



FOR IMMEDIATE RELEASE

The J. Craig Venter Institute improves its metagenomics annotation pipeline with high-performance computing solution from CLC bio

Boston, Massachusetts, USA -- July 14, 2009 -- The J. Craig Venter Institute (JCVI) in Rockville, Massachusetts, has recently incorporated CLC bio's accelerated versions of the algorithms Hmmpfam and Hmmsearch into their bioinformatics pipeline for functional annotation of proteins identified in metagenomics data. The algorithms originate from Dr. Sean Eddy's popular HMMER package but their core parts have been accelerated by CLC bio using SIMD technology.

Director of Bioinformatics Software at JCVI, Dr. Saul Kravitz, states *"Given the ongoing acceleration in DNA sequencing capacity it is imperative for us to ensure that the bioinformatics pipelines we use to analyze sequencing data do not become bottlenecks to our researchers. The SIMD accelerated tools from CLC bio have given us a significant increase in analysis capacity that we could easily implement and take advantage of in our annotation pipeline without any further hardware investments."*

CEO of CLC bio USA, Jan Lomholdt, continues *"We have worked closely with the scientists at JCVI and have used their input to expand the functionality of our algorithms to make them better suited for metagenomics analysis. Furthermore, it is a great confirmation of the level of our technology, to see our command-line tools incorporated in a professional high-throughput analysis pipeline at a leading research institution such as JCVI."*

CLC bio's command-line tool, CLC Bioinformatics Cell, uses the Single Instruction, Multiple Data (SIMD) technology to parallelize and thereby accelerate bioinformatics algorithms - like Hmmpfam, Hmmsearch, ClustalW, and Smith-Waterman - on Intel and AMD computer processors.

To read more about CLC bio's high-performance computing solutions, go to:
www.clcbio.com/hpc



About CLC bio

<http://www.clcbio.com/index.php?id=17>

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