

Istvan Bartha

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

2,251
citations

361413

20
h-index

434195

31
g-index

40
all docs

40
docs citations

40
times ranked

5266
citing authors

#	ARTICLE	IF	CITATIONS
1	Predicting the mutational drivers of future SARS-CoV-2 variants of concern. <i>Science Translational Medicine</i> , 2022, 14, eabk3445.	12.4	101
2	Transfer transcriptomic signatures for infectious diseases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	8
3	Broad sarbecovirus neutralization by a human monoclonal antibody. <i>Nature</i> , 2021, 597, 103-108.	27.8	220
4	Broad betacoronavirus neutralization by a stem helix-specific human antibody. <i>Science</i> , 2021, 373, 1109-1116.	12.6	262
5	Functional characterization of 3D protein structures informed by human genetic diversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 8960-8965.	7.1	33
6	The human noncoding genome defined by genetic diversity. <i>Nature Genetics</i> , 2018, 50, 333-337.	21.4	137
7	Precision medicine screening using whole-genome sequencing and advanced imaging to identify disease risk in adults. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 3686-3691.	7.1	76
8	Human gene essentiality. <i>Nature Reviews Genetics</i> , 2018, 19, 51-62.	16.3	213
9	Correcting for Population Stratification Reduces False Positive and False Negative Results in Joint Analyses of Host and Pathogen Genomes. <i>Frontiers in Genetics</i> , 2018, 9, 266.	2.3	14
10	Genome-to-genome analysis highlights the effect of the human innate and adaptive immune systems on the hepatitis C virus. <i>Nature Genetics</i> , 2017, 49, 666-673.	21.4	129
11	Evaluating the Impact of Functional Genetic Variation on HIV-1 Control. <i>Journal of Infectious Diseases</i> , 2017, 216, 1063-1069.	4.0	20
12	Severe viral respiratory infections in children with <i>IFIH1</i> loss-of-function mutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 8342-8347.	7.1	111
13	Estimating the Respective Contributions of Human and Viral Genetic Variation to HIV Control. <i>PLoS Computational Biology</i> , 2017, 13, e1005339.	3.2	28
14	Exome Sequencing Reveals Primary Immunodeficiencies in Children with Community-Acquired <i>Pseudomonas aeruginosa</i> Sepsis. <i>Frontiers in Immunology</i> , 2016, 7, 357.	4.8	21
15	Privacy-preserving genomic testing in the clinic: a model using HIV treatment. <i>Genetics in Medicine</i> , 2016, 18, 814-822.	2.4	36
16	Role of APOBEC3F Gene Variation in HIV-1 Disease Progression and Pneumocystis Pneumonia. <i>PLoS Genetics</i> , 2016, 12, e1005921.	3.5	17
17	The Characteristics of Heterozygous Protein Truncating Variants in the Human Genome. <i>PLoS Computational Biology</i> , 2015, 11, e1004647.	3.2	34
18	Adaptation on a genomic scale. <i>ELife</i> , 2015, 4, e06193.	6.0	2

#	ARTICLE	IF	CITATIONS
19	Polymorphisms of large effect explain the majority of the host genetic contribution to variation of HIV-1 virus load. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14658-14663.	7.1	154
20	The Interplay Between Host Genetic Variation, Viral Replication, and Microbial Translocation in Untreated HIV-Infected Individuals. <i>Journal of Infectious Diseases</i> , 2015, 212, 578-584.	4.0	20
21	Amino Acid Variation in HLA Class II Proteins Is a Major Determinant of Humoral Response to Common Viruses. <i>American Journal of Human Genetics</i> , 2015, 97, 738-743.	6.2	63
22	Dynamics of HIV Latency and Reactivation in a Primary CD4+ T Cell Model. <i>PLoS Pathogens</i> , 2014, 10, e1004156.	4.7	70
23	Analysis of Stop-Gain and Frameshift Variants in Human Innate Immunity Genes. <i>PLoS Computational Biology</i> , 2014, 10, e1003757.	3.2	32
24	GuavaH: a compendium of host genomic data in HIV biology and disease. <i>Retrovirology</i> , 2014, 11, 6.	2.0	13
25	Structural Insights into the Trp-Cage Folding Intermediate Formation. <i>Chemistry - A European Journal</i> , 2013, 19, 2628-2640.	3.3	49
26	24 Hours in the Life of HIV-1 in a T Cell Line. <i>PLoS Pathogens</i> , 2013, 9, e1003161.	4.7	134
27	A genome-to-genome analysis of associations between human genetic variation, HIV-1 sequence diversity, and viral control. <i>ELife</i> , 2013, 2, e01123.	6.0	126
28	Mapping of positive selection sites in the HIV-1 genome in the context of RNA and protein structural constraints. <i>Retrovirology</i> , 2011, 8, 87.	2.0	51
29	Joint analysis of host and pathogen genomes. , 2011, , .		0
30	Has HIV evolved to induce immune pathogenesis?. <i>Trends in Immunology</i> , 2008, 29, 322-328.	6.8	17