Angela J Rogers

List of Publications by Year in descending order

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Version: 2024-02-01

73 papers 12,831 citations

33 h-index 102304 66 g-index

92 all docs 92 docs citations 92 times ranked 18914 citing authors

#	Article	IF	CITATIONS
1	SARS-CoV-2 RNAemia Predicts Clinical Deterioration and Extrapulmonary Complications from COVID-19. Clinical Infectious Diseases, 2022, 74, 218-226.	2.9	51
2	COVID-19 ARDS: One Pathogen, Multiple Phenotypes. Critical Care Clinics, 2022, , .	1.0	6
3	Association Between SARS-CoV-2 RNAemia and Postacute Sequelae of COVID-19. Open Forum Infectious Diseases, 2022, 9, ofab646.	0.4	14
4	Machine learning approaches to the human metabolome in sepsis identify metabolic links with survival. Intensive Care Medicine Experimental, $2022,10,10$	0.9	7
5	Biochemical, biophysical, and immunological characterization of respiratory secretions in severe SARS-CoV-2 infections. JCI Insight, 2022, 7, .	2.3	16
6	Anti-nucleocapsid antibody levels and pulmonary comorbid conditions are linked to post–COVID-19 syndrome. JCI Insight, 2022, 7, .	2.3	18
7	Prolonged Hospitalization Following Acute Respiratory Failure. Chest, 2021, 159, 1867-1874.	0.4	5
8	Network study of nasal transcriptome profiles reveals master regulator genes of asthma. Journal of Allergy and Clinical Immunology, 2021, 147, 879-893.	1.5	22
9	Synthetic Siglec-9 Agonists Inhibit Neutrophil Activation Associated with COVID-19. ACS Central Science, 2021, 7, 650-657.	5.3	39
10	Integrated analysis of multimodal single-cell data. Cell, 2021, 184, 3573-3587.e29.	13.5	5,912
10		13.5	5,912 4
	Integrated analysis of multimodal single-cell data. Cell, 2021, 184, 3573-3587.e29. Prospective validation of an 11-gene mRNA host response score for mortality risk stratification in the		5,912
11	Integrated analysis of multimodal single-cell data. Cell, 2021, 184, 3573-3587.e29. Prospective validation of an 11-gene mRNA host response score for mortality risk stratification in the intensive care unit. Scientific Reports, 2021, 11, 13062. Multi-omic profiling reveals widespread dysregulation of innate immunity and hematopoiesis in	1.6	4
11 12	Integrated analysis of multimodal single-cell data. Cell, 2021, 184, 3573-3587.e29. Prospective validation of an 11-gene mRNA host response score for mortality risk stratification in the intensive care unit. Scientific Reports, 2021, 11, 13062. Multi-omic profiling reveals widespread dysregulation of innate immunity and hematopoiesis in COVID-19. Journal of Experimental Medicine, 2021, 218, .	1.6	139
11 12 13	Integrated analysis of multimodal single-cell data. Cell, 2021, 184, 3573-3587.e29. Prospective validation of an 11-gene mRNA host response score for mortality risk stratification in the intensive care unit. Scientific Reports, 2021, 11, 13062. Multi-omic profiling reveals widespread dysregulation of innate immunity and hematopoiesis in COVID-19. Journal of Experimental Medicine, 2021, 218, . Plasma Metabolites in Early Sepsis Identify Distinct Clusters Defined by Plasma Lipids. , 2021, 3, e0478. A Perspective on the Role of Point-of-Care "lmmuno-Triaging―to Optimize COVID-19 Vaccination	1.6 4.2	139
11 12 13 14	Integrated analysis of multimodal single-cell data. Cell, 2021, 184, 3573-3587.e29. Prospective validation of an 11-gene mRNA host response score for mortality risk stratification in the intensive care unit. Scientific Reports, 2021, 11, 13062. Multi-omic profiling reveals widespread dysregulation of innate immunity and hematopoiesis in COVID-19. Journal of Experimental Medicine, 2021, 218, . Plasma Metabolites in Early Sepsis Identify Distinct Clusters Defined by Plasma Lipids. , 2021, 3, e0478. A Perspective on the Role of Point-of-Care "Immuno-Triaging―to Optimize COVID-19 Vaccination Distribution in a Time of Scarcity. Frontiers in Public Health, 2021, 9, 638316. The COVID-19 Outpatient Pragmatic Platform Study (COPPS): Study design of a multi-center pragmatic	1.6 4.2	139
11 12 13 14	Integrated analysis of multimodal single-cell data. Cell, 2021, 184, 3573-3587.e29. Prospective validation of an 11-gene mRNA host response score for mortality risk stratification in the intensive care unit. Scientific Reports, 2021, 11, 13062. Multi-omic profiling reveals widespread dysregulation of innate immunity and hematopoiesis in COVID-19. Journal of Experimental Medicine, 2021, 218, . Plasma Metabolites in Early Sepsis Identify Distinct Clusters Defined by Plasma Lipids. , 2021, 3, e0478. A Perspective on the Role of Point-of-Care "lmmuno-Triaging―to Optimize COVID-19 Vaccination Distribution in a Time of Scarcity. Frontiers in Public Health, 2021, 9, 638316. The COVID-19 Outpatient Pragmatic Platform Study (COPPS): Study design of a multi-center pragmatic platform trial. Contemporary Clinical Trials, 2021, 108, 106509. Active surveillance of serious adverse events following transfusion of COVID â€19 convalescent	1.6 4.2 1.3	4 139 10 3

