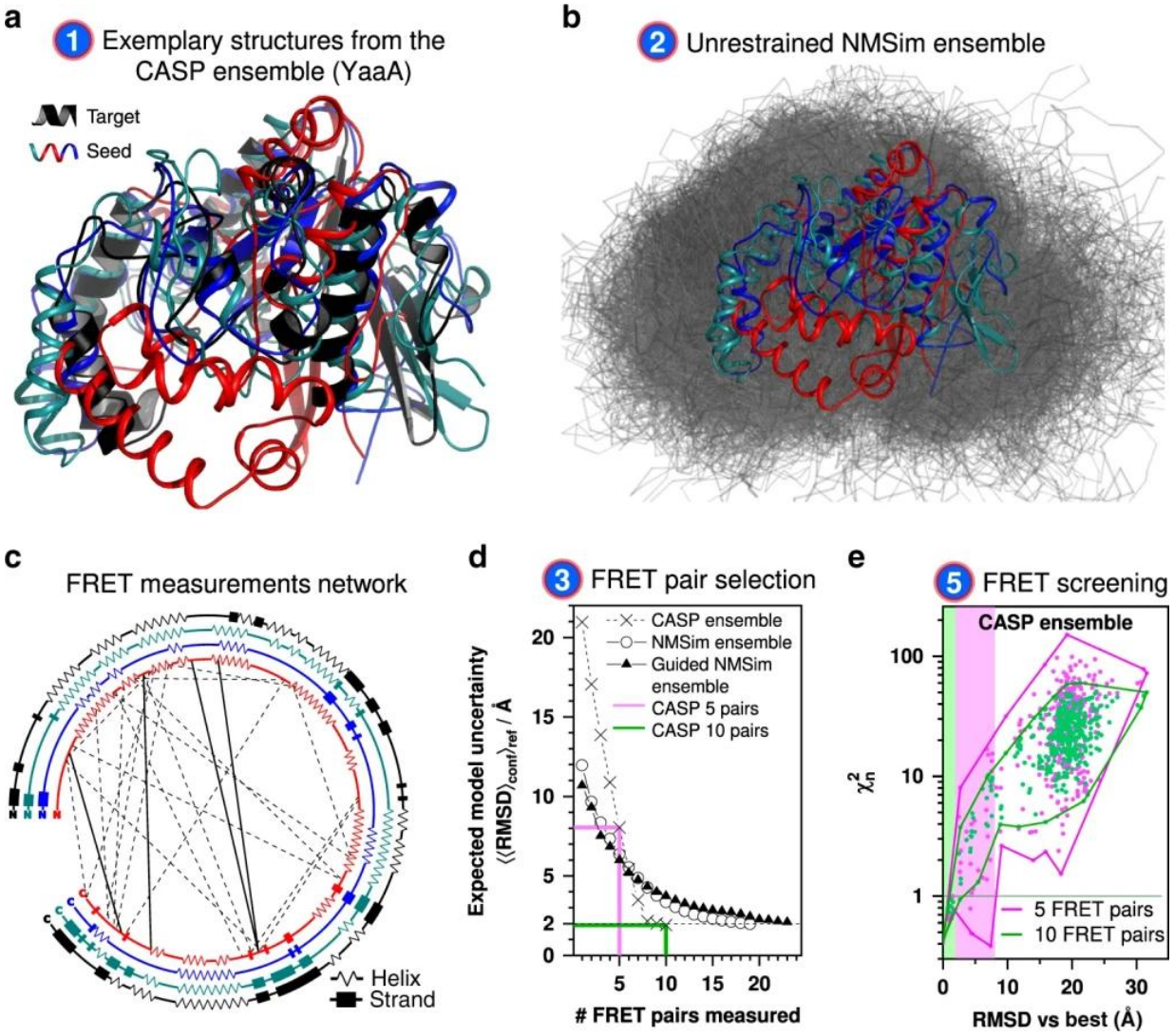


FRET experiments can provide state-specific structural information of complex dynamic biomolecular assemblies. However, to overcome the sparsity of FRET experiments, they need to be combined with computer simulations. We introduce a program suite with (i) an automated design tool for FRET experiments, which determines how many and which FRET pairs should be used to minimize the uncertainty and maximize the accuracy of an integrative structure, (ii) an efficient approach for FRET-assisted coarse-grained structural modeling, and all-atom molecular dynamics simulations-based refinement, and (iii) a quantitative quality estimate for judging the accuracy of FRET-derived structures as opposed to precision. We benchmark our tools against simulated and experimental data of proteins with multiple conformational states and demonstrate an accuracy of ~3 Å RMSDCα against X-ray structures for sets of 15 to 23 FRET pairs. Free and open-source software for the introduced workflow is available at https://github.com/Fluorescence-Tools. A web server for FRET-assisted structural modeling of proteins is available at http://nmsim.de.