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OMNI™ Technology Platform

Superior Performance through AI-Driven Design

Anges

About EmendoBio

- Founded in U.S. in 2016 by scientists from the Weizmann Institute, Israel
- Founding investors: OrbiMed and Takeda Ventures
- AnGes became a majority shareholder in December 2020

Management

Naoya Satoh, PhD
President & CEO

Assaf Sarid
CFO

Idit Buch, PhD
VP, Computational Biology

Ella Segal
VP, Research and Analytical Sciences

Board of Directors

Ei Yamada, PhD
AnGes

Naoya Satoh, PhD
AnGes

David C. Dale, MD
Former Dean
UW Medical School

Stephen Tsang, MD
Clinical Geneticist
Columbia University

Harry Malech, MD
Chief Genetic Immunotherapy, NIH

David Rawlings, MD
Director Immunity and Immunotherapies, SCRI

Andrew Kung, MD PhD
Chair Dept. Peds. Sloan Kettering

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Current Limitations of Gene Editing

Safety

- Off-target effects
- Translocations

Editing Strategy

- PAM availability
- Allele specific editing
  - Mutations
  - SNPs
  - Enhancer sites
  - Splice donor / acceptor

Delivery

- Packaging limitations
- Tissue specificity

Immunogenicity

- Anti-nuclease antibodies
- Cytotoxic T cells

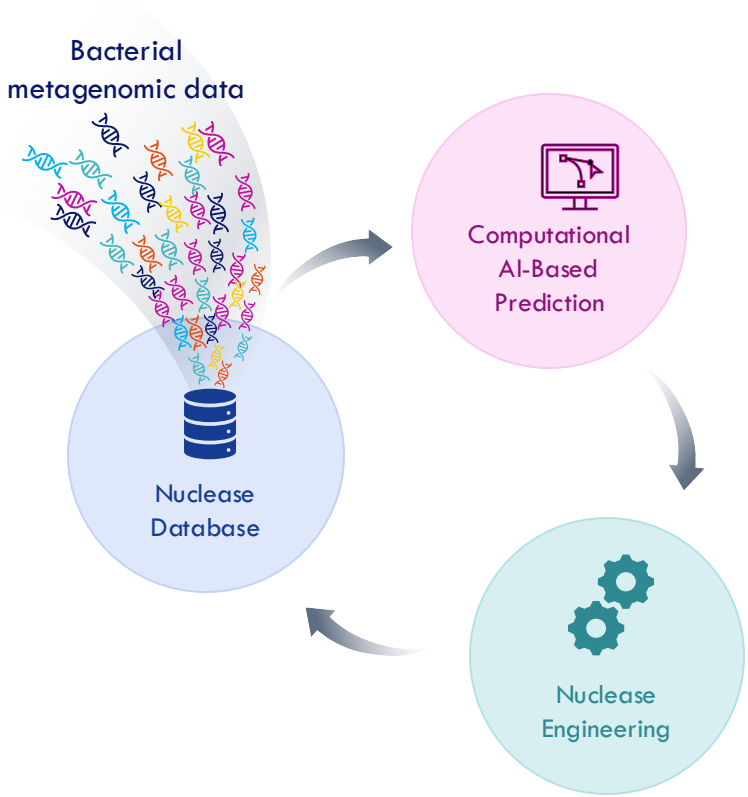
IP

- Nuclease
- Guide RNA (gRNA)

OMNI™ Platform Offers a Variety of Gene-Editing Solutions

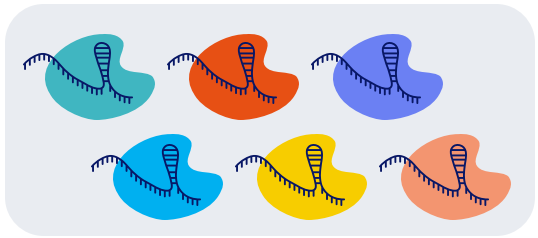
Synergistic discovery, engineering and computational technologies combine to produce a portfolio of high-performance OMNI™ type-II nucleases

