

# Reconstruction and analysis of the gene network of hepatocellular carcinoma under mechanical stress of the cell

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**Motivation and Aim:** Hepatocellular carcinoma is a leading cancer worldwide. Its incidence is increasing, and is closely related to advanced liver disease. Cirrhosis represents the greatest risk factor for this malignancy, and is the main indication for screening and surveillance. Due to the absence of symptoms in 60 % of patients, hepatocellular carcinoma is diagnosed late, cases – against the background of multiorgan metastasis. Despite advances in medical, locoregional and surgical therapies, hepatocellular carcinoma remains one of the most common causes of cancer-related death globally [1]. Alterations to the mechanical properties of the microenvironment are a hallmark of cancer. Elevated mechanical stresses exist in many solid tumors and elicit responses from cancer cells. Uncontrolled growth in confined environments gives rise to elevated solid compressive stress on cancer cells. Cancer cells in the tumor respond to elevated mechanical stresses, and these responses are important for cancer cell survival. Solid compressive stress alters cancer cell behaviors such as proliferation, invasion, and apoptosis. Mechanical stress in tissue cells should lead to apoptosis. However, this is not observed in tumor cells [2]. The aim of this work was to reconstruct and analyze the gene network of hepatocellular carcinoma under mechanical stress of the cell and to build frame models of the regulation of apoptosis by hepatocellular carcinoma.

**Methods and Algorithms:** The gene networks were built using the ANDSystem system for automatic reconstruction of associative gene networks. The databases of Gene Ontology were used to search for genes associated with cell response to mechanical stress and ClinVar to search for single nucleotide polymorphisms associated with hepatocellular carcinoma.

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## References

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