Monther Alhamdoosh

List of Publications by Year
in descending order

16 papers	1,612 citations

840776
11 h-index

996975
15 g-index

20 all docs	20 docs citations	20 times ranked	3009 citing authors

#	Article	IF	Citations
1	Targeting the Human Î²c Receptor Inhibits Contact Dermatitis in a Transgenic Mouse Model. Journal of Investigative Dermatology, 2022, 142, 1103-1113.e11.	0.7	4
2	Antiâ€Î²_c mAb CSL311 inhibits human nasal polyp pathophysiology in a humanized mouse xenograft model. Allergy: European Journal of Allergy and Clinical Immunology, 2020, 75, 475-478.	5.7	10
3	Blockade of the G-CSF Receptor Is Protective in a Mouse Model of Renal Ischemiaâ€"Reperfusion Injury. Journal of Immunology, 2020, 205, 1433-1440.	0.8	8
4	Cellular Microenvironment Stiffness Regulates Eicosanoid Production and Signaling Pathways. American Journal of Respiratory Cell and Molecular Biology, 2020, 63, 819-830.	2.9	25
5	A guide to creating design matrices for gene expression experiments. F1000Research, 2020, 9, 1444.	1.6	25
6	Topical application of human-derived Ig isotypes for the control of acute respiratory infection evaluated in a human CD89-expressing mouse model. Mucosal Immunology, 2019, 12, 1013-1024.	6.0	8
7	Machine learning applied to wholeâ€blood RNAâ€sequencing data uncovers distinct subsets of patients with systemic lupus erythematosus. Clinical and Translational Immunology, 2019, 8, e01093.	3.8	43
8	Combining multiple tools outperforms individual methods in gene set enrichment analyses. Bioinformatics, 2017, 33, 414-424.	4.1	141
9	Four simple recommendations to encourage best practices in research software. F1000Research, 2017, 6, 876.	1.6	88
10	Easy and efficient ensemble gene set testing with EGSEA. F1000Research, 2017, 6, 2010.	1.6	53
11	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. F1000Research, 2016, 5, 1408.	1.6	368
12	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. F1000Research, 2016, 5, 1408.	1.6	394
13	Fast decorrelated neural network ensembles with random weights. Information Sciences, 2014, 264, 104-117.	6.9	163
14	Evolutionary extreme learning machine ensembles with size control. Neurocomputing, 2013, 102, 98-110.	5.9	88
15	Improving the prediction of disulfide bonds in Eukaryotes with machine learning methods and protein subcellular localization. Bioinformatics, 2011, 27, 2224-2230.	4.1	37
16	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. F1000Research, 0, 5, 1408.	1.6	149