

# Identification of a novel human immunodeficiency enables mechanistic dissection of a previously unknown regulator of NK and CD8+ T-cell cytotoxicity

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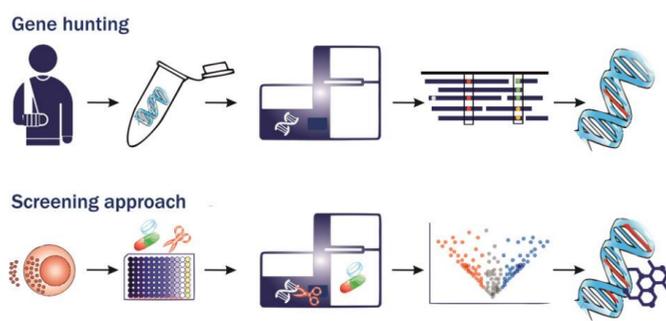
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## INTRODUCTION

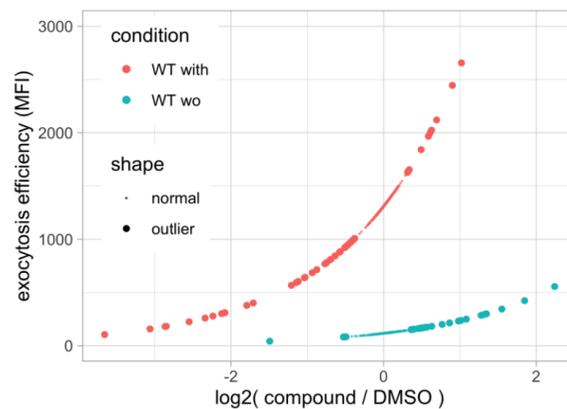
The investigation of genetic inborn errors have greatly enhanced our understanding of disease pathology & immunity. In addition to a targeted single-gene centered disease study we aim to gain systematic understanding of immune function by deciphering the key molecules using high-throughput CRISPR/ drug screens.

## AIMS

- Identification of novel disease-causing entities<sup>1</sup>
- Functional screening for primary immunodeficiency<sup>2,3</sup>

