



GenScript

OmniGuide RNA Design Tool Protocol

Enabling Easy & Precise Design

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Please send an Email to crispr@genscript.com for additional support

Applications & Advantages – OmniGuide RNA Design Tool

What is OmniGuide RNA design tool?

- Design gRNA sequences for CRISPR knockout experiments, provide gRNA parameters, and enable downstream OmniGuide RNA ordering

Resources > Bioinformatics Tools

EasyEdit sgRNA Now Starting at Only \$79/2nmol! User Guide

Design high-performance CRISPR guide RNAs using the most up-to-date design algorithm, for effective gene editing. Select Gene / Design / Order

Nuclease: SpCas9

Target Species: Homo sapiens (GRCh38.p13)

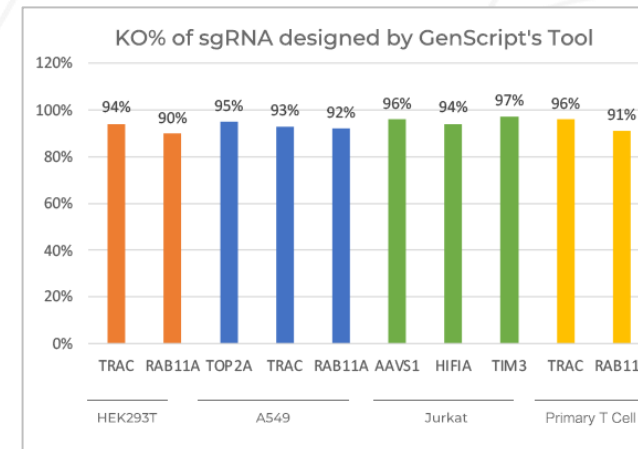
Number of gRNAs Per Gene: 6

Input Format: Gene Symbol

Submit

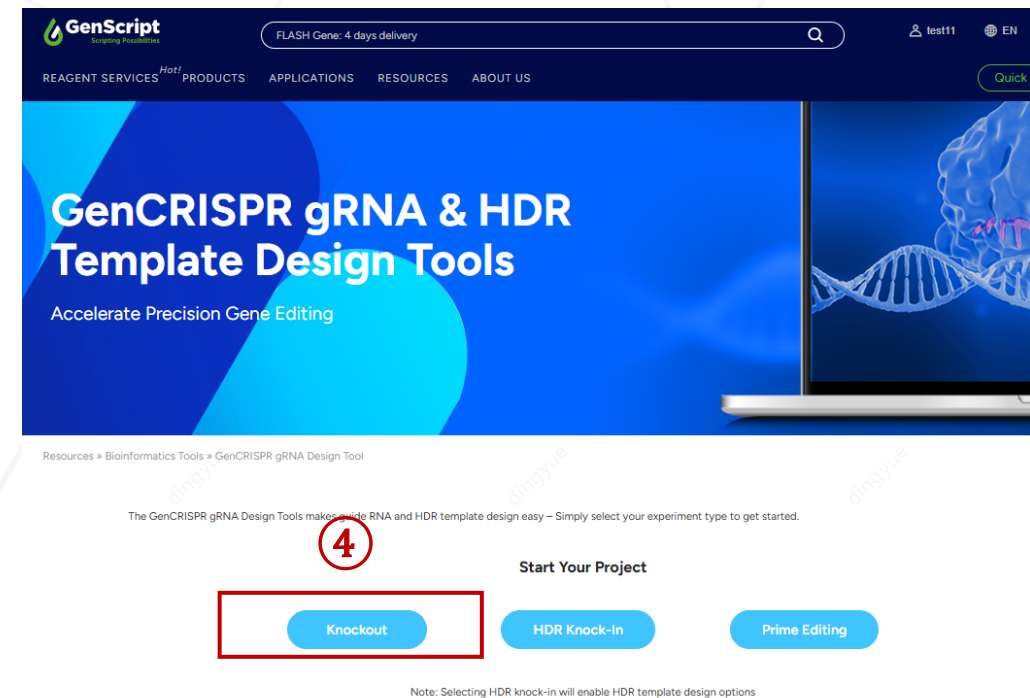
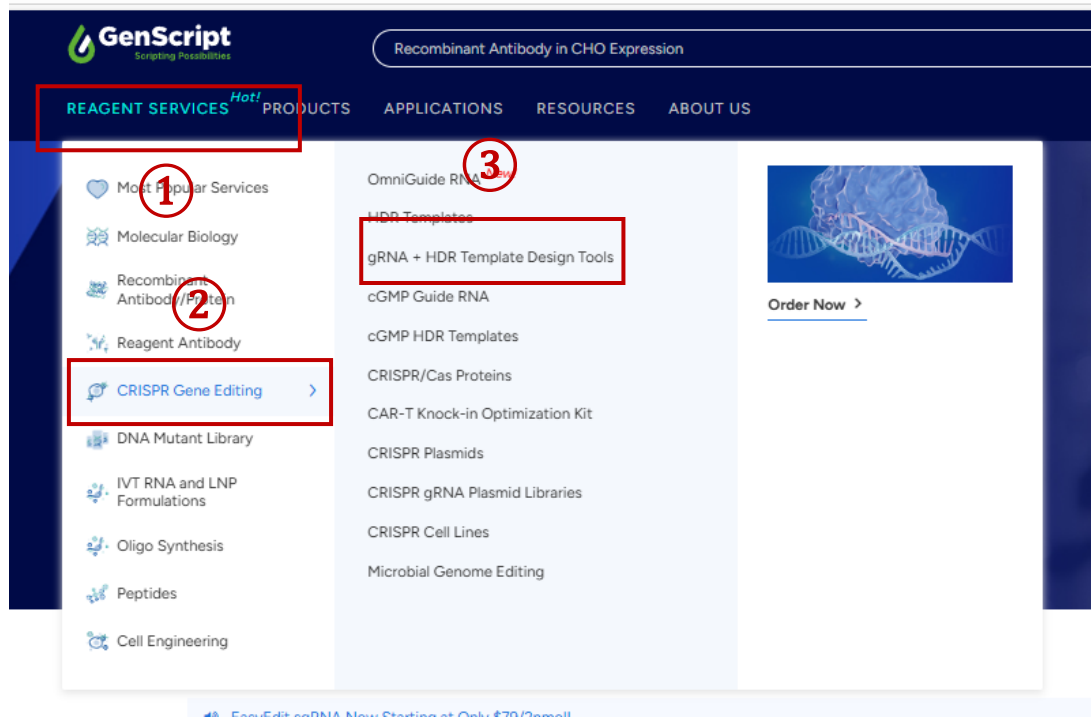
Advantages of OmniGuide RNA design tool

