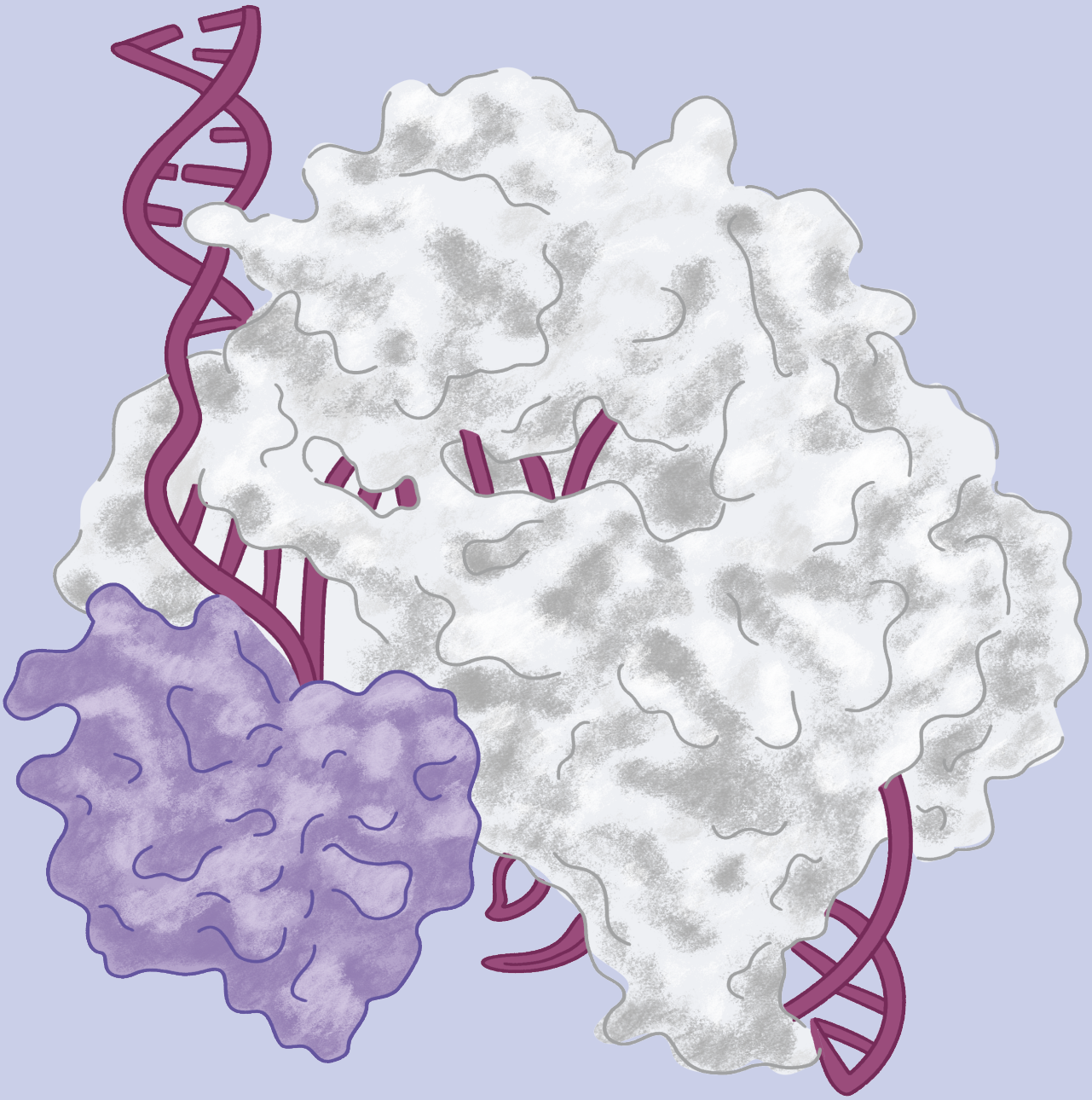
KACTUS

supra-ABE

A novel adenine base editor



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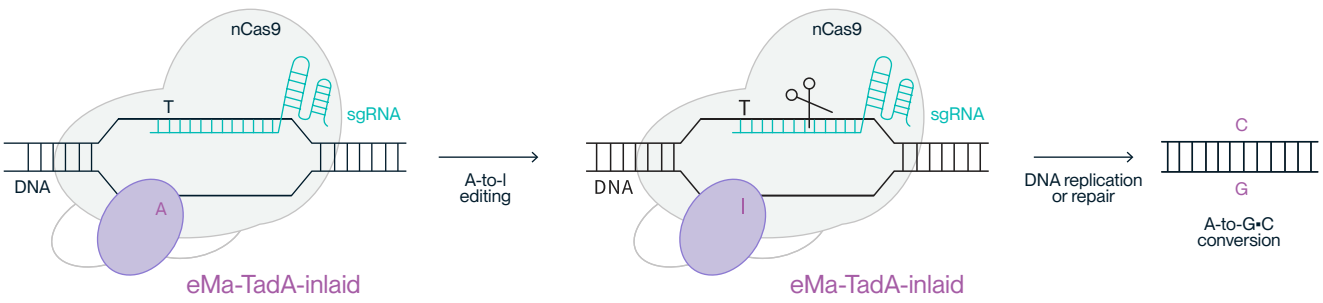
About supra-ABE Base Editor

supra-ABE is a novel adenine base editor consisting of a patented adenine deaminase eMa-TadA fused with Cas9 nickase (Cas9n), where eMa-TadA is chimerically embedded in Cas9n. The supra-ABE base editor features high editing activity, a broad effective editing window, and low off-target rates, making it flexible for applications in cellular and gene therapy.

