THE TOPOGRAPHY OF PORCINE RELAXIN:

LOCATION OF THE TRYPTOPHAN RESIDUES

R. James⁺, H. D. Niall* and R. A. Bradshaw⁺

Howard Florey Institute, University of Melbourne,
Parkville, Victoria, Australia*

Department of Biological Chemistry, Washington
University School of Medicine
St. Louis, MO⁺

The amino acid sequence of porcine relaxin is distinctly similar to that of insulin, particularly in regard to the placement of the cystine residues, suggesting the likelihood of three-dimensional homology as well. Two computer-modeling studies have produced structures consistent with this possibility. While the overall correctness of these predictions can only be adequately tested by x-ray crystallographic analyses, solution methods can determine if the placement of certain side chains is compatible. By use of charge transfer titrations, the solvent availability of the two tryptophan residues located in the B chain has been examined. N-Methylnicotinamide chloride forms weak complexes with indole moieties that are readily detected by visible absorption measurements. Such reactions occur in proteins if the tryptophan residues are fully exposed which was found to be the case in relaxin. Furthermore, Trp B-18 was also fully available, by this criterion, when the Trp-Gly-Arg sequence was removed from the carboxyl terminus of the B chain by carboxypeptidase Y. These results clearly favor only one of the predicted orientations of Trp B-18 and suggest an altered position of the carboxyl terminal region of the B chain than that previously proposed. (RAB was a Josiah Macy Jr. Foundation Faculty Scholar at the HFI during the tenure of these studies).