1. **Comprehensive applications:** Support 14 species, Cas9, Cas12a base editing, and prime editing
2. **More precise design:** updated on-target and off-target scores
3. **Enhance editing efficiency:**
 - Designs target early exons to avoid truncated functional proteins
 - Higher transcripts coverage
 - Ideal GC% for gRNA
4. **Validated efficiency:** Indel% up to 97% validated by experiments



Where can we find OmniGuide RNA Design Tool?

1. Visit the address: <https://www.genscript.com/tools/gRNA-design-tool>
2. Find the tool in [GenScript website](#):



Cas9 / Cas12 Design Processes

Nuclease: SpCas9
Target Species: Homo sapiens (GRCh38.p13)
Number of gRNAs Per Gene: 6
Input Format: Gene Symbol (selected) ADAR
Submit

Nuclease: SpCas9
Target Species: Homo sapiens (GRCh38.p13)
Number of gRNAs Per Gene: 6
Input Format: Specific Sequence (selected)
Format: Enter Sequence
Specific Sequence: Enter up to 10 Specific Sequence. The number of bases in each sequence should be between 500nt and 2000 nt.
>Name
ATGAAACCGCTGGAACGTATTCTGGCTACCGCCCGTGCCACCCGCGTCACATC
CTGCTGCCGGAAGGCGAAGACCCGCGTGTGCCAGGCGGCCCGTCGCCTGA
CCGAAGAAGGTCTGGCACGTGTCTACTGATGAACGGTCCGGAAATGCCGGC
GTTACGCGCATCTGCCCGGCTGAAGCGTCGGATCTGCCGGAACCTGGCGGACCG
TTGCCATCTGATGCCGCGCAGCTAAAGGCATGACCCGGTGCCAGGCACTGATTGA
Submit

Step 1. Enter your request

1. Select Nuclease / Species

2. Choose Input Format

- Gene Symbol / Gene ID (the image above)
- Specific Sequence (the image below)
 - 500-2000 nt
 - Sequence format (enter directly or upload file)
>Name
ATCGATGAGATGA
 - Up to 10 specific sequence, more sequences lead to slower designs

