



# BOOSTING HPC FOR BIOTECHNOLOGY

## BIELEFELD UNIVERSITY'S BIOTECHNOLOGY CENTER TRANSCENDS RESEARCH BOUNDARIES

### About the Customer

Widely recognized for its interdisciplinary research-oriented teaching, Germany's Bielefeld University encompasses humanities, technology, and natural and social sciences. The university's Center for Biotechnology (CeBiTec) bundles the institution's biotechnological activities and research projects, fostering cross-field collaboration and innovation. As part of CeBiTec, the Bioinformatics Resource Facility (BRF), led by Dr. Stefan Albaum, provides a high-performance compute infrastructure for hundreds of faculty members and 1,000+ researchers from global academia and industry.



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Dr. Stefan Albaum, leader,  
Bioinformatics Resource  
Facility at CeBiTec



Hundreds of bioinformatics tools enable sequencing data evaluation, assembly, read mapping, gene prediction, functional annotation, and analysis, including NCBI Blast, SPAdes, SOAPDenovo, Abyss, Canu, HMMer, Glimmer, Prodigal, Quast, Bowtie, and DESeq2. CeBiTec's biologists and bioinformaticians process and share generated data within their fields. Faculty of Technology users develop applications and scripts using Python, C++, Perl, or Java. Facilitating it all is the BRF's HPC cluster, with more than 100 servers, nearly 3,000 CPU cores, and about 15.5 TB of RAM.

The Bioinformatics Resource Facility at CeBiTec needed a powerful, efficient workload manager to handle massive data and meet growing demand

### Their Challenge

**Massive volumes of data and growing user demand** meant the BRF needed a powerful, efficient workload orchestrator. They were using an earlier version of Grid Engine, but increasing demand meant workloads were no longer being processed efficiently. Generating enormous amounts of data — as with high-throughput DNA sequencing — heavily burdens the HPC clusters tasked with storage, processing, visualization, and integration. Multiple such workloads were creating inefficient resource usage and bottlenecks at Bielefeld University, and they needed an **enterprise-grade workload management solution that would deliver orders-of-magnitude performance improvements**.

### Our Solution

Altair® Grid Engine® delivers **superior workload orchestration** so scientists can focus on their ground-breaking research and teaching. The BRF team selected Altair Grid Engine for its **optimized throughput and performance, rich features, reliability, expert support, and no learning curve**. As the de-facto standard workload orchestration solution in biotechnology, Altair Grid Engine offers deeply integrated tools, applications, and libraries for CeBiTec's user base. "Right away, Altair Grid Engine enabled highly efficient usage of our compute resources with a very small footprint," explains Dr. Albaum. "We like the fact that users who do not have experience can quickly submit jobs to the cluster." Dr. Albaum cites Altair's 100% DRMAA2 support as a critical feature. In addition to the many bioinformatics tools maintained on their servers, the BRF team designs and develops their own applications for analysis and processing of large-scale -omics datasets such as QuPE, MeltDB, and Fusion, applications that rely on workload submission via the DRMAA2 interface.

### Results

With Altair Grid Engine, the BRF is enabling CeBiTec to **move biotechnology forward**. Dr. Albaum calls it "an established, easy-to-use system for managing the largest-scale processing of huge datasets," and adds that Altair's expertise and support is a major plus: "Support requests are always handled immediately." He believes BRF's HPC environment with Altair Grid Engine will play a key role in Bielefeld University's success for many years to come.