



## Molecular pathology

### Dataome and MH Guide: Making knowledge clinically relevant

In the first five months of 2020, 2,655 medical publications were published on ovarian cancer alone.<sup>1</sup> Have you read them all? Which of these are relevant for your clinical practice? Curated knowledge databases, such as those used in the Molecular Health Guide (MH Guide), may be useful for you.



#### Medical knowledge doubles every 73 days

Medical and clinical knowledge is constantly increasing worldwide: A study predicted a doubling time of about 2.5 months in 2020, down from an estimated 3.5 years in 2010.<sup>2</sup> This is associated with several challenges, such as advancing specialization, increasingly data-intensive diagnostic tests, and the demand for personalized medicine.

Specific software solutions may help link this ever-evolving medical knowledge with clinical relevance and integrate it into one's daily routine. MH Guide supports doctors in identifying individual, optimally effective tumor therapies for patients.<sup>3,4</sup>

#### MH Guide uses information provided by Dataome

The partially curated knowledge database Dataome helps bundle together daily increasing medical knowledge. Complex genetic tumor data, such as NGS data, are efficiently and automatically collated by MH Guide with information obtained from Dataome. MH Guide interprets clinically relevant gene variants and annotates these with clinico-molecular variant interpretations with regard to response or resistance to drug therapy.<sup>3,4</sup>

## MH Guide



- is a CE-marked in vitro diagnostic (IVD) software.<sup>3,4</sup>
- is continuously updated with the latest data from the Dataome knowledge platform, which is evaluated by scientific and medical experts.<sup>3,4</sup>
- contains clinico-molecular variant interpretations (CVIs) for 5,490 variants in 491 genes (as of 06/2020).
- offers the possibility to integrate your own clinico-molecular variant interpretations.<sup>3,4</sup>

## How the Dataome knowledge base works

Dataome technology, developed over more than a decade, is characterized by 3 innovations:

### 1. Dataome capture:<sup>5,6</sup>

Acquisition: Freely accessible and proprietary molecular and clinical data sources are searched in real time and processed in the Dataome knowledge platform.

Quality assurance: Gene variants are interpreted by targeted curating by scientific (molecular biologists) and medical experts (molecular pathologists and oncologists).

### Which sources are integrated?

Dataome integrates data from a variety of structured and unstructured sources. These include published scientific and biomedical findings on cancer therapies, signaling pathways and clinico-molecular variant interpretations (CVIs) as well as clinical (genome) studies and drug data.<sup>5,6</sup>

### 2. Dataome knowledge base:<sup>5,6</sup>

The knowledge database Dataome bundles and structures clinico-molecular data and current molecular biological literature from across the world. Dataome thus enables data to be classified in a medically relevant context.

### 3. Dataome analytics:<sup>5,6</sup>

The Dataome knowledge database provides content for analysis platforms, such as MH Guide, and thus enables clinically relevant gene variants to be identified and interpreted from complex genetic tumor information.

The identification of variants and annotations of biomarkers is based on:<sup>5</sup>

ACMG variants classification, COSMIC, BRCA exchange, CVIs (Molecular Health's Proprietary CVI Database), AMP/CAP/ASCO Classification, gnomAD based population frequencies

Recommendations for therapy and clinical studies are based on:<sup>5</sup>

CVIs (Molecular Health's proprietary CVI database), WHO and NCT clinical studies, drug approval status (global data), NCCN guidelines, curated ESMO guidelines, clinical trial NGS biomarkers

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## Sources

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