3. Click “submit”



Cas9 / Cas12 Design Processes (for gene symbol / ID)

Top-ranked guide RNAs for knocking out the ADAR gene

Top-ranked guide RNAs and parameters

| Option | Rank | Gene Symbol | Gene ID | Sequence | PAM | Strand | Location | On Target Score | Off Target Score | Overall Score | Primer Design |
|-------------------------------------|------|-------------|---------|----------------------|-----|--------|----------------------|-----------------|------------------|---------------|--|
| <input checked="" type="checkbox"/> | 1 | ADAR | 103 | AATAGTATCCGGCAGCACC | CCG | - | 154601230..154601252 | 0.60 | 0.00 | 77.00 | <input checked="" type="checkbox"/> Yes Options |
| <input checked="" type="checkbox"/> | 2 | ADAR | 103 | ATGATGGCTCGAACTCACC | TGG | + | 154601212..154601234 | 0.47 | 0.18 Detail | 52.00 | <input checked="" type="checkbox"/> Yes Options |
| <input checked="" type="checkbox"/> | 3 | ADAR | 103 | CAGCTGAAGAATCCCATCAG | CCG | - | 154601122..154601144 | 0.56 | 0.40 Detail | 34.00 | <input checked="" type="checkbox"/> Yes Options |
| <input type="checkbox"/> | 4 | ADAR | 103 | TGGGGAGGGCAGCACTCCA | TGG | - | 154597137..154597159 | 0.67 | 0.37 Detail | 56.00 | <input type="checkbox"/> Yes Options |
| <input type="checkbox"/> | 5 | ADAR | 103 | CTCGCCATTGATGACACACC | TGG | + | 154598554..154598576 | 0.14 | 0.00 | 37.00 | <input type="checkbox"/> Yes Options |
| <input type="checkbox"/> | 6 | ADAR | 103 | TTGGAGTACGCCGCTCCCA | TGG | - | 154596859..154596881 | 0.40 | 0.00 | 63.00 | <input type="checkbox"/> Yes Options |

Back Design more sgRNA for ADAR Order gRNA plasmid construct Order sgRNA oligo

Step 2. Select your sequences

1. We recommend top 3 sequences for one gene
2. Selected desired sgRNA and click “order sgRNA oligo” for chemical synthetic sgRNA or “order gRNA plasmid construct”

Parameter's introduction

- On target score (from -1.5 to 1.5): higher score means higher editing efficiency. Some gRNAs have penalty factors that lead to negative On-Target Scores. Below 0.2 will be marked in red, typically indicating low editing efficiency. Consider using them only if no better options are available
- Off target score (from 0 to 1): lower score means lower off target effects
- Over all score: higher score means higher on target score, lower off target score and cover more transcripts
- Primer design: we provide primer design for verifying editing efficiency. Click "Option" to select or deselect primers
- **Ranking (most comprehensive evaluation)**: Higher over all score and target earlier exon to avoid truncated functional protein

Notes:

- Click the black question marks to see the explanations (red labeled box)
- Click the sequence to view its position in sequence map (green labeled box)
- Click “download selected results” to download the sequences (blue labeled box)

Cas9 / Cas12 Design Processes (for Specific Sequences)

Top-ranked guide RNAs for knocking out

Jump to Gene: Select a gene...

Gene: Gene 1

Target Sequence: sgRNA (blue), sgRNA (orange), sgRNA (yellow)

Gene 1

Top-ranked guide RNAs and parameters

| Option | Rank | Sequence Name | Sequence | PAM | Strand | Location | On Target Score | Off Target Score | Overall Score | Primer Design |
|-------------------------------------|------|---------------|----------------------|-----|--------|----------|-----------------|--------------------------------|---------------|---------------|
| <input checked="" type="checkbox"/> | 1 | Gene 1 | ACGAGCCTGCCCCAGGGTCA | GGG | - | 8,30 | 0.81 | 0.29 Detail | 42.00 | |
| <input checked="" type="checkbox"/> | 2 | Gene 1 | GCCCGGAMGGCTTCGGGCA | TGG | - | 26,57 | 0.96 | 0.00 | 67.00 | |
| <input checked="" type="checkbox"/> | 3 | Gene 1 | AGCGCCACDCCCTGCGGGA | CGG | - | 62,84 | 0.82 | 0.07 Detail | 60.00 | |

