

Defining and characterizing the components of a CRISPR-Cas9 genomic medicine

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Platform for CRISPR medicines

RNP based Lead Discovery platform

Fully synthetic modular dgRNA

Ex-vivo T-cell and HSC editing with Cpf1

O Pipeline strategy to enable successful medicines

Medical Need

- Severe diseases where current treatments, if any, are poor
- Potential for durable therapies to provide unique benefit

Biology & Clinical

- Clear biological hypothesis for genomic intervention
- Favorable clinical and regulatory path

Technical

- Validated delivery approaches
- Mutation feasibly corrected



Eye

- Leber Congenital Amaurosis 10
- Ocular HSV
- Additional ocular indications

Lung

Cystic Fibrosis

Muscle

Duchenne Muscular Dystrophy

Liver

- Alpha-1 Antitrypsin Deficiency
- Infectious diseases of liver

Bone Marrow & Blood

- Hemoglobinopathies
- Engineered T cells for cancer
- Additional bone marrow and blood indications

CO Scalable, Consistent Engineered Cell Therapies

Platform for CRISPR Medicines



Engineer multiple components to T-cell & HSC sensitivity (maintain cell viability, potency)

O | Defining every component : key to a successful CRISPR medicine

Aspects of a Ribonucleoprotein medicine



- Efficacy: well optimized cellular and well characterized in vitro efficacy
- Stability: track RNP activity through gene-editing workflow and therapeutic window
- Fidelity: Define every component and characterize trace elements
- Pharmacokinetics



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⊘ | RNP lead discovery

Wealth of standardized data across cell types, nucleases, gRNA formats



Many factors influence gRNA efficacy: gRNA sequence, Nuclease type, cell type

Cell type dependence

T-cells skew to deletions as compared to insertions in HEK-293T cells



Guide dependence of edit

Normalized indel distributions display range of levels of control





CO Indel pattern dependence on nuclease choice

Spy-Cas9 shows the +1 insertion more often than Spy-Cas9



(1) +1 overhangs a result of nuclease properties

Pyogenes cuts with a 1bp stagger more often than Sau Cas9



as fraction of total reads

Extended Data Figure 2 | **Cas9 orthologue cleavage pattern** *in vitro*. Stacked bar graph indicates the fraction of targets cleaved at 2, 3, 4, or 5 bp upstream of PAM for each Cas9 orthologue; most Cas9 enzymes cleave stereotypically at 3 bp upstream of PAM (red triangle).

3' 5' TGTCAGAAC ACAGTCTTG 3' 5′ 5 AGAAC GTCA ACAGT TCTTG 21 5' 5' 3' TGTCAAGAAC ACAGTTCTTG 31 5'

+1 insertions come from base 5' of cut site

In vivo genome editing using Staphylococcus aureus Cas9.

Ran FA, Cong L, Yan WX, Scott DA, Gootenberg JS, Kriz AJ, Zetsche B, Shalem O, Wu X, Makarova KS, Koonin EV, Sharp PA, Zhang F. Nature. 2015 Apr 9;520(7546):186-91. doi: 10.1038/nature14299.



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O GRNA component at the core of the RNP medicine

Maturation of the synthetic gRNA field allow for multiple formats

- Chemical synthesis of gRNA allows for greater flexibility, fidelity, scale and purity
- Synthetic chemistry goes from 3' to 5', 100-mers were challenging till recently
- Safety and Specificity of a medicine rely on a precise characterization and control of every component



100-mer sgRNA

Generating Synthetic Covalently-Coupled Dual gRNA

A completely non-enzymatic process for guide production

Why make a synthetic guide?

