

# Target protein quantification

## exogenous gene

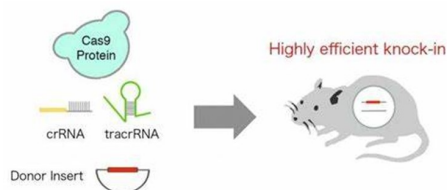
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#### Technical details

The protein quantification technology based on mass spectrometry typically involves enzymatic digestion of samples into peptide for analysis. After digesting either purified standard proteins or samples with high abundance of target proteins (such as cells/tissues), specific peptides of the target protein are identified for qualitative and quantitative analysis. During method development, optimization of parameters for liquid chromatography and mass spectrometry is necessary. Additionally, stability and matrix effects of specific peptide need to be evaluated. After estimating the approximate concentration of the target protein, a calibration curve is constructed by adding target peptide segments to blank matrices, enabling absolute quantification of the target protein in the samples.

#### Application

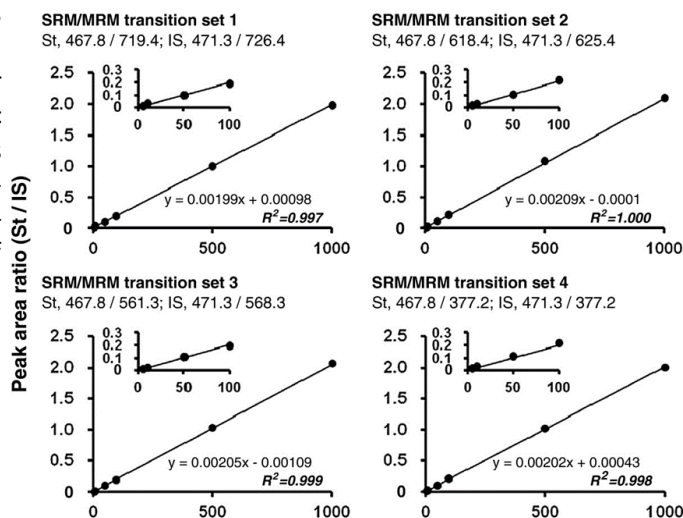
##### 1. Quantification of protein expressed by exogenous gene



Due to some research needs, exogenous gene of interest may be knocked in or some endogenous genes may be knocked out in mouse or other model species. Whether the target gene is

knocked out/knocked in successfully or not can be observed at the protein level. In addition, after mRNA vaccines are administered in vivo, it is often necessary to quantify their expression products, so as to respond to their transformation efficiency in vivo as well as survival time, and for some gene editing drugs, the difference between the wild type and the mutant type of the target protein may only be a few amino acids, which cannot be effectively differentiated by western blot, and our mass spectrometry

platform allows for highly specific characterization as well as quantification of the expression products of the target gene.



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