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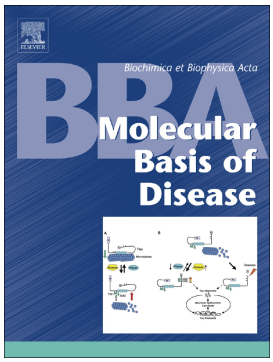

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Prediction of potential drivers connecting different dysfunctional levels in lung adenocarcinoma via a protein–protein interaction network

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