

Conformational Analysis in Solution of Protein Kinase C bII V5-1 peptide

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Abstract

One of protein kinase C (PKC) isozymes, PKC b binds to receptor for activated C kinase 1 (RACK1), and their complex is suggested to be translocated to melanosomes. The binding site of PKC b for RACK1 is considered one of its catalytic domains, V5 domain which consists of three motifs such as V5-1, V5-2, and V5-3. Among these, V5-1 region, extreme C-terminal residues of PKC b showed the highest RACK1 binding affinity. PKC b can be classified into PKC bI and PKC bII based on their different V5 domain. RACK1 binding affinity of PKC bII is five times greater than that of PKC bI. The structures of PKC bI, PKC bII, and RACK1 are not known. However, the conformational study on PKC bII V5-1 region showing high RACK1 binding selectivity may help us understanding interaction between RACK1 and PKC bII.

Reference

1. W. S. Liu, C. A. Heckman, The sevenfold way of PKC regulation, (1998) *Cell. Signal.* 10, 529-542.