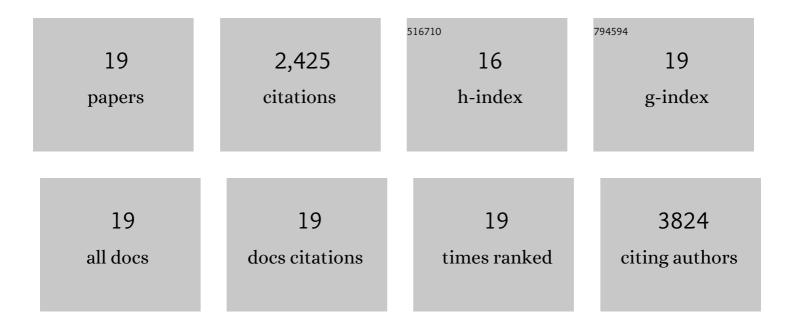
## Mohamed Uduman

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/11176936/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	MicroRNA signatures discriminate between uterine and ovarian serous carcinomas. Human Pathology, 2018, 76, 133-140.	2.0	11
2	Spatiotemporal segregation of human marginal zone and memory B cell populations in lymphoid tissue. Nature Communications, 2018, 9, 3857.	12.8	78
3	Characterization of Diabetogenic CD8+ T Cells. Journal of Biological Chemistry, 2016, 291, 11230-11240.	3.4	25
4	VDJML: a file format with tools for capturing the results of inferring immune receptor rearrangements. BMC Bioinformatics, 2016, 17, 333.	2.6	16
5	Automated analysis of high-throughput B-cell sequencing data reveals a high frequency of novel immunoglobulin V gene segment alleles. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E862-70.	7.1	215
6	Change-O: a toolkit for analyzing large-scale B cell immunoglobulin repertoire sequencing data. Bioinformatics, 2015, 31, 3356-3358.	4.1	643
7	The KRAS-Variant and miRNA Expression in RTOG Endometrial Cancer Clinical Trials 9708 and 9905. PLoS ONE, 2014, 9, e94167.	2.5	17
8	High-resolution antibody dynamics of vaccine-induced immune responses. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 4928-4933.	7.1	186
9	pRESTO: a toolkit for processing high-throughput sequencing raw reads of lymphocyte receptor repertoires. Bioinformatics, 2014, 30, 1930-1932.	4.1	417
10	Influence of seasonal exposure to grass pollen on local and peripheral blood IgE repertoires in patients with allergic rhinitis. Journal of Allergy and Clinical Immunology, 2014, 134, 604-612.	2.9	55
11	Integrating B Cell Lineage Information into Statistical Tests for Detecting Selection in Ig Sequences. Journal of Immunology, 2014, 192, 867-874.	0.8	32
12	Shared VH1-46 gene usage by pemphigus vulgaris autoantibodies indicates common humoral immune responses among patients. Nature Communications, 2014, 5, 4167.	12.8	63
13	Models of Somatic Hypermutation Targeting and Substitution Based on Synonymous Mutations from High-Throughput Immunoglobulin Sequencing Data. Frontiers in Immunology, 2013, 4, 358.	4.8	197
14	Quantifying selection in high-throughput Immunoglobulin sequencing data sets. Nucleic Acids Research, 2012, 40, e134-e134.	14.5	179
15	Gene Expression Gradients along the Tonotopic Axis of the Chicken Auditory Epithelium. JARO - Journal of the Association for Research in Otolaryngology, 2011, 12, 423-435.	1.8	29
16	Detecting selection in immunoglobulin sequences. Nucleic Acids Research, 2011, 39, W499-W504.	14.5	83
17	Gene Expression Analysis of Forskolin Treated Basilar Papillae Identifies MicroRNA181a as a Mediator of Proliferation. PLoS ONE, 2010, 5, e11502.	2.5	18
18	Taking Advantage: High-Affinity B Cells in the Germinal Center Have Lower Death Rates, but Similar Rates of Division, Compared to Low-Affinity Cells. Journal of Immunology, 2009, 183, 7314-7325.	0.8	86

#	Article	IF	CITATIONS
19	Improved methods for detecting selection by mutation analysis of Ig V region sequences. International Immunology, 2008, 20, 683-694.	4.0	75