Show More >>

Gene 2: Gene 2

Target Sequence: sgRNA (blue), sgRNA (orange), sgRNA (yellow)

Gene 2

Top-ranked guide RNAs and parameters

| Option | Rank | Sequence Name | Sequence | PAM | Strand | Location | On Target Score | Off Target Score | Overall Score | Primer Design |
|-------------------------------------|------|---------------|----------------------|-----|--------|----------|-----------------|--------------------------------|---------------|---------------|
| <input checked="" type="checkbox"/> | 1 | Gene 2 | GCGGATCANNCGGANCSSGG | CGG | - | 21,43 | 0.77 | 0.12 Detail | 70.00 | |
| <input checked="" type="checkbox"/> | 2 | Gene 2 | ACAGCGGATCANNCGGANC | GGG | - | 26,46 | 0.87 | 0.38 Detail | 56.00 | |
| <input checked="" type="checkbox"/> | 3 | Gene 2 | TCCGCTGATGATCCGATGA | CGG | - | 28,47 | 1.12 | 0.00 | 108.00 | |

Show More >>

Back

[Design more sgRNAs](#) [Order gRNA plasmid construct](#) [Order sgRNA oligo](#)

Step 2. Select your sequences

1. We recommend top 3 sequences for one gene
2. Selected desired sgRNA and click “order sgRNA oligo” for chemical synthetic sgRNA or “order gRNA plasmid construct”

Parameter's introduction & Notes

- Parameter meanings, comments, and result downloads are the same as on the previous page ([Page 5](#))

How to find multiple design results for multiple target sequences?

- Check target sequence names and design results. (red labeled box)
- Select a name from the dropdown for quick access to design results. (green labeled box)
- Click "Show More" for additional gRNA designs. (blue labeled box)

Cas9 / Cas12 Design Processes

GenScript
Make Research Easy

test11 CONTACT US MY ORDER

sgRNA Ordering (* Required Fields) Information Cart Confirm Order Result Feedback

* Delivery Format: Dry Powder

* Format: Single Tubes

Enter the sgRNA sequence(s) into the spreadsheet below. Clear Table

| | * Name | * Input Sequence | Final sgRNA Sequence | Length | *Quantity | *Purity | *Aliquoting Into |
|----|--------|-----------------------------------|---|--------|-----------|----------|------------------|
| 1 | ADAR-1 | AATAGTATCCCGCAGCACC | m ^A m ^A m ^U *rArGrUrArUrCrCrGrCrGrCrArGrC | 20 nt | 2 nmol | EasyEdit | 1 |
| 2 | ADAR-2 | ATGATGGCTCGA ^A ACTCACC | m ^A m ^U *m ^G *rArUrGrGrCrUrCrGrArArArCrUrC | 20 nt | 2 nmol | EasyEdit | 1 |
| 3 | ADAR-3 | CAGCTGAAGA ^A CCCCATCAG | m ^C *m ^A *m ^G *rCrUrGrArArGrArArCrCrCrArL | 20 nt | 2 nmol | EasyEdit | 1 |
| 4 | | | | | | | |
| 5 | | | | | | | |
| 6 | | | | | | | |
| 7 | | | | | | | |
| 8 | | | | | | | |
| 9 | | | | | | | |
| 10 | | | | | | | |

Add rows Apply

Custom Primer for Assessing Editing Efficiency

Enter the primer sequence(s) into the spreadsheet below. Clear Table

| | * Primer Name | * Primer Sequence(5'->3') | Length | Quantity |
|---|------------------------|-----------------------------------|--------|----------|
| 1 | ADAR-1 Pr1 LeftPrimer | AAAGAAACCGCAGATTCCTC | 20 nt | 2 nmol |
| 2 | ADAR-1 Pr1 RightPrimer | ATATTCTACAGCCCGCTGA | 20 nt | 2 nmol |
| 3 | ADAR-2 Pr1 LeftPrimer | TCACCTGTATATACCACA | 20 nt | 2 nmol |
| 4 | ADAR-2 Pr1 RightPrimer | TTGACTAGCGA ^A CTGGGCAT | 20 nt | 2 nmol |
| 5 | ADAR-3 Pr1 LeftPrimer | AGAAACAGGCAAGAGCCCA | 20 nt | 2 nmol |

Add rows Apply

Add To Cart

Step 3. Order your gRNA

1. Select quantity, purity, aliquoting tubes
2. Click “Add to cart”
3. Click “Continue” → “Get a quote” → “Thank you for your Quotation!”

