Supporting Information

Unveiling Medin Folding and Dimerization Dynamics and Conformations via Atomistic Discrete Molecular Dynamics Simulations

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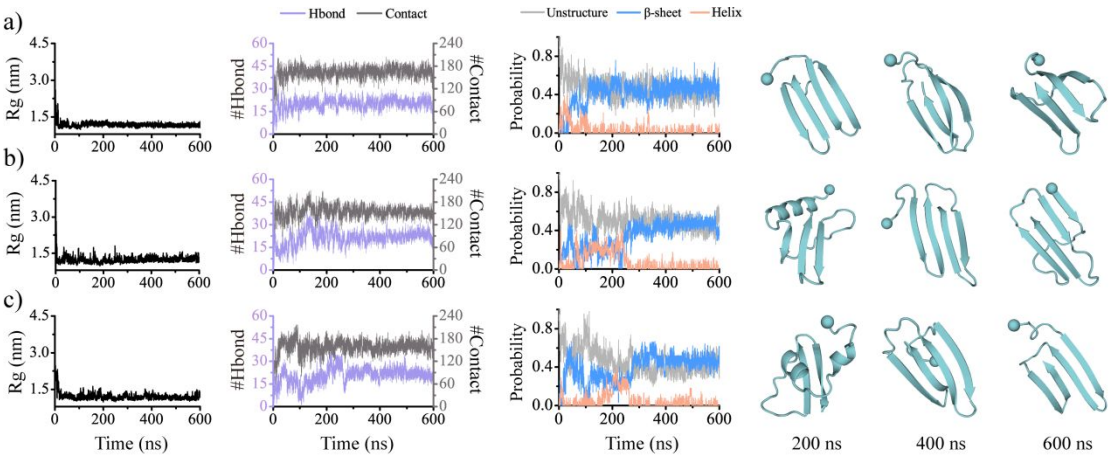

Figure S1. Assessment of equilibrium for the folding dynamics of the medin monomer. The first panel shows the time evolution of the radius of gyration (Rg). The second panel displays the number of intra-molecular backbone hydrogen bonds and contacts as a function of the simulation time. The third panel depicts the probabilities of unstructured (random coil and bend), β-sheet, and helix conformations. Three trajectories, randomly selected from thirty independent DMD simulations, are represented as **a-c)**. Snapshots at 200 ns intervals, highlighting the N-terminal Cα atom as a bead, provide a visual representation of the folding dynamics on the right.

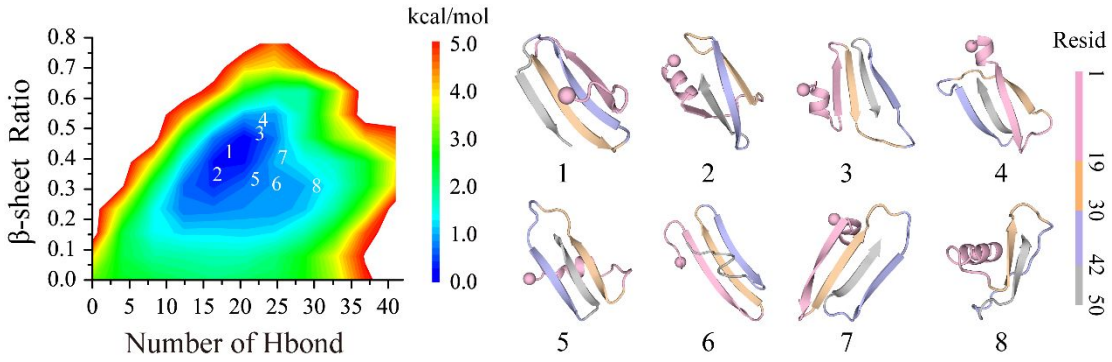

Figure S2. Conformational free energy landscape analysis of the medin monomer. The free energy landscape of the medin monomer is plotted as a function of the total number of hydrogen bonds formed by main-chain atoms and the average β-sheet ratio. Representative conformations, scattered in the energy basin and labeled as 1-8, are shown on the right.