EmendoBio's Platform



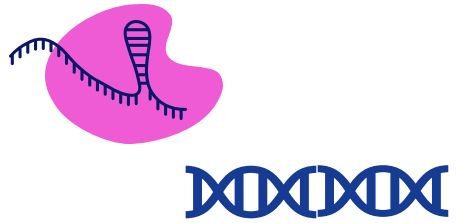
Panel of Engineered OMNI™ Nucleases

- Novel
- Highly active
- Highly specific



Optimal Therapeutic Compositions per target

- High safety profile
- Expanded range of applications
- Freedom to operate



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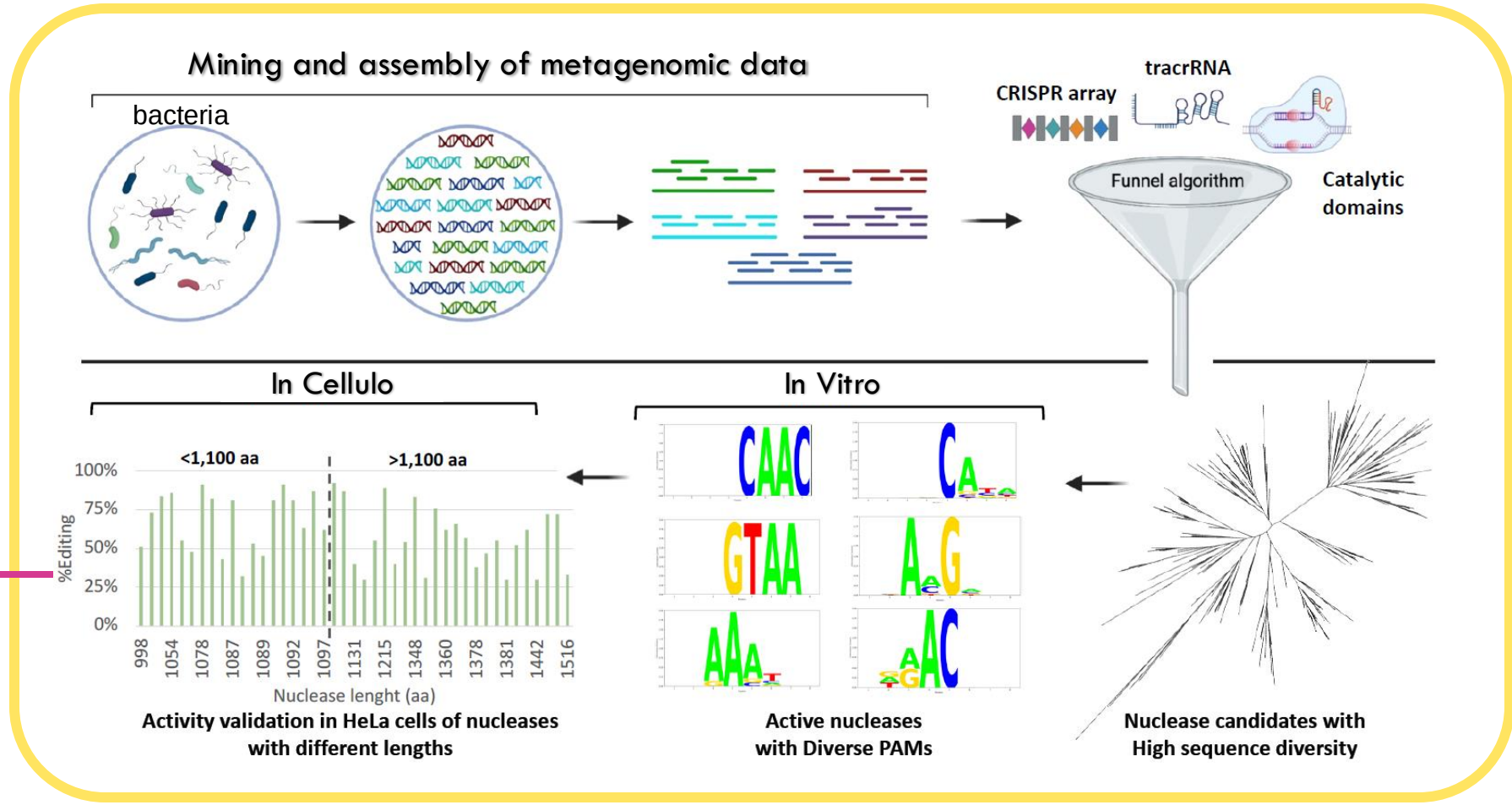
Nuclease Discovery