Notes:

- Click “Clear Table” if you do not need product in the table. (red labeled box)

Base Editing gRNA Design Processes

Base Editing Design Tool

① Target Species: Homo sapiens (GRCh38.p13) ▼

① Nuclease: ABE (A to G) ▼

PAM: Cas9-NGG ▼

② Editing Window: 4 to 8 ?

③ * Select CDS frame: +0 ▼ ?

④ Target Sequence: Please input a sequence containing ATCG, supporting 40-1000 nt.

> Name
Sequence
It is recommended to input a 40–50 nt target sequence (sense strand) that contains the desired editing site, keeping about 20 nt on each side of the site. Excessively long sequences may result in too many design outputs.

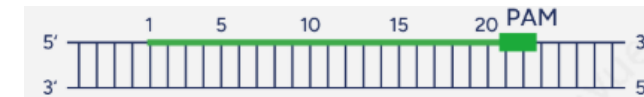
Submit

Step 1. Choose Editing System

ABE (A to G) or CBE (C to T)

Step 2. Select Editing Window

The specific region on target DNA where base conversion occurs



- Recommend 4–8, and no wider than 2–12 to maintain editing efficiency.
- If you need a window beyond 2–12, consider switching to prime editing or HDR knock-in.

Step 3. Select CDS frame

- +0: Start codons from base 1
- +1: Start codons from base 2
- +2: Start codons from base 3

Step 4. Input Target Sequence

40-50 nt target sequence (sense strand) that contains the desired editing site, keeping about 20 nt on each side of the site.

Base Editing gRNA Design Processes

Base Editing guide RNAs Design Results and Distribution

Original sequence ATCG/N | Edited sequence ATCG/N | Original amino acid A | Edited amino acid A

W R L A Q S *

T T G C C G G C T A G C T C A G T C C T A G G

G A A T T C G C G G C C G C T T C T A G A T T G A C G G C T A G C T C C T A G T A C A G T G C T A C T A G A G A A A G A G G A G

N S R P L L D * R L A Q S * V Q C * L L E K E E

A A A T A C T A G A T G A G C G G C A A C C G T G G T G T G G T T T A C C T G G G T C G C G G C A A G G T T G A G G T G C A G A A A A T C G A C T A T

K Y * M S G N R G V V Y L G A G K V E V Q K I D Y

C C G A A G A T G C A A G A T C C G C G T G G T A A G A A A A T C G A A C A C G G C G T G A T T C I G A A A G T G G T T A G C A C C A A C A T T T G C

P K M Q D P R G K K I E H G V I L K V V S T N I C

G G T A G C G A T C A G C A C A T G G T T C G T G G C A C C A A C C A C A C A C A C A A C C A C A C A C A C A C A C A A C A C C A C A C A C A A

G S D Q H M V R G T N H T H H N H T H T Q H H T Q

AA

Base Editing guide RNAs and Parameters

Selecting a gRNA sequence highlights it in blue and shows its editing effect on the map. Tick the checkbox to use the sequence for ordering.

| Option | gRNA Sequence | Editing Window Sequence | Target Sequence | Position | Direction | GC% | On Target Score | Off Target Score | Validation Primer |
|--------------------------|-----------------------|-------------------------|---------------------|----------|-----------|------|-----------------|--------------------------------|-------------------|
| <input type="checkbox"/> | GCTAGCCGTC AATCTAGAAG | AGC CG | CGG CCA GCT | 11 | - | 0.5 | 1.06 | 0.00 | |
| <input type="checkbox"/> | TTGACGGCTAGCTCAGTCCT | AC GGC | GA TTG GCG G L A | 22 | + | 0.55 | 0.25 | 0.22 Detail | |
| <input type="checkbox"/> | TAGTAGCTAGCACTGTACCT | I AGC I | I AGC CAC TA S H | 39 | - | 0.45 | 0.57 | 0.42 Detail | |

Back

Order gRNA oligo

Download results

Step 1. Choose desired gRNA

- The tool shows nucleotide and amino acid changes before and after gRNA editing
- Click different gRNAs sequence to find those that meet your needs. (Green box)

Step 2. Review related parameters

On-target, off-target, and validation primers are provided. (If on-target score <0 or off-target score >0.95, and these parameters are critical for your application, you may try base editing, or switch to prime editing, or an HDR knock-in system for better efficiency.)

