



Structural insight into an ankyrin-sensitive lipid-binding site of erythroid β -spectrin.

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It was recently shown that the region within β -spectrin responsible for interactions with ankyrin includes a lipid-binding site which displayed sensitivity to inhibition by ankyrin. We studied its structure by constructing a series of single and double spin-labeled β -spectrin-derived peptides and analyzing their spin-spin distances via electron paramagnetic resonance spectroscopy and the Fourier deconvolution method. The results indicate that the whole ankyrin-sensitive lipid-binding site of β -spectrin exhibits a helical conformation revealing a distinct 3_{10} -helix contribution at its N-terminus. The start of the helix was located five residues upstream along the sequence compared to the theoretical predictions. A model based on the obtained data provides direct evidence that the examined lipid-binding site is a highly amphipathic helix, which is correlated with the specific conformation of its N-terminal fragment

Słowa kluczowe

Site-directed spin labeling, electron paramagnetic resonance spectroscopy, β -spectrin, lipid-binding domain, helical structure

Adres publiczny

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