

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

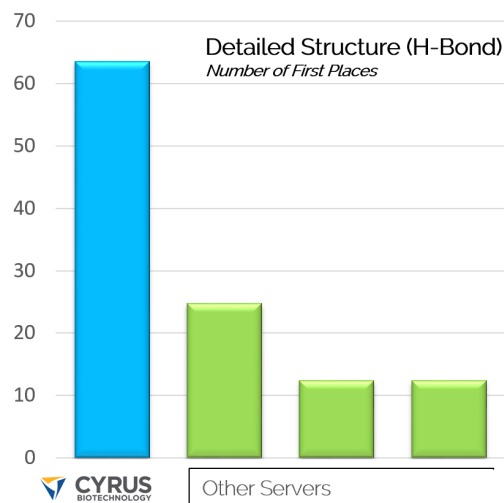
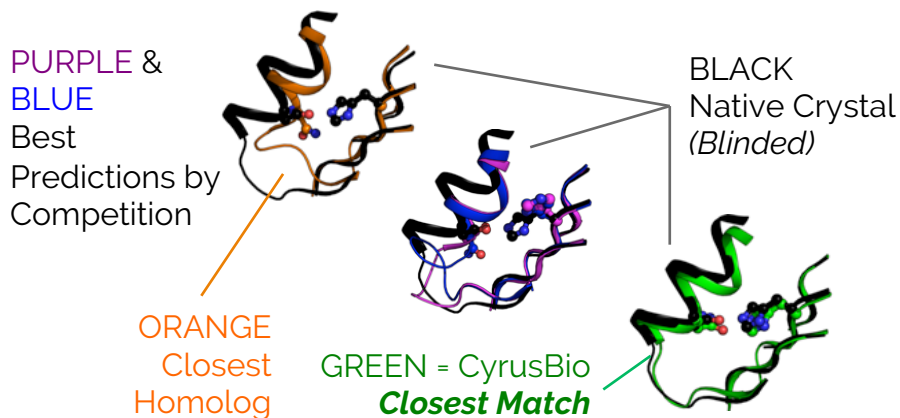
Cyrus manages RosettaCM's dependencies with several other software packages and custom scripts.

Cloud Based

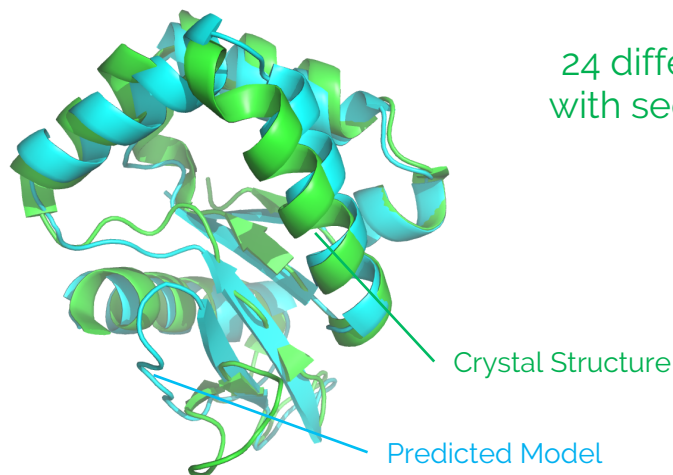
Instantly harness the power of thousands of processors.

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

More Accurate Details vs. popular software
 Swiss-prot, IntFOLD, Schrodinger, BIOVIA, etc.



Accurate Models of Very Low Homology Structures



24 different templates
 with sequence ID $\leq 18\%$

RMSD
 = 1.9Å

Template PDB_ID	Coverage	Sequence Identity
4q6tA	67.24	15.38
2ddxA	62.93	16.44
3aquD	64.66	10.67
1ydoB	61.21	7.04
5jh8A	66.38	10.39
3wjjA	70.69	10.98
4f9dA	57.76	17.91
4uriB	69.83	12.35
1hxB	67.24	11.54
1v47A	56.03	12.31
2ftpA	62.07	8.33
3co4A	66.38	5.19
1hjb	66.38	11.69
5hclD	62.93	1.37
3bg9C	62.93	10.96
4zquA	70.69	13.29
1ljjA	67.24	12.82
1m03A	62.93	8.22
1owqA	66.38	12.99
3cz8A	67.24	8.97
4s3jA	64.66	6.67
5jd3H	62.07	9.72
1hjwB	67.24	11.54
4g6uA	72.41	13.1