Angiogenin

Josette Badet

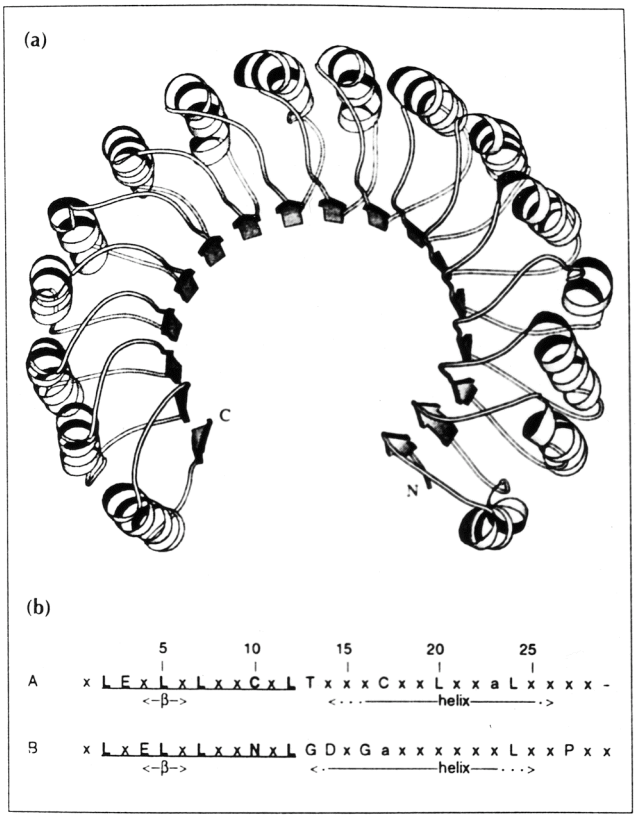

Figure 3. Structure of ribonuclease inhibitor (RI). (a) Ribbon diagram of the structure of porcine RI generated using the program MOLSCRIPT. (b) Consensus sequences and secondary structure of leucine-rich repeats (LRRs) of porcine RI. The sequence of RI was aligned so that two types of repeats (A and B) alternate in the sequence. One-letter amino acid code is used. 'x' indicates any amino acid and 'a' denotes an aliphatic amino acid. The part of the repeat that is strongly conserved in all LLR proteins is underlined, and the conserved residues are shown in bold. Below the sequence, solid lines mark the core region of ß-sheet and helix; dots denote extensions of helix in different repeats. Reproduced with permission from [54].