The structure of bovine seminal ribonuclease (RNAse BS) and bovine pancreatic enzyme (RNAse A), has been refined to 2 Å resolution to a final R factor of 0.205 based on 14300 reflections with I > σ(I) (~ 80 % of the total). The final model includes all the non-hydrogen atoms of the two subunits, related by a local twofold axis, 6 sulphate anions and 135 water molecules. The outstanding features of the model are: a) the sixteen-membered cycle linking the two subunits and involving residues Cys30 and Cys31 of the two chains; b) the two active sites formed by residues belonging to different chains. The twofold symmetry is well preserved throughout the structure, but marked deviations are observed for the hinge peptide (residues 15-21) and the external loop (65-72). In the last case the differences are propagated to the two active sites: in one subunit the aspartate 121 is hydrogen bonded to His 119, whereas in the other subunit it is bonded to the main chain NH group of lysine 66. In both subunits the side chain group of His 119 has been treated as a mixture of two different specific conformations. The structural features in the region of the active sites permitted us to implement the widely accepted mechanism of action of ribonucleases.