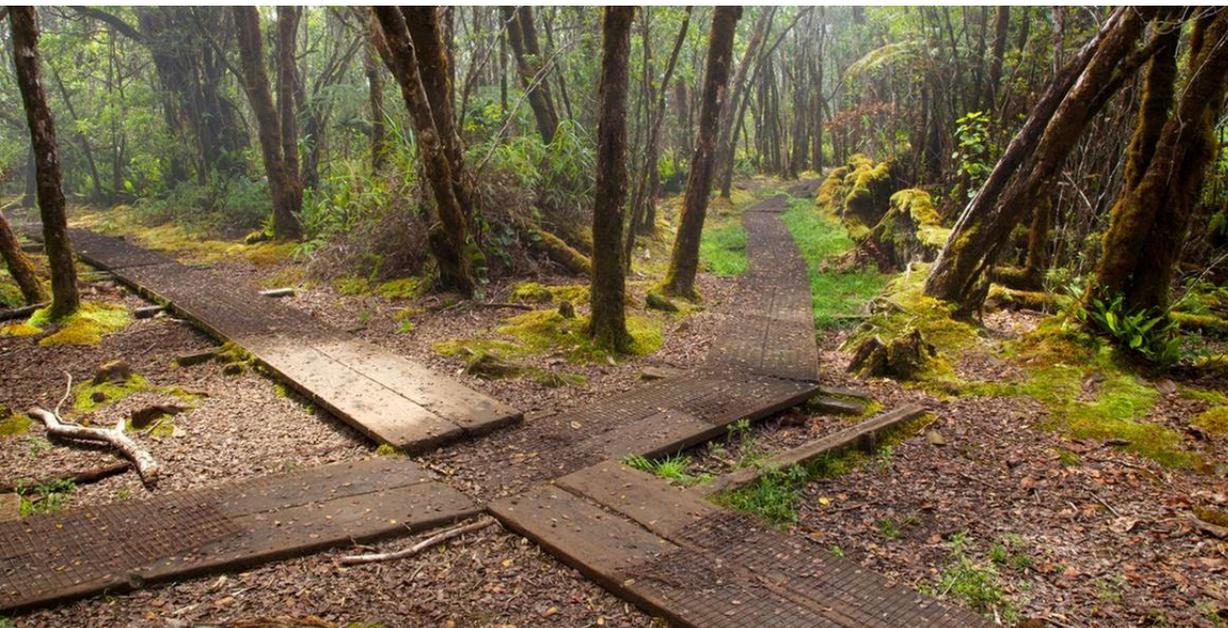




Derive treatment options from NGS data

MH Guide: Finding one's way through the oncological therapy jungle

Molecular tumor analyses are relevant to therapy in an increasing number of indications. But what treatment options are available for the identified molecular changes? The use of the MH Guide provides you with concrete and patient-specific answers for therapy decisions.



More than half of oncology studies with biomarkers

Since 2011, an average of about one oncology drug per month has been approved in Germany.¹ By the end of 2023, another 206 projects could lead to approval or approval extension of cancer therapies, according to an October 2019 survey by the research-based pharmaceutical companies (vfa).² Also, the proportion of clinical trials worldwide investigating new anticancer drugs that have used biomarkers is steadily increasing: while this was 15% in 2000, by 2018 biomarkers were used in 55% of oncology trials.³