Step 3. Get sequence and order

Select a gRNA, then click the Excel icon to download or "Order gRNA oligo" to order online.

Base Editing gRNA Design Processes

GenScript Empowering Possibilities test11 CONTACT US MY ORDER

OmniGuide RNA Online Order (* Required Fields) 1 Information > 2 Cart > 3 Confirm Order > 4 Result Feedback

Order Information

* **Editing System**: Base Editing

* **Type**: Conventional

* **Delivery Format**: Dry Powder

* **Container**: Single Tubes

96-well plate display area (shown when 96-well plates are selected)

Bulk Order

[Download Template](#) [Upload Template](#)

Drag & Drop or Click [Choose Files](#)

Form instructions: Bulk copy/paste from an Excel sheet here ↓ Number in sequence ☑ Fill according to first row ☑ Clear all values [Clear Table](#) [User Guide](#)

| | * Name | * Input Sequence | Length | Final sequence | *Purification | *Quantity | *Aliquoting Into | Price | Option |
|----|---------------|----------------------|--------|-------------------------|---------------|-----------|------------------|---------|--------|
| 1 | BaseEditing-2 | UUGACGGCUAGCUCAGUCCU | 20 nt | mU*mU*mG*ACGGCUAGCUCAGI | Desalt | 2 nmol | 1 | \$79.00 | |
| 2 | | | | | | | | | |
| 3 | | | | | | | | | |
| 4 | | | | | | | | | |
| 5 | | | | | | | | | |
| 6 | | | | | | | | | |
| 7 | | | | | | | | | |
| 8 | | | | | | | | | |
| 9 | | | | | | | | | |
| 10 | | | | | | | | | |

Add rows [Apply](#)

If you have any special requirements, for example adding any modifications to the RNA sequence, please describe them here.

Contract Save: \$0.00 Coupon Save: \$0.00 [Discount Details](#)

Production Time: 4 Business Days Total Amount: \$79.00

[Add To Cart](#)

[Add-on Items \(Custom Primer for Assessing Editing Efficiency\)](#)

Order your gRNA

1. Select quantity, purity, aliquoting tubes
2. Click “Add to cart”
3. Click “Continue” → “Get a quote” → “Thank you for your Quotation!”

Prime Editing gRNA Design Processes

Step 1. Select Gene

Option 1: 'Enter Gene Symbol' tab

- **Required:** gene symbol or transcript ID of interest, editing system
- **Optional:** Edit locations (base or amino acid), design nicking sgRNA ^[1], 3' extension ^[2] (added by default), add gRNA spacer sequence

Enter Gene Symbol | Enter Sequence

* Target Species: Homo sapiens (GRCh38.p13)

* Editing System: PE2/PE3/PE4/PE5/PE Max

* Gene Symbol: ADAR

* Transcript ID: NM_001025107

* Select CRISPR Nuclease: Cas9-NGG

* Design nicking sgRNA: Yes

* Max nick distance to edit site: 90

* Add 3' Extension: Yes

* Export Design Number: 1

Edit Location: Base Position

gRNA(spacer) sequence within pegRNA(optional): Sequence length between 17nt to 23nt.

Submit

Click the black question marks for detailed explanations of each option.

Option 2: 'Enter Sequence' tab

- **Required:** wildtype & desired sequence, CDS frame, editing system
- **Optional:** 3' extension (added by default), design nicking sgRNA

Enter Gene Symbol | Enter Sequence

* Target Species: Homo sapiens (GRCh38.p13)

* Editing System: PE2/PE3/PE4/PE5/PE Max

* Enter sequence:

* Wildtype sequence before editing: 5' → 3'

Please fill in the sequence according to the following rules:
1. The wildtype sequence and the desired sequence must be different and both should exceed 102 nt and include the PAM sequence.
2. The maximum insertion length is 100 nt, so the desired sequence can be up to 100 nt longer than the wildtype sequence.
3. There must be a 51 nt sequence on both the left and right sides of the edit site.

* Desired sequence after editing: 5' → 3'

Please fill in the sequence according to the following rules:
1. The wildtype sequence and the desired sequence must be different and both should exceed 102 nt and include the PAM sequence.
2. The maximum insertion length is 100 nt, so the desired sequence can be up to 100 nt longer than the wildtype sequence.
3. There must be a 51 nt sequence on both the left and right sides of the edit site.

