

# **GenCRISPR sgRNA Design Tool Protocol** Enabling Easy & Precise Design

Presenter:

Date:

www.genscript.com

# Applications & Advantages – sgRNA design tool

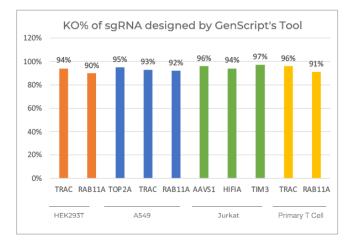
### What is sgRNA design tool?

Design sgRNA sequences for knock-out experiment, downstream order EasyEdit sgRNA / SafeEdit sgRNA

		A Design Tool	The Second
SALA -			
ioinformatics Tools			
EasyEdit sgRNA Now Starting at Only \$79/2	llome		
Design high-performance CRISPR guide RNAs u	ing the most up-to-date design algorithm,	for effective gene editing.	Select Gene / Design / Order
Nucl	ase: SpCas9		
Target Spe	cies: Homo sapiens (GRCh38.p13)		~
	ene: 6		
Number of a DNAs Per C	one. O		
Number of gRNAs Per G			
Number of gRNAs Per C	mat: Gene Symbol	• 0	
	mat: Gene Symbol	• @	

### Advantages of sgRNA design tool

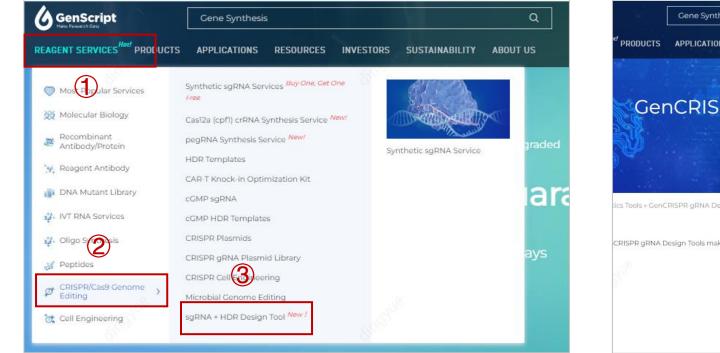
- 1. Comprehensive applications: Support 10 species, Cas9 and Cas12a
- 2. More prices design: updated on-target and off-target scores
- 3. Enhance editing efficiency:
  - Designs target early exons to avoid truncated functional proteins
  - Higher transcript coverage
  - Ideal GC% for sgRNA
- 4. Validated efficiency: Indel% up to 97% validated by experiments

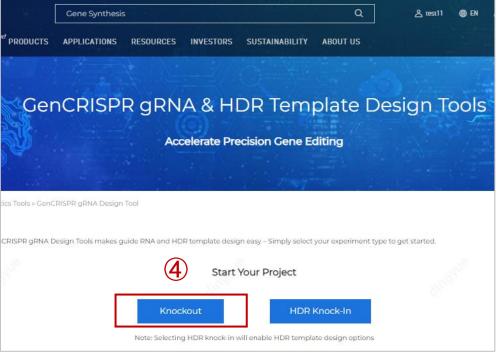




### Where can we find sgRNA design tool?

- 1. Visit the address: <u>https://www.genscript.com/tools/gRNA-design-tool</u>
- 2. Find the tool in official site:







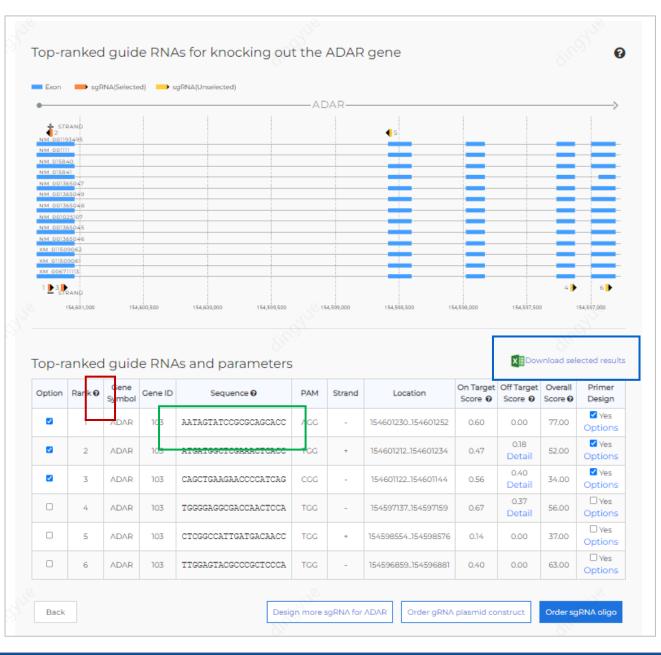
### sgRNA design tool design process

Nuclease:	SpCas9	~
Target Species:	Homo sapiens (GRCh38.pl3)	~
Number of gRNAs Per Gene:	6	
Input Format:	Gene Symbol 🗸 💿	
	Submit	

### Step 1. Enter your request

- 1. Select Nuclease / Select species / Enter Gene symbol
- 2. Click "submit"





## 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"

#### **Parameters introduction**

- <u>On target score</u>: higher score means higher editing efficiency
- <u>Off target score:</u> lower score means lower off target effects
- <u>Over all score:</u> higher score means higher on target score, lower off target score and cover more transcripts
- <u>Ranking (most comprehensive evaluation)</u>: 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)

N/	A Ordering (* Required I	Fields)			formation >	2 Cart > 3	Confirm Order	Result Feedback
	ery Format: Dry Powder		•					
	at: Single Tubes 🖌	to the spreadsheet	below.					📋 Clear Table
	* Name	*1	nput Sequence 😔	Final sgRNA Sequence 😣	Length 😏	*Quantity	*Purity	*Aliquoting Into
	ADAR-1	AATAGTATCCG	GCAGCACC	mA*mA*mU*rArGrUrArUrCrCrGrCrGrCrArGrC	20 nt	2 nmol v	EasyEdit	1
2	ADAR-2	ATGATGGCTCG	WACTCACC	mA*mU*mG*rArUrGrGrCrUrCrGrArArArCrUrC	20 nt	2 nmol 🔹	EasyEdit	1
5	ADAR-3	СЛЕСТЕЛЛЕЛЛ	CCCCATCAG	mC*mA*mG*rCrUrGrArArGrArArCrCrCrCrArL	20 nt	2 nmol 🔹	EasyEdit	1
-						Y		
						×		
						Y		,
						×		
						Y		·
)						*		,
)						×		,
	m Primer for Assessing						S	📋 Clear Table
	* Primer N	* Primer Name		^ Primer Sequence(5'->3')		Length		Quantity
	ADAR-1 Pr1 LeftPrimer		AAAGAAACGCAGAGTTCCTC			20 nt	2 nmol	
	ADAR-1 Pr1 RightPrimer		ATATTCTAACAGCCCGCTGA			20 nt	2 nmol	
	ADAR-2 Prl LeftPrimer		TCACCTGTAATATACCCACA			20 nt	2 nmol	
	ADAR-2 Pr1 RightPrime	r	TTGACTAGCGAACTGGGCAT			20 nt	2 nmol	
	ADAR-3 Pr1 LeftPrimer		АБЛАЛАСАББСАЛБАББССА	<i>.</i>		20 nt	2 nmol	
		SUL STORE		100 100	+			

### Step 3. Order your sgRNA

- 1. Select quantity, purity, aliquoting tubes
- 2. Click "Add to cart"
- 3. Click "Continue"  $\rightarrow$  "Get a quote"  $\rightarrow$ " Thank you for your Quotation!"

#### Notes:

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

