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## 5 - 51 The Function of RPS27a in Apoptosis of Non-small Cell Lung Carcinoma Cells Induced by Carbon Ion Radiation\*

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Lung adenocarcinoma (LUAD) is the main histological subtype of lung cancer, and the 5-year overall survival rate of LUAD is less than 20%<sup>[1]</sup>. However, the mechanism of LUAD development is complex, and the effect of oncogenes on LUAD is still unknown. This study used the A549 cells of non-small cell lung carcinoma cells (NSCLC) as a model to address these questions. The present study revealed that ribosomal protein S27a (RPS27a) directly bound RPL11, and RPS27a knockdown enhanced the binding of RPL11 and MDM2, thereby inhibiting MDM2-mediated p53 ubiquitination and degradation in A549 cells.

The silver stained image of the binding proteins revealed a band at approximately 18 kDa (Fig. 1(a)). The band was further analyzed by MS, and a total of 133 proteins were identified in the IP protein sample. Among which 43 interactors were RPs (Fig. 1(b)). The combined degree of RPS27a was highest. 4 Gy carbon ion irradiation (CIR), a common experimental dose<sup>[2]</sup>, was used to induce apoptosis of A549 cells. Then, the increased apoptosis of A549 induced by CIR was observed and the decreased expression of RPS27a were time dependent. The correlation analysis suggested that the RPS27a level was related to the late apoptotic ratio after CIR. Therefore, A549 cell apoptosis may be associated with decreased RPS27a expression, and we were able to induce apoptosis of A549 cells by decreasing RPS27a expression. The knockdown of RPS27a increased in MDM2 and p21 protein levels, G1-phase arrest and apoptosis of A549 cells. Therefore, RPS27a might be a potential target in the treatment of NSCLC.

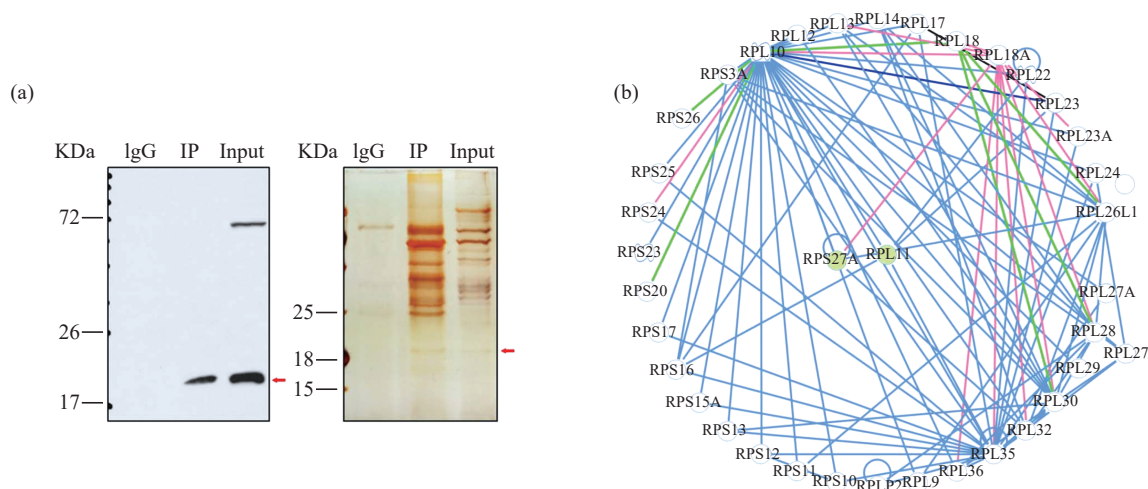


Fig. 1 (color online) Identification of RPs interacting with RPL11 in A549 cells. (a) The endogenous RPL11-interacting proteins were pulled down by anti-RPL11 antibody. The immunoprecipitates were separated by SDS-PAGE, then silver stained. The band (approximately 18 kDa) containing proteins strongly bound to RPL11 was digested with trypsin and analyzed with LC-MS/MS, (b) Interaction network of RPs with RPL11, on the basis of the STRING database.

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