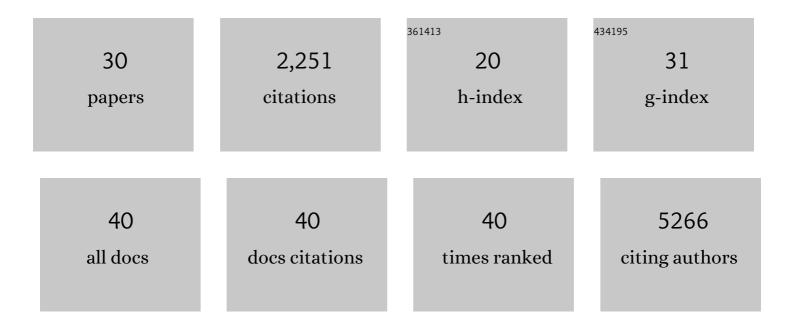
Istvan Bartha

List of Publications by Year in descending order

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Ιςτιλη Βάρτηλ

#	Article	IF	CITATIONS
1	Broad betacoronavirus neutralization by a stem helix–specific human antibody. Science, 2021, 373, 1109-1116.	12.6	262
2	Broad sarbecovirus neutralization by a human monoclonal antibody. Nature, 2021, 597, 103-108.	27.8	220
3	Human gene essentiality. Nature Reviews Genetics, 2018, 19, 51-62.	16.3	213
4	Polymorphisms of large effect explain the majority of the host genetic contribution to variation of HIV-1 virus load. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14658-14663.	7.1	154
5	The human noncoding genome defined by genetic diversity. Nature Genetics, 2018, 50, 333-337.	21.4	137
6	24 Hours in the Life of HIV-1 in a T Cell Line. PLoS Pathogens, 2013, 9, e1003161.	4.7	134
7	Genome-to-genome analysis highlights the effect of the human innate and adaptive immune systems on the hepatitis C virus. Nature Genetics, 2017, 49, 666-673.	21.4	129
8	A genome-to-genome analysis of associations between human genetic variation, HIV-1 sequence diversity, and viral control. ELife, 2013, 2, e01123.	6.0	126
9	Severe viral respiratory infections in children with <i>IFIH1</i> loss-of-function mutations. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 8342-8347.	7.1	111
10	Predicting the mutational drivers of future SARS-CoV-2 variants of concern. Science Translational Medicine, 2022, 14, eabk3445.	12.4	101
11	Precision medicine screening using whole-genome sequencing and advanced imaging to identify disease risk in adults. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 3686-3691.	7.1	76
12	Dynamics of HIV Latency and Reactivation in a Primary CD4+ T Cell Model. PLoS Pathogens, 2014, 10, e1004156.	4.7	70
13	Amino Acid Variation in HLA Class II Proteins Is a Major Determinant of Humoral Response to Common Viruses. American Journal of Human Genetics, 2015, 97, 738-743.	6.2	63
14	Mapping of positive selection sites in the HIV-1 genome in the context of RNA and protein structural constraints. Retrovirology, 2011, 8, 87.	2.0	51
15	Structural Insights into the Trp age Folding Intermediate Formation. Chemistry - A European Journal, 2013, 19, 2628-2640.	3.3	49
16	Privacy-preserving genomic testing in the clinic: a model using HIV treatment. Genetics in Medicine, 2016, 18, 814-822.	2.4	36
17	The Characteristics of Heterozygous Protein Truncating Variants in the Human Genome. PLoS Computational Biology, 2015, 11, e1004647.	3.2	34
18	Functional characterization of 3D protein structures informed by human genetic diversity. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 8960-8965.	7.1	33

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#	Article	IF	CITATIONS
19	Analysis of Stop-Gain and Frameshift Variants in Human Innate Immunity Genes. PLoS Computational Biology, 2014, 10, e1003757.	3.2	32
20	Estimating the Respective Contributions of Human and Viral Genetic Variation to HIV Control. PLoS Computational Biology, 2017, 13, e1005339.	3.2	28
21	Exome Sequencing Reveals Primary Immunodeficiencies in Children with Community-Acquired Pseudomonas aeruginosa Sepsis. Frontiers in Immunology, 2016, 7, 357.	4.8	21
22	The Interplay Between Host Genetic Variation, Viral Replication, and Microbial Translocation in Untreated HIV-Infected Individuals. Journal of Infectious Diseases, 2015, 212, 578-584.	4.0	20
23	Evaluating the Impact of Functional Genetic Variation on HIV-1 Control. Journal of Infectious Diseases, 2017, 216, 1063-1069.	4.0	20
24	Has HIV evolved to induce immune pathogenesis?. Trends in Immunology, 2008, 29, 322-328.	6.8	17
25	Role of APOBEC3F Gene Variation in HIV-1 Disease Progression and Pneumocystis Pneumonia. PLoS Genetics, 2016, 12, e1005921.	3.5	17
26	Correcting for Population Stratification Reduces False Positive and False Negative Results in Joint Analyses of Host and Pathogen Genomes. Frontiers in Genetics, 2018, 9, 266.	2.3	14
27	GuavaH: a compendium of host genomic data in HIV biology and disease. Retrovirology, 2014, 11, 6.	2.0	13
28	Transfer transcriptomic signatures for infectious diseases. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	8
29	Adaptation on a genomic scale. ELife, 2015, 4, e06193.	6.0	2

30 Joint analysis of host and pathogen genomes. , 2011, , .

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