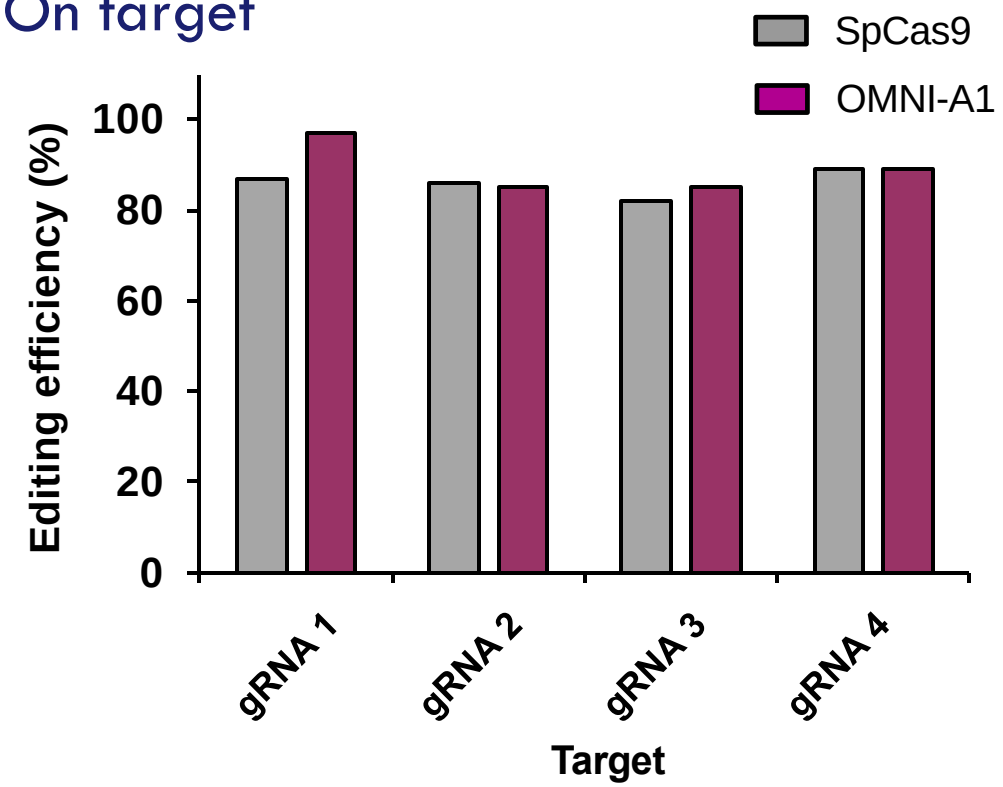


OMNI™ Type-II Nuclease Panel
with Diverse Characteristics

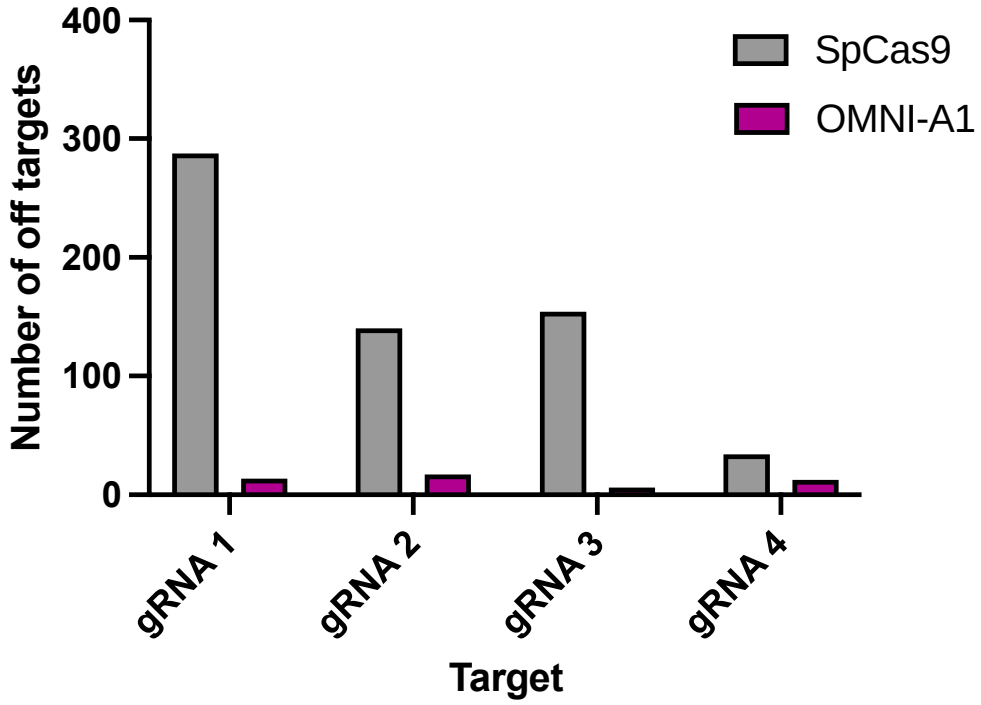
Activity and Specificity of OMNI-A1™ (1,370aa)

OMNI-A1™ vs SpCas9

On target



Off target



OMNI-A1™ has higher specificity compared to SpCas9

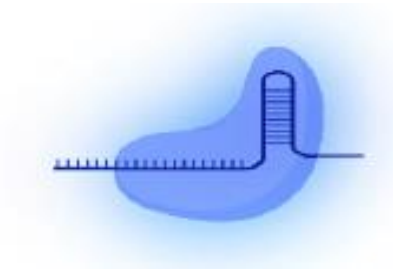
Nuclease Engineering Platform

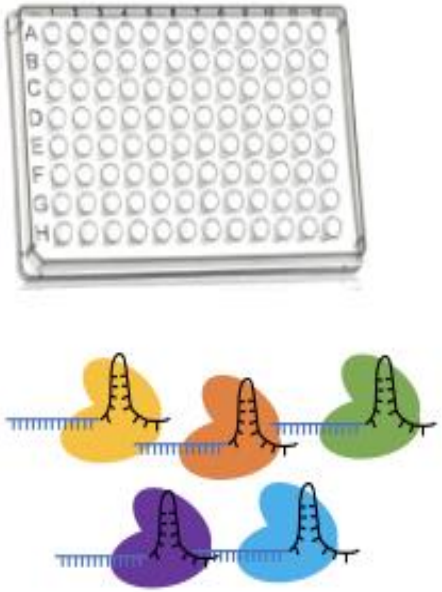
OMNI™ nuclease (from panel)

AI based engineering for variant library generation

Libraries of nuclease variants

Screening in mammalian cell line



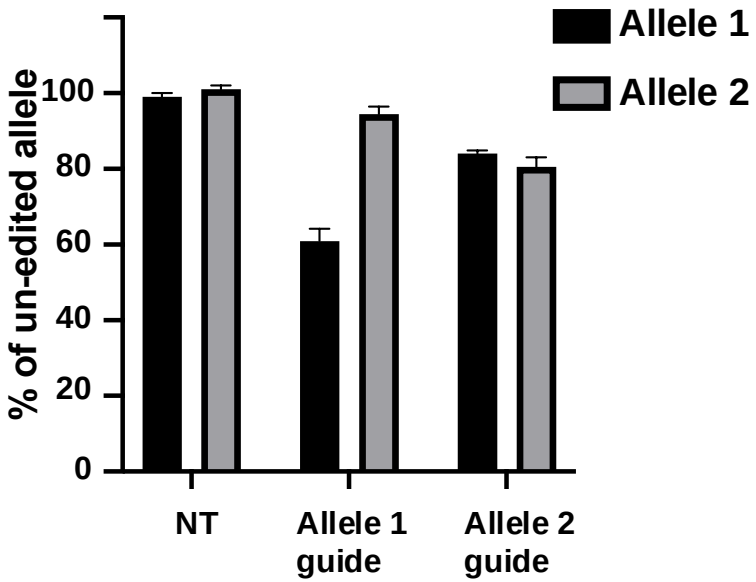


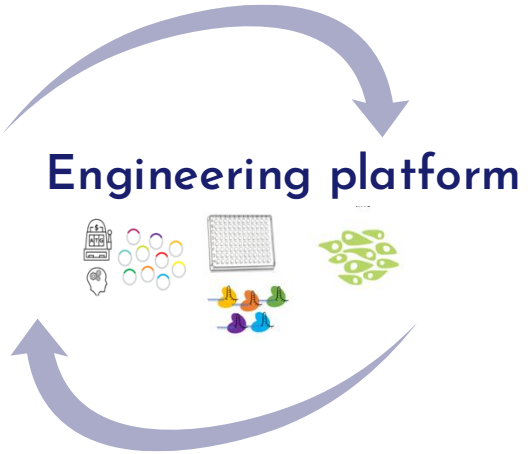
Highly Active and Specific
Optimized OMNI™ Variants

