proportions, with a standard deviation per residue of less than 5%.

Amino acids were also released quantitatively from bradykinin and [5-valine]-angiotensin II amide.

Incubations of two D-residue analogues of [5-valine]-angiotensin II amide ([6-D-histidine]- and [2-D-arginine]-angiotensin II amide) showed that bonds adjacent to D-amino acid residues were not cleaved.

Enzyme digestion was applied to Synacthen that had been partially racemized by alkali treatment (Lee & Buettner-Janusch, 1963). The results indicated where extensive racemization had probably occurred.

Incubation of performic acid-oxidized ribonuclease showed that aspartic acid and glutamic acid could be detected separately from asparagine and glutamine. Glutamine and methionine sulphone were not released quantitatively, and the amounts of these amino acids did not increase when the time of incubation was increased.

Hydrolysis by bound peptidases might be a useful method both as a purity check for synthetic peptides and in the elucidation of peptide and protein amino acid sequences.

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Model of an Insulin Dimer and Tetramer, and a Hypothetical Proinsulin

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Revised X-ray co-ordinates for insulin giving data for both the main chain and R-group atoms have become available (Blundell *et al.* 1971), and from these a number of atomic models of the monomer have been built. However, as the molecule crystallizes as a hexamer composed of three identical dimer pairs, I have constructed a Biobits model (Smith & Smith, 1970; Smith, Smith & Roberts, 1970) illustrating various points that will not be seen from the atomic monomer model.

First, a complete insulin dimer showing both α - and β -chains together with all R groups was constructed. Secondly, a single-backbone-only mono-

mer was built on each side of the complete dimer, thus enabling a tetramer to be examined from all sides. The two zinc atoms are included so that a complete idea of the hexamer can be visualized.

The model is extremely lightweight and stable so that it can be turned and examined from all directions. Possible peptide chain interactions can be considered as well as R-group interactions and, because each R group is represented by a single bit, such groups can be readily inserted or removed without disturbing the basic molecular structure. It is also possible to insert the proinsulin intermediate peptide and to hypothesize on the three-dimensional structure of this molecule, on the different immunological and other observed reactions between the two etc.

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Antimicrobial Proteins in Bovine Neutrophils

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Milk of cows with mild mastitis has greater antimicrobial activity than has normal milk (Derbyshire, 1964). The phagocytic activity of the cellular factor has been described (Elek, 1959), but there has been less definition of the antimicrobial humoral factors in mastitis milk. One of the humoral factors described is a basic protein fraction with antimicrobial activity isolated from the cells in bulk milk samples (Hibbitt, Brownlie & Cole, 1971). It was stable to heating at 70°C for 30 min. The present work indicates that an acid-extractable fraction is obtainable from the cells of mastitis milk, consisting of 95–99% neutrophils, with activity against streptococci and both coagulase-positive and coagulase-negative staphylococci.

A sterile mild mastitis was induced in the cow by infusion of 1 μ g of an *Escherichia coli* lipopolysaccharide endotoxin through the teat canal and the milk was collected 16h later. Cells were removed from the milk by centrifuging at 400g_{av}. and washed three times in a cold iso-osmotic saline. The cells were homogenized in ice-cold 0.2M-hydrochloric acid in a Waring Blendor at full speed for 2min, then centrifuged at 20 000g_{av}. for 10min. The clear supernatant was dialysed against five changes of double-glass-distilled water, and any