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Solution structure and membrane-binding property of the N-terminal tail domain of human Annexin I

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ANNEXINs are a family of ubiquitous proteins that bind to negatively charged phospholipids in a calcium-dependent manner, and are involved in many important cellular processes such as anti-inflammation, anti-coagulation, *etc.* Each annexin is composed of two parts, a major C-terminal core domain and a minor N-terminal tail domain. The similar properties of all annexins regarding Ca^{2+} and phospholipid seem to be due to the former that show highly conserved sequences and structures. Since the latter differ widely in length and sequence, it has been proposed that the structurally distinct N-terminal domain of each annexin may impart functional specificity. However, no structural evidence has been reported for whether the N-terminal tail of annexin I itself binds to membrane, despite many reports demonstrating its regulatory role in the membrane interaction properties. In this work, we report the conformational preferences of the partial N-terminal domain of annexin I at membrane-mimetic environments by using a peptide corresponding to residues 2 to 26 of human annexin I ($AnxI^{N26}$). The results of present report provide structural evidences for the membrane-binding properties of $AnxI^{N26}$, including the role of the hydrophobic cluster containing the unique tryptophan of annexin I. Additionally, the effect of Ca^{2+} on the membrane binding property of the peptide is investigated.