

# CodeQuest™ with PipeWorks

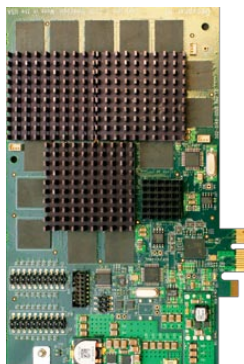


## High Throughput Genomics Workstation

CodeQuest™ is an accelerated biocomputing workstation that puts you in control of next-generation genomics—without having to build and administer a cluster.

CodeQuest includes SeqCruncher™, an accelerator based upon field programmable gate array (FPGA) technology. With each SeqCruncher, CodeQuest processes Tera-BLAST, Smith-Waterman and HMM with the performance of 62-471X CPU cores.

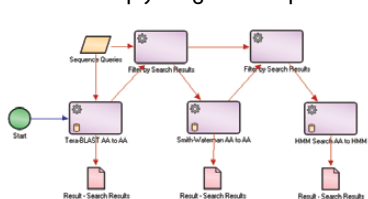
Sensitive mapping of short sequences to a genome is important for siRNA studies, motif exploration and probe design, and can be accomplished with Tera-Probe™ or Smith-Waterman. The SeqCruncher architecture improves these searches by up to 15X compared to our prior-generation accelerator.



SeqCruncher™ FPGA Accelerator

Categorizing millions of novel sequences using known protein family databases like PFAM is essential for metagenomics research. CodeQuest is 300-800X faster than running HMMER software on a single 3 GHz CPU core.


The PipeWorks™ visual environment enables non-programmers to build multi-step sequence analysis pipelines with unparalleled ease-of-use. Simply drag-and-drop to connect accelerated sequence



analysis tools, data sources and filters into a workflow, then process with CodeQuest. This eliminates the need to manually integrate results from dozens of web sites or

individual programs. Workflows can be saved as XML files and shared with other CodeQuest users.

When cooler heads prevail, more science gets done. CodeQuest won't heat your entire lab, yet can rival the performance of hundreds of CPUs. Simply plug CodeQuest into a standard power outlet, connect to your network, and your team can start running advanced analyses for fast, accurate answers to their next-generation genomics questions.



**hp**  
xw8600  
Workstation

### Accelerated Genomic Algorithm Suites

- TeraBLAST™ speeds genome annotation and SNP mapping
- TeraProbe™ speeds short-sequence mapping with high sensitivity
- DeCypherHMM™ delivers powerful Hidden Markov Model and ProfileSearch analyses for protein classification
- GeneDetective™ allows you to model genes by mapping EST, cDNA, HMMs or protein sequences to genomic DNA
- DeCypherSW™ offers Smith-Waterman and Framesearch for cross-genome protein comparisons

### Technical Specifications

- 1 or 2 SeqCruncher™ FPGA Accelerators (PCIe)
- PipeWorks™ visual pipeline-building interface (Windows models only, 5 named users)
- Includes a scriptable command line interface and an intuitive web interface
- HP® xw8600 workstation with 2 dual-core Xeon CPUs, 4 GB RAM, 1 TB SATA storage, DVD writer, 19" monitor

CodeQuest™ Products	Next Engines	PipeWorks Seats	Operating System	Cat. No.
CodeQuest Z1	1	5 users	Win2003 Server	75008
CodeQuest Z2	2	5 users	Win2003 Server	75016
SeqCruncher Upgrade 1P (for X8)	1	5 users	Win2003 Server	inquire
SeqCruncher Upgrade 1L (for X8)	1	n.a.	Red Hat (RHE4)	inquire
SeqCruncher Upgrade 2P (for X8, X9)	2	5 users	Win2003 Server	inquire



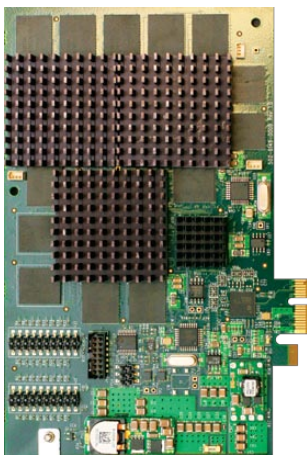
# CodeQuest™ for Linux



## Next-Generation Genomics Workstation

CodeQuest™ for Linux is an accelerated biocomputing workstation that puts you in control of next-generation genomics—without having to build and administer a cluster.

### SeqCruncher™ FPGA Accelerator



CodeQuest includes SeqCruncher™, an accelerator based upon field programmable gate array (FPGA) technology. With each SeqCruncher, CodeQuest processes Tera-BLAST, Smith-Waterman and HMM with the performance of 62-471X CPU cores.

