Damien Chaussabel

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5330306/publications.pdf

Version: 2024-02-01

160 17,579 papers citations

58 h-index 126 g-index

182 all docs 182 docs citations 182 times ranked

23349 citing authors

#	Article	IF	CITATIONS
1	An interferon-inducible neutrophil-driven blood transcriptional signature in human tuberculosis. Nature, 2010, 466, 973-977.	27.8	1,632
2	Pyogenic Bacterial Infections in Humans with MyD88 Deficiency. Science, 2008, 321, 691-696.	12.6	844
3	Molecular signatures of antibody responses derived from a systems biology study of five human vaccines. Nature Immunology, 2014, 15, 195-204.	14.5	672
4	A Modular Analysis Framework for Blood Genomics Studies: Application to Systemic Lupus Erythematosus. Immunity, 2008, 29, 150-164.	14.3	623
5	<i>IRF8</i> Mutations and Human Dendritic-Cell Immunodeficiency. New England Journal of Medicine, 2011, 365, 127-138.	27.0	564
6	Functional Specializations of Human Epidermal Langerhans Cells and CD14+ Dermal Dendritic Cells. Immunity, 2008, 29, 497-510.	14.3	539
7	Influence of the transcription factor RORγt on the development of NKp46+ cell populations in gut and skin. Nature Immunology, 2009, 10, 75-82.	14.5	507
8	Gene expression patterns in blood leukocytes discriminate patients with acute infections. Blood, 2007, 109, 2066-2077.	1.4	462
9	A multicentre, randomised, double-blind, placebo-controlled trial with the interleukin-1 receptor antagonist anakinra in patients with systemic-onset juvenile idiopathic arthritis (ANAJIS trial). Annals of the Rheumatic Diseases, 2011, 70, 747-754.	0.9	462
10	Global Analyses of Human Immune Variation Reveal Baseline Predictors of Postvaccination Responses. Cell, 2014, 157, 499-513.	28.9	424
11	Immunodeficiency, autoinflammation and amylopectinosis in humans with inherited HOIL-1 and LUBAC deficiency. Nature Immunology, 2012, 13, 1178-1186.	14.5	410
12	Life-threatening influenza and impaired interferon amplification in human IRF7 deficiency. Science, 2015, 348, 448-453.	12.6	389
13	Nasopharyngeal Microbiota, Host Transcriptome, and Disease Severity in Children with Respiratory Syncytial Virus Infection. American Journal of Respiratory and Critical Care Medicine, 2016, 194, 1104-1115.	5.6	337
14	TLR recognition of self nucleic acids hampers glucocorticoid activity in lupus. Nature, 2010, 465, 937-941.	27.8	320
15	Unique gene expression profiles of human macrophages and dendritic cells to phylogenetically distinct parasites. Blood, 2003, 102, 672-681.	1.4	305
16	Modular Transcriptional Repertoire Analyses of Adults With Systemic Lupus Erythematosus Reveal Distinct Type I and Type II Interferon Signatures. Arthritis and Rheumatology, 2014, 66, 1583-1595.	5.6	302
17	Human TYK2 deficiency: Mycobacterial and viral infections without hyper-lgE syndrome. Journal of Experimental Medicine, 2015, 212, 1641-1662.	8.5	293
18	Systems Scale Interactive Exploration Reveals Quantitative and Qualitative Differences in Response to Influenza and Pneumococcal Vaccines. Immunity, 2013, 38, 831-844.	14.3	284

