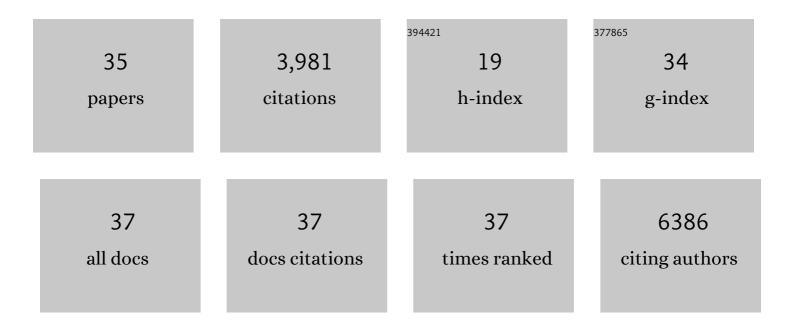
Scott R Presnell

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Seasonal airway microbiome and transcriptome interactions promote childhood asthma exacerbations. Journal of Allergy and Clinical Immunology, 2022, 150, 204-213.	2.9	31
2	Chemokines, soluble PD-L1, and immune cell hyporesponsiveness are distinct features of SARS-CoV-2 critical illness. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2022, 323, L14-L26.	2.9	15
3	Endotype of allergic asthma with airway obstruction in urban children. Journal of Allergy and Clinical Immunology, 2021, 148, 1198-1209.	2.9	32
4	Inducible expression quantitative trait locus analysis of the MUC5AC gene in asthma in urban populations of children. Journal of Allergy and Clinical Immunology, 2021, 148, 1505-1514.	2.9	14
5	Development of a fixed module repertoire for the analysis and interpretation of blood transcriptome data. Nature Communications, 2021, 12, 4385.	12.8	29
6	A pro-inflammatory CD8+ T-cell subset patrols the cervicovaginal tract. Mucosal Immunology, 2019, 12, 1118-1129.	6.0	12
7	Transcriptome networks identify mechanisms of viral and nonviral asthma exacerbations in children. Nature Immunology, 2019, 20, 637-651.	14.5	106
8	Chronic TLR7 and TLR9 signaling drives anemia via differentiation of specialized hemophagocytes. Science, 2019, 363, .	12.6	82
9	Allergen-induced activation of natural killer cells represents an early-life immune response in the development of allergic asthma. Journal of Allergy and Clinical Immunology, 2018, 142, 1856-1866.	2.9	26
10	A collection of annotated and harmonized human breast cancer transcriptome datasets, including immunologic classification. F1000Research, 2017, 6, 296.	1.6	14
11	A collection of annotated and harmonized human breast cancer transcriptome datasets, including immunologic classification. F1000Research, 2017, 6, 296.	1.6	14
12	Transcriptomic evidence for modulation of host inflammatory responses during febrile Plasmodium falciparum malaria. Scientific Reports, 2016, 6, 31291.	3.3	85
13	A curated compendium of monocyte transcriptome datasets of relevance to human monocyte immunobiology research. F1000Research, 2016, 5, 291.	1.6	20
14	A curated transcriptome dataset collection to investigate the immunobiology of HIV infection. F1000Research, 2016, 5, 327.	1.6	10
15	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
16	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
17	A curated transcriptome dataset collection to investigate the functional programming of human hematopoietic cells in early life. F1000Research, 2016, 5, 414.	1.6	12
18	A compendium of monocyte transcriptome datasets to foster biomedical knowledge discovery. F1000Research, 2016, 5, 291.	1.6	4

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19	An interactive web application for the dissemination of human systems immunology data. Journal of Translational Medicine, 2015, 13, 196.	4.4	49
20	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
21	Molecular signatures of antibody responses derived from a systems biology study of five human vaccines. Nature Immunology, 2014, 15, 195-204.	14.5	672
22	Systems Scale Interactive Exploration Reveals Quantitative and Qualitative Differences in Response to Influenza and Pneumococcal Vaccines. Immunity, 2013, 38, 831-844.	14.3	284
23	IL-28, IL-29 and their class II cytokine receptor IL-28R. Nature Immunology, 2003, 4, 63-68.	14.5	1,385
24	Four helix bundle diversity in globular proteins. Journal of Molecular Biology, 1994, 236, 1356-1368.	4.2	151
25	Origins of structural diversity within sequentially identical hexapeptides. Protein Science, 1993, 2, 2134-2145.	7.6	94
26	MacMatch: a tool for pattern-based protein secondary structure prediction. Bioinformatics, 1993, 9, 373-374.	4.1	5
27	A segment-based approach to protein secondary structure prediction. Biochemistry, 1992, 31, 983-993.	2.5	49
28	[13] Pattern-based approaches to protein structure prediction. Methods in Enzymology, 1991, 202, 252-268.	1.0	12
29	Experimental and theoretical studies of the three-dimensional structure of human interleukin-4. Proteins: Structure, Function and Bioinformatics, 1991, 11, 111-119.	2.6	39
30	A hybrid of bovine pancreatic ribonuclease and human angiogenin: an external loop as a module controlling substrate specificity?. Protein Engineering, Design and Selection, 1991, 4, 831-835.	2.1	25
31	The ribonuclease from an extinct bovid ruminant. FEBS Letters, 1990, 262, 104-106.	2.8	115
32	Topological distribution of four-alpha-helix bundles. Proceedings of the National Academy of Sciences of the United States of America, 1989, 86, 6592-6596.	7.1	193
33	The design of syntetic genes. Nucleic Acids Research, 1988, 16, 1693-1702.	14.5	18
34	Expression of bovine pancreatic ribonuclease A in Escherichia coli. FEBS Journal, 1987, 163, 67-71.	0.2	28
35	Evolutionary Guidance and the Engineering of Enzymes. , 1986, , 325-340.		Ο