Single-Step Method to Fragment and Tag Both Ends of DNA Molecules with Arbitrary Nucleotide Sequences

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Technology description

Researchers in the Lewis-Sigler Institute for Integrative Genomics at Princeton University have developed a new simplified method to fragment and tag both ends of DNA molecules with arbitrary nucleotide sequences for Next Generation Sequencing as well as other high-throughput DNA processing.

This invention combines all reagents in a single step to fragment and tag both ends of DNA molecules with desired nucleotide sequences with optional PCR amplification, while all other existing NGS library preparation methods involve multiple steps which use different reagents.

This invention not only reduces the hands-on sample processing time, but also greatly facilitates the high-throughput compartmentalized DNA processing, such as water-in-oil emulsion droplets, which are not amenable to using different reagents in multiple steps. This invention can potentially be used in other types of compartmentalized micro-reactors and nano-biotechnologies.

Application area

- DNA library preparation for Next-Generation Sequencing
- Emulsion droplet based DNA processing
- Nano-biotechnologies and other micro-reactors on DNA

Advantages

- Simplest 1-step method
- Single reaction mixture including all reagents and DNA sample
- Reaction controlled by a series of incubation temperatures
- Reduced sample processing time
- Optional final PCR amplification

Institution

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