HSMD Solution Overview for Clinical Labs

The Human Somatic Mutation Database (HSMD) is a web-based application that allows you to harness genetic insights from QIAGEN's real-world oncology dataset combined with knowledge from 2 decades of expert curation. HSMD contains over 300,000 clinical oncology cases and over 1.3 million mutations associated with over 3.4 million relationships from PubMed, drug labels, clinical trials, clinical guidelines and public databases such as gnomAD and HGMD.

The comprehensive, weekly updated aggregation of structured content delivers valuable scientific information that enables scientists to search and explore biological, clinical, and disease-relevant mutations and genes. HSMD covers content for spontaneous mutations as well as cancer-associated inherited variants, to give full insights into the complexity of cancer genetics, and the oncogenic potential of a mutation.

Value	Benefits	Features
Spot key findings from tumor molecular profile	Gain insights into clinically observed mutation and gene prevalence and drill down into the biological, clinical and disease specific role.	Industry's largest cancer genomic knowledge base integrating content from over 300,000 observed clinical cases and over 1.3 million mutations with associated content from over 3.4 million structured relationships.
Reduce operational bottlenecks	Search, explore and synthesize weekly updated key findings about genes, diseases, variants, clinical trials and drugs from a single integrated database.	Users can flexibly search high-quality, in-depth variant, gene and disease specific information online.
Accelerate drug development programs	Make better-informed decisions on the significance of variants by accessing quality somatic cancer driver information.	Offers deep insights into expertly curated and clinically observed somatic variants to facilitate understanding of the classifications and precise functions of variants during precision medicine R&D.