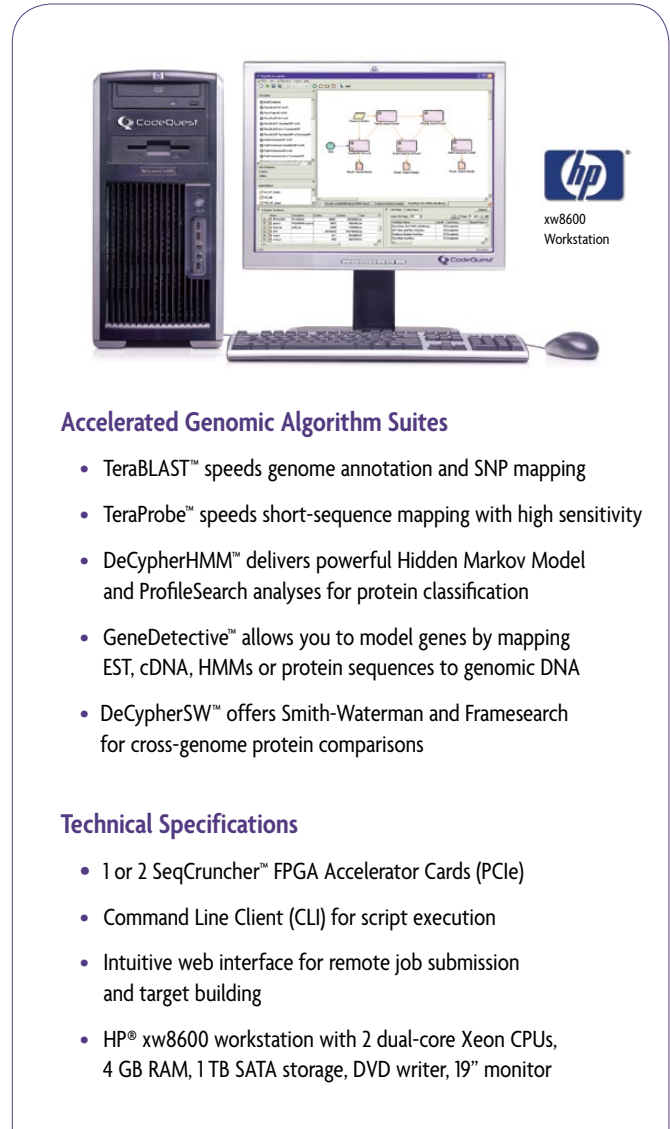
Sensitive mapping of short query sequences to a genome is extremely valuable for siRNA studies, motif exploration and probe design. SeqCruncher's architecture improves these Smith-Waterman and HMM searches by up to 15X compared to our prior generation accelerator.

Categorizing millions of novel sequences using known protein family databases like PFAM is essential for metagenomics research. CodeQuest is 300-800X faster than running HMMER software on a 3 GHz CPU core.

CodeQuest for Linux includes an intuitive web interface to provide easy searching. Additionally, the command line interface makes it easy to harness accelerated searches within your own bioinformatics applications. The powerful HP workstation includes a terabyte of storage and server-grade processing to serve as a high-performance computing resource for your entire lab. Plus, with Redhat Linux, it's even easier to integrate your favorite open source tools.



When cooler heads prevail, more science gets done. CodeQuest won't heat your entire lab, yet can rival the performance of hundreds of CPUs. Simply plug CodeQuest into a standard power outlet, connect to your network, and your team can run advanced analyses for fast, accurate answers to their next-generation genomics questions.



### Accelerated Genomic Algorithm Suites

- TeraBLAST™ speeds genome annotation and SNP mapping
- TeraProbe™ speeds short-sequence mapping with high sensitivity
- DeCypherHMM™ delivers powerful Hidden Markov Model and ProfileSearch analyses for protein classification
- GeneDetective™ allows you to model genes by mapping EST, cDNA, HMMs or protein sequences to genomic DNA
- DeCypherSW™ offers Smith-Waterman and Framesearch for cross-genome protein comparisons

### Technical Specifications

- 1 or 2 SeqCruncher™ FPGA Accelerator Cards (PCIe)
- Command Line Client (CLI) for script execution
- Intuitive web interface for remote job submission and target building
- HP® xw8600 workstation with 2 dual-core Xeon CPUs, 4 GB RAM, 1 TB SATA storage, DVD writer, 19" monitor

CodeQuest™ Products	Next Engines	PipeWorks Software	Operating System	Catalog No.
CodeQuest for Linux - ZL1	1	not available	Red Hat (RHE4)	75017
CodeQuest for Linux - ZL2	2	not available	Red Hat (RHE4)	75018
SeqCruncher Upgrade 1L (for X8)	1	not available	Red Hat (RHE4)	inquire

Contact your local TimeLogic representative for details on CodeQuest™ today by visiting: [www.timelogic.com/distributors.html](http://www.timelogic.com/distributors.html)



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