

Cyrus implements the *Rosetta* Homology Modeling tool (*RosettaCM*) as an easy-to-use, SaaS offering to computationally predict protein structures.

### Highest Accuracy Prediction

Accelerate structure-guided design, protein engineering and structure determination (molecular replacement)

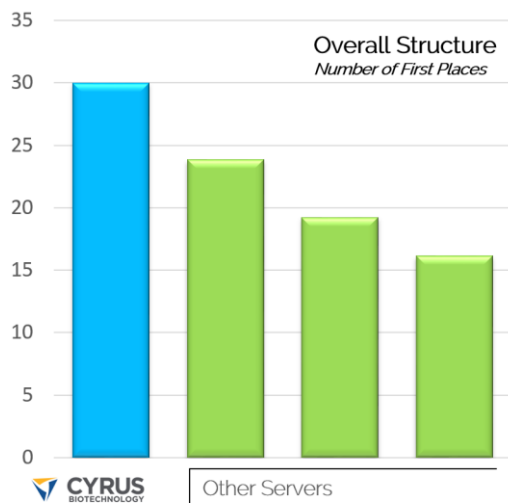
### Fully Automated Workflow - Sequence In, Structure Out

Cyrus manages RosettaCM's dependencies with several other software packages and custom scripts.

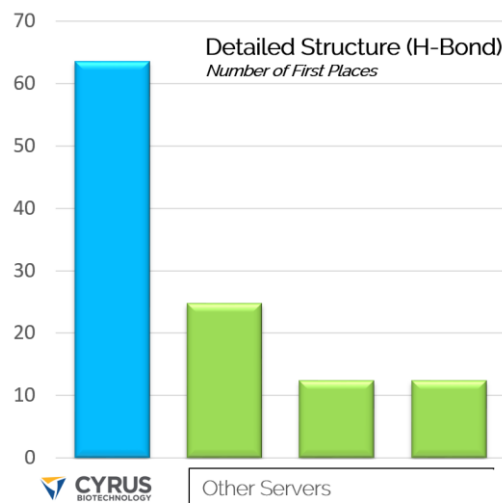
### Cloud Based

Instantly harness the power of thousands of processors

*Rosetta* is the known innovator and leader in protein structure prediction and design. It consistently earns **first place** at CASP and CAMEO - blind, fully automated protein structure prediction tests using both homology and ab initio methods.



### CASP First Place



### CAMEO First Place

