

# Alt-R™ CRISPR-Cas9 sgRNAs

Chemically synthesized and modified single guide RNAs for outstanding CRISPR performance and quality



**sgRNAs in days, not weeks,**  
with fast synthesis time (3–5  
business days\*)



**Guaranteed performance**  
with predesigned sgRNAs



**Custom features to meet  
your needs,** such as a  
variety of deliverable sizes,  
chemical modifications, and  
purification



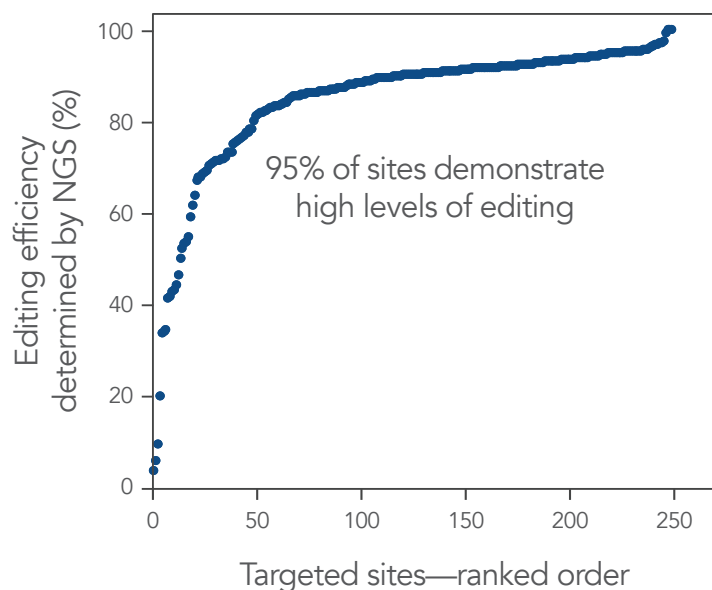
**Trusted quality and  
manufacturing,** delivering  
optimized synthesis and  
purification to mitigate oligo  
cross contamination risk

\* 3–5 business days for most standard requests. Custom requests may require additional manufacturing time.

Alt-R CRISPR-Cas9 single guide RNAs (sgRNAs) comprise both crRNA and tracrRNA sequences within a single molecule. Outstanding editing performance is observed at >95% of sites in Jurkat cells (Figure 1). Alt-R Cas9 sgRNAs are ideal for challenging conditions such as high nuclease environments or when co-delivered with Cas9 mRNA. They contain chemical modifications that provide increased stability, potency, and resistance against nuclease activity (Figure 2).

## CUSTOMIZABLE sgRNAs TO FIT EVERY PROJECT AND EVERY BUDGET

Available in a wide range of deliverable sizes, Alt-R Cas9 sgRNAs can be customized to suit small and large experiments. They are available in tube or plate format in a variety of scales from 2 nmol and up. Further options for custom chemical modifications, additional purification, and custom formulation provide unparalleled flexibility to meet your experimental needs.



**Figure 1. Alt-R CRISPR-Cas9 sgRNAs provide remarkable editing potency in Jurkat cells.** Ribonucleoprotein (RNP) complexes were formed with Alt-R S.p. WT Cas9 Nuclease V3, combined with Alt-R Cas9 sgRNAs synthesized for 255 randomly selected Cas9 guide RNA sites across the human genome. RNP complexes (4  $\mu$ M) were delivered into Jurkat cells (human T lymphocyte-derived cancer cells) via a Nucleofector™ system (Lonza) in the presence of Alt-R Cas9 Electroporation Enhancer. Genome editing efficiencies were determined by target amplification followed by next generation sequencing on an Illumina instrument.

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