Finite size effect on hydrogen bond cooperativity in (Ala)$_n$ polypeptides: A DFT study using numeric atom-centered orbitals

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— An accurate representation of the energetic contribution $E_{\text{hb}}$ of hydrogen bonds to structure formation is paramount to understand the secondary structure stability of proteins, both qualitatively and quantitatively. However, $E_{\text{hb}}$ depends strongly on its environment, and even on the surrounding peptide conformation itself. For instance, a short $\alpha$-helical polypeptide (Ala)$_4$ can not be stabilized by its single hydrogen bond, whereas an infinite $\alpha$-helical chain (Ala)$_\infty$ is clearly energetically stable over a fully extended conformation. We here use all-electron density functional calculations in the PBE generalized gradient approximation by a recently developed, computationally efficient numeric atom-centered orbital based code$^1$ to investigate this H-bond cooperativity that is intrinsic to Alanine-based polypeptides (Ala)$_n$ ($n=1$-20,$\infty$). We compare finite and infinite prototypical helical conformations ($\alpha$, $\pi$, $3_{10}$) on equal footing, with both neutral and ionic termination for finite (Ala)$_n$ peptides. Moderately sized NAO basis sets allow to capture $E_{\text{hb}}$ with meV accuracy, revealing a clear jump in $E_{\text{hb}}$ (cooperativity) when two H-bonds first appear in line, followed by slower and more continuous increase of $E_{\text{hb}}$ towards $n \to \infty$.