

Anglique B Van t Wout

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

14
papers

405
citations

11
h-index

14
g-index

14
ext. papers

540
ext. citations

7
avg, IF

2.97
L-index

#	Paper	IF	Citations
14	Anti-TNF therapy in IBD exerts its therapeutic effect through macrophage IL-10 signalling. <i>Gut</i> , 2020 , 69, 1053-1063	19.2	37
13	Transient opening of trimeric prefusion RSV F proteins. <i>Nature Communications</i> , 2019 , 10, 2105	17.4	29
12	Development of Reliable, Valid and Responsive Scoring Systems for Endoscopy and Histology in Animal Models for Inflammatory Bowel Disease. <i>Journal of Crohn's and Colitis</i> , 2018 , 12, 794-803	1.5	36
11	Structural basis for recognition of the central conserved region of RSV G by neutralizing human antibodies. <i>PLoS Pathogens</i> , 2018 , 14, e1006935	7.6	35
10	Antibiotic-induced acceleration of type 1 diabetes alters maturation of innate intestinal immunity. <i>ELife</i> , 2018 , 7,	8.9	41
9	DYRK1A Controls HIV-1 Replication at a Transcriptional Level in an NFAT Dependent Manner. <i>PLoS ONE</i> , 2015 , 10, e0144229	3.7	14
8	Contribution of genetic background, traditional risk factors, and HIV-related factors to coronary artery disease events in HIV-positive persons. <i>Clinical Infectious Diseases</i> , 2013 , 57, 112-21	11.6	45
7	The presence of CXCR4-using HIV-1 prior to start of antiretroviral therapy is an independent predictor of delayed viral suppression. <i>PLoS ONE</i> , 2013 , 8, e76255	3.7	3
6	Genome-wide association studies on HIV susceptibility, pathogenesis and pharmacogenomics. <i>Retrovirology</i> , 2012 , 9, 70	3.6	39
5	Reconstructing the dynamics of HIV evolution within hosts from serial deep sequence data. <i>PLoS Computational Biology</i> , 2012 , 8, e1002753	5	37
4	HIV-1 envelope diversity 1 year after seroconversion predicts subsequent disease progression. <i>Aids</i> , 2012 , 26, 1517-22	3.5	6
3	Rising HIV-1 viral load set point at a population level coincides with a fading impact of host genetic factors on HIV-1 control. <i>Aids</i> , 2011 , 25, 2217-26	3.5	10
2	Detection of inferred CCR5- and CXCR4-using HIV-1 variants and evolutionary intermediates using ultra-deep pyrosequencing. <i>PLoS Pathogens</i> , 2011 , 7, e1002106	7.6	43
1	Genome-wide association study identifies single nucleotide polymorphism in DYRK1A associated with replication of HIV-1 in monocyte-derived macrophages. <i>PLoS ONE</i> , 2011 , 6, e17190	3.7	30