse. <i>Frontiers in Immunology</i> , <b>2020</b> , 11, 1636	8.4	62
50	Transcriptional Correlates of Tolerance and Lethality in Mice Predict Ebola Virus Disease Patient Outcomes. <i>Cell Reports</i> , <b>2020</b> , 30, 1702-1713.e6	10.6	9
49	Pathway mapping of leukocyte transcriptome in influenza patients reveals distinct pathogenic mechanisms associated with progression to severe infection. <i>BMC Medical Genomics</i> , <b>2020</b> , 13, 28	3.7	6
48	How do I identify pathologic organisms in the 21st century?. <b>2020</b> , 299-306.e1		
47	Human Respiratory Syncytial Virus-Induced Immune Signature of Infection Revealed by Transcriptome Analysis of Clinical Pediatric Nasopharyngeal Swab Samples. <i>Journal of Infectious Diseases</i> , <b>2021</b> , 223, 1052-1061	7	1
46	Identification of key candidate biomarkers for severe influenza infection by integrated bioinformatical analysis and initial clinical validation. <i>Journal of Cellular and Molecular Medicine</i> , <b>2021</b> , 25, 1725-1738	5.6	3
45	Validation of a Host Gene Expression Test for Bacterial/Viral Discrimination in Immunocompromised Hosts. <i>Clinical Infectious Diseases</i> , <b>2021</b> , 73, 605-613	11.6	5
44	Identification of a Minimal 3-Transcript Signature to Differentiate Viral from Bacterial Infection from Best Genome-Wide Host RNA Biomarkers: A Multi-Cohort Analysis. <i>International Journal of Molecular Sciences</i> , <b>2021</b> , 22,	6.3	2
43	Discriminating Bacterial and Viral Infection Using a Rapid Host Gene Expression Test. <i>Critical Care Medicine</i> , <b>2021</b> , 49, 1651-1663	1.4	11

42	Localized skin inflammation during cutaneous leishmaniasis drives a chronic, systemic IFN- signature. <i>PLoS Neglected Tropical Diseases</i> , <b>2021</b> , 15, e0009321	4.8	8
41	Multi-cohort analysis of host immune response identifies conserved protective and detrimental modules associated with severity across viruses. <i>Immunity</i> , <b>2021</b> , 54, 753-768.e5	32.3	17
40	VB, a new blood biomarker for differential diagnosis and recovery monitoring of acute viral and bacterial infections. <i>EBioMedicine</i> , <b>2021</b> , 67, 103352	8.8	2
39	A single transcript for the prognosis of disease severity in COVID-19 patients. <i>Scientific Reports</i> , <b>2021</b> , 11, 12174	4.9	O
38	Blood transcriptomics reveal the evolution and resolution of the immune response in tuberculosis. <i>Journal of Experimental Medicine</i> , <b>2021</b> , 218,	16.6	5
37	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
36	A curated transcriptome dataset collection to investigate the blood transcriptional response to viral respiratory tract infection and vaccination. <i>F1000Research</i> , <b>2019</b> , 8, 284	3.6	4
35	Abundance of ADAM9 transcripts increases in the blood in response to tissue damage. <i>F1000Research</i> , <b>2015</b> , 4, 89	3.6	14
34	Increased abundance of ADAM9 transcripts in the blood is associated with tissue damage. <i>F1000Research</i> , <b>2015</b> , 4, 89	3.6	14
33	microRNAs in circulation are altered in response to influenza A virus infection in humans. <i>PLoS ONE</i> , <b>2013</b> , 8, e76811	3.7	75
32	Anomaly Detection in Host Signaling Pathways for the Early Prognosis of Acute Infection. <i>PLoS ONE</i> , <b>2016</b> , 11, e0160919	3.7	7
31	Host Transcriptional Response to Influenza and Other Acute Respiratory Viral InfectionsA Prospective Cohort Study. <i>PLoS Pathogens</i> , <b>2015</b> , 11, e1004869	7.6	78
30	Sepsis Diagnostics in the Era of "Omics" Technologies. <i>Prague Medical Report</i> , <b>2018</b> , 119, 9-29	0.7	7
29	The Host Response to Viral Infections Reveals Common and Virus-Specific Signatures in the Peripheral Blood. <i>Frontiers in Immunology</i> , <b>2021</b> , 12, 741837	8.4	3
28	Whole blood transcriptomic analysis to identify clinical biomarkers of drug response. <i>Methods in Molecular Biology</i> , <b>2014</b> , 1175, 35-43	1.4	О
27	Human Susceptibility and Response to Viral Diseases. 567-578		
26	Human Respiratory Syncytial Virus-induced immune signature of infection revealed by transcriptome analysis of clinical pediatric nasopharyngeal swab samples.		
25	A multi-tissue study of immune gene expression profiling highlights the key role of the nasal epithelium in COVID-19 severity.		Ο

