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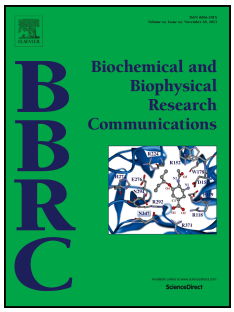

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Coatomer subunit beta 2 (COPB2), identified by label-free quantitative proteomics, regulates cell proliferation and apoptosis in human prostate carcinoma cells

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Abstract

Label-free quantitative proteomics has broad applications in the identification of differentially expressed proteins. Here, we applied this method to identify differentially expressed proteins (such as coatomer subunit beta 2 [COPB2]) and evaluated the functions and molecular mechanisms of these proteins in prostate cancer (PCA) cell proliferation. Proteins extracted from surgically resected PCA tissues and adjacent tissues of 3 patients were analyzed by label-free quantitative proteomics. The target protein was confirmed by bioinformatics and GEO dataset analyses. To investigate the role of the target protein in PCA, we used lentivirus-mediated small-interfering RNA (siRNA) to knockdown protein expression in the prostate carcinoma cell line, CWR22RV1 cells and assessed gene and protein expression by reverse transcription quantitative polymerase chain reaction and western blotting. CCK8 and colony formation assays were conducted to evaluate cell proliferation. Cell cycle distributions and apoptosis were assayed by flow cytometry. We selected the differentiation-related protein COPB2 as our target protein based on the results of label-free quantitative proteomics. High expression of COPB2 was found in PCA tissue and was related to poor overall survival based on a public dataset. Cell