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19	Whole Blood Gene Expression Profiles to Assess Pathogenesis and Disease Severity in Infants with Respiratory Syncytial Virus Infection. PLoS Medicine, 2013, 10, e1001549.	8.4	273
20	Herpes simplex virus encephalitis in a patient with complete TLR3 deficiency: TLR3 is otherwise redundant in protective immunity. Journal of Experimental Medicine, 2011, 208, 2083-2098.	8.5	262
21	Transcriptional Blood Signatures Distinguish Pulmonary Tuberculosis, Pulmonary Sarcoidosis, Pneumonias and Lung Cancers. PLoS ONE, 2013, 8, e70630.	2.5	254
22	Herpes simplex encephalitis in children with autosomal recessive and dominant TRIF deficiency. Journal of Clinical Investigation, 2011, 121, 4889-4902.	8.2	254
23	Assessing the human immune system through blood transcriptomics. BMC Biology, 2010, 8, 84.	3.8	235
24	Heterozygous <i>TBK1</i> mutations impair TLR3 immunity and underlie herpes simplex encephalitis of childhood. Journal of Experimental Medicine, 2012, 209, 1567-1582.	8.5	231
25	Blood leukocyte microarrays to diagnose systemic onset juvenile idiopathic arthritis and follow the response to IL-1 blockade. Journal of Experimental Medicine, 2007, 204, 2131-2144.	8.5	215
26	Gene Expression in Peripheral Blood Mononuclear Cells from Children with Diabetes. Journal of Clinical Endocrinology and Metabolism, 2007, 92, 3705-3711.	3.6	201
27	Copy Number Loss of the Interferon Gene Cluster in Melanomas Is Linked to Reduced T Cell Infiltrate and Poor Patient Prognosis. PLoS ONE, 2014, 9, e109760.	2.5	192
28	Detectable Changes in The Blood Transcriptome Are Present after Two Weeks of Antituberculosis Therapy. PLoS ONE, 2012, 7, e46191.	2.5	190
29	Democratizing systems immunology with modular transcriptional repertoire analyses. Nature Reviews Immunology, 2014, 14, 271-280.	22.7	190
30	Association of RNA Biosignatures With Bacterial Infections in Febrile Infants Aged 60 Days or Younger. JAMA - Journal of the American Medical Association, 2016, 316, 846.	7.4	180
31	Systemic sclerosis and lupus: Points in an interferonâ€mediated continuum. Arthritis and Rheumatism, 2010, 62, 589-598.	6.7	177
32	Genomic transcriptional profiling identifies a candidate blood biomarker signature for the diagnosis of septicemic melioidosis. Genome Biology, 2009, 10, R127.	9.6	176
33	Plasticity and Virus Specificity of the Airway Epithelial Cell Immune Response during Respiratory Virus Infection. Journal of Virology, 2012, 86, 5422-5436.	3.4	176
34	CD2 Distinguishes Two Subsets of Human Plasmacytoid Dendritic Cells with Distinct Phenotype and Functions. Journal of Immunology, 2009, 182, 6815-6823.	0.8	162
35	Life-threatening influenza pneumonitis in a child with inherited IRF9 deficiency. Journal of Experimental Medicine, 2018, 215, 2567-2585.	8.5	146
36	A Genomic Approach to Human Autoimmune Diseases. Annual Review of Immunology, 2010, 28, 535-571.	21.8	137

