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Computational model of siRNA regulation in p53 signaling pathway

p53 is a transcriptional factor kept in healthy cells at low level under the control of its inhibitor Mdm2, but activated (phosphorylated) in response to DNA damage. When activated and present in high concentration, it induces transcription of numerous genes involved in cell cycle arrest and DNA repair. If the last fails, p53 final job is to trigger the cell-death program called apoptosis. It is known that almost all cancers have some irregularities in the p53 module. Especially breast cancer cells MCF-7 which have blocked PTEN gene resulting in the inability to trigger apoptosis. In this work we show the possibility of using proper siRNA to omit this weakness and by that to push cancer cells into the apoptotic state.