Increased Specificity

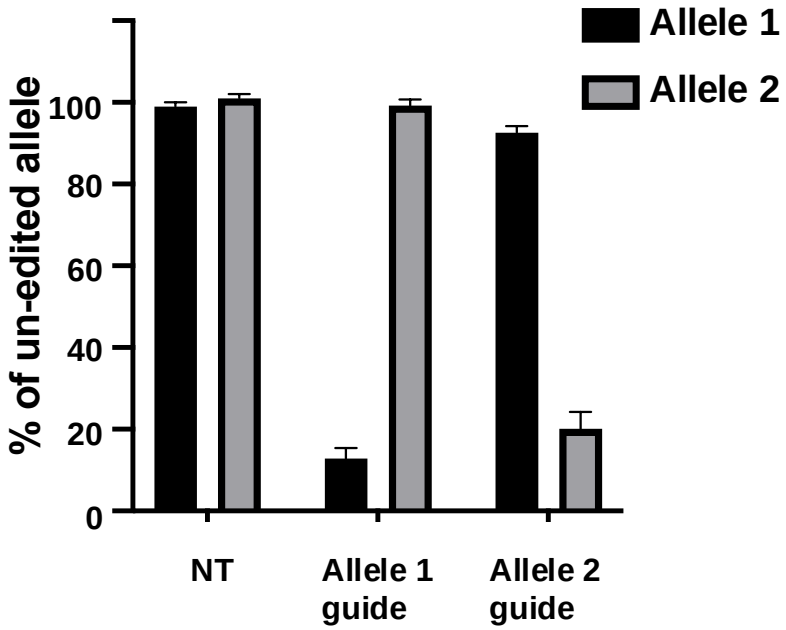
OMNI-A1 ™ – powerful engineering platform

OMNI-A1™





OMNI-A1 V10™



Non-Compromised Nuclease Safety

Engineering platform achieves systematic elimination of off-targets

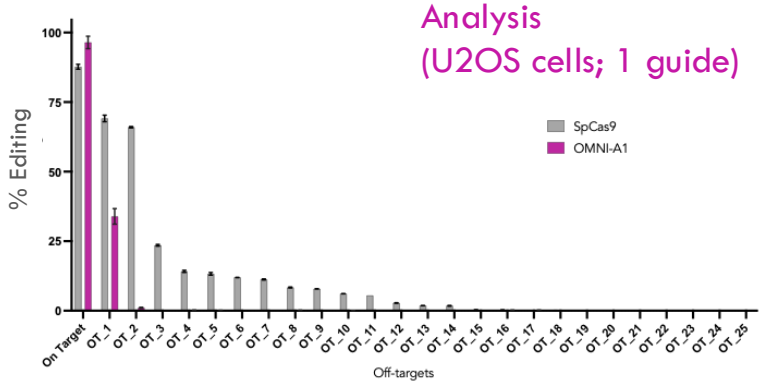
Optimized to be highly active and specific

Engineering further eliminates off-targets

Limits potential for off-target mediated translocations (OMTs)

