

AngÃ©lique B Van 't Wout

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8954920/publications.pdf>

Version: 2024-02-01

14
papers

664
citations

758635

12
h-index

1058022

14
g-index

14
all docs

14
docs citations

14
times ranked

1334
citing authors

#	ARTICLE	IF	CITATIONS
1	Anti-TNF therapy in IBD exerts its therapeutic effect through macrophage IL-10 signalling. <i>Gut</i> , 2020, 69, 1053-1063.	6.1	109
2	Transient opening of trimeric prefusion RSV F proteins. <i>Nature Communications</i> , 2019, 10, 2105.	5.8	71
3	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.	0.6	88
4	Structural basis for recognition of the central conserved region of RSV G by neutralizing human antibodies. <i>PLoS Pathogens</i> , 2018, 14, e1006935.	2.1	50
5	Antibiotic-induced acceleration of type 1 diabetes alters maturation of innate intestinal immunity. <i>ELife</i> , 2018, 7, .	2.8	70
6	DYRK1A Controls HIV-1 Replication at a Transcriptional Level in an NFAT Dependent Manner. <i>PLoS ONE</i> , 2015, 10, e0144229.	1.1	24
7	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, 112-121.	2.9	56
8	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.	1.1	3
9	Reconstructing the Dynamics of HIV Evolution within Hosts from Serial Deep Sequence Data. <i>PLoS Computational Biology</i> , 2012, 8, e1002753.	1.5	42
10	HIV-1 envelope diversity 1 year after seroconversion predicts subsequent disease progression. <i>Aids</i> , 2012, 26, 1517-1522.	1.0	7
11	Genome-wide association studies on HIV susceptibility, pathogenesis and pharmacogenomics. <i>Retrovirology</i> , 2012, 9, 70.	0.9	48
12	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, 2217-2226.	1.0	13
13	Detection of Inferred CCR5- and CXCR4-Using HIV-1 Variants and Evolutionary Intermediates Using Ultra-Deep Pyrosequencing. <i>PLoS Pathogens</i> , 2011, 7, e1002106.	2.1	52
14	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.	1.1	31