# 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 function** 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. High editing levels are 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**) [**1**].

## Customizable sgRNAs to fit every project and every budget

Available in a wide range of deliverable yields, 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 flexibility to meet your experimental needs.

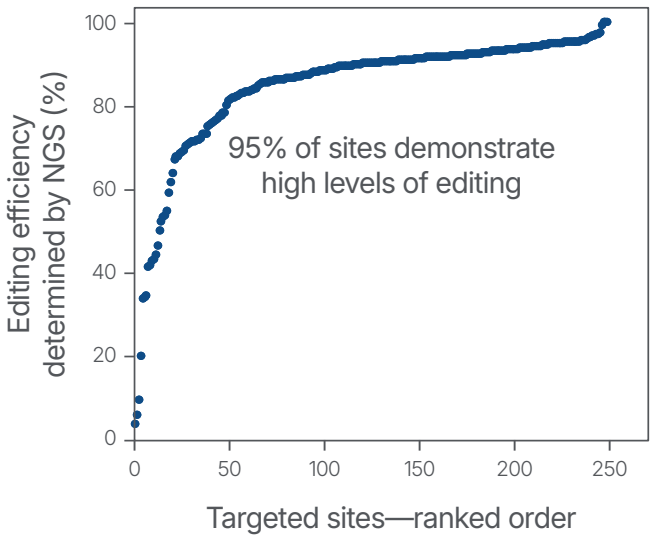
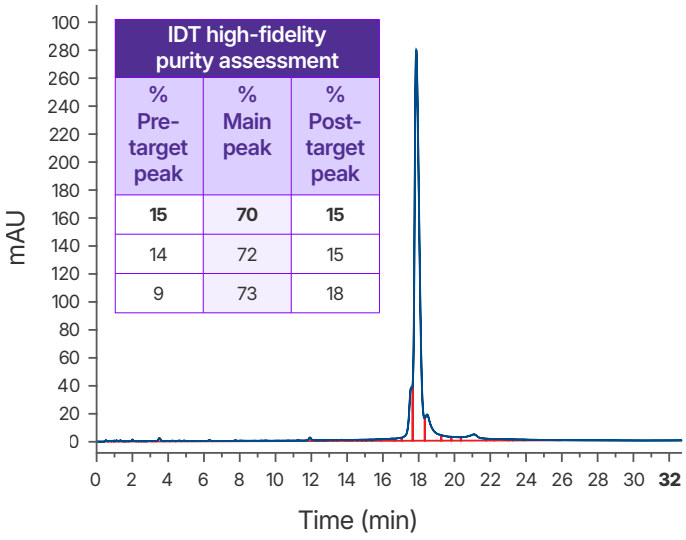


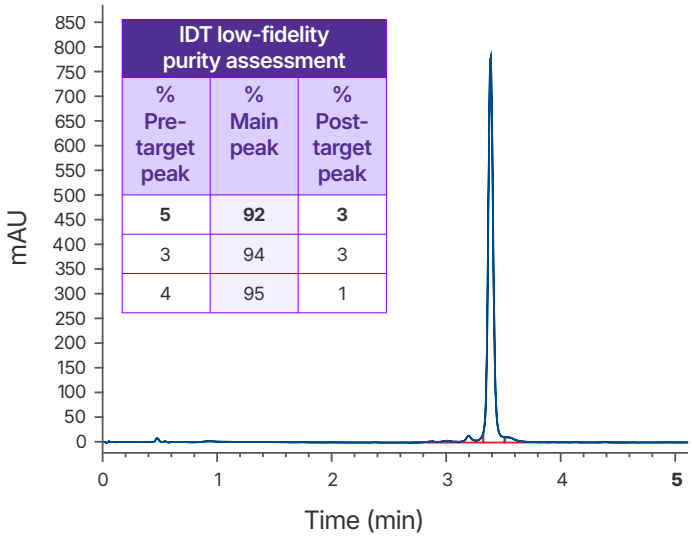

**Figure 1. Alt-R CRISPR-Cas9 sgRNAs result in high editing rates in Jurkat cells.** Ribonucleoprotein (RNP) complexes were formed with Alt-R S.p. WT Cas9 Nuclease V3, combined with Alt-R Cas9 sgRNAs synthesized for 255 randomly selected Cas9 guide RNA sites (*n* = 1 per site) across the human genome. RNP complexes (4 µM) 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.