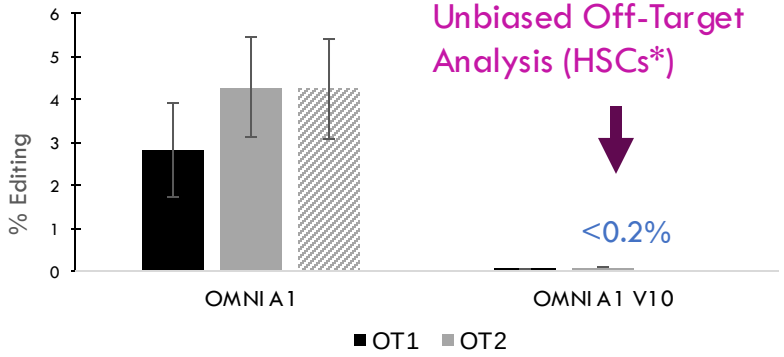
OMNI-A1™ vs SpCas9

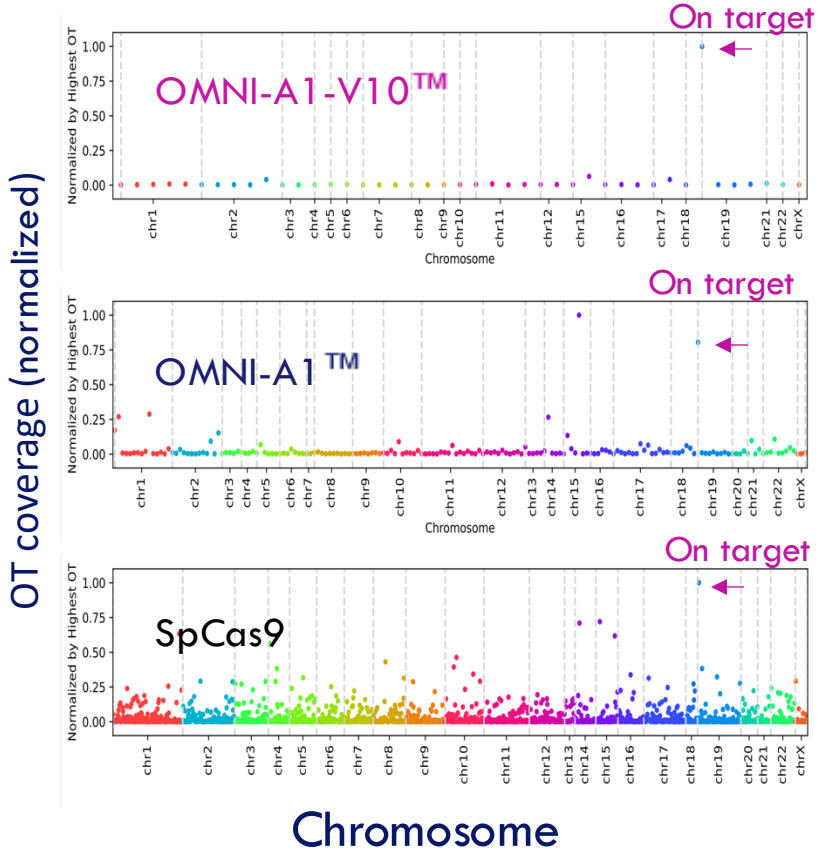
Unbiased Off-Target Analysis (U2OS cells; 1 guide)



OMNI-A1™ vs OMNI-A1-V10™

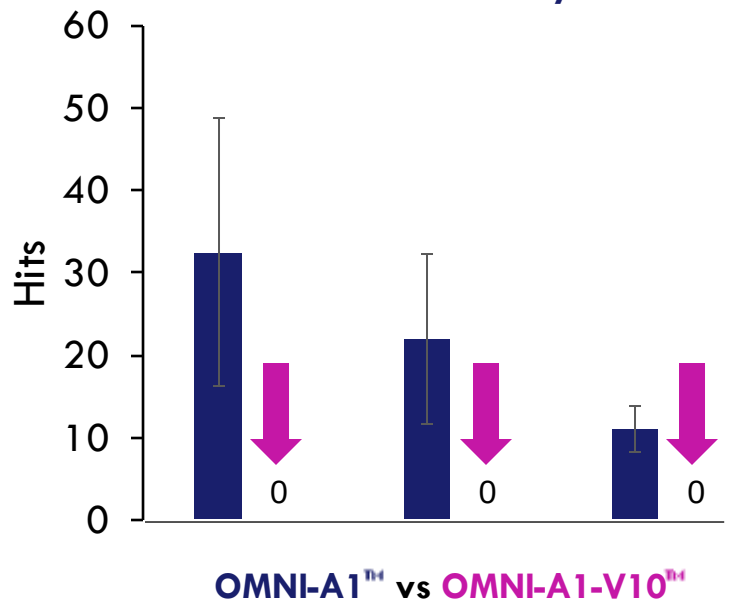
Unbiased Off-Target Analysis (HSCs*)





