Vladimir Jojic

List of Publications by Year
in descending order

17 papers	3,959 citations	623734 14 h-index	996975 15 g-index
20 all docs	20 docs citations	20 times ranked	8922 citing authors

#	Article	IF	Citations
1	Variation in the Human Immune System Is Largely Driven by Non-Heritable Influences. Cell, 2015, 160, 37-47.	28.9	828
2	Deciphering the transcriptional network of the dendritic cell lineage. Nature Immunology, 2012, 13, 888-899.	14.5	688
3	Systems analysis of sex differences reveals an immunosuppressive role for testosterone in the response to influenza vaccination. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 869-874.	7.1	542
4	Expression of specific inflammasome gene modules stratifies older individuals into two extreme clinical and immunological states. Nature Medicine, 2017, 23, 174-184.	30.7	304
5	Conservation and divergence in the transcriptional programs of the human and mouse immune systems. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 2946-2951.	7.1	296
6	Cytomegalovirus infection enhances the immune response to influenza. Science Translational Medicine, 2015, 7, 281ra43.	12.4	277
7	An inflammatory aging clock (iAge) based on deep learning tracks multimorbidity, immunosenescence, frailty and cardiovascular aging. Nature Aging, 2021, 1, 598-615.	11.6	202
8	Design of synthetic bacterial communities for predictable plant phenotypes. PLoS Biology, 2018, 16, e2003962.	5.6	182
9	Identification of transcriptional regulators in the mouse immune system. Nature Immunology, 2013, 14, 633-643.	14.5	179
10	Apoptosis and other immune biomarkers predict influenza vaccine responsiveness. Molecular Systems Biology, 2013, 9, 659.	7.2	173
11	The immunoregulatory landscape of human tuberculosis granulomas. Nature Immunology, 2022, 23, 318-329.	14.5	110
12	ImmGen at 15. Nature Immunology, 2020, 21, 700-703.	14.5	55
13	Modeling Multiplexed Images with <i>Spatial-LDA</i> Reveals Novel Tissue Microenvironments. Journal of Computational Biology, 2020, 27, 1204-1218.	1.6	42
14	Learning Microbial Interaction Networks from Metagenomic Count Data. Journal of Computational Biology, 2016, 23, 526-535.	1.6	39
15	Tradict enables accurate prediction of eukaryotic transcriptional states from 100 marker genes. Nature Communications, 2017, 8, 15309.	12.8	18
16	DRUG-INDUCED mRNA SIGNATURES ARE ENRICHED FOR THE MINORITY OF GENES THAT ARE HIGHLY HERITABLE. , 2014, , .		1
17	Reconstructing Tissue Properties From Medical Images With Application in Cancer Screening. IEEE Transactions on Medical Robotics and Bionics, 2019, 1, 6-13.	3.2	0