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37	A recessive form of hyper-IgE syndrome by disruption of ZNF341-dependent STAT3 transcription and activity. Science Immunology, 2018, 3, .	11.9	132
38	Multicohort analysis reveals baseline transcriptional predictors of influenza vaccination responses. Science Immunology, 2017, 2, .	11.9	122
39	Induction of B7-H6, a ligand for the natural killer cell–activating receptor NKp30, in inflammatory conditions. Blood, 2013, 122, 394-404.	1.4	120
40	Relationships Among Murine CD11chigh Dendritic Cell Subsets as Revealed by Baseline Gene Expression Patterns. Journal of Immunology, 2003, 171, 47-60.	0.8	119
41	Progression of whole-blood transcriptional signatures from interferon-induced to neutrophil-associated patterns in severe influenza. Nature Immunology, 2018, 19, 625-635.	14.5	119
42	Improving Efficacy of Clinical Islet Transplantation with Iodixanol-Based Islet Purification, Thymoglobulin Induction, and Blockage of IL- $1\hat{1}^2$ and TNF- $\hat{1}\pm$. Cell Transplantation, 2011, 20, 1641-1647.	2.5	113
43	The immunity-related GTPase Irgm1 promotes the expansion of activated CD4+ T cell populations by preventing interferon-l̂3-induced cell death. Nature Immunology, 2008, 9, 1279-1287.	14.5	110
44	Assessment of immune status using blood transcriptomics and potential implications for global health. Seminars in Immunology, 2015, 27, 58-66.	5.6	110
45	Programmed death ligand 1 is overâ€expressed by neutrophils in the blood of patients with active tuberculosis. European Journal of Immunology, 2011, 41, 1941-1947.	2.9	104
46	Mining microarray expression data by literature profiling. Genome Biology, 2002, 3, RESEARCH0055.	9.6	102
47	Host Immune Transcriptional Profiles Reflect the Variability in Clinical Disease Manifestations in Patients with Staphylococcus aureus Infections. PLoS ONE, 2012, 7, e34390.	2.5	100
48	A novel form of human STAT1 deficiency impairing early but not late responses to interferons. Blood, 2010, 116, 5895-5906.	1.4	93
49	Influence of Coinfecting Pathogens on HIV Expression: Evidence for a Role of Toll-Like Receptors. Journal of Immunology, 2004, 172, 7229-7234.	0.8	92
50	Systems Biology Approaches Reveal a Specific Interferon-Inducible Signature in HTLV-1 Associated Myelopathy. PLoS Pathogens, 2012, 8, e1002480.	4.7	92
51	Transcriptomic evidence for modulation of host inflammatory responses during febrile Plasmodium falciparum malaria. Scientific Reports, 2016, 6, 31291.	3.3	85
52	TPL-2–ERK1/2 Signaling Promotes Host Resistance against Intracellular Bacterial Infection by Negative Regulation of Type I IFN Production. Journal of Immunology, 2013, 191, 1732-1743.	0.8	84
53	HIV–tuberculosis-associated immune reconstitution inflammatory syndrome is characterized by Toll-like receptor and inflammasome signalling. Nature Communications, 2015, 6, 8451.	12.8	81
54	The Transcriptional Signature of Active Tuberculosis Reflects Symptom Status in Extra-Pulmonary and Pulmonary Tuberculosis. PLoS ONE, 2016, 11, e0162220.	2.5	81

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55	Enhanced Monocyte Response and Decreased Central Memory T Cells in Children with Invasive Staphylococcus aureus Infections. PLoS ONE, 2009, 4, e5446.	2.5	79
56	A narrow repertoire of transcriptional modules responsive to pyogenic bacteria is impaired in patients carrying loss-of-function mutations in MYD88 or IRAK4. Nature Immunology, 2014, 15, 1134-1142.	14.5	75
57	How the study of children with rheumatic diseases identified interferonâ€Î± and interleukinâ€1 as novel therapeutic targets. Immunological Reviews, 2008, 223, 39-59.	6.0	68
58	Human Adaptive Immunity Rescues an Inborn Error of Innate Immunity. Cell, 2017, 168, 789-800.e10.	28.9	68
59	Multicenter Systems Analysis of Human Blood Reveals Immature Neutrophils in Males and During Pregnancy. Journal of Immunology, 2017, 198, 2479-2488.	0.8	66
60	Transcriptional profiling unveils type I and II interferon networks in blood and tissues across diseases. Nature Communications, 2019, 10, 2887.	12.8	65
61	Interferon Signature in the Blood in Inflammatory Common Variable Immune Deficiency. PLoS ONE, 2013, 8, e74893.	2.5	64
62	TLR3 controls constitutive IFN- \hat{l}^2 antiviral immunity in human fibroblasts and cortical neurons. Journal of Clinical Investigation, 2021, 131, .	8.2	64
63	Haploinsufficiency at the human IFNGR2 locus contributes to mycobacterial disease. Human Molecular Genetics, 2013, 22, 769-781.	2.9	58
64	Dissection of Immune Gene Networks in Primary Melanoma Tumors Critical for Antitumor Surveillance of Patients with Stage II–III Resectable Disease. Journal of Investigative Dermatology, 2014, 134, 2202-2211.	0.7	51
65	Transcriptional specialization of human dendritic cell subsets in response to microbial vaccines. Nature Communications, 2014, 5, 5283.	12.8	51
66	A 380-gene meta-signature of active tuberculosis compared with healthy controls. European Respiratory Journal, 2016, 47, 1873-1876.	6.7	51
67	Ribosomal protein mRNAs are translationally-regulated during human dendritic cells activation by LPS. Immunome Research, 2009, 5, 5.	0.1	49
68	An interactive web application for the dissemination of human systems immunology data. Journal of Translational Medicine, 2015, 13, 196.	4.4	49
69	Inherited human IRAK-1 deficiency selectively impairs TLR signaling in fibroblasts. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E514-E523.	7.1	49
70	Diarrheagenic Escherichia coli Carrying Supplementary Virulence Genes Are an Important Cause of Moderate to Severe Diarrhoeal Disease in Mexico. PLoS Neglected Tropical Diseases, 2015, 9, e0003510.	3.0	46
71	A systematic approach to biomarker discovery; Preamble to "the iSBTc-FDA taskforce on immunotherapy biomarkers". Journal of Translational Medicine, 2008, 6, 81.	4.4	45
72	Three Copies of Four Interferon Receptor Genes Underlie a Mild Type I Interferonopathy in Down Syndrome. Journal of Clinical Immunology, 2020, 40, 807-819.	3.8	44

