

Docket #: S00-132

Multiplex Pyrosequencing for Typing

Stanford researchers at the Genome Technology Center have developed a simple, reliable, and accurate method for obtaining sequencing information for multiple sites within target nucleic acid. Since each pattern contains more than one unique peak for each genotype, the analysis time is shortened thus reducing costs while providing more accurate data. The method is useful for microbial typing or analysis of more than one single-nucleotide polymorphisms in one pool.

Applications

- Genotyping
- Microbial typing and analysis

Advantages

- Shortened analysis time
- Reduced cost
- Improved data

Patents

- Published Application: [WO2002020837](#)
- Published Application: [20050084851](#)

Innovators

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