

Istvan Bartha

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8789258/publications.pdf>

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 | Broad betacoronavirus neutralization by a stem helix-specific human antibody. <i>Science</i> , 2021, 373, 1109-1116. | 12.6 | 262 |
| 2 | Broad sarbecovirus neutralization by a human monoclonal antibody. <i>Nature</i> , 2021, 597, 103-108. | 27.8 | 220 |
| 3 | Human gene essentiality. <i>Nature Reviews Genetics</i> , 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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14658-14663. | 7.1 | 154 |
| 5 | The human noncoding genome defined by genetic diversity. <i>Nature Genetics</i> , 2018, 50, 333-337. | 21.4 | 137 |
| 6 | 24 Hours in the Life of HIV-1 in a T Cell Line. <i>PLoS Pathogens</i> , 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. <i>Nature Genetics</i> , 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. <i>ELife</i> , 2013, 2, e01123. | 6.0 | 126 |
| 9 | 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 |
| 10 | Predicting the mutational drivers of future SARS-CoV-2 variants of concern. <i>Science Translational Medicine</i> , 2022, 14, eabk3445. | 12.4 | 101 |
| 11 | 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 |
| 12 | Dynamics of HIV Latency and Reactivation in a Primary CD4+ T Cell Model. <i>PLoS Pathogens</i> , 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. <i>American Journal of Human Genetics</i> , 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. <i>Retrovirology</i> , 2011, 8, 87. | 2.0 | 51 |
| 15 | Structural Insights into the TrpCage Folding Intermediate Formation. <i>Chemistry - A European Journal</i> , 2013, 19, 2628-2640. | 3.3 | 49 |
| 16 | Privacy-preserving genomic testing in the clinic: a model using HIV treatment. <i>Genetics in Medicine</i> , 2016, 18, 814-822. | 2.4 | 36 |
| 17 | The Characteristics of Heterozygous Protein Truncating Variants in the Human Genome. <i>PLoS Computational Biology</i> , 2015, 11, e1004647. | 3.2 | 34 |
| 18 | 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 |

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|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 19 | Analysis of Stop-Gain and Frameshift Variants in Human Innate Immunity Genes. <i>PLoS Computational Biology</i> , 2014, 10, e1003757. | 3.2 | 32 |
| 20 | Estimating the Respective Contributions of Human and Viral Genetic Variation to HIV Control. <i>PLoS Computational Biology</i> , 2017, 13, e1005339. | 3.2 | 28 |
| 21 | 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 |
| 22 | 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 |
| 23 | Evaluating the Impact of Functional Genetic Variation on HIV-1 Control. <i>Journal of Infectious Diseases</i> , 2017, 216, 1063-1069. | 4.0 | 20 |
| 24 | Has HIV evolved to induce immune pathogenesis?. <i>Trends in Immunology</i> , 2008, 29, 322-328. | 6.8 | 17 |
| 25 | Role of APOBEC3F Gene Variation in HIV-1 Disease Progression and Pneumocystis Pneumonia. <i>PLoS Genetics</i> , 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. <i>Frontiers in Genetics</i> , 2018, 9, 266. | 2.3 | 14 |
| 27 | GuavaH: a compendium of host genomic data in HIV biology and disease. <i>Retrovirology</i> , 2014, 11, 6. | 2.0 | 13 |
| 28 | 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 |
| 29 | Adaptation on a genomic scale. <i>ELife</i> , 2015, 4, e06193. | 6.0 | 2 |
| 30 | Joint analysis of host and pathogen genomes. , 2011, , . | | 0 |