24	A Study Based on Metabolomics, Network Pharmacology, and Experimental Verification to Explore the Mechanism of Qinbaiqingfei Concentrated Pills in the treatment of Mycoplasma Pneumonia. <i>Frontiers in Pharmacology</i> , <b>2021</b> , 12, 761883	5.6	0
23	A Robust Host-Response-Based Signature Distinguishes Bacterial and Viral Infections Across Diverse Global Populations. <i>SSRN Electronic Journal</i> ,	1	O
22	A 6-mRNA host response classifier in whole blood predicts outcomes in COVID-19 and other acute viral infections <i>Scientific Reports</i> , <b>2022</b> , 12, 889	4.9	2
21	Gene Expression Scoring of Immune Activity Levels for Precision Use of Hydrocortisone In Vasodilatory Shock <i>Shock</i> , <b>2022</b> , 57,	3.4	1
20	Systematic comparison of published host gene expression signatures for bacterial/viral discrimination <i>Genome Medicine</i> , <b>2022</b> , 14, 18	14.4	3
19	A multi-tissue study of immune gene expression profiling highlights the key role of the nasal epithelium in COVID-19 severity <i>Environmental Research</i> , <b>2022</b> , 210, 112890	7.9	2
18	A comparison of host response strategies to distinguish bacterial and viral infection <i>PLoS ONE</i> , <b>2021</b> , 16, e0261385	3.7	1
17	Data_Sheet_1.XLSX. <b>2018</b> ,		
16	Data_Sheet_2.XLSX. <b>2018</b> ,		
15	Data_Sheet_3.XLSX. <b>2018</b> ,		
14	Data_Sheet_4.XLSX. <b>2018</b> ,		
13	Data_Sheet_5.XLSX. <b>2018</b> ,		
12	Presentation_1.PDF. <b>2018</b> ,		
11	A protein signature associated with active tuberculosis identified by plasma profiling and network-based analysis.		
10	Mortality Prediction in Sepsis With an Immune-Related Transcriptomics Signature: A Multi-Cohort Analysis. <i>Frontiers in Medicine</i> , 9,	4.9	O
9	Evaluation and validation of the increased annexin A3 (ANXA3) as a novel biomarker to predict sepsis in critically ill patients.		
8	Construction of gene network database, and identification of key genes for diagnosis, prognosis, and treatment in sepsis.		О
7	Co-expression network analysis identifies potential candidate hub genes in severe influenza patients needing invasive mechanical ventilation. <b>2022</b> , 23,		1

## CITATION REPORT

6	Cytokine Storm <b>D</b> efinition, Causes, and Implications. <b>2022</b> , 23, 11740	5
5	Role of gene sequencing for the diagnosis, tracking and prevention of ocular infections. <b>2022</b> , 24, 36	O
4	An automated DNA computing platform for rapid etiological diagnostics. 2022, 8,	О
3	A protein signature associated with active tuberculosis identified by plasma profiling and network-based analysis. <b>2022</b> , 25, 105652	O
2	Benchmarking transcriptional host response signatures for infection diagnosis. <b>2022</b> , 13, 974-988.e7	О
1	A robust host-response-based signature distinguishes bacterial and viral infections across diverse global populations. <b>2022</b> , 3, 100842	0