Recent developments in "omics" technologies have revolutionized how biomedical research is conducted. These approaches enable unbiased analyses of biological samples and can be used to generate novel hypotheses. Proteins are the molecular effectors how biomedical research is conducted. These approaches enable to identify RNA binding proteins and determined that arginine-rich peptides lead to a generalised differential regulation of these variants. With the help of systematic mapping of substrates of DNA replication group, we used targeted proteomics to accurately identify and quantify different Kras isoforms, which provide valuable information to understand the interplay between these variants. With the help of systematic mapping of substrates of DNA replication group, we used targeted proteomics to accurately identify and quantify different Kras isoforms, which provide valuable information to understand the interplay between these variants. With the help of systematic mapping of substrates of DNA replication group, we used targeted proteomics to accurately identify and quantify different Kras isoforms, which provide valuable information to understand the interplay between these variants. With the help of systematic mapping of substrates of DNA replication group, we used targeted proteomics to accurately identify and quantify different Kras isoforms, which provide valuable information to understand the interplay between these variants. With the help of systematic mapping of substrates of DNA replication group, we used targeted proteomics to accurately identify and quantify different Kras isoforms, which provide valuable information to understand the interplay between these variants. With the help of systematic mapping of substrates of DNA replication group, we used targeted proteomics to accurately identify and quantify different Kras isoforms, which provide valuable information to understand the interplay between these variants. With the help of systematic mapping of substrates of DNA replication group, we used targeted proteomics to accurately identify and quantify different Kras isoforms, which provide valuable information to understand the interplay between these variants. With the help of systematic mapping of substrates of DNA replication group, we used targeted proteomics to accurately identify and quantify different Kras isoforms, which provide valuable information to understand the interplay between these variants. With the help of systematic mapping of substrates of DNA replication group, we used targeted proteomics to accurately identify and quantify different Kras isoforms, which provide valuable information to understand the interplay between these variants.