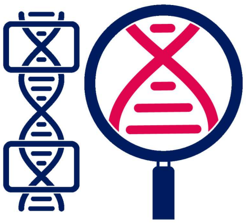
GENERAL *DETAIL* *REPORT*

Choose efficient, cost-effective sequencing focused on protein-coding regions. Our whole exome sequencing (WES) service lets you choose from a range of industry-leading library prep kits for hybridization enrichment – including those from Agilent and Twist – to make sure you get the reliable libraries you need.



Whole exome sequencing (WES) is a targeted approach that makes it possible to identify variations in the protein-coding part of a genome. In humans, only around 1% of the genome consists of exomes. However, **most disease-related genetic variants occur in exons, making these regions crucial to many genetic studies.**

Because the sequenced region is narrowed down from gigabasepairs to megabasepairs, **sequencing throughput required per sample per analysis is much smaller**. **This makes exome sequencing unbeatable in terms of precision and economy and method of choice for many researchers and clinicians.**

APPLICATIONS

WES can provide insights into the **genetic origins of Mendelian diseases** or traits that are hard to study with conventional gene discovery strategies. Exome sequencing of parent–child trios is also a highly effective approach for **identifying de novo coding mutations of a disease**, as it is very unlikely that multiple de novo events occur in one specific gene.