Chromosome

Unbiased OMT analysis



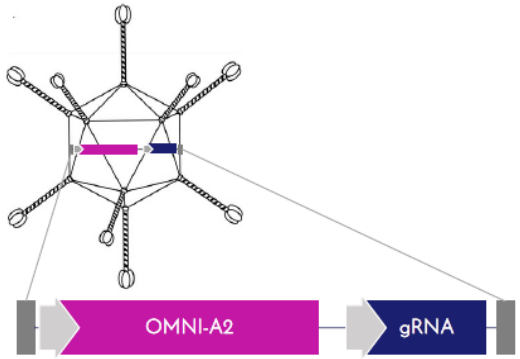
OMNI-A1™ vs OMNI-A1-V10™

HSCs - hematopoietic stem cells

OMNI-A2™ (1,050aa): Short AAV-Deliverable Nuclease

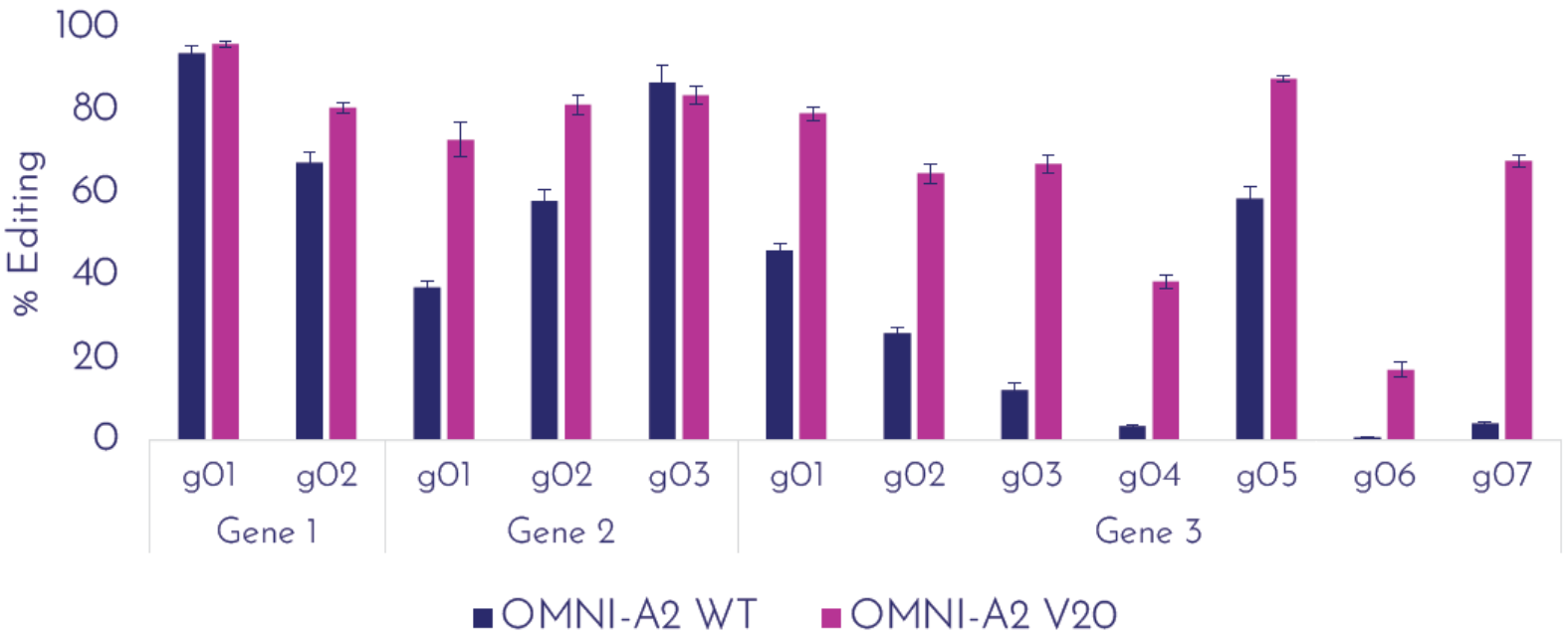
Short, highly active, AAV packaging compatible nucleases available

AAV-based vectors



Limited payload capacity

Editing by OMNI-A2-V20™



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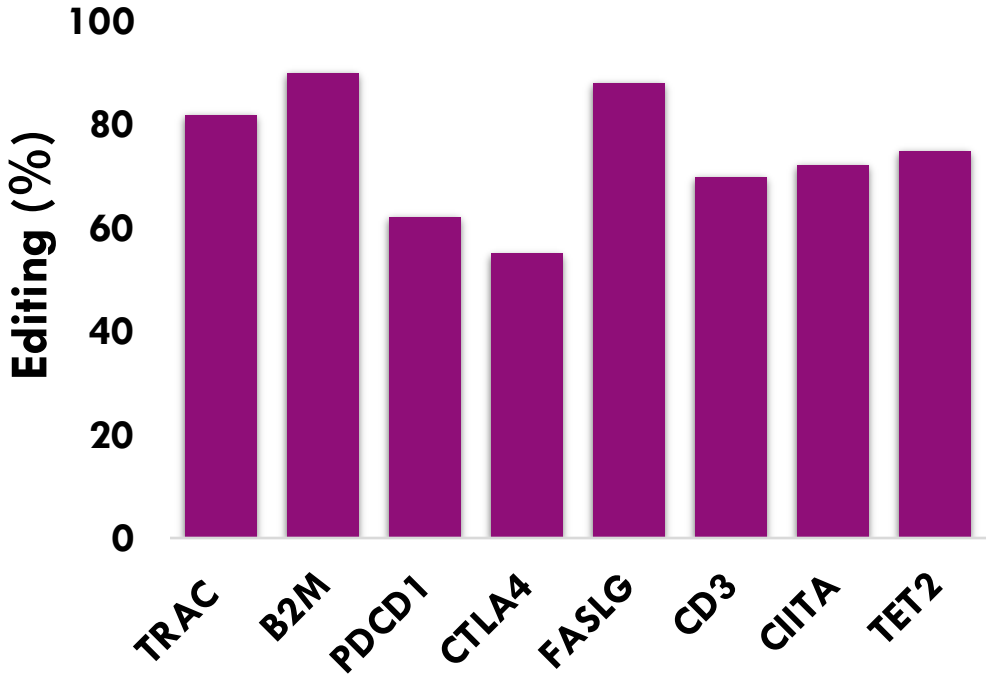
OMNI-A4™ Presents High Activity and Specificity Profile

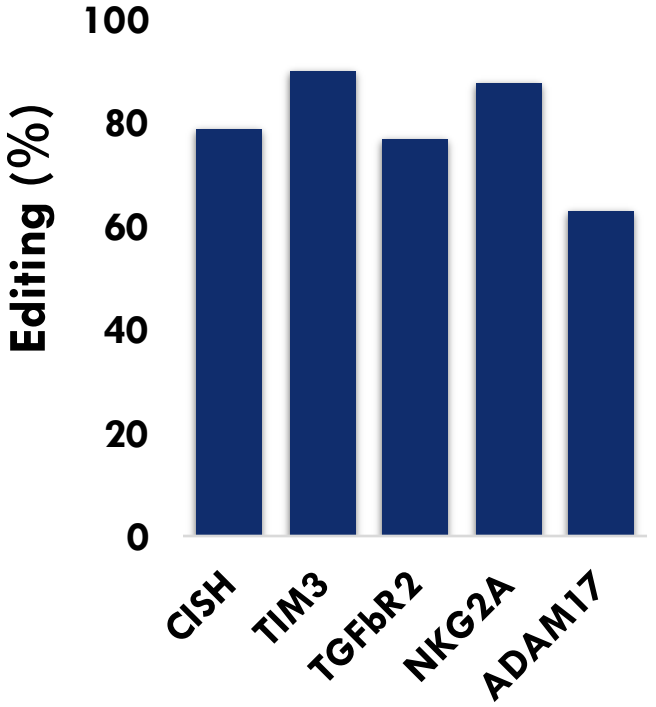
Non-NGG PAM nuclease compositions for major cell therapy and immuno-oncology targets