Developed exclusively by Lumiere Therapeutics and licensed for commercial development to KACTUS, supra-ABE has been optimized using KACTUS' proprietary SAMS™ (Structure-Aided Multiplex Screening) technology platform. Through advanced optimization of expression, purification, and formulation, KACTUS delivers a DNA adenine base editor with high purity, exceptional stability, superior editing efficiency, and minimal off-target activity.

Mechanism of Action

The engineered adenine deaminase eMa-TadA in supra-ABE catalyzes the deamination of adenine (A) in DNA, converting it to inosine (I), During DNA replication, inosine is recognized as guanine (G), enabling precise A-to-G substitution within editing window positions 4–14, This process operates without requiring donor templates or inducing double-strand DNA breaks.



Advantages

Proprietary Patent: A commercialized adenine base editor with independent intellectual property rights.

High Editing Efficiency: supra-ABE can efficiently screen gene targets, enabling effective editing of more gene loci.

Broad Editing Window: Compared to the classic ABE8e, the chimeric supra-ABE has a wider editing window (positions 4-14).

More Flexible Target Selection: Suitable for a wider range of application scenarios, including gene therapy, cell therapy, epigenetic suppression, and many other application targets. It can efficiently edit the start codon ATG and intron/exon splicing sites GU-AG, achieving efficient gene knockout and exon skipping.

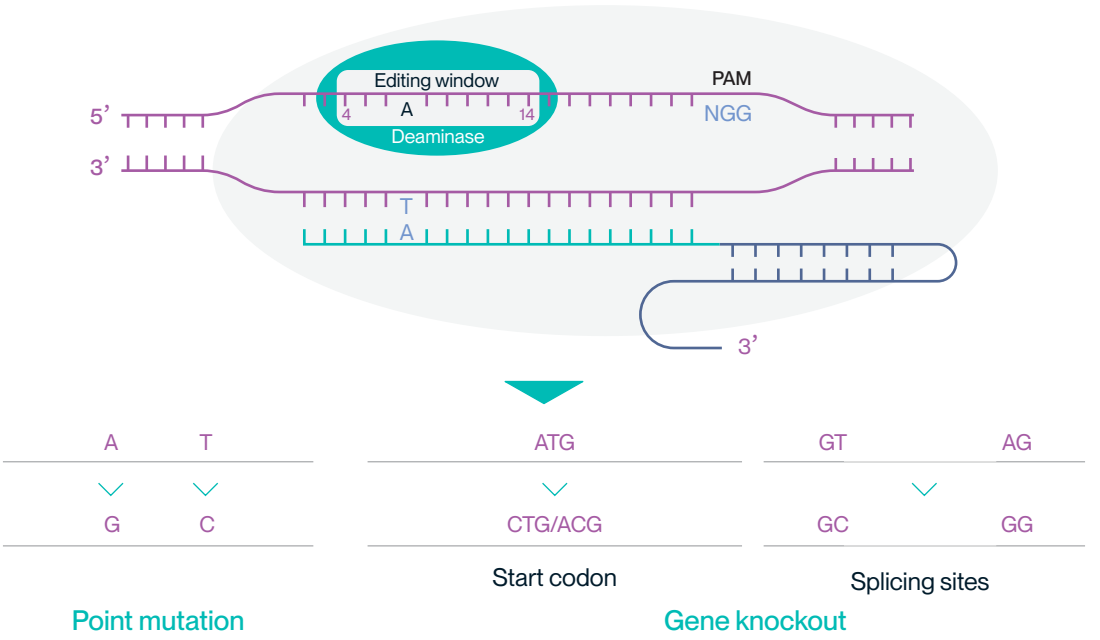
Applications

Gene Knockout

Gene knockout is achieved by mutating the start codon ATG or altering the canonical splice sites GT-AG through A-to-G or T-to-C substitutions, thereby disrupting gene function.

Gene Correction

Precise repair of pathogenic single-base mutations (A-to-G or T-to-C substitutions at specific adenine or thymine sites) enables restoration of normal gene function through single-base editing.