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73	CD40 Ligation Prevents <i>Trypanosoma cruzi </i> Infection through Interleukin-12 Upregulation. Infection and Immunity, 1999, 67, 1929-1934.	2.2	44
74	Analysis of Significance Patterns Identifies Ubiquitous and Disease-Specific Gene-Expression Signatures in Patient Peripheral Blood Leukocytes. Annals of the New York Academy of Sciences, 2005, 1062, 146-154.	3.8	43
75	SP100 inhibits ETS1 activity in primary endothelial cells. Oncogene, 2005, 24, 916-931.	5.9	43
76	IRF4 haploinsufficiency in a family with Whipple's disease. ELife, 2018, 7, .	6.0	43
77	IL-10 up-regulates nitric oxide (NO) synthesis by lipopolysaccharide (LPS)-activated macrophages: improved control of Trypanosoma cruzi infection. Clinical and Experimental Immunology, 1998, 113, 59-64.	2.6	39
78	Whole blood transcriptional profiles as a prognostic tool in complete and incomplete Kawasaki Disease. PLoS ONE, 2018, 13, e0197858.	2.5	39
79	Ductal Injection of JNK Inhibitors Before Pancreas Preservation Prevents Islet Apoptosis and Improves Islet Graft Function. Human Gene Therapy, 2009, 20, 73-85.	2.7	38
80	Production of interleukinâ€27 by human neutrophils regulates their function during bacterial infection. European Journal of Immunology, 2012, 42, 3280-3290.	2.9	37
81	Microarray-based identification of novel biomarkers in IL-1-mediated diseases. Current Opinion in Immunology, 2007, 19, 623-632.	5.5	35
82	Low HERV-K(C4) Copy Number Is Associated With Type 1 Diabetes. Diabetes, 2014, 63, 1789-1795.	0.6	34
83	A transcriptomic reporter assay employing neutrophils to measure immunogenic activity of septic patients' plasma. Journal of Translational Medicine, 2014, 12, 65.	4.4	34
84	A vision and a prescription for big data–enabled medicine. Nature Immunology, 2015, 16, 435-439.	14.5	34
85	Modular transcriptional repertoire analyses identify a blood neutrophil signature as a candidate biomarker for lupus nephritis. Rheumatology, 2017, 56, kew439.	1.9	34
86	Vaginal Microbiota and Cytokine Levels Predict Preterm Delivery in Asian Women. Frontiers in Cellular and Infection Microbiology, 2021, 11, 639665.	3.9	34
87	Biomedical Literature Mining. Molecular Diagnosis and Therapy, 2004, 4, 383-393.	3.3	33
88	Long-Chain Acyl-CoA Synthetase 1 Role in Sepsis and Immunity: Perspectives From a Parallel Review of Public Transcriptome Datasets and of the Literature. Frontiers in Immunology, 2019, 10, 2410.	4.8	33
89	Blood Interferon Signatures Putatively Link Lack of Protection Conferred by the RTS,S Recombinant Malaria Vaccine to an Antigen-specific IgE Response. F1000Research, 2015, 4, 919.	1.6	33
90	Annexin A3 in sepsis: novel perspectives from an exploration of public transcriptome data. Immunology, 2020, 161, 291-302.	4.4	32

