

Quakecon Folding@Home Challenge FAQ

Team Name: Quakecon&NVIDIA

Team Number: 169355

What are the minimum system requirements to run Folding@Home?

Almost all computers can contribute to Folding@Home. However, if the computer is too slow (e.g. wasn't bought in the last 3-4 years or so), the computer might not be fast enough to make the deadlines of typical work units.

Pretty much any 1GHz+ machine can run Folding@Home. The slower the machine, the longer it will take you to finish processing an individual work unit.

Can I use an ATI GPU or Intel /AMD CPU for the Quakecon Folding@Home Challenge

Of course! You can use any GPU and any CPU for the Quakecon Folding@Home Challenge. However, computers with NVIDIA GPUs will calculate work units fastest as NVIDIA GPUs are up to 140x faster than traditional CPUs and more than twice as fast as ATI GPUs in Folding@Home.

Why does my computer run slow when I am running Folding@Home?

Running the Folding@Home client a very resource intensive task and will take up most of your computer's processing power. Unless you have an extreme performance PC, only basic applications like word, firefox, irc, ftp clients, etc. will be able to run concurrently with Folding@Home. If you are going to game, make sure that you Pause your Folding@Home work unit calculations so you can dedicate your PC's resources to gaming. Also, Folding@Home can be running in the background even though the Folding@Home visualization screen is not turned on. The best way to make sure

Therefore, we would recommend you turn on Folding@Home only when you're planning to do things away from your PC – like visit the exhibit area, participate in the tournaments, etc.

How do I get one of the cool NVIDIA Folding@Home Wristbands?

Once you successfully complete your first Folding@Home work unit, your statistics will automatically be added to the Quakecon&NVIDIA stats page (the page updates every 2 hours). Once you see yourself up on the page, come by the NVIDIA booth and you will receive the NVIDIA Folding@Home Wristband. The wristband will make you eligible for special activities and prizes at the NVIDIA booth – which will be announced later in the BYOC.

Is Folding@Home a bandwidth hog?

The short answer is No. Folding@Home only requires about 5MB of bandwidth (2.5mb up, 2.5mb down) per work unit. Most work units will take anywhere from 2 hrs – 6 hrs to process (depending on the configuration of your PC) so bandwidth is not an issue.

Which ports does Folding@Home use?

Folding@Home uses ports 80 and ports 8080.

What is protein folding?

Proteins are biology's workhorses -- its "nanomachines." Before proteins can carry out these important functions, they assemble themselves, or "fold." The process of protein folding, while critical and fundamental to virtually all of biology, in many ways remains a mystery.

What is distributed computing?

Distributed Computing is a method of computer processing in which different parts of a program, or different portions of data, are processing simultaneously on two or more computers that are communicating with each other over a network or through the Internet.

How long does it take to finish a work unit? How do you measure a work unit?

This varies, of course, on the speed of the computer and the size of the protein under study. Depending on the protein and the properties studied, different size work units may be used. The general rule is that the faster the PC you are using, the less time it will take

About the Folding@Home Visualization Screensaver

Our screen saver shows real time visualizations of the simulations being performed. The molecule drawn is the current atomic configuration ("fold") of the protein being simulated on your computer and the pie chart the left shows the current progress on the work unit.

There are currently four visualization modes: Space-filling, ball-and-stick, wireframe, and alpha-trace. In ball-and-stick, each small ball represents an atom, and the sticks represent bonds between atoms. In the space-filling model, each filled sphere represents the approximate volume that the electrons occupy around each atom. In wireframe mode, only the bonds are drawn, but with the vertices colored to indicate atom identity. In all but alpha-trace mode, carbon atoms are drawn in dark gray, hydrogen atoms are drawn in light gray (although some hydrogen atoms are not drawn at all), oxygen atoms are drawn in red, nitrogen atoms are drawn in blue, and sulfur atoms are drawn in yellow. In the alpha-trace model, only one atom (the alpha-carbon) is shown per amino acid residue, in order to emphasize the overall arrangement of the peptide or protein.

For a complete list of Folding@Home FAQs, please visit the Folding@Home website here:
<http://folding.stanford.edu/English/FAQ-NVIDIA>