

**Detection of single nucleotide polymorphisms in virus genomes assembled from high-throughput sequencing data: large-scale performance testing of sequence analysis strategies**

Rollin, Johan; Bester, Rachelle; Brostaux, Yves; Caglayan, Kadriye; De Jonghe, Kris; Eichmeier, Ales; Foucart, Yoika; Haegeman, Annelies; Koloniuk, Igor; Kominek, Petr; Maree, Hans; Onder, Serkan; Posada Cespedes, Susana; Rouni, Vahid; Šafarova, Dana; Schumpp, Olivier; Ulubas Serce, Cigdem; **Sömera, Merike**; Tamisier, Lucie; Vainio, Eeva; van der Vlugt, Rene AA; Massart, Sebastien PeerJ 2023 / art. e15816 <https://doi.org/10.7717/peerj.15816> [Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

**A high-performance MEMRISTOR-based Smith-Waterman DNA sequence alignment using FPNI structure**

**Taheri, Mahdi**; Zandevakili, Hamed; Mahani, Ali Journal of Applied Research in Electrical Engineering 2021 / p. 59-68 <https://doi.org/10.22055/jaree.2021.36117.1016>

**Lowering uncertainty of cancer classification**

Okun, O.; **Priisalu, Helen** Proceedings of IPMU'08 2008 / p. 543-550 : ill

**Top-K formal concepts for identifying positively and negatively correlated biclusters**

Houari, Amina; **Ben Yahia, Sadok** Model and Data Engineering : 10th International Conference, MEDI 2021, Tallinn, Estonia, June 21–23, 2021 : proceedings 2021 / p. 156-172 [https://doi.org/10.1007/978-3-030-78428-7\\_13](https://doi.org/10.1007/978-3-030-78428-7_13) [Conference Proceedings at Scopus](#) [Article at Scopus](#)