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Recent Selected Publications by EVBC Members

A DNA-based vaccine protects against Crimean-Congo haemorrhagic fever virus disease in a Cynomolgus macaque model. *Nat Microbiol* [10.1038/s41564-020-00815-6](https://doi.org/10.1038/s41564-020-00815-6)

Direct RNA sequencing reveals m6A modifications on adenovirus RNA are necessary for efficient splicing. *Nat Commun* [10.1038/s41467-020-19787-6](https://doi.org/10.1038/s41467-020-19787-6)

The European Bioinformatics Institute: empowering cooperation in response to a global health crisis. *Nucleic Acids Res* [10.1093/nar/gkaa1077](https://doi.org/10.1093/nar/gkaa1077)

Re-assembly of nineteenth-century smallpox vaccine genomes reveals the contemporaneous use of horsepox and horsepox-related viruses in the USA. *Genome Biol* [10.1186/s13059-020-02202-0](https://doi.org/10.1186/s13059-020-02202-0)

Multi-Omic Data Integration Allows Baseline Immune Signatures to Predict Hepatitis B Vaccine Response in a Small Cohort. *Front Immunol* [10.3389/fimmu.2020.578801](https://doi.org/10.3389/fimmu.2020.578801)

Systems Biology Methods Applied to Blood and Tissue for a Comprehensive Analysis of Immune Response to Hepatitis B Vaccine in Adults. *Front Immunol* [10.3389/fimmu.2020.580373](https://doi.org/10.3389/fimmu.2020.580373)

Sequencing facility and DNA source associated patterns of virus-mappable reads in whole-genome sequencing data. *Genomics* [10.1016/j.ygeno.2020.12.004](https://doi.org/10.1016/j.ygeno.2020.12.004)

Full-genome sequencing of German rabbit haemorrhagic disease virus uncovers recombination between RHDV (GI.2) and EBHSV (GI.1). *Virus Evol* [10.1093/ve/veaa080](https://doi.org/10.1093/ve/veaa080)

Establishment of a Challenge Model for Sheeppox Virus Infection. *Microorganisms* [10.3390/microorganisms8122001](https://doi.org/10.3390/microorganisms8122001)

Recommendations for the introduction of metagenomic high-throughput sequencing in clinical virology, part I: Wet lab procedure. *J Clin Virol* [10.1016/j.jcv.2020.104691](https://doi.org/10.1016/j.jcv.2020.104691)

Reviews and more

Epidemiology and Sequence-Based Evolutionary Analysis of Circulating Non-Polio Enteroviruses. *Microorganisms* [10.3390/microorganisms8121856](https://doi.org/10.3390/microorganisms8121856)

Preprints

Validation of molecular clock inferred HIV infection ages: evidence for accurate estimation of infection dates. *medRxiv* [10.1101/2020.12.11.20247601](https://doi.org/10.1101/2020.12.11.20247601)

The influence of human genetic variation on Epstein-Barr virus sequence diversity. *medRxiv* [10.1101/2020.12.02.20242370](https://doi.org/10.1101/2020.12.02.20242370)

The Dutch Microbiome Project defines factors that shape the healthy gut microbiome. *Research Square* [10.21203/rs.3.rs-117376/v1](https://doi.org/10.21203/rs.3.rs-117376/v1)

Estimating the Distribution of Viral Taxa in Next-generation Sequencing data using Artificial Neural Networks. *Research Square* [10.21203/rs.3.rs-127809/v1](https://doi.org/10.21203/rs.3.rs-127809/v1)

 [EVBC publications website](https://www.evbc.org/)

EVBC Special Issues

Virus Bioinformatics 2020 in *Viruses*

Advances in the Bioinformatics Knowledge of mRNA Polyadenylation in Baculovirus Genes. *Viruses* [10.3390/v12121395](https://doi.org/10.3390/v12121395)

The International Virus Bioinformatics Meeting 2020. *Viruses* [10.3390/v12121398](https://doi.org/10.3390/v12121398)

NCBI's Virus Discovery Codeathon: Building "FIVE" —The Federated Index of Viral Experiments API Index. *Viruses* [10.3390/v12121424](https://doi.org/10.3390/v12121424)

Characterization and Diversity of 243 Complete Human Papillomavirus Genomes in Cervical Swabs Using Next Generation Sequencing. *Viruses* [10.3390/v12121437](https://doi.org/10.3390/v12121437)

Natural Selection Plays an Important Role in Shaping the Codon Usage of Structural Genes of the Viruses Belonging to the Coronaviridae Family. *Viruses* [10.3390/v13010003](https://doi.org/10.3390/v13010003)

Characterization of a Novel Mitovirus of the Sand Fly *Lutzomyia longipalpis* Using Genomic and Virus-Host Interaction Signatures. *Viruses* [10.3390/v13010009](https://doi.org/10.3390/v13010009)

Upcoming Events

EVBC does not endorse any of the listings and is only involved in events marked as **EVBC Events** ★.

EMBL-EBI: Introduction to RNA-seq and functional interpretation

16–19 March 2021

online

Gain an introduction to the technology, data analysis, tools, and resources used in RNA sequencing and transcriptomics.

Application deadline:

22 January 2021

ISMB/ECCB 2021

25–29 July 2021, Lyon, France

online

ISMB joining forces with the ECCB will be the year's most important computational biology event globally.

Proceedings Submission Deadline: 28 January 2021

International Conference on Research in Computational Molecular Biology (RECOMB)

18–21 April, Padova, Italy

Algorithmic computational biology conference bridging the areas of computational, mathematical, statistical and biological sciences.

Highlights submission deadline: 29 January 2021

Poster submission deadline: 01 February 2021

A Practical Introduction to NGS Data Analysis

01–03 March 2021

online

Get a deeper understanding in Next-Generation Sequencing (NGS) with a special focus on bioinformatics issues.

Registration Deadline:

01 February 2021

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