OMNI-A4™	
CRISPR type	II-A
Protein length	1,348 aa (161.9 Kda)
gRNA length	101 nt
PAM	NNRACT
hg38 coverage	0.77%

T cells



NK cells



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A Portfolio of "Off-the-Shelf" Editing Solutions

SAFE HARBOR

#	Target Gene	Computational	Cell Line	Target Cells
1	AAVS1	•	•	
2	ROSA26	•	•	
3	C3	•	•	
4	APLP2	•	•	•

HEMATOPOETIC STEM CELLS

#	Target Gene	Disease	Computational	Cell Line	Target Cells
5	ELANE	Severe Congenital Neutropenia	•	•	•
6	SAMD9L	Myeloid malignancies	•	•	
7	GATA2	Myeloid malignancies	•	•	
8	SAMD9	Myeloid malignancies	•	•	
9	RPS19	Diamond Blackfan Anemia	•	•	

IMMUNO-ONCOLOGY

#	Target Gene	Computational	Cell Line	Target Cells
10	PDCD1	•	•	•
11	TRAC	•	•	•
12	TRBC1	•	•	•
13	TRBC2	•	•	•
14	B2M	•	•	•
15	CTLA4	•	•	•
16	TET2	•	•	•
17	CD3E	•	•	•
18	LAG3	•	•	•
19	FAS	•	•	•
20	HAVCR2 (TIM3)	•	•	•
21	HLAE	•	•	•
22	CIITA	•	•	•
23	FASLG	•	•	•
24	IL15	•	•	•
25	TIGIT	•	•	•
26	CISH	•	•	•

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A Portfolio of "Off-the-Shelf" Editing Solutions

LIVER

#	Target Gene	Disease	Computational	Cell Line	Target Cells
27	SERPINA1	A1AD	•	•	•
28	ANGPTL3	Dyslipidemia including homozygous familial hypercholesterolemia	•	•	•
29	LDLR	Atherosclerotic cardiovascular disease	•	•	•
30	HBV	Hepatitis	•	•	

CNS

#	Target Gene	Disease	Computational	Cell Line	Target Cells
31	LRRK2	Parkinson's disease	•	•	

OPHTHALMOLOGY

#	Target Gene	Disease	Computational	Cell Line	Target Cells
32	TCF4	Fuchs Endothelial Corneal Dystrophy	•	•	
33	TGFBi	Corneal Dystrophies	•	•	
34	SARM1	Neuronal and macular degeneration	•	•	
35	RPE65	Retinitis Pigmentosa	•	•	
36	RHO	Retinitis Pigmentosa	•	•	
37	FLG	Ichthyosis vulgaris	•	•	
38	BEST1	Autosomal dominant vitreoretinochoroidopathy	•	•	
39	PRPH2	Retinitis Pigmentosa	•	•	

OMNI™ Panel Genome Accessibility

Nuclease Portfolio

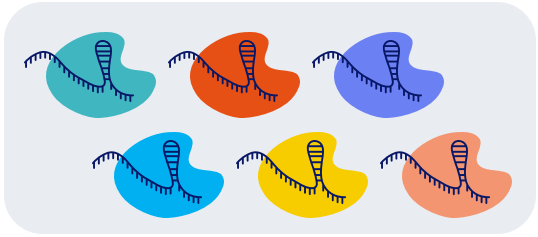
10,000 discovered nucleases

300 validated in vitro

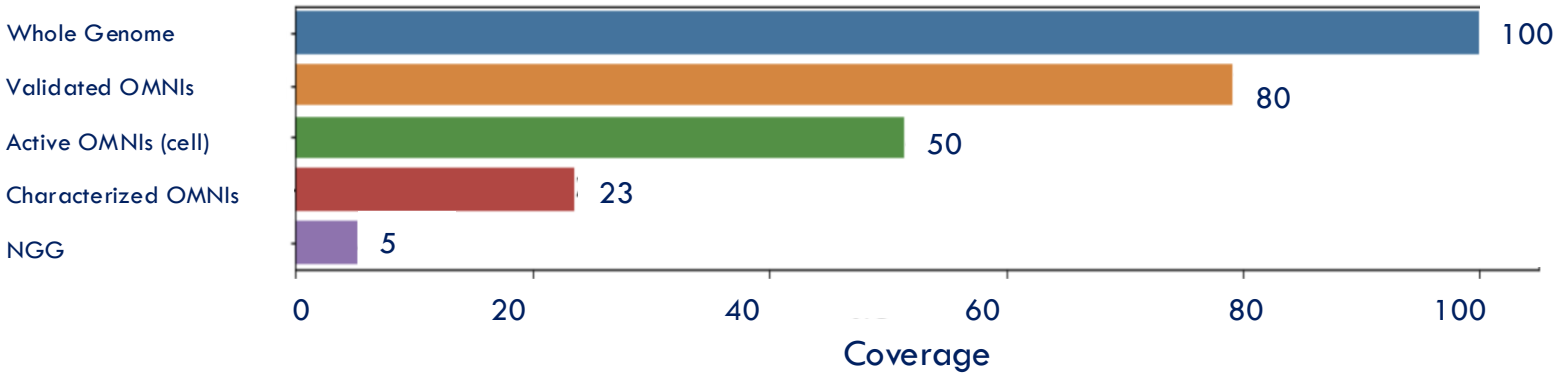
80 shown active in cells

12 characterized

2 engineered



OMNI™ Genomic PAM Coverage



The diversity of PAM sites of the OMNI™ nucleases overcomes PAM constraints and significantly widens genome accessibility, making **any gene targetable**

