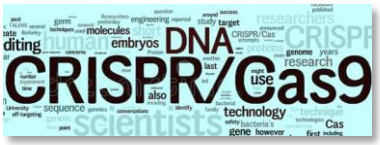
NEWS:



Untargeted nanoLC-MS/MS proteomics is a good tool to check your CRISPR-Cas9 modifications.

As the most recent new technology, CRISPR-Cas9 has revolutionized conventional genetic engineering methods and unprecedentedly facilitated cell engineering. Like any new impacting technology, CRISPR-Cas9 induced fears about the life management and controversial debates. (see Unexpected mutations after CRISPR–Cas9 editing *in vivo* by Schaefer KA and all. Nature Methods 14, 547–548 (2017) - Retracted online 30 March 2018)

So it seems necessary and prudent to check what are the consequences on the cell/organ metabolism as widely as possible and to extend controls to be sure that the observed mutations generated by the tool are those expected.

Quantitative untargeted LC-MS/MS proteomics is a good tool to check the induced modifications as it is focused **at the functional level** and **as it is untargeted, so hypothesis free**. With this method, you can access to operational impacted pathways and detect unexpected effects. Numerous applications have been described at the protein level (2) (3) and even now at the Post Pranslational Modifications level.(1)

(1)Degradation of PHLPP2 by KCTD17, via a Glucagon-Dependent Pathway, Promotes Hepatic Steatosis. Kim K and all., Gastroenterology. 2017 Dec;153(6):1568-1580.e10. doi: 10.1053/j.gastro.2017.08.039. Epub 2017 Aug 30.
https://www.ncbi.nlm.nih.gov/pubmed/28859855

(2)Establishment of a CRISPR/Cas9-Mediated Cysltr1 Knockout Mouse Model and iTRAQ-Based Proteomic Analysis. Mao J and all. Proteomics Clin Appl. 2018 Jan 26. doi: 10.1002/prca.201700087.
https://www.ncbi.nlm.nih.gov/pubmed/29377627

(3)CRISPR/Cas9-mediated genomic editing of Cluap1/IFT38 reveals a new role in actin arrangement. Beyer T and all. Mol Cell Proteomics. 2018 Apr 3. pii: mcp.RA117.000487. doi: 10.1074/mcp.RA117.000487.
https://www.ncbi.nlm.nih.gov/pubmed/29615496

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