CONFORMATION-SPECIFIC IR AND UV SPECTROSCOPY OF THE AMINO ACID GLUTAMINE: AMIDE-STACKING AND HYDROGEN BONDING IN AN IMPORTANT RESIDUE IN NEURODEGENERATIVE DISEASES

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Glutamine plays an important role in several neurodegenerative diseases including Huntington’s disease (HD) and Alzheimer’s disease (AD). An intriguing aspect of the structure of glutamine is its incorporation of an amide group in its side chain, thereby opening up the possibility of forming amide-amide H-bonds between the peptide backbone and side chain. In this study the conformational preferences of two capped glutamines Z(carboxybenzyl)-Glutamine-X (X=OH, NHMe) are studied under jet-cooled conditions in the gas phase in order to unlock the intrinsic structural motifs that are favored by this flexible sidechain. Conformational assignments are made by comparing the hydride stretch (3100-3700 cm\(^{-1}\)) and amide I and II (1400-1800 cm\(^{-1}\)) resonant ion-dip infrared spectra with predictions from harmonic frequency calculations. Assigned structures will be compared to previously published results on both natural and unnatural residues. Particular emphasis will be placed on the comparison between glutamine and unconstrained \(\gamma\)-peptides due to the similar three-carbon spacing between backbone and side chain in glutamine to the backbone spacing in \(\gamma\)-peptides. The ability of the glutamine side-chain to form amide stacked conformations will be a main focus, along with the prevalence of extended backbone type structures.\(^a\)