

# Thermodynamics and kinetics of amphotericin B self-association in aqueous solution characterized in molecular detail

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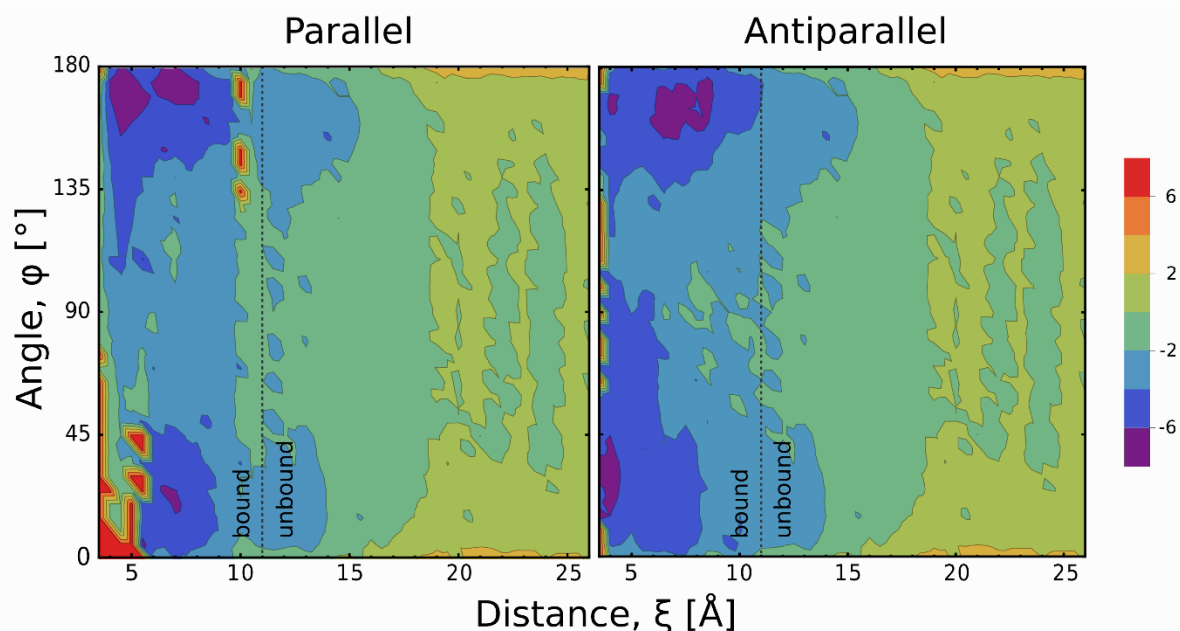
