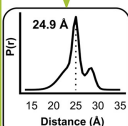


**CONE model**

Conversion to distance distribution

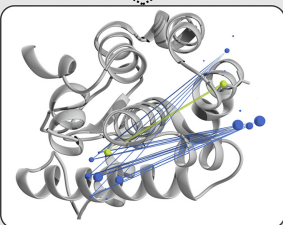


Conversion to restraints

CB 93 CB 123 24.9  
...

Comparison to restraints using CONE model

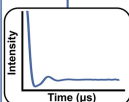
CB distance calculation



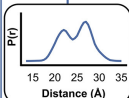
**RosettaDEER**

Comparison to experimental decay trace

Background calculation



Conversion to time domain

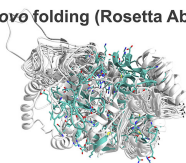


Distance measurements

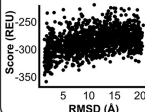
Pseudorotamer calculation

**B**

**De novo folding (Rosetta AbInitio)**



**Scoring**



**Clustering**

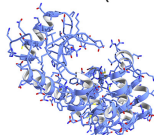


**Backbone refinement (RosettaCM)**

**Scoring**

**Clustering**

**Full-atom refinement (Rosetta Relax)**



**C**