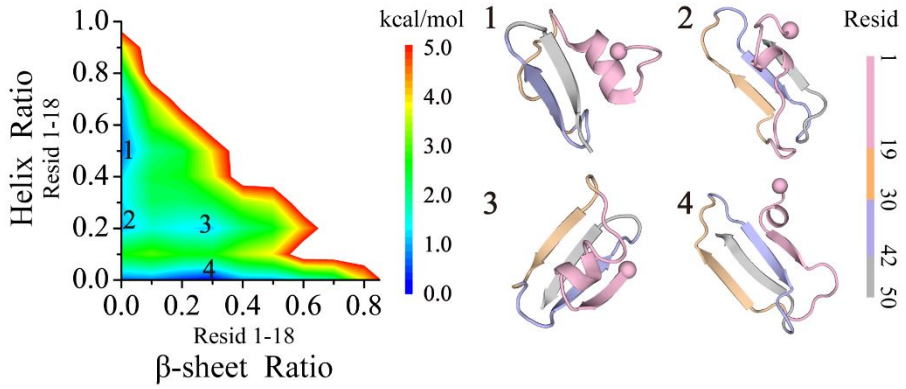

Figure S3. Structural analysis of the N-terminus of the medin monomer. The structural potential mean force is plotted as a function of the β-sheet and helix ratio for residues 1-18 of medin. Four representative structures, labeled 1-4 on the free energy landscape surface, with low free energy and varying helix and β-sheet contents, are also presented.

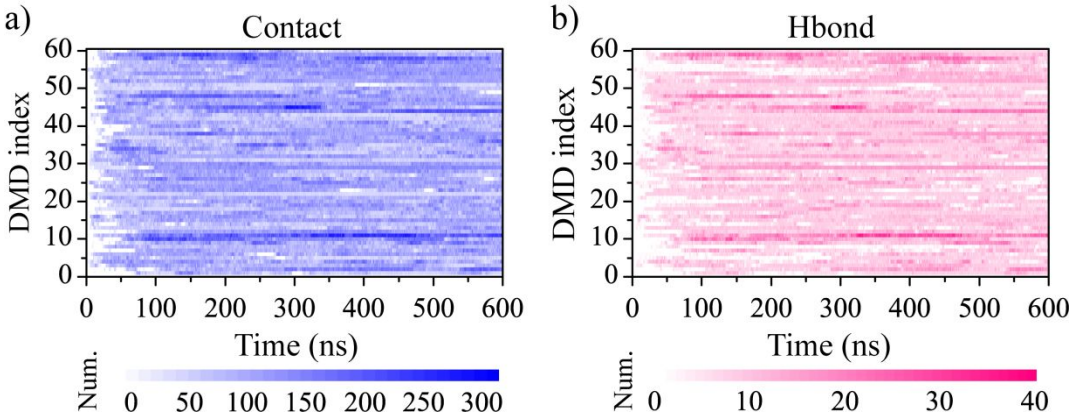

Figure S4. Dimerization dynamics analysis. The time evolution of the number of inter-peptide contacts **a)** and hydrogen bonds **b)** in each independent DMD simulation**.**

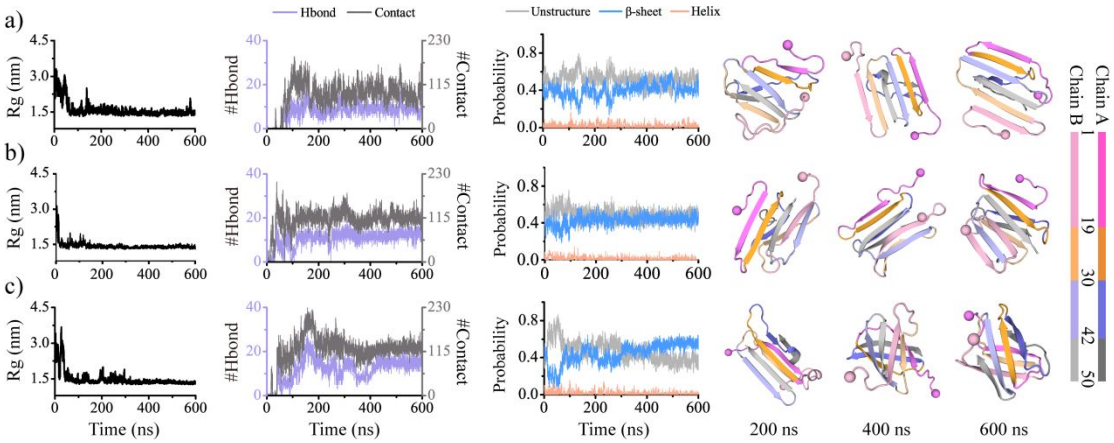

Figure S5. Equilibrium analysis of the dimerization simulation of medin peptides. The first panel presents the time evolution of the radius of gyration (Rg). The second panel shows the time evolution of the total number of the backbone hydrogen bonds and contacts. The third panel displays the probabilities of unstructured (random coil and bend), β-sheet, and helix conformations as a function of simulation time. Trajectories **a-c)** represent three randomly selected simulations out of fifty independent DMD simulations. Snapshots, highlighting the N-terminal Cα atom as a bead, are illustrated on the right at 200 ns intervals.

