Exploring Protein Conformational Heterogeneity with CryoEM and Enhanced Sampling Molecular Dynamics

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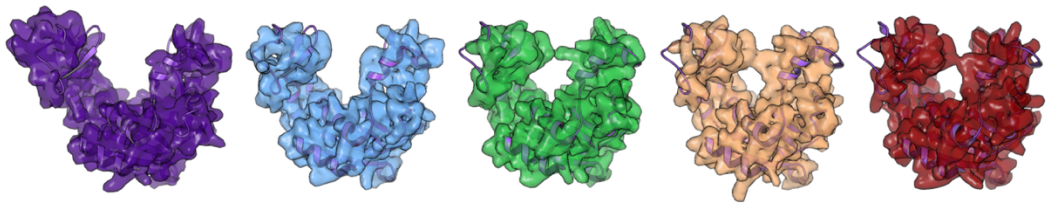
Summary:

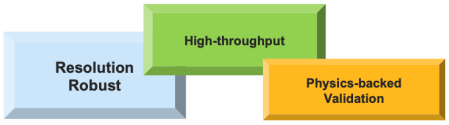
- Understand biomolecular structural heterogeneity from CryoEM maps using Weighted Ensemble Molecular Dynamics (WEMD)
- Automated workflows accelerate identification of structures best matching multiple target maps
- Eigen-maps help scientists visualize and perform quantitative comparison of dynamic behavior captured by both simulation and CryoEM methods

Product Keywords: Orion®, CryoEM, WEMD



OpenEye's Orion Structural Biology workflows integrate Weighted Ensemble MD Simulation and CryoEM data by guiding simulations based on CryoEM maps derived from heterogeneity analysis.

CryoEM provides revolutionary high-resolution snapshots of macromolecules in near-native conformational states. However, modeling the resulting large number of maps requires substantial manual input, particularly when the protein exhibits loop or domain movement.



OpenEye is accelerating CryoEM fitting with fast, robust, physics-based solutions.

To address this, OpenEye's Orion Structural Biology workflows (Floes) offer a powerful solution - CryoEM guided Molecular Dynamics (MD) simulations. These Floes automate map fitting using Weighted Ensemble MD via two key methods: efficiently identifying simulated structures that best match multiple CryoEM maps simultaneously, and projecting protein motion onto the heterogeneity space from CryoEM particle stacks via PCA eigen-maps for direct comparison of simulated motion to that seen in the CryoEM experiment.

Combining atomic models with CryoEM density and map-guided WEMD simulations allows drug discovery scientists to model flexible regions/loops and account for conformational heterogeneity, accelerating their research.

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