Challenge: Finding therapeutic options available from biomarkers

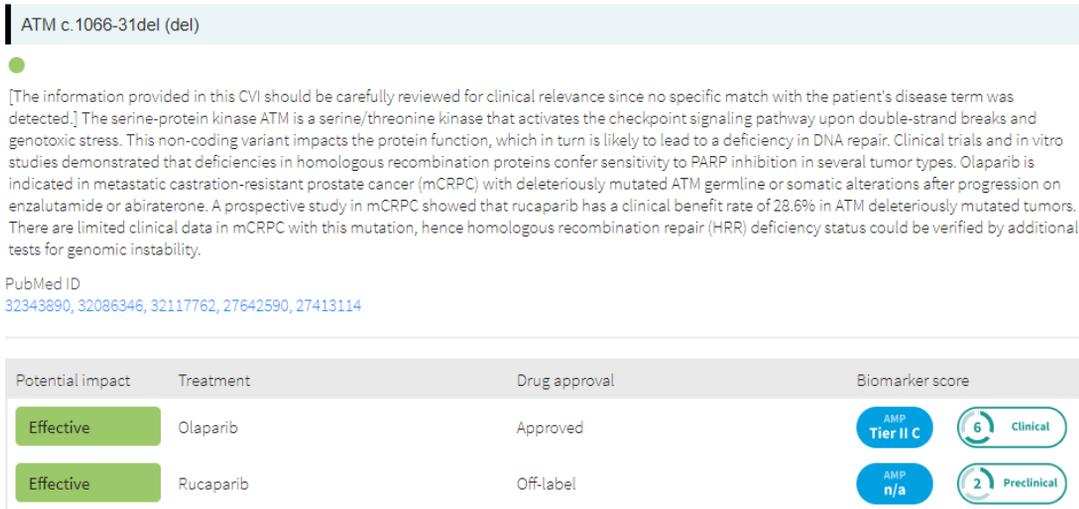
The increasing number of molecular-stratified therapy options presents physicians and members of (molecular) tumor boards with the difficulty of interpreting the results of a molecular tumor analysis and finding appropriate therapy options for their patients. According to a colloquium survey, 41% of oncologists and pathologists see the clinical consequence of a molecular tumor diagnosis for the patient as the greatest challenge.⁴

MH Guide helps with biomarker-based therapy decision

Software solutions like MH Guide help evaluate clinical options. MH Guide comprehensively analyzes the data of a molecular tumor diagnosis and links it with information on possible therapy options that match the individual tumor profile and appropriate clinical studies. Thus, the CE-marked software supports^{5, 6}

- Molecular pathologists in the evaluation of complex genetic tumor data and
- The treating oncologists in clinical therapy decisions.

Figure 1



All clinically relevant variant interpretations are evidence-based and transparent for physicians through source links, e. g. to PubMed ID (**Fig. 1**). This allows physicians to make well-informed treatment decisions with MH Guide.^{5, 7}

Analyzing tumor genetic data in an evidence-based manner with MH Guide

MH Guide automatically analyzes tumor genetic data from data in FASTQ or VCF format, for example from NGS* sequencing, and matches it with biomedical knowledge. For this purpose, MH Guide uses data obtained from the continuously updated knowledge database Dataome. This brings together a wide range of peer-reviewed information from recognized literature sources, genomic studies and reference databases.^{5,6}

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* Next-generation sequencing

Figure 2: Interpretation of the gene variants found according to the ACMG classification.

ACMG criteria <small>highlighted = activated, bullet = automatically calculated</small>	Pathogenic criteria										Benign criteria										Final ACMG classification and active criteria								
Evidence	VERY STRONG				STRONG				MODERATE				SUPPORTING				STAND-ALONE				STRONG				SUPPORTING				Pathogenic
Predictive data	✓ PVS1*	✗ PS1*	✗ PM4*	✗ PM5*	✗ PP3*																				✓ PVS1*	Potentially truncating variant in a gene where loss of function is a known mechanism of disease.			
Functional data		✓ PS3*	✓ PM1*		✗ PP2*																				✓ PS3*	The variant has a damaging effect on the gene product according to functional studies curated and stored in the MH Variant annotation database.			
Population data		✗ PS4	✓ PM2*																						✓ PM1*	The variant is in a mutational hot spot or a well-established functional domain where more than 66.6% of variants are pathogenic.			
De novo data		✗ PS2	✗ PM6																						✓ PM2*	The variant is absent from population frequency databases such as the Genome Aggregation Database.			
Allelic data			✗ PM3																						✓ PM5*	The variant was reported as pathogenic in variant classification databases such as ClinVar.			
Segregation data					✗ PP1																								
Other databases					✓ PP5*																								
Other data					✗ PP4																								

From the annotated clinical variant interpretation, MH Guide derives individual therapy options.^{5,6} The user can customize the analysis e. g.

- interactively select or deselect variants if further information is available
- Add your own clinical molecular variant interpretations.
- Integrate other biomarkers, e. g. from non-NGS methods⁵

MH Guide Report: Biomarkers and treatment options at a glance

The software derives personalized treatment options from your patient’s molecular tumor profile. From this, MH Guide automatically generates a report that can be specified and customized by the user (**Fig. 3**). This contains a clear overview of ^{5,6}

- the therapy-relevant biomarkers