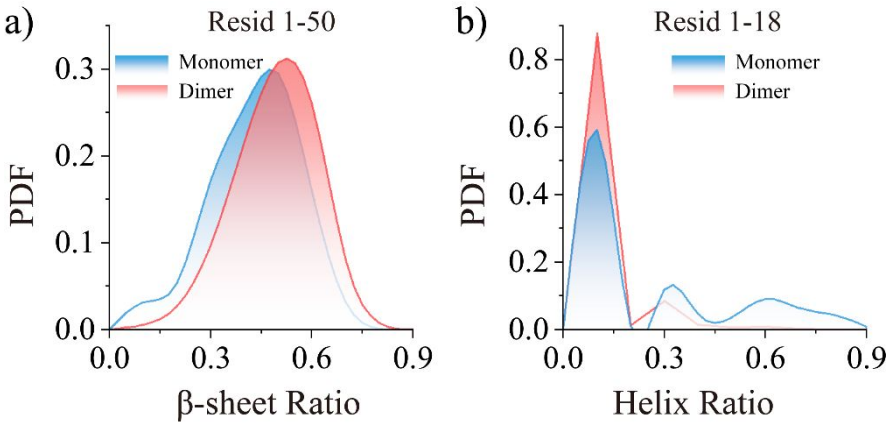

Figure S6. Comparing the conformation of medin peptide within dimer and monomer. The probability distribution function of the average β-sheet content for each medin peptide in monomer and dimer **a)**. The probability distribution function of the average helix content for the segment of medin1-18 in each medin monomer and dimer **b)**.

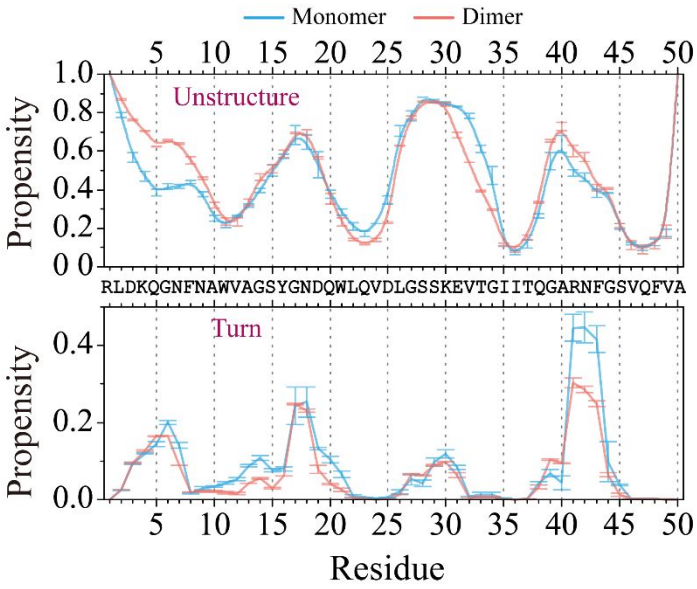

Figure S7. Secondary structure analysis for each residue. The average propensity of each residue adopts unstructured (top) and turn (bottom) conformations within the medin monomer and dimer.

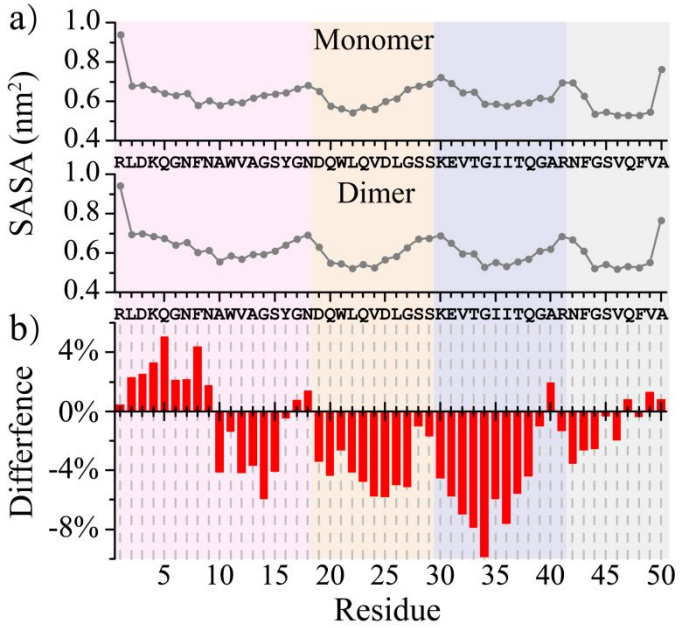

Figure S8. Solvent accessible surface area analysis. The solvent accessible surface area (SASA) values for each residue within the medin monomer and dimer are illustrated upper and bottom **a)**. The relatively different ratio for each residue SASA in the medin dimer compared to the monomer **b)**.