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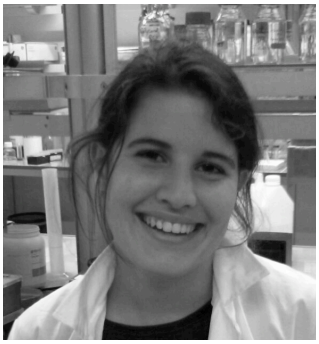
Creating a reporter system for the analysis of p53 mutations



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Cancer is responsible for more than 15% of human deaths. Activation of oncogenes and inactivation of tumor suppressor genes contribute to malignant transformation of cells. Mutations of the tumor suppressor gene TP53 are observed in about 50% of human cancers. Therefore, it is of high interest to understand functional consequences of TP53 mutations in order to develop biological tests that allow targeting mutant p53 for oncotherapy.
In this study we use CRISPR-Cas9, the latest genome editing technique, for introducing specific TP53 mutations into the genome of a non-tumoral fibroblast cell line. We analyze the effects of p53 mutations at the transcriptomic and proteomic level. These analyses will help identifying gene- and pathway-specific effects of distinct p53 mutations.
These results will be used for establishing cell lines that allow high throughput screening, in order to discover new chemical compounds that are able to restore crucial functions of mutant p53 proteins.

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