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19	Delving beneath the surface of hyperinflammation in COVID-19. Lancet Rheumatology, The, 2020, 2, e578-e579.	2.2	14
20	Defining the features and duration of antibody responses to SARS-CoV-2 infection associated with disease severity and outcome. Science Immunology, 2020, 5, .	5.6	404
21	A single-cell atlas of the peripheral immune response in patients with severe COVID-19. Nature Medicine, 2020, 26, 1070-1076.	15.2	1,300
22	Electrical Storm in COVID-19. JACC: Case Reports, 2020, 2, 1256-1260.	0.3	4
23	A generalizable 29-mRNA neural-network classifier for acute bacterial and viral infections. Nature Communications, 2020, 11, 1177.	5.8	77
24	Gender Differences in Authorship of Critical Care Literature. American Journal of Respiratory and Critical Care Medicine, 2020, 201, 840-847.	2.5	44
25	Cytokine profile in plasma of severe COVID-19 does not differ from ARDS and sepsis. JCI Insight, 2020, 5, .	2.3	196
26	Association Between Peripheral Blood Oxygen Saturation (SpO ₂)/Fraction of Inspired Oxygen (FiO ₂) Ratio Time at Risk and Hospital Mortality in Mechanically Ventilated Patients. , 2020, 24, .		20
27	Precision Medicine in Critical Illness: Sepsis and Acute Respiratory Distress Syndrome. Respiratory Medicine, 2020, , 267-288.	0.1	2
28	Association of Elevated Plasma Interleukin-18 Level With Increased Mortality in a Clinical Trial of Statin Treatment for Acute Respiratory Distress Syndrome*. Critical Care Medicine, 2019, 47, 1089-1096.	0.4	70
29	Treatment with allogeneic mesenchymal stromal cells for moderate to severe acute respiratory distress syndrome (START study): a randomised phase 2a safety trial. Lancet Respiratory Medicine, the, 2019, 7, 154-162.	5.2	443
30	Genome-Wide Association Study in Acute Respiratory Distress Syndrome. Finding the Needle in the Haystack to Advance Our Understanding of Acute Respiratory Distress Syndrome. American Journal of Respiratory and Critical Care Medicine, 2018, 197, 1373-1374.	2.5	6
31	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
32	Plasma mitochondrial DNA and metabolomic alterations in severe critical illness. Critical Care, 2018, 22, 360.	2.5	31
33	Current Status and Future Opportunities in Lung Precision Medicine Research with a Focus on Biomarkers. An American Thoracic Society/National Heart, Lung, and Blood Institute Research Statement. American Journal of Respiratory and Critical Care Medicine, 2018, 198, e116-e136.	2.5	49
34	<i>MUC5B</i> Promoter Polymorphism and Development of Acute Respiratory Distress Syndrome. American Journal of Respiratory and Critical Care Medicine, 2018, 198, 1342-1345.	2.5	9
35	A Nasal Brush-based Classifier of Asthma Identified by Machine Learning Analysis of Nasal RNA Sequence Data. Scientific Reports, 2018, 8, 8826.	1.6	51
36	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