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91	Alteration of Migration and Maturation of Dendritic Cells and T-Cell Depletion in the Course of Experimental Trypanosoma cruzi Infection. Laboratory Investigation, 2003, 83, 1373-1382.	3.7	31
92	Neuroinvasive West Nile Infection Elicits Elevated and Atypically Polarized T Cell Responses That Promote a Pathogenic Outcome. PLoS Pathogens, 2016, 12, e1005375.	4.7	31
93	Development of a fixed module repertoire for the analysis and interpretation of blood transcriptome data. Nature Communications, 2021, 12, 4385.	12.8	29
94	Induction of TRAIL- and TNF-α-Dependent Apoptosis in Human Monocyte-Derived Dendritic Cells by Microfilariae of Brugia malayi. Journal of Immunology, 2008, 181, 7081-7089.	0.8	28
95	ZnT8-Specific CD4+ T Cells Display Distinct Cytokine Expression Profiles between Type 1 Diabetes Patients and Healthy Adults. PLoS ONE, 2013, 8, e55595.	2.5	28
96	Mutations of HNRNPAO and WIF1 predispose members of a large family to multiple cancers. Familial Cancer, 2015, 14, 297-306.	1.9	28
97	Incidence, clinical presentation, and antimicrobial resistance trends in Salmonella and Shigella infections from children in Yucatan, Mexico. Frontiers in Microbiology, 2013, 4, 288.	3.5	26
98	The Relationship of Immune Cell Signatures to Patient Survival Varies within and between Tumor Types. PLoS ONE, 2015, 10, e0138726.	2.5	24
99	Adult-onset type 1 diabetes patients display decreased IGRP-specific Tr1 cells in blood. Clinical Immunology, 2015, 161, 270-277.	3.2	23
100	Shared and organism-specific host responses to childhood diarrheal diseases revealed by whole blood transcript profiling. PLoS ONE, 2018, 13, e0192082.	2.5	23
101	Definition of erythroid cellâ€positive blood transcriptome phenotypes associated with severe respiratory syncytial virus infection. Clinical and Translational Medicine, 2020, 10, e244.	4.0	22
102	Disease Mechanisms in Rheumatologyâ€"Tools and Pathways: Current Perspectives on Systems Immunology Approaches to Rheumatic Diseases. Arthritis and Rheumatism, 2013, 65, 1407-1417.	6.7	21
103	The Blood Transcriptome of Experimental Melioidosis Reflects Disease Severity and Shows Considerable Similarity with the Human Disease. Journal of Immunology, 2015, 195, 3248-3261.	0.8	20
104	A curated compendium of monocyte transcriptome datasets of relevance to human monocyte immunobiology research. F1000Research, 2016, 5, 291.	1.6	20
105	A Neutrophil-Driven Inflammatory Signature Characterizes the Blood Transcriptome Fingerprint of Psoriasis. Frontiers in Immunology, 2020, 11, 587946.	4.8	19
106	Increased abundance of ADAM9 transcripts in the blood is associated with tissue damage. F1000Research, 2015, 4, 89.	1.6	19
107	Blood Interferon Signatures Putatively Link Lack of Protection Conferred by the RTS,S Recombinant Malaria Vaccine to an Antigen-specific IgE Response. F1000Research, 2015, 4, 919.	1.6	19
108	Data management: it starts at the bench. Nature Immunology, 2009, 10, 1225-1227.	14.5	18