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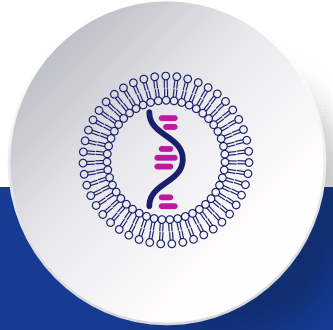
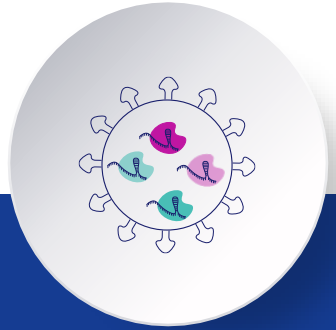
OMNI™-Generated Nucleases

Compatible with all commonly used delivery platforms

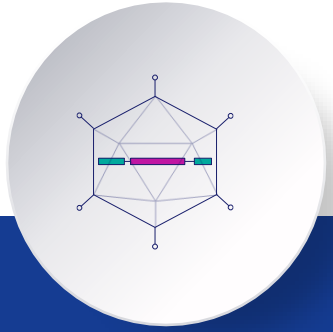
Ribonucleoprotein (RNPs)



Lipid nano particles (LNPs)



Lenti Virus Like Particles (LVLPs)

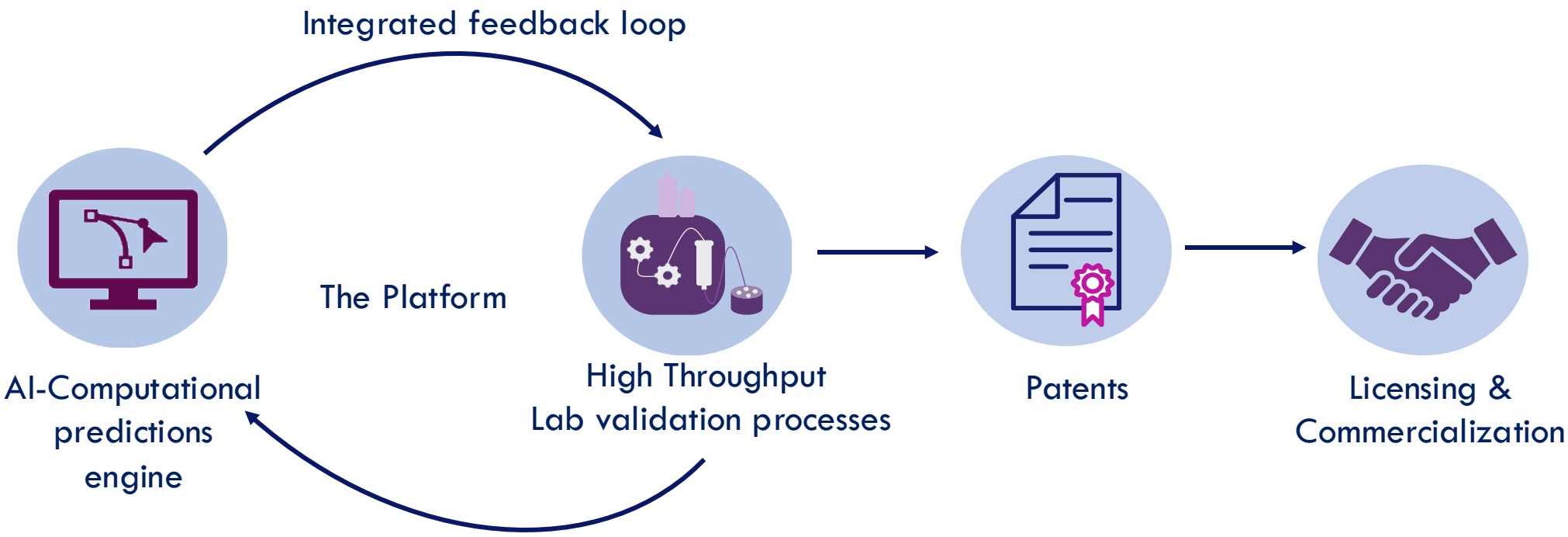


Adeno Associated Virus (AAV)

Extensive Intellectual Property Portfolio

- Strong IP position – 191 patents/applications worldwide
- Coverage extending to 2041
- Gene Editing Techniques
- Compositions for gene editing
  - Knock-out and knock-in compositions
  - Allele-specific compositions
  - Numerous target genes & indications
- Novel CRISPR nucleases
  - OMNI™ Panel Nucleases
  - High-fidelity variants
  - Variants with increased activity, specificity

EmendoBio's Business Model



Collaboration Work Plan

Upon transfer of gene sequence:	Time
○ EmendoBio assesses licensee needs and optimizes OMNI™ nuclease	2-4 weeks
○ EmendoBio provides nuclease and recommended guide RNA sequence	6-8 weeks

Summary

EmendoBio's platform

- AI-based nuclease discovery and engineering platform
- Precision, diversity, efficiency and safety superior to conventional CRISPR
- Compatible with all commonly used delivery platforms

Strong IP position

- Patent families covering all aspects of gene editing

Custom-designed and off-the-shelf nucleases

- Available for exclusive or nonexclusive licensing

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