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37	Profiling of ARDS pulmonary edema fluid identifies a metabolically distinct subset. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2017, 312, L703-L709.	1.3	36
38	New Strategies and Challenges in Lung Proteomics and Metabolomics. An Official American Thoracic Society Workshop Report. Annals of the American Thoracic Society, 2017, 14, 1721-1743.	1.5	44
39	Metabolites Associated With Malnutrition in the Intensive Care Unit Are Also Associated With 28â€Day Mortality. Journal of Parenteral and Enteral Nutrition, 2017, 41, 188-197.	1.3	26
40	Metabolome alterations in severe critical illness and vitamin D status. Critical Care, 2017, 21, 193.	2.5	40
41	A resident-created hospitalist curriculum for internal medicine housestaff. Journal of Hospital Medicine, 2016, 11, 646-649.	0.7	8
42	ATS Core Curriculum 2016: Part II. Adult Critical Care Medicine. Annals of the American Thoracic Society, 2016, 13, 731-740.	1.5	0
43	Proteomic study of acute respiratory distress syndrome: current knowledge and implications for drug development. Expert Review of Proteomics, 2016, 13, 457-469.	1.3	15
44	16 Years and Counting? Time toÂlmplement Noninvasive Screening for ARDS. Chest, 2016, 150, 266-267.	0.4	1
45	A computational approach to mortality prediction of alcohol use disorder inpatients. Computers in Biology and Medicine, 2016, 75, 74-79.	3.9	17
46	Metabolism, Metabolomics, and Nutritional Support of Patients with Sepsis. Clinics in Chest Medicine, 2016, 37, 321-331.	0.8	64
47	Expression Quantitative Trait Loci Information Improves Predictive Modeling of Disease Relevance of Non-Coding Genetic Variation. PLoS ONE, 2015, 10, e0140758.	1.1	17
48	Mesenchymal stem (stromal) cells for treatment of ARDS: a phase 1 clinical trial. Lancet Respiratory Medicine, the, 2015, 3, 24-32.	5.2	614
49	Finding an Early Warning Signal for Acute Respiratory Distress Syndrome. Critical Care Medicine, 2015, 43, 721-722.	0.4	0
50	Increased expression of neutrophil-related genes in patients with early sepsis-induced ARDS. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2015, 308, L1102-L1113.	1.3	137
51	Factors associated with bronchiolitis obliterans syndrome and chronic graftâ€versusâ€host disease after allogeneic hematopoietic cell transplantation. American Journal of Hematology, 2014, 89, 404-409.	2.0	46
52	Pharmacogenomics: novel loci identification via integrating gene differential analysis and eQTL analysis. Human Molecular Genetics, 2014, 23, 5017-5024.	1.4	24
53	Design and implementation of the START (STem cells for ARDS Treatment) trial, a phase 1/2 trial of human mesenchymal stem/stromal cells for the treatment of moderate-severe acute respiratory distress syndrome. Annals of Intensive Care, 2014, 4, 22.	2.2	53
54	Applying metabolomics to uncover novel biology in ARDS. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2014, 306, L957-L961.	1.3	34

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55	Integrative "Omic―Analysis of Experimental Bacteremia Identifies a Metabolic Signature That Distinguishes Human Sepsis from Systemic Inflammatory Response Syndromes. American Journal of Respiratory and Critical Care Medicine, 2014, 190, 445-455.	2.5	100
56	Metabolomic Derangements Are Associated with Mortality in Critically Ill Adult Patients. PLoS ONE, 2014, 9, e87538.	1.1	127
57	Copy number variation genotyping using family information. BMC Bioinformatics, 2013, 14, 157.	1.2	7
58	Airway dilation in bronchiolitis obliterans after allogeneic hematopoietic stem cell transplantation. Respiratory Medicine, 2013, 107, 276-283.	1.3	18
59	Circulating Mitochondrial DNA in Patients in the ICU as a Marker of Mortality: Derivation and Validation. PLoS Medicine, 2013, 10, e1001577.	3.9	354
60	An Integrated Clinico-Metabolomic Model Improves Prediction of Death in Sepsis. Science Translational Medicine, 2013, 5, 195ra95.	5.8	380
61	Inflammasome-regulated Cytokines Are Critical Mediators of Acute Lung Injury. American Journal of Respiratory and Critical Care Medicine, 2012, 185, 1225-1234.	2.5	469
62	Low Dose Busulfan Is Associated with Bronchiolitis Obliterans Syndrome Following Allogeneic Hematopoietic Stem Cell Transplantation Blood, 2012, 120, 3128-3128.	0.6	0
63	Airway Dilation in Bronchiolitis Obliterans After Allogeneic Hematopoietic Stem Cell Transplantation Blood, 2012, 120, 3058-3058.	0.6	5
64	The CD4+ T-cell transcriptome and serum IgE in asthma: IL17RB and the role of sex. BMC Pulmonary Medicine, 2011, 11, 17.	0.8	23
65	A Role for Wnt Signaling Genes in the Pathogenesis of Impaired Lung Function in Asthma. American Journal of Respiratory and Critical Care Medicine, 2010, 181, 328-336.	2.5	94
66	Stronger Evidence for Replication of NPPA Using Genome-wide Genotyping Data. American Journal of Respiratory and Critical Care Medicine, 2010, 181, 96-96.	2.5	0
67	Assessing the Reproducibility of Asthma Candidate Gene Associations, Using Genome-wide Data. American Journal of Respiratory and Critical Care Medicine, 2009, 179, 1084-1090.	2.5	99
68	Predictors of poor response during asthma therapy differ with definition of outcome. Pharmacogenomics, 2009, 10, 1231-1242.	0.6	54
69	Asthma genetics and genomics 2009. Current Opinion in Genetics and Development, 2009, 19, 279-282.	1.5	102
70	Genetic association analysis of copy-number variation (CNV) in human disease pathogenesis. Genomics, 2009, 93, 22-26.	1.3	177
71	The interaction of glutathione <i>S</i> àêtransferase M1â€null variants with tobacco smoke exposure and the development of childhood asthma. Clinical and Experimental Allergy, 2009, 39, 1721-1729.	1.4	38
72	Filaggrin mutations confer susceptibility to atopic dermatitis but not to asthma. Journal of Allergy and Clinical Immunology, 2007, 120, 1332-1337.	1.5	67