Research outputs:

Contaminating viral sequences in high-throughput sequencing viromics: a linkage study of 700 sequencing libraries
Research output: Contribution to journal › Journal article – Annual report year: 2019 › Research › peer-review

High-throughput sequencing-based investigation of viruses in human cancers by multi-enrichment approach
Research output: Contribution to journal › Journal article – Annual report year: 2019 › Research › peer-review

Cutavirus in Cutaneous Malignant Melanoma
Research output: Contribution to journal › Journal article – Annual report year: 2017 › Research › peer-review

Identification of Known and Novel Recurrent Viral Sequences in Data from Multiple Patients and Multiple Cancers
Research output: Contribution to journal › Journal article – Annual report year: 2016 › Research › peer-review

Propionibacterium acnes: disease-causing agent or common contaminant? Detection in diverse patient samples by next generation sequencing
Research output: Contribution to journal › Journal article – Annual report year: 2016 › Research › peer-review

Species-independent identification of known and novel recurrent genomic entities in multiple cancer patients
Research output: Contribution to journal › Conference abstract in journal – Annual report year: 2016 › Research › peer-review

Investigation of Human Cancers for Retrovirus by Low-Stringency Target Enrichment and High-Throughput Sequencing
Research output: Contribution to journal › Journal article – Annual report year: 2015 › Research › peer-review

Traces of ATCV-1 associated with laboratory component contamination
Research output: Contribution to journal › Letter – Annual report year: 2015 › Research › peer-review