Our Experience

We have helped many companies under NDA, and cannot mention them here. Below are public examples.

Memorial Sloan Kettering Cancer Center

We helped the Memorial Sloan-Kettering Cancer Center with improving a tool they used daily. Where it previously took one hour, it now takes just two minutes ? a speed-up of 30x. Their productivity rose, as they did not need to wait for results so long anymore and could get more done without buying new computers.

Gromacs
fast
flexible
free

We ported GROMACS to OpenCL and optimised the code for usage with AMD FirePro accelerators. This resulted in code that is as fast with CUDA. Gromacs is used world-wide by over 5000 research centers, from simulating molecular docking to examining the hydrogen bonds in a falling water drop. Read more...

STANFORD UNIVERSITY
DEPARTMENT OF CHEMISTRY

For the university of Stanford we optimised a part of TeraChem, a general purpose quantum chemistry software designed to run on NVIDIA GPU architectures. Our work resulted in adding an extra 70% performance to the already optimised CUDA-code.

MANCHESTER 1824
The University of Manchester

For the University of Manchester we got a large speedup with UNIFAC when going from OpenMP code to optimised OpenCL. Where OpenMP could get the single threaded code down to about 8 seconds, we brought it down to 0.062 seconds. Read more...