

# **AQuaRef: QM-based atomic model refinement becomes reality**

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BNL

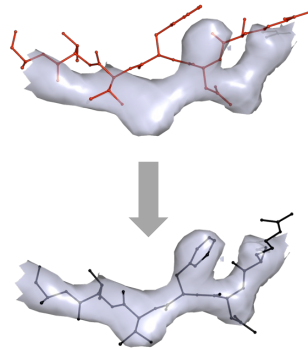
# Atomic model refinement

**T**

Optimize  
consensus  
between model-  
to-data fit and  
prior information

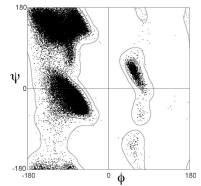
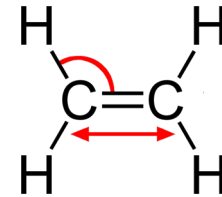
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**T<sub>DATA</sub>**



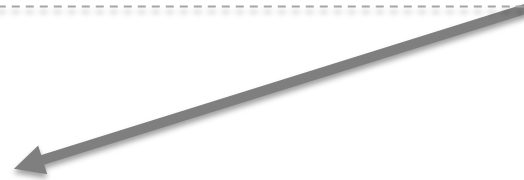
+

**W \* T<sub>RESTRAINTS</sub>**



# Restraints

$$T = T_{\text{DATA}} + W * T_{\text{RESTRAINTS}}$$



$$T_{\text{RESTRAINTS}} = T_{\text{BOND}} + T_{\text{ANGLE}} + T_{\text{DIHEDRAL}} + T_{\text{PLANE}} + T_{\text{REPULSION}} + T_{\text{CHIRALITY}}$$

- Too simplistic:
  - No attraction terms (electrostatics, etc)
  - Not using information about protein structure (secondary structure, rotamers)
  - Limited to tabulated entities in the libraries (e.g., Monomer Library, GeoStd)

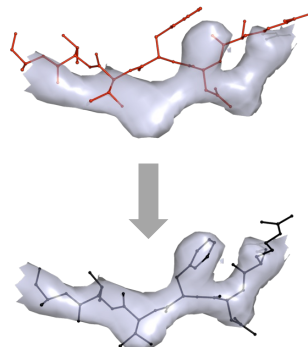
# A better solution

**T**

Optimize  
consensus  
between model-  
to-data fit and...  
common sense

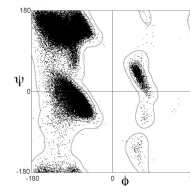
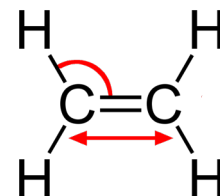
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**T<sub>DATA</sub>**



+

**W \* T<sub>RESTRAINTS</sub>**

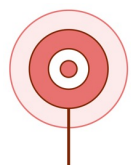


Bonds, angles, planes,  
torsions, chirality, non-  
bonded repulsion

**Replace with  
energies/gradients  
from QM calculations**

**AQuaRef:** AI-enabled Quantum Refinement

# QM calculations for proteins structures<sup>\*</sup>: history of progress

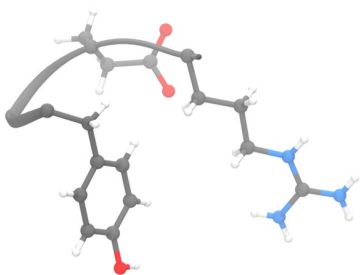


**Impossible**

**2010**

## QM Calculations

Impossible for proteins.  
Limited to small molecules  
only

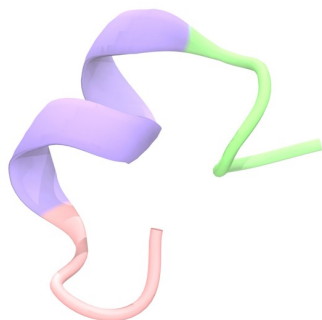


**Limited**

**2012**

## GPU Accelerated QM

Limited to peptides and very small  
proteins (~hundreds of atoms)

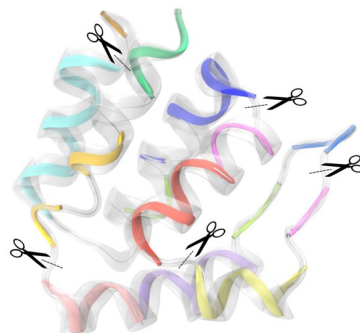


**Possible**

**2017**

## Q|R with Fragmentation

QM-based protein refinement. Slow,  
resource-intensive, no inherent size  
limit