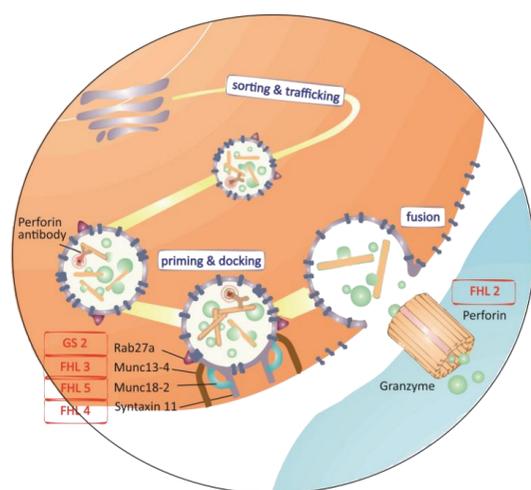


## High-throughput chemical probing of granule exocytosis



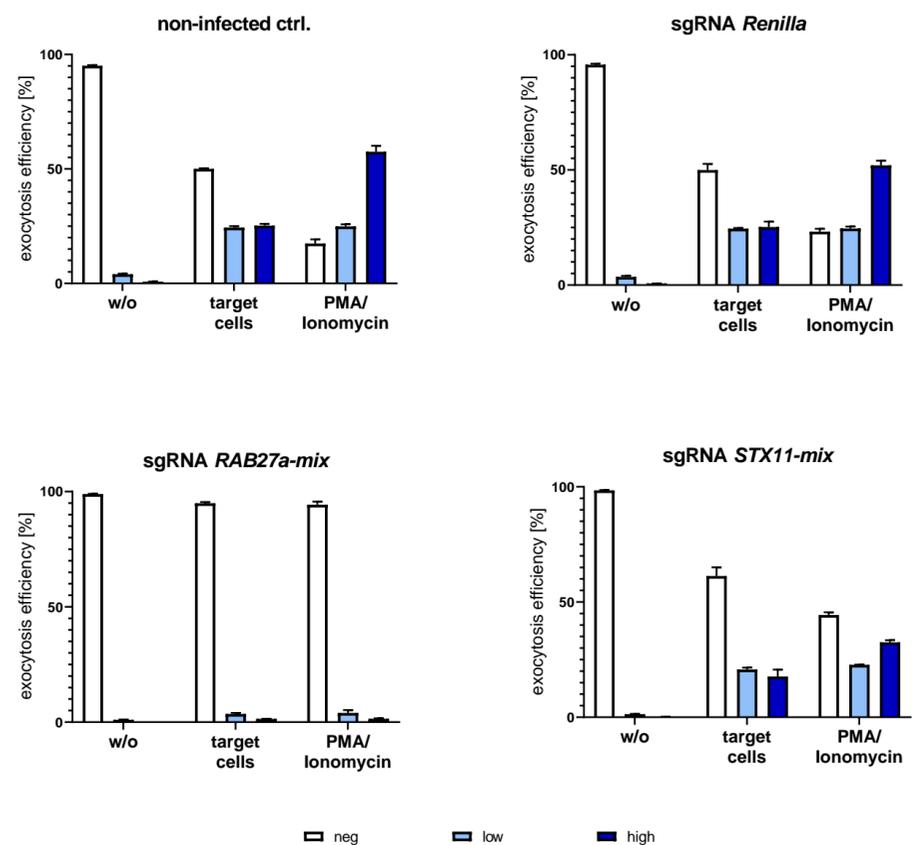
**Figure 4.** High-throughput granule exocytosis compound screen using NK92 WT with a library of >300 different drugs<sup>3</sup>. NK92 WT with target cells (red), NK92 without target cells (turquoise). Hits are indicated as outliers.

## Functional NK-cell deficiencies



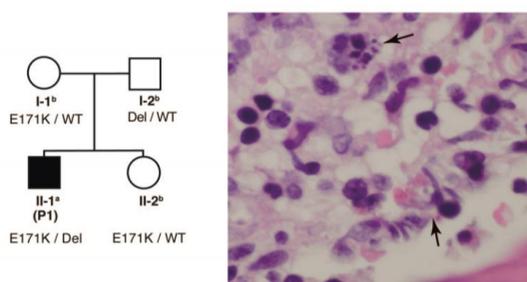
**Figure 1.** Functional NK-cell immunodeficiencies impairing lytic granule convergence towards target cells and thus hindering the effector cell's cytotoxic activity leading to primary/familial hemophagocytic lymphohistiocytosis (FHL) or HLH-related syndromes<sup>4</sup>.

## Targeted small-scale knockout screen sets basis for systematic genome-wide approach

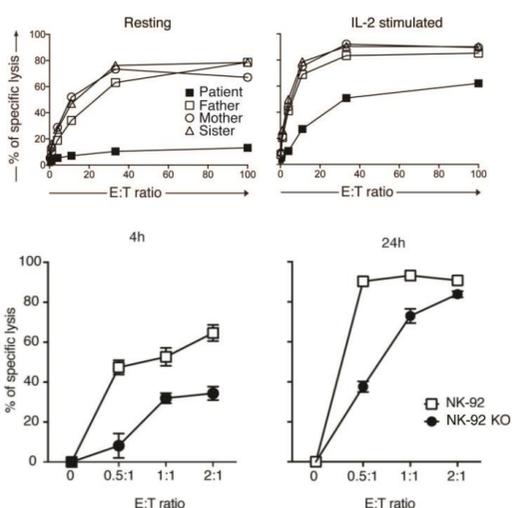


**Figure 5.** The effect of CRISPR-mediated gene ablation on exocytosis efficiency in NK92 cells upon stimulation with target cells or PMA/Ionomycin.

## Novel human immunodeficiency with FHL phenotype



**Figure 2.** Index patient with novel mutation presenting with diagnostic HLH criteria<sup>5</sup>.



**Figure 3.** Primary NK cells and NK92 KO cell line show diminished cytotoxic activity towards target cells – a hallmark of HLH.

## FUTURE DIRECTIONS

- Use targeted approaches to dissect the cellular pathways & key molecules responsible for rescue & pathology-causing mechanisms
- Probe & validate drug screen hits with help of pathway annotation
- Perform CRISPR screen and validate candidate genes identified

## REFERENCES

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