FABI BIOINFORMATICS TOOL, THE RIPPER, SELECTED FOR THE PEERJ FEATURE COLLECTION

The prestigious PeerJ feature collection highlights novel and innovative developments in the field of biotechnology. The collection, curated by senior academic editors from the peer-reviewed scientific mega-journal PeerJ, features selected features to showcase exceptional resources that contribute to the broader scientific community.

The RIPper was chosen for the PeerJ bioinformatics feature collection by senior editors Professors Claus Wilke and Keith Crandall. The design and development of The RIPper is part of FABIan Stephanie van Wyk's PhD research project. The RIPper is a web-based tool specifically designed to allow the automation of laborious techniques to study Repeat-Induced Point (RIP) mutations. The RIPper applies these techniques to generate data to answer pressing questions about pathogen development and genome evolution. This technology has been well-received by the scientific community and data generated using The RIPper is currently being applied to both local and international fungal genomics research.