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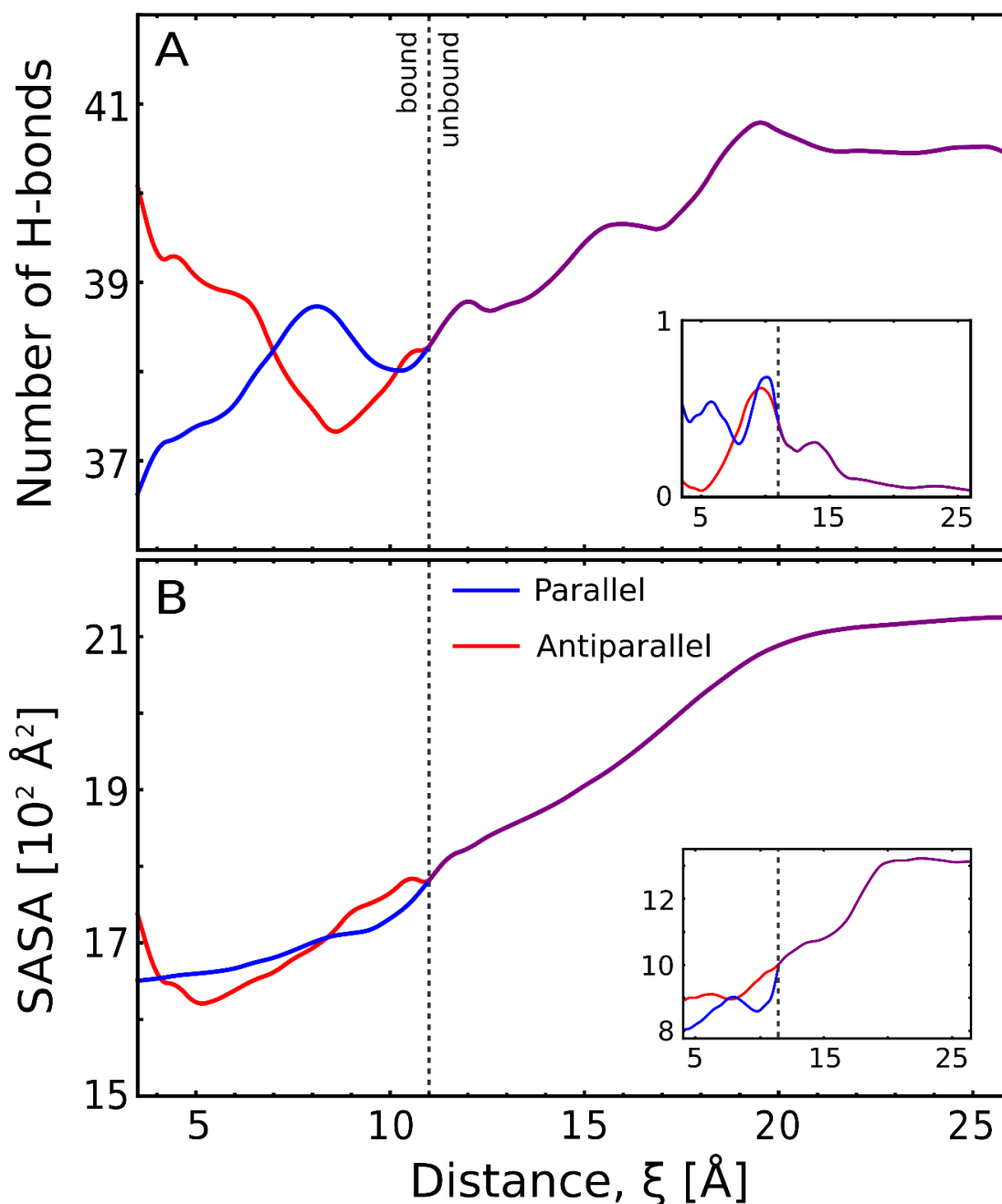
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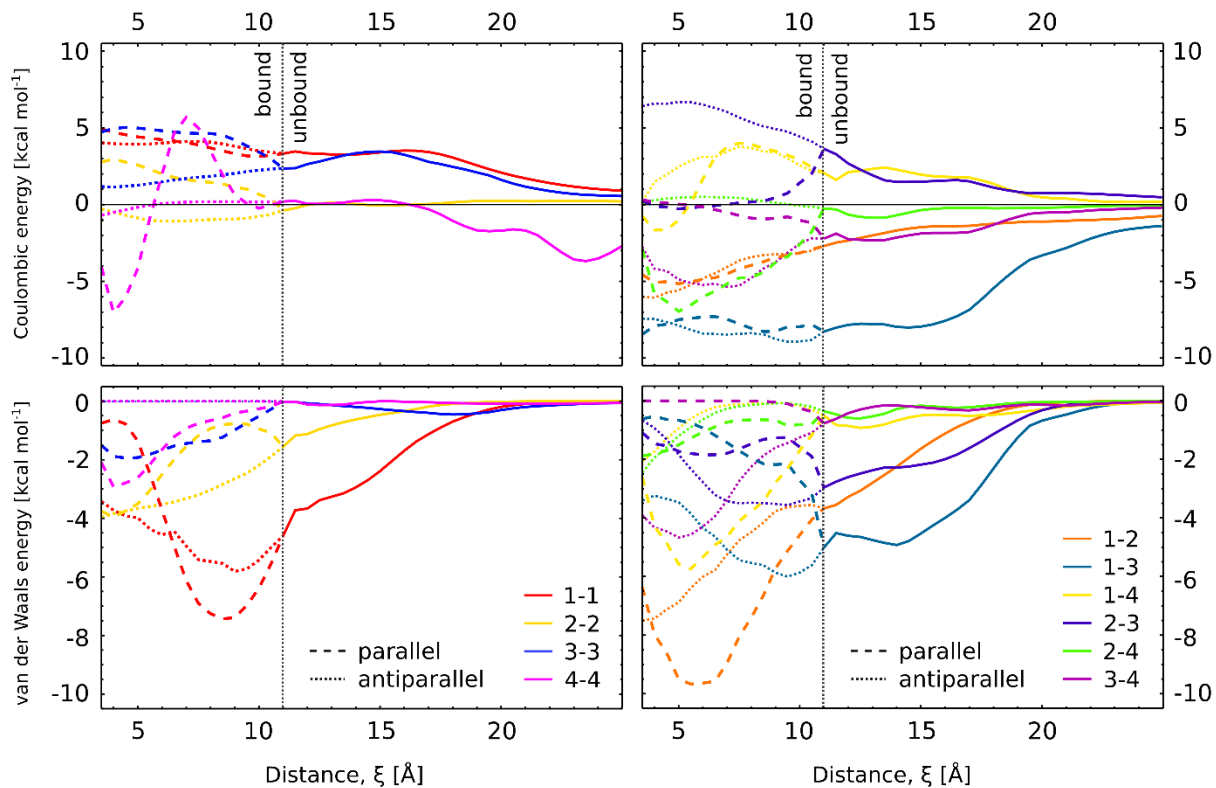
## Supplementary Information



