

# Why OpenMM?

- Many choices of software for molecular dynamics
  - [https://en.wikipedia.org/wiki/Comparison\\_of\\_software\\_for\\_molecular\\_mechanics\\_modeling](https://en.wikipedia.org/wiki/Comparison_of_software_for_molecular_mechanics_modeling)
  - [https://www.rcsb.org/pages/thirdparty/modeling\\_and\\_simulation](https://www.rcsb.org/pages/thirdparty/modeling_and_simulation)
- OpenMM is
  - free
  - GPU-accelerated
  - can be used in python scripts/C++ programs

# **Interactive MD exercise**