Greater than 95% Purity

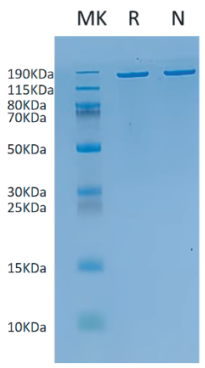


Figure. 1 Bis-Tris PAGE analysis confirms supra-ABE purity exceeding 95.0%

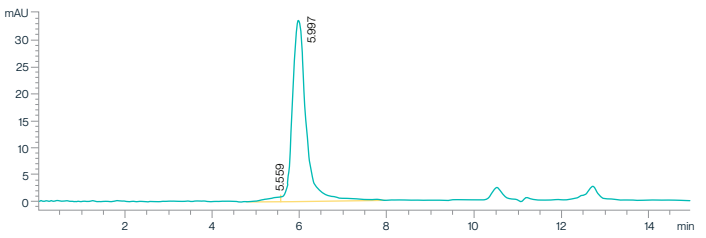


Figure 2. SEC-HPLC analysis confirms supra-ABE purity exceeding 95.0%

High Base Editing Efficiency

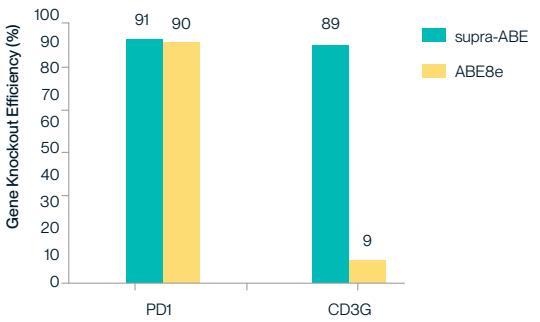


Figure 3. Sanger sequencing and EditR analysis demonstrate that supra-ABE efficiently mediates A-to-G conversion in the start codon (ATG) of PD1 and CD3G genes, disrupting translation initiation and achieving approximately 90% knockout efficiency.

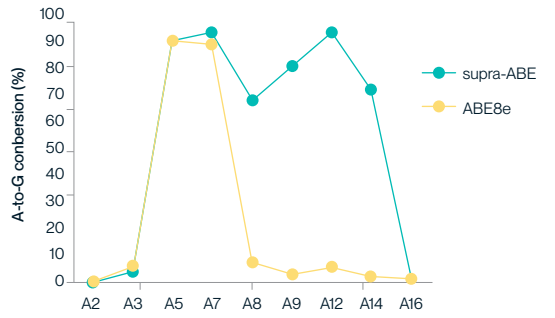


Figure 4. Sanger sequencing and EditR analysis results show that supra-ABE can convert A to G within the editing window, with varying editing efficiencies for adenine (A) bases at different positions—the highest editing efficiency exceeds 90%. Additionally, the editing window of supra-ABE is wider than that of ABE8e.

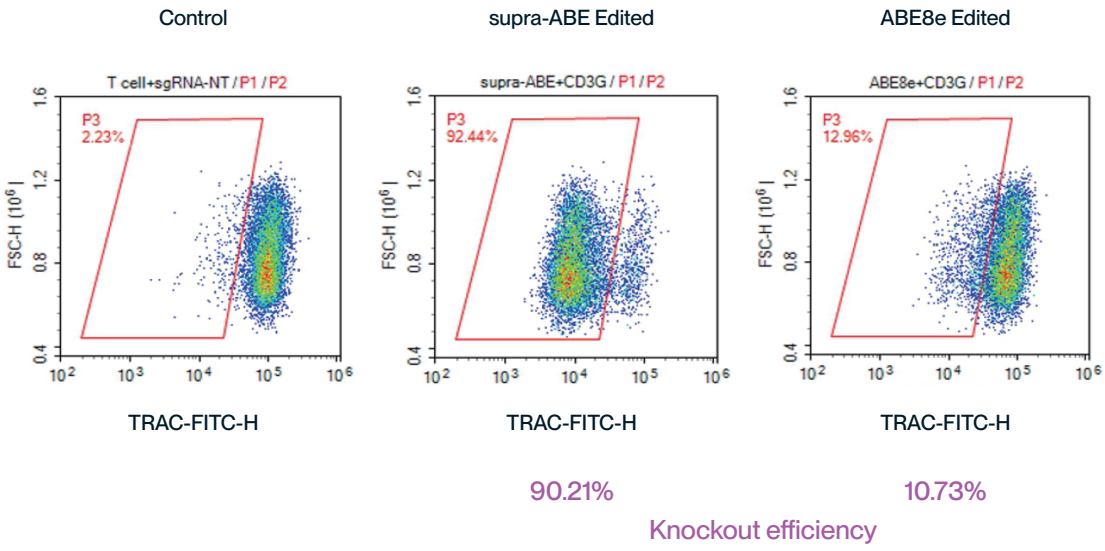


Figure 5. FACS analysis demonstrated that supra-ABE efficiently knocked out the CD3G protein, achieving a knockout efficiency of 90.21%, whereas ABE8e exhibited no editing activity within the editing range at this site.

Quality Specifications

Item	Acceptance Criteria
Concentration	9.0-11.0mg/mL
Purity (Bis-Tris PAGE)	≥ 80.0%
Purity (SEC-HPLC)	≥ 80.0%
Endotoxin	≤ 10.0EU/mg

Ordering Information

Product Name: supra-ABE

Catalog No. CAS-EE145

Available Sizes: 100UG / 1MG

To request a quote, please contact us at support@kactusbio.us

Learn More