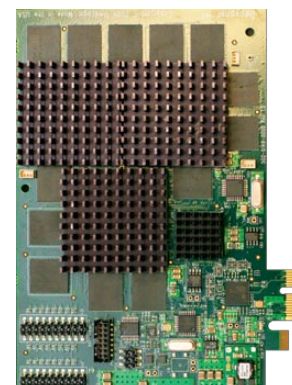


SeqCruncher™ FPGA Accelerator



The SeqCruncher™ accelerator is designed to handle the growing data volumes of metagenomics and downstream annotation of next-generation sequence data. Based upon TimeLogic's field programmable gate array (FPGA) technology, SeqCruncher powers the DeCypher and CodeQuest biocomputing solutions. Both solutions speed comparisons of gene and protein sequence data in a small form-factor solution.

SeqCruncher™ brings 3-20X improved performance over our DeCypher Engine™ G4 systems for Tera-BLAST, Smith-Waterman, HMM and GeneDetective™ comparisons. Compared to running HMMer software on a 2.66 GHz Intel Xeon CPU core, a SeqCruncher-powered CodeQuest workstation delivers 450-900X better performance.

The SeqCruncher also speeds the comparison of millions of short sequence reads or SNPs to a genome. Smith-Waterman and HMM comparisons of query sequences as short as 16 symbols are now up to 15X faster than our prior accelerator. Additionally, DeCypher users have access to Tera-Probe™, which approximates Smith-Waterman sensitivity at accelerated BLAST speeds for 16-50 bp sequence queries.

Up to 20 SeqCruncher cards can be installed in a DeCypher Enterprise system. Each SeqCruncher can outperform hundreds of CPUs, yet most DeCypher systems require only inches of rack space. The DeCypher management software automatically handles job management and target database distribution across all nodes. TimeLogic will help configure each node of your DeCypher system nodes for optimal performance and search-type priority.

SeqCruncher™ systems help you analyze data from next-generation sequencers, such as systems from Illumina, Roche and ABI.

The 400 next-gen instruments currently deployed could generate 41 terabases of data in one year—or 550-fold more data than is currently stored in Genbank!

Designed for comparisons of tremendous size, SeqCruncher can help you leverage the knowledge stored in hundreds of sequence databases to discover more from your sequencing endeavors.

SeqCruncher™ Performance

Performance

Tera-BLASTN Mapped 100,000 Solexa reads (49-mers) to Arabidopsis genome in 2.3 minutes with a 2U DeCypher server (2 SeqCruncher accelerators)

Tera-BLASTN Compared 100,000 ESTs to Arabidopsis genome in 1.3 minutes using a 2U DeCypher server (2 SeqCruncher cards)

Tera-BLASTN Compared Human chromosome X to Y in 3:48 minutes (92.7 trillion cells/second) with a 2U DeCypher server (3 SeqCruncher accelerators)

Tera-Probe™ Compared 125,000 50-mers (direct & complement) to the Human genome in 4 minutes (permitting up to 5 mismatches/gaps) with a CodeQuest Z1-P workstation (1 SeqCruncher)

Tera-BLASTP Compared 10,000 protein sequences to UniProt in 1 minute, 5 seconds using a 2U DeCypher server (2 SeqCruncher accelerators)

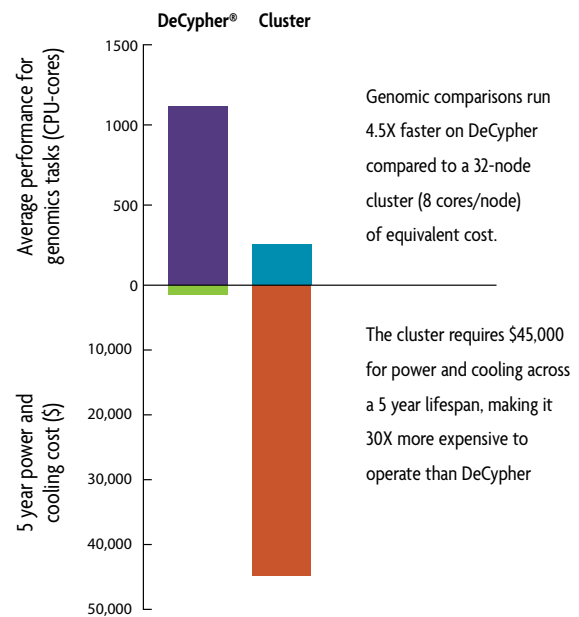
Smith-Waterman Compared one thousand 49-mers to a small genome of 119 million symbols in 3.5 minutes (84 billion cells/second) using a 2U DeCypher server (3 SeqCruncher accelerators)

Smith-Waterman, Double Affine Compared 5000 sequences vs Chromosome 22 in 1 hour, 41 minutes with a 2U DeCypher server (2 SeqCruncher accelerators)

HMM Compared 1,000 GOS sequences to PFAM: 2 minutes, 48 seconds (26 billion cells/second) using a 2U DeCypher server (2 SeqCruncher accelerators)

HMM Compared 5,000 EST sequences to PFAM in 2 minutes, 11 seconds (14 billion cell/second) with a 2U DeCypher server (2 SeqCruncher accelerators)

Higher Performance, Lower Operational Costs



Custom Benchmarks at Your Request

Want to know how long these searches would take on your current cluster or DeCypher system? Contact us today for access to our query sets and try them yourself! Or send us sample data and we'll run a custom benchmark for you.

The SeqCruncher solutions are ideally suited to cope with your rapidly growing next-gen data analysis needs and we look forward to demonstrating their performance.

DeCypher SeqCruncher Products	Catalog No
SeqCruncher™ PCIe accelerator	75006
Host server (Dell 2950, RHE4 64-bit OS, 8 GB RAM, 5 x 146 GB SAS drives)	75220
Host server (Dell 2950, Win2003 32-bit, 8 GB RAM, 5 x 146 GB SAS drives)	75200
Tera-BLAST Module (with Tera-Probe)	75100
Smith-Waterman Module (Framesearch and Symmetric Framesearch)	75101
HMM Module (HMM-Framesearch, Profilesearch and Profile-Framesearch)	75102
GeneDetective Module for gene modeling	75103