SIDE CHAIN EFFECT ON IR SPECTRA OF HETEROGENEOUS PEPTIDE SEQUENCE. THEORETICAL INVESTIGATION OF A SERIES OF TRIPEPTIDES (A-X-A)

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IR, Raman and VCD studies of peptides and proteins are often focused on the amide I at $\sim$1650 cm^{-1} (mainly amide C=O stretch), but the lower energy amide II ($\sim$1550 cm $^{-1}$) and III ($\sim$1300 cm^{-1}) transitions (mixes of NH deformation and C-N stretch) also give conformationally sensitive IR and Raman bands, respectively. Conventional, theoretical models have focused on the amide functional group and have ignored the side chains, often representing them as Ala oligopeptides. We have studied the effect of the side chain on the spectra of a series of tripeptides AXA, (X=G, V, L, F, W, S, K, Y, N), which are capped at N- and C- termini to yield Ac-Ala-Xxx-Ala-NHMe. The geometry of the tripeptides was constrained (in terms of, ϕ, ψ torsional angles) to either α-helical, (-57, -47), 3_{10}-helical (-60, -30) or PPII-helical (-78, 149) conformations by fully optimizing all the coordinates except (ϕ, ψ, and ω which are fixed) at the DFT BPW91/6-31G* level of theory. The harmonic force field (FF), atomic polar tensor (APT) and atomic axial tensor (AAT) values were calculated at the same level for frequency and intensity (IR and VCD evaluation). Since the amide modes are mixed among the residues, ^{13}C=^{18}O labeling of the A-X-A amide group was used to simulate a shift of that amide I frequency down by between 40 to 60 cm^{-1} thereby resolving the contribution of such labeled residues from the rest of the amide groups (^{12}C=^{16}O). Comparison of these results for the AXA series showed distinct patterns of side chain impact on the diagonal force constants for the X residue. Transfer of these parameters onto larger peptides was used to simulate spectra for realistic sequence studied experimentally.