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109	Blood-Borne RNA Correlates with Disease Activity and IFN-Stimulated Gene Expression in Systemic Lupus Erythematosus. Journal of Immunology, 2016, 197, 2854-2863.	0.8	18
110	BloodGen3Module: blood transcriptional module repertoire analysis and visualization using R. Bioinformatics, 2021, 37, 2382-2389.	4.1	18
111	Dendritic Cells, Therapeutic Vectors of Immunity and Tolerance. American Journal of Transplantation, 2005, 5, 205-206.	4.7	17
112	Quiescent Innate Response to Infective Filariae by Human Langerhans Cells Suggests a Strategy of Immune Evasion. Infection and Immunity, 2013, 81, 1420-1429.	2.2	17
113	Identification of the Key Differential Transcriptional Responses of Human Whole Blood Following TLR2 or TLR4 Ligation In-Vitro. PLoS ONE, 2014, 9, e97702.	2.5	17
114	Finger stick blood collection for gene expression profiling and storage of tempus blood RNA tubes. F1000Research, 2016, 5, 1385.	1.6	17
115	Transforming Growth Factor \hat{l}^2 Signaling Controls Activities of Human Intestinal CD8+T Suppressor Cells. Gastroenterology, 2013, 144, 601-612.e1.	1.3	16
116	Transketolase and vitamin B1 influence on ROS-dependent neutrophil extracellular traps (NETs) formation. PLoS ONE, 2019, 14, e0221016.	2.5	16
117	Finger stick blood collection for gene expression profiling and storage of tempus blood RNA tubes. F1000Research, 2016, 5, 1385.	1.6	16
118	Using  collective omics data' for biomedical research training. Immunology, 2018, 155, 18-23.	4.4	15
119	A prospective cohort for the investigation of alteration in temporal transcriptional and microbiome trajectories preceding preterm birth: a study protocol. BMJ Open, 2019, 9, e023417.	1.9	15
120	Blood genome expression profiles in infants with congenital cytomegalovirus infection. Nature Communications, 2020, 11 , 3548.	12.8	15
121	Abundance of ADAM9 transcripts increases in the blood in response to tissue damage. F1000Research, 2015, 4, 89.	1.6	15
122	A collection of annotated and harmonized human breast cancer transcriptome datasets, including immunologic classification. F1000Research, 2017, 6, 296.	1.6	14
123	Transcriptomic Profiling Identifies Neutrophil-Specific Upregulation of Cystatin F as a Marker of Acute Inflammation in Humans. Frontiers in Immunology, 2021, 12, 634119.	4.8	14
124	Prospective validation study of prognostic biomarkers to predict adverse outcomes in patients with COVID-19: a study protocol. BMJ Open, 2021, 11, e044497.	1.9	14
125	A collection of annotated and harmonized human breast cancer transcriptome datasets, including immunologic classification. F1000Research, 2017, 6, 296.	1.6	14
126	A modular framework for the development of targeted Covid-19 blood transcript profiling panels. Journal of Translational Medicine, 2020, 18, 291.	4.4	13

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127	Gene Expression Profiling of Human Pancreatic Islets Undergoing a Simulated Process of Instant Blood-Mediated Inflammatory Reaction. Transplantation Proceedings, 2008, 40, 430-432.	0.6	12
128	Transcriptional network predicts viral set point during acute HIV-1 infection. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, 1103-1109.	4.4	12
129	A curated transcriptome dataset collection to investigate the development and differentiation of the human placenta and its associated pathologies. F1000Research, 2016, 5, 305.	1.6	12
130	A curated transcriptome dataset collection to investigate the functional programming of human hematopoietic cells in early life. F1000Research, 2016, 5, 414.	1.6	12
131	Paradoxical association between blood modular interferon signatures and quality of life in patients with systemic lupus erythematosus. Rheumatology, 2020, 59, 1975-1983.	1.9	10
132	Connection of BANK1, Tolerance, Regulatory B cells, and Apoptosis: Perspectives of a Reductionist Investigation. Frontiers in Immunology, 2021, 12, 589786.	4.8	10
133	A curated transcriptome dataset collection to investigate the immunobiology of HIV infection. F1000Research, 2016, 5, 327.	1.6	10
134	A curated transcriptome dataset collection to investigate the development and differentiation of the human placenta and its associated pathologies. F1000Research, 2016, 5, 305.	1.6	10
135	Analysis of Transcriptional Signatures in Response to Listeria monocytogenes Infection Reveals Temporal Changes That Result from Type I Interferon Signaling. PLoS ONE, 2016, 11, e0150251.	2.5	10
136	Gene expression changes in human islets exposed to type 1 diabetic serum. Islets, 2012, 4, 312-319.	1.8	9
137	A curated transcriptome dataset collection to investigate the blood transcriptional response to viral respiratory tract infection and vaccination F1000Research, 2019, 8, 284.	1.6	9
138	Introducing a New Dimension to Molecular Disease Classifications. Trends in Molecular Medicine, 2016, 22, 451-453.	6.7	7
139	Differential regulation of the immune system in a brain-liver-fats organ network during short-term fasting. Molecular Metabolism, 2020, 40, 101038.	6.5	7
140	ÂA curated transcriptomic dataset collection relevant to embryonic development associated with in vitro fertilization in healthy individuals and patients with polycystic ovary syndrome. F1000Research, 2017, 6, 181.	1.6	7
141	Cohort profile: molecular signature in pregnancy (MSP): longitudinal high-frequency sampling to characterise cross-omic trajectories in pregnancy in a resource-constrained setting. BMJ Open, 2020, 10, e041631.	1.9	6
142	A protocol for extraction of total RNA from finger stick whole blood samples preserved with TempusTM solution. F1000Research, 0, 7, 1739.	1.6	6
143	Transcriptomic profile investigations highlight a putative role for NUDT16 in sepsis. Journal of Cellular and Molecular Medicine, 2022, 26, 1714-1721.	3.6	5
144	A curated collection of transcriptome datasets to investigate the molecular mechanisms of immunoglobulin E-mediated atopic diseases. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	4

