

# Base Editing

## Pin-point™ base editing CBE and ABE reagents

Revvity's Pin-point base editing platform offers a unique and powerful approach for safe and efficient complex genetic engineering. Available in both Cytosine Base Editor (CBE) and Adenine Base Editor (ABE) formats for research use, with flexible licensing options for subsequent therapeutic development.

### SINGLE NUCLEOTIDE CHANGE

- Correct disease SNP mutation
- Disrupt gene enhancer or promoter regions

C>T } CBE  
 G>A }  
 A>G } ABE  
 T>C }

### GENE KNOCKOUT

Stop codon introduction  
(Only possible with CBE)

CAA (Gln) → TAA (stop)  
 CAG (Gln) → TAG (stop)  
 CGA (Arg) → TGA (stop)  
 TGG (Trp) → TAG (stop)  
 TGG (Trp) → TGA (stop)  
 TGG (Trp) → TAA (stop)

Splice donor (SD) or  
splice acceptor (SA) mutation  
(ABE or CBE)

SD SA  
 exon GT intron AG exon  
 CA TC

## Pin-point base editing CBE and ABE reagents enable a wide range of applications

	ABE	CBE
mRNA and validated sgRNA controls available off-the-shelf as inventoried solutions	X	X
Achieve gene knockout through disrupting splice donor and splice acceptor sites	X	X
Achieve gene knockout through introduction of premature stop codons		X
Precise and flexible deaminase options available for optimized use cases	X	
Custom sgRNAs available	X	X
Custom sgRNA design tool available for designing gene KO guides	X	X
Licenses for therapeutic development available	X	X

Example of published research applications using Pin-point base editing reagents

Allogeneic CAR-T cell generation from simultaneous gene knockin and multiplex knockout  
(Porreca et al., Mol. Ther., 2024), <https://pubmed.ncbi.nlm.nih.gov/38937969/>

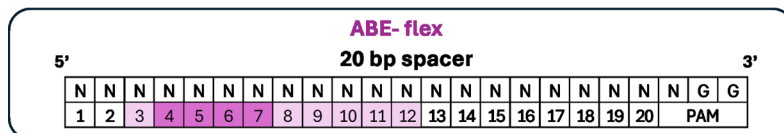
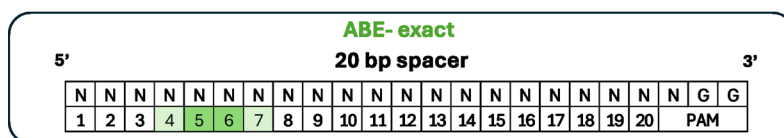
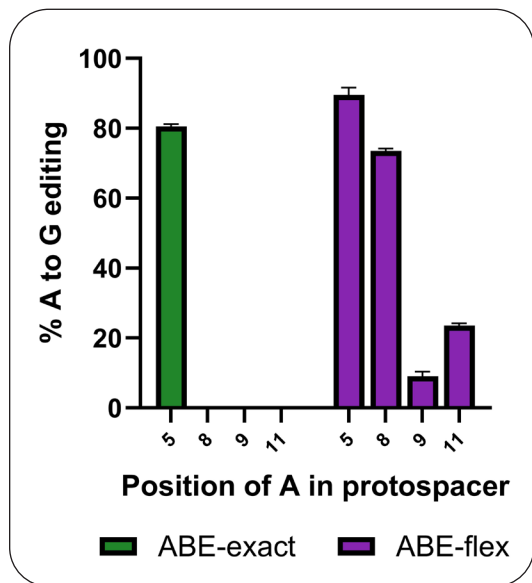
Efficient multiplex base editing in iPSCs with minimal p53 activation and low DNA Damage  
(Blassberg et al., bioRxiv, 2025), <https://www.biorxiv.org/content/10.1101/2025.06.05.656583v1>

## Multiple formats of mRNA and sgRNA solutions are available to empower your research

	CBE	ABE
Nickase ( <i>unmod or 5moU-modified mRNAs</i> )	CBE nCas9	ABE nCas9
Deaminase ( <i>unmod or 5moU-modified mRNAs</i> )	CBE rAPOBEC deaminase	ABE-exact and ABE-flex deaminases
sgRNAs + analysis primers	CBE CD52	ABE CD52
	CBE PDCD1	ABE PDCD1
	CBE TRAC	ABE TRAC
	CBE Site2	ABE Site2
	CBE CD58	ABE CD58
	CBE CIITA	ABE HBG1/2
	CBE HBG1/2	ABE BCL11a
	CBE BCL11a	
CBE PCSK9		
Custom sgRNA ( <i>Standard purification or HPLC</i> )	<a href="https://horizondiscovery.com/en/ordering-and-calculation-tools/pin-point-base-editing-design-tool">Use our custom sgRNA design tool to target your gene of interest! horizondiscovery.com/en/ordering-and-calculation-tools/pin-point-base-editing-design-tool</a>	

The Pin-point base editing mRNAs are provided in both unmodified and 5moU-modified formats to enable optimal use in your cell type of interest. The Pin-point synthetic sgRNA validated controls include gene or locus specific controls validated for assessment of base editing and phenotypic protein knockout where applicable. These include a set of well-defined targets associated with CAR-T therapies, cardiovascular disease,  $\beta$ -thalassemia, or loci characterized in the literature for evaluation of base editors.

**New!** The enzymes to match your editing needs: **Exact** or **Flexible** editing using **ABE-exact** or **ABE-flex** deaminases designed using Profluent's frontier AI models.



ABE-exact and ABE-flex deaminases are designed using Profluent's frontier AI models, and have been biologically validated to deliver enhanced base editing with distinct editing profiles tailored to your experimental needs. Use ABE-exact for precise, single-base edits within a defined editing window, or ABE-flex to access target bases located further from the nearest PAM.

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