* Select CDS frame: +0

* Select CRISPR Nuclease: Cas9-NGG

* Design nicking sgRNA: Yes

* Max nick distance to edit site: 90

* Add 3' Extension: Yes

* Export Design Number: 1

Submit

Input sequence rules:

1. The wildtype sequence and desired sequence must be different and both should exceed 102 nt.
2. Both the wildtype sequence and desired sequence must include the PAM sequence.
3. There must be a 51 nt sequence on both the left and right sides of the edit site.

Please choose your open reading frames as shown below:

CDS+0
Base: ACA TTT GCT TCT ...
amino acid: T FAS ...

CDS+1
Base: A CAT TTG CTT CT ...
amino acid: I LL ...

CDS+2
Base: AC ATT TGC TTC T ...
amino acid: I CF ...

[1] Nicking sgRNA induces a single-strand break on the opposite DNA strand to promote repair, enhancing editing efficiency.

[2] Add 3'Extension: an extension sequence at 3'end protecting the 3' end from degradation which will improve prime editing efficiency. Reference: Nelson,J.W. et al, 2022.

Prime Editing gRNA Design Processes

Step 2. Edit Mutations

- Select the editing site:** The green bar in the sequence map indicates the editing site. Click the 'Zoom to Edit' button to display the bases in the target sequence. Enter the desired deletion length in the 'Deletion Length' box or left-click the green bar and hold to drag it across the nucleotide/sequence to be modified.
 - For a deletion edit: Delete the original sequence in the 'Mutation' box.
 - For a nucleotide substitution: Delete the original sequence and rewrite the desired sequence in the 'Mutation' box.
 - For a sequence insertion: Enter the insertion sequence in the 'Mutation' box.Click the left mouse button in any area outside the Mutation Box to see the effective editing request on the sequence map.
- Optional- Insert a tag:** Nine commonly used tags can be selected and inserted during the pegRNA design process. Find the desired tag in the dropdown menu and click the 'Insert' button to add it.

Note: If the arrow in the sequence map points to the left, indicating the gene is on the - strand, choose the (- strand) tag option. If the arrow points to the right, choose the (+ strand) tag option.
- Optional- Add a silent mutation** to the RTT region to prevent Cas9 recutting while preserving the translated amino acid sequence.
- Click 'Submit'

The screenshot shows the 'pegRNA design tool' interface. At the top, there's a navigation bar with 'Select Gene > Mutation > Design Results'. Below it, a sequence map for the 'adar' gene is displayed with a green bar indicating the editing site. The sequence map includes coordinates from 154,001,720 to 154,001,780. Below the sequence map, there are input fields for 'Start Edit' (154607754) and 'Deletion Length' (0), along with a 'Zoom to Edit' button. A 'Mutation' box is visible, and a 'Submit' button is at the bottom right.

This screenshot shows the 'pegRNA design tool' interface with a dropdown menu open for tag selection. The menu lists various tags: FLAG (- strand), FLAG (+ strand), HA (- strand), HA (+ strand), Myc (- strand), Myc (+ strand), 3xGS (- strand), 3xGS (+ strand), 3xGS (- strand), 3xGS (+ strand), H1BIT (- strand), H1BIT (+ strand), V5 (- strand), V5 (+ strand), Kozak (- strand), and Kozak (+ strand). The 'Mutation' box contains the text 'ATC'. The 'Submit' button is visible at the bottom right.

Prime Editing gRNA Design Processes

Step 3. Select Your Sequence

1. Select sgRNA (spacer) sequence

Parameters:

- On-target score (from -1.5 to 1.5): A higher score indicates higher editing efficiency. Some gRNAs have penalty factors that lead to negative On-Target Scores. Below 0.2 will be marked in red, typically indicating low editing efficiency. Consider using them only if no better options are available. [1]
- Off-target score (from 0 to 1): A lower score indicates fewer off-target effects [2]
- Distance to mutation: The distance from actual cutting site to your desired cutting site. Generally, the smaller the distance, the better.
- Ranking: Sequences with a smaller 'Distance to mutation' will have a higher ranking. (If the 'Distance to mutation' is within 20, we recommend sequences with a high on-target score and 40-80% GC content. If experimental editing efficiency is poor, please consider another design).

2. Select pegRNA:

Click "Show more" to select pegRNAs with different PBS and RTT lengths. Authoritative literature recommends testing several pegRNA to determine the best choice.