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145	Transcriptome and Literature Mining Highlight the Differential Expression of ERLIN1 in Immune Cells during Sepsis. Biology, 2021, 10, 755.	2.8	4
146	A compendium of monocyte transcriptome datasets to foster biomedical knowledge discovery. F1000Research, 2016, 5, 291.	1.6	4
147	Blood gene transcript signature profiling in pregnancies resulting in preterm birth: A systematic review. European Journal of Obstetrics and Gynecology and Reproductive Biology: X, 2020, 8, 100118.	1.1	3
148	Integrated transcriptionalâ€phenotypic analysis captures systemic immunomodulation following antiangiogenic therapy in renal cell carcinoma patients. Clinical and Translational Medicine, 2021, 11, e434.	4.0	3
149	A curated transcriptome dataset collection to investigate inborn errors of immunity. F1000Research, 2019, 8, 188.	1.6	3
150	SysInflam HuDB, a Web Resource for Mining Human Blood Cells Transcriptomic Data Associated with Systemic Inflammatory Responses to Sepsis. Journal of Immunology, 2021, 207, 2195-2202.	0.8	3
151	A curated transcriptome dataset collection to investigate inborn errors of immunity. F1000Research, 2019, 8, 188.	1.6	3
152	Characterization of peripheral blood mononuclear cells gene expression profiles of pediatric Staphylococcus aureus persistent and non-carriers using a targeted assay. Microbes and Infection, 2020, 22, 540-549.	1.9	2
153	Influence of storage conditions of small volumes of blood on immune transcriptomic profiles. BMC Research Notes, 2020, 13, 150.	1.4	2
154	Organizing gene literature retrieval, Âprofiling, and visualization training workshops for early career researchers. F1000Research, 0, 10, 275.	1.6	2
155	Blood Transcriptional Fingerprints to Assess the Immune Status of Human Subjects., 2011, , 105-125.		1
156	Mapping the Road of Gvhd and GVT: A Longitudinal Study of Immune-Transcriptome Signatures As Novel Approach to Solve Post-Allogeneic Hematopoietic Cell Transplantation Dilemmas. Blood, 2019, 134, 4550-4550.	1.4	1
157	Blood leukocyte microarrays to diagnose systemic onset juvenile idiopathic arthritis and follow the response to IL-1 blockade. Journal of Experimental Medicine, 2009, 206, 2299-2299.	8.5	O
158	A Web-Based Systems Immunology Toolkit Allows the Visualization and Analysis of Public Collective Data to Decipher Immunity in Early Life. , 2016 , , .		0
159	Big Data as the Foundation of a Novel Training Platform for Biomedical Researchers in Qatar. , 2016, , .		0
160	Understanding the Mechanism of Diabetes Mellitus in a LRBA-Deficient Patient. Biology, 2022, 11, 612.	2.8	0