- Targeted chemistries anywhere in the molecule
- Unhindered ends and modifications
- Scale up and purity are more compatible with CMC requirements



covalently-coupled dual gRNA (dgRNA)





Cellular Editing Activity

In vitro transcribed and synthetic covalently-coupled dgRNA are equivalent in cells



- --- IVT purified by vendor
- → IVT purified by collaborator
- --- covalently-coupled dgRNA
- 2-part synthetic



(C) gRNA purity and sequence fidelity

Covalently-coupled dgRNA result in greater sequence fidelity in target region



Covalently-Coupled dgRNA



Α

(C) gRNA Purity and Sequence Fidelity

Covalently-coupled dgRNA result in fewer truncated molecules



Α

5 -						0.0049	2e-04			9e-04		2e-04	5e-04		5e-04	5e-04		2e-04	0.0012	0.0021		7e-04	0.0014		0.0012	2e-04	2e-04			2e-04
4-		2e-04		2e-04	2e-04	0.0012				0.0019	9e-04	2e-04	5e-04	2e-04	0.0082	5e-04	2e-04		9e-04	5e-04	0.0023		7e-04	0.0012			0.0075	0.0026	5e-04	
'3-		5e-04		0.0105	5e-04	2e-04			5e-04	0.007	26-04		0.0016		0.0156	7e-04	7e-04		0.0026	0.0014	0.0044	0.0016	0.0028		7e-04	2e-04	0.0016	2e-04	0.0019	5e-04
2-			2e-04	0.0279	2e-04	2e-04	0.0028		5e-04	7e-04	5e-04	0.0126	0.004	2e-04	0.007	0.0026	0.0014	7e-04	0.0082	0.0061	0.0016	0.0033	2e-04	5e-04	2e-04	9e-04	0.003	0.0037	0.0033	0.0016
1 -		2e-04	0.1642	0.0338	0.0398	0.2042	0.1094		0.0326	0.1479	0.0696	0.6543	0.0028	0.0587	0.0917	0.3644	0.1693	0.0012	0.2387	0.0955	0.2352	0.1982	0.0035	7e-04		0.0608	0.2056	0.0652	0.2603	0.0349
-1-			0.0824		0,0813	0,1472	0,1565		0,115	0,1092	0,1195	0,3407		0.099	0.1327	0,1726	0,2804		0,1481	0,2361	0.4466	0,6248				0.2385	0.0685	0,3991	0,1325	0,1742
-2 -		0.0058	9e-04	0.0405		0.0289	0.0037	0.0051	0.024	0.0289		0,0361	0.0263	0.0366	0.1281	0.0424	0.0238	0,027	0,2189			0,1614			0.0263	0.1896			0.034	0,064
-3 -	0.0382	9e-04	0.0056		0.0072	7e-04	0.0021	0.004	0.0091	0.0179		0.0021	0.0813			0.024		0.0119	0.0112	0.0354		0.0414		0.0109	0.0142	0.0196	0.0154	0.0123	0.0221	0.0366
-4 -	0.0221	0.0037	2e-04	0.0028	0.0016	0.003		0.0058	0.0116	0.0088	0.0403			0.0226		0.0077	0.0116	0.0061	0.0033	0.0321		0.013	0.024	0.0056	0.0063	0.0175	0.0033	0.0424		
-5 -	0.2282	7e-04		5e-04	0.0016	0.0014	0.0051	0.0026	0.0047	0.0014	0.0065	0.0035	0.0044	0.0079	0.0161			0.0019	0.0019	0.0256		0.0144	0.0026	0.0061	0.0093	0.0077	0.003	0.0144	0.0151	0.0047

Covalently-Coupled dgRNA





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CO | Type VI nuclease Cpf1 with many benefits

- Smaller gRNA just 44 nucleotides
- The business end of gRNA is at 3'
- dsDNA Cutting profile different from Spy and Sau Cas9
- More targets with enzyme and evolved variants



CO Screening of multiple Cpf-1 orthologs and variants

AsCpf1 emerging as the "go to" Cpf1 with Robust activity



Cpf1 editing at T-cell targets



Ex-vivo editing of Cpf1 at sample locus

Sample editing by AsCPf1 in HSCs





- A flexible platform allows for lead discovery screening and optimization at scale
- Wealth of standardized data allows for insights into nuclease function and its interplay with biology to engineer a therapeutic outcome
- Modular gRNA allow for controlling the core of the RNP medicine
- Cpf1 editing points to greater flexibility in developing CRISPR medicines

Poster: 7, 33 and 68