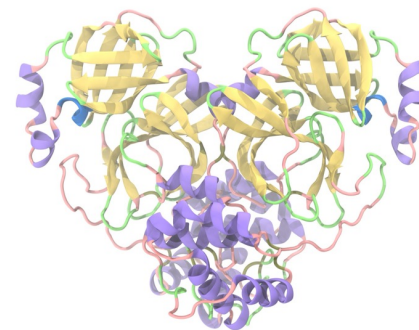


**Practical**

**2024**

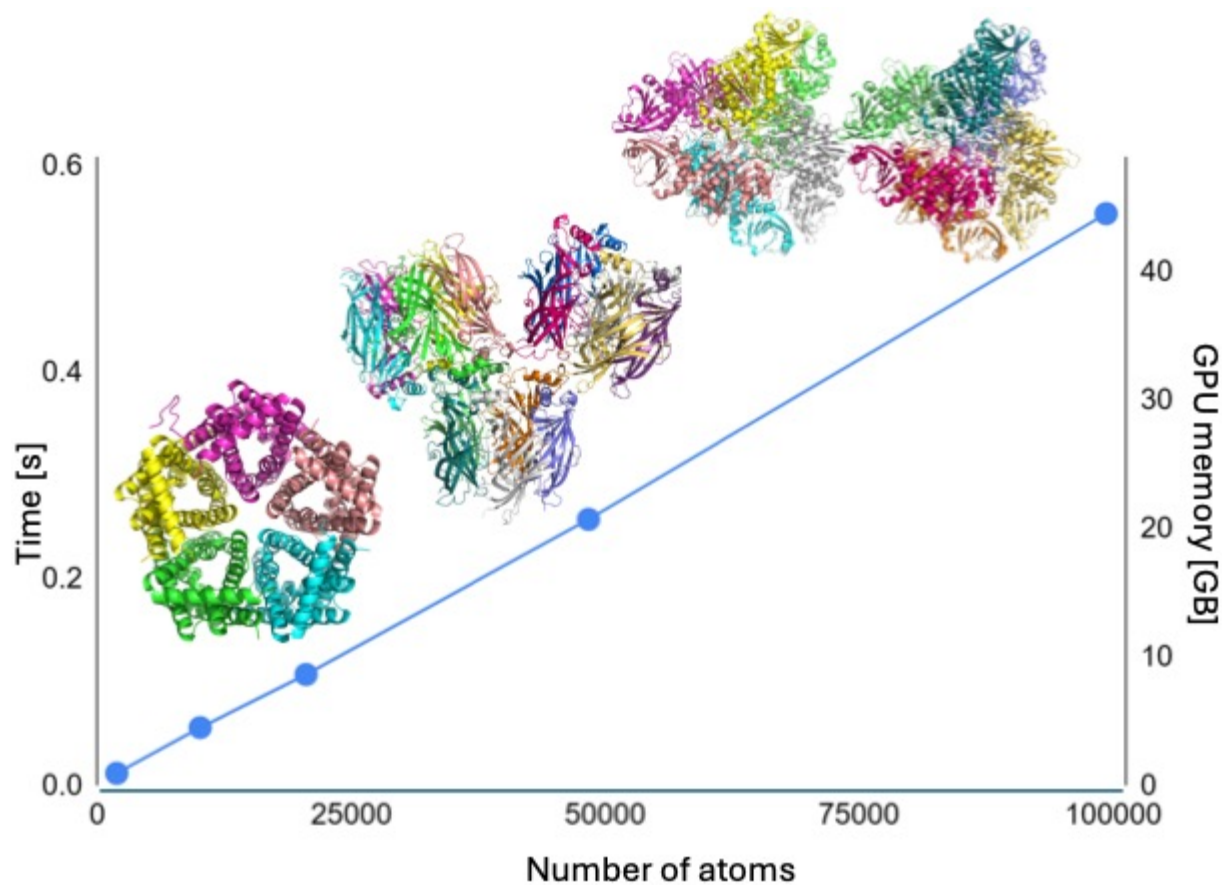
## ML Potentials

Fast, rivaling classical force fields,  
with QM-level accuracy and no  
fragmentation required