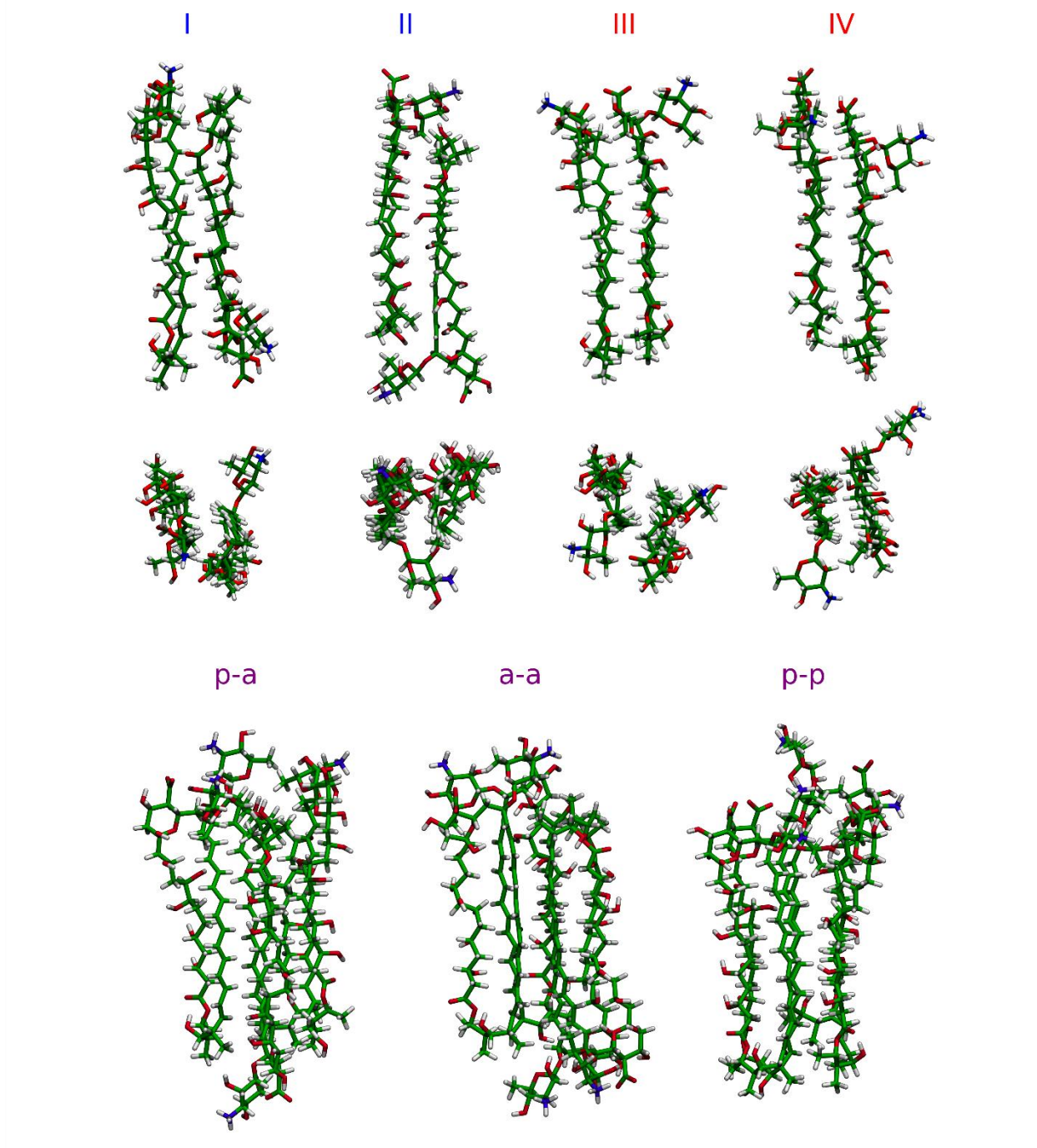
**Supplementary Figure S1.** 2D free energy profiles of two AmB molecules in a parallel and antiparallel geometry, as a function of the interchromophore distance,  $\xi$ , and the angle between the 2<sup>nd</sup> main axes of both monomers,  $\phi$  (see Fig. 1 for a depiction of the coordinates). The minima are marked as I-IV according to Fig. 2B.



**Supplementary Figure S2. A:** Number of hydrogen bonds formed between AmB and water molecules (main panel) and two AmB monomers (inset) as a function of the intermonomer distance  $\xi$ . A hydrogen bond was defined by a D-A distance threshold of 3.5  $\text{\AA}$  and a D-H-A angle threshold of 40°, where D, A and H are the donor, acceptor and hydrogen atoms, respectively. **B:** Overall and hydrophobic (inset) solvent accessible surface area as a function of  $\xi$ . For the bound state ( $\xi < 11$   $\text{\AA}$ ), parallel and antiparallel dimers were considered separately.



**Supplementary Figure S3.** Decomposed intermolecular interaction energies (Coulombic and van der Waals) between the respective parts of AmB monomers. Contributions are labeled according to the numbering scheme in Fig. 1. (polyol chain, 1; polyene chain, 2; polar tail, 3; mycosamine head, 4).



**Supplementary Figure S4.** High-resolution visualisation of identified stable dimer structures (I-IV) and representative tetramer structures (p-a: parallel-antiparallel; a-a: antiparallel-antiparallel; p-p: parallel-parallel).