## Better QC for more accurate purity

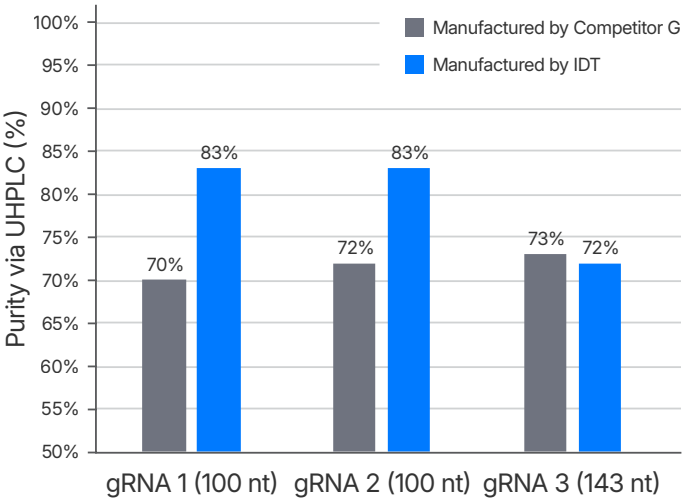
A1. **High-fidelity** purity assessment




A2. **Low-fidelity** purity assessment




B1. Purity comparison via IDT's high-fidelity UHPLC




B2. Average HPLC gRNA purity comparison

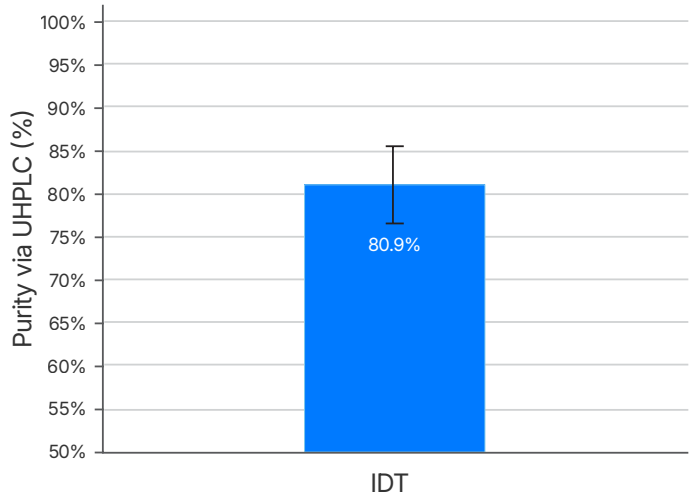



**Figure 2.IDT's gRNA UHPLC purity assessment method vs a leading competitor**. Left chromatogram (**A1**) represents purity of competitor G sgRNA using IDT's high-fidelity QC method. Right chromatogram (**A2**) is purity as reported by a low-fidelity QC method performed at IDT which does not allow enough time for sample separation and indicates artificially high purity. This low-fidelity method was developed to demonstrate the importance of a longer run time for purity accuracy. It was repeated for 3 guides ranging from 100–143 nt (one representative chromatogram shown). (**B1**) Average gRNA purity of three gRNAs of identical sequence from a competitor and IDT using IDT's **high-fidelity QC** to eliminate inflated purity estimates. (**B2**) Average purity of IDT HPLC gRNAs with a range of chemical modification patterns *n* = 102.

## Increased stability and efficiency with chemical modifications

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|---|---|
| **Available modifications*** | RNA, 2′O-Methyl, phosphorothioate bonds, DNA, 2′ Fluoro, Affinity Plus™ Locked Nucleic Acids |

* Not all modifications are available in combination and on all types of guide RNAs.

## For more information, visit **idtdna.com/CRISPR**

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