**\* Whole protein structures, not QM/MM and other ONIOM like methods!**

# Time & Memory Scaling: single energy calculation



# Q|R: Quantum Refinement project

Blend of expertise and background

Crystallography  
methods



Software  
development



QM  
expertise

[www.qrefine.com](http://www.qrefine.com)



Quantum Refinement

<http://qrefine.com>

[qrefine@googlegroups.com](mailto:qrefine@googlegroups.com)

Q|R @ GitHub

Pending.AI (Australia)



Mark Waller



Holger Kruse

Uni of Wrocław

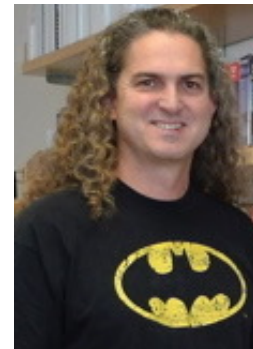


Malgorzata  
Biczysko

LBNL (USA)



Pavel Afonine



Nigel Moriarty



# The Team: crystallography + chemistry + AI expertise

Carnegie Mellon University



Olexandr Isayev



Roman Zubatyuk



Hatice Gökcan

Uni. of Florida



Adrian Roitberg

Blend of expertise and background

Crystallography  
methods



Software  
development



QM  
expertise



ML / AI  
expertise

Pending AI



Marl Waller



Holger Kruse

Uni of Wrocław



Malgo Biczysko

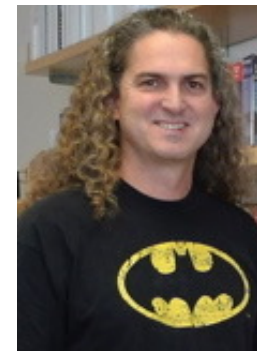
LBNL



Billy Poon



Pavel Afonine



Nigel Moriarty



- Limitations
  - Proteins only. Including other types of molecules is work in progress
  - No alternative conformations
- Timing
  - Same as standard refinement or 2-3 times slower
- Hardware requirement:
  - GPU laptop or a workstation
- Availability
  - AQuaRef is now available in Phenix nightly builds and Q|R

# Availability

phenix-online.org/download/phenix/nightly/?version=dev-5430

## Installers for Phenix version dev-5430 (development version)

For a summary of possible errors and/or bugs, please see the build and testing logs:

[ci](#), [mac-intel-osx-x86 64](#), [intel-linux-2.6-x86 64-centos6](#)

[Version documentation](#)

[Summary of changes](#)

### Linux

Kernel 2.6 (64-bit; CentOS 6) [ [download command-line installer](#) ]

CentOS 6 is the earliest linux distribution supported. This installer will work with newer linux distributions.

### macOS

OS X 10.9+ (64-bit Intel) [ [download point-and-click installer](#) ]

OS X 10.9+ (64-bit Intel) [ [download command-line installer](#) ]

The graphical installer will install to /Applications; the command-line installer may be relocated with the --prefix argument.

On macOS 12 and later, you will need to run "xattr -c " to avoid errors about untrusted files

For Phenix 1.20.1 and before, the Phenix GUI will crash on macOS Sonoma (14). Please download this [fix](#) to fix your Phenix installation. Extract the tarball and run "sudo ./fix\_wxpython.sh /Applications/phenix-1.20.1-4487". You will need administrative access to modify files in /Applications.

### Windows [\(partially supported\)](#)

For full functionality, you should run the Python 2.7 linux installer on Windows using WSL. Instructions for setting up Phenix with WSL can be found [here](#).

A native Windows build is only available for Python 3, but you will encounter crashes. See below for the link to the Windows installer.

The next official release of Phenix will be in Python 3 and Windows will have a working installer again.

### Python 3.9 (Alpha) - CUDA 11 and CUDA 12 support only for quantum refinement on Linux, general Phenix GUI is still in testing and does not have full functionality

Linux (CUDA 12) [ [download command-line installer](#) ]

Linux (CUDA 11) [ [download command-line installer](#) ]

### Python 3.9 (Alpha) - For testing and development, do not expect full functionality in the Phenix GUI

Linux [ [download command-line installer for development builds and modifications \(contains "modules" directory\)](#) ]

Linux [ [download command-line installer](#) ]

macOS (Intel) [ [download graphical installer](#) ]

macOS (Intel) [ [download command-line installer](#) ]

macOS (Apple Silicon) [ [download graphical installer](#) ]

macOS (Apple Silicon) [ [download command-line installer](#) ]

Windows [ [download graphical installer](#) ]