Docket #: S16-025

High-throughput precision genome editing

Researchers at Stanford have developed a rapid and efficient method for high-throughput genome editing using CRISPR/Cas9. The CRISPR/Cas9 system allows researchers to edit any site in an organism's genome. However, in many organisms there are a large number of diseases or traits that are moderated by multiple genetic loci and thus many loci would need to be altered. Currently, it is too time consuming to precisely perform each edit. To overcome this limitation the inventors have developed this technology which enables precise, high-throughput genomic editing with CRISPR/Cas9. To increase the efficiency, it uses modified guide RNAs (gRNAs) that are tethered to the donor DNA sequence that serves as the repair template. This fast, multi-location, genome-wide precision editing technology opens the door to innumerable research applications in medicine and bioengineering.

Note: This technology is available for licensing in the plant field of use.

Stage of research
Validation studies have been performed in yeast and show great promise.

Applications

- High-throughput genomic editing for:
    - Research
    - Bioengineering

Advantages

- Rapid, multi-location, genome-wide precision editing.

Publications

- Published PCT application: WO 2018/049168

Patents

- Published Application: WO2018049168
- Published Application: 20190330619
- Published Application: 20230383290
- Issued: 11,760,998 (USA)

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