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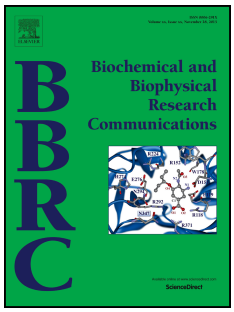

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Identification of Cep169-interacting proteins and the *in vivo* modification sites of Cep169 via proteomic analysis

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Abstract

Cep169 is a microtubule plus-end tracking and centrosomal protein that interacts with CDK5RAP2. Cep169 is known to regulate microtubule dynamics and stability; however, its other cellular functions remain largely elusive. In this study, we identified novel Cep169-interacting proteins from HeLa cell extracts. Proteomic analysis via LC-MS/MS helped to identify approximately 400 novel Cep169-interacting proteins, including centrosomal proteins, cilium proteins, microtubule-associating proteins, and several E3 ubiquitin ligases. In addition, we identified *in vivo* posttranslational modification sites of Cep169, namely, 27 phosphorylation sites, five methylation sites, and four ubiquitination sites. Of these, 14 phosphorylated residues corresponding to the consensus Cdk phosphorylation sites may be required for Cdk1-mediated dissociation of Cep169 from the centrosome during mitosis and Cdk regulation during the G1/S phase. Furthermore, siRNA-induced Cep169 depletion was found to inhibit the growth of RPE1 cells. Our findings suggest that Cep169 regulates cell growth by interacting with multiple proteins.

Keyword

Cep169, Mass spectrometry analysis, Cdk, Centrosome, Modification