- Click the black question marks to view each full sequence (red-labeled box)
- Click 'Download Results' to download the sequences (green-labeled box)

2. Select Nicking sgRNA:

Nicking sgRNA will help enhance editing efficiency in a PE3 system. Please choose a pegRNA and nicking sgRNA from the same group.

3. Click 'Place Order'

pegRNA design tool

Select Gene > Mutation > Design Results

Output for Gene Symbol ADAR (Transcript ID NM_001025107) Download Result

Design #1

| Component | Sequence(5'->3') | Length | On-target Score | Off-target Score | Distance to mutation | GC% |
|----------------|----------------------|--------|-----------------|------------------|----------------------|-----|
| sgRNA (Spacer) | UCCUCUUGAGUUUUUAGACA | 20 | 1.17 | 0.5 | 4 | 35 |

Show More >

| Select | Item | RTT Sequence | RTT Length | PBS Sequence | PBS Length | Final Sequence | Final Sequence Length | GC% |
|--------------------------|-------------------------|------------------------------------|------------|------------------|------------|-------------------------|-----------------------|-------|
| <input type="checkbox"/> | pegRNA1_RTT38nt_PBS10nt | CUCCUUGAUCUCGGC <u>ADGGUG</u> ... | 38 | CUAAAAACUC | 10 | UCCUCUUGAGUUUUUAGACA... | 195 | 42.05 |
| <input type="checkbox"/> | pegRNA2_RTT42nt_PBS13nt | UUUUUCUCCUUGAUCUCGG <u>CAU</u> ... | 42 | CUAAAAACUCAAG | 13 | UCCUCUUGAGUUUUUAGACA... | 202 | 41.09 |
| <input type="checkbox"/> | pegRNA3_RTT48nt_PBS16nt | CGCAGAUUUUCUCCUUGAUCU... | 48 | CUAAAAACUCAAGAGG | 16 | UCCUCUUGAGUUUUUAGACA... | 211 | 42.18 |

Show More >

Design #2

| Component | Sequence(5'->3') | Length | On-target Score | Off-target Score | Distance to mutation | GC% |
|----------------|----------------------|--------|-----------------|------------------|----------------------|-----|
| sgRNA (Spacer) | GCAGAUUUUCUCCUUGAUCU | 20 | -0.03 | 0.42 | 25 | 40 |

Show More >

Back Place Order

Reference

[1] Doench's Rule Set 3 <https://pubmed.ncbi.nlm.nih.gov/36068235/>

[2] Doench's CFD score <https://pubmed.ncbi.nlm.nih.gov/26780180/>

Prime Editing gRNA Design Processes

Step 4. Select Specifications

- Select the desired delivery format and container
- Select the quantity and purity for pegRNA and nicking sgRNA
- Add PE mRNA / protein or PE Positive control if needed
- Click "Add to Cart"
- Select the desired items in the cart, then click "Continue" → "Get a Quote" → "Thank you for your quotation!"

pegRNA Ordering

* Delivery Format:

* Editing System:

* Format:

Enter the RNA sequence(s) into the spreadsheet below. How to add customized modification? [Clear Table](#)

| | Extension | * Default Modification | * Final sequence | Length | *Quantity | *Purity | *Aliquoting Into |
|---|-----------|------------------------|---|--------|-----------|---------|------------------|
| 1 | | Yes | mU ^{mC} mC ^U CUUGAGUUUUUACACAGUUUUACAGCUAGA | 219 nt | | | |

Add rows Comments:

sgRNA Ordering

* Delivery Format:

* Format:

Enter the sgRNA sequence(s) into the spreadsheet below. [Clear Table](#)

| | * Name | * Input Sequence | Final sgRNA Sequence | Length | *Quantity | *Purity | *Aliquoting Into |
|---|----------------------|---------------------|--|--------|-----------|----------|------------------|
| 1 | Nicking_sgRNA_1_adar | AGGGUUUGAGUCUGGGUCC | m ^A mC ^{mC} *GrGRUUrGrArGrUcUrGrGr | 20 nt | | EasyEdit | 1 |

Add rows Comments:

Add-On Items

| Cat. No. | Name | Quantity | Price | Numbers |
|----------|--------------|----------|--------|--------------------------------|
| SC2346 | PE2/PE3 mRNA | 0.2 mg | \$350 | <input type="text" value="0"/> |
| | | 1 mg | \$1300 | <input type="text" value="0"/> |