Sanger Sequencing Recap

Method

Chain termination sequencing using dideoxynucleotides (ddNTPs)

Year Introduced

1977 by Frederick Sanger (Nobel Prize 1980)

Read Length

400-900 base pairs per read

Accuracy

99.9% accuracy (very high)

Key Characteristics

- Gold standard for verification and validation
- Low throughput - sequences one fragment at a time
- Relatively expensive per base (~$500 per sample)
- Takes several hours to complete
- Best for targeted sequencing of specific genes

Clinical Use Today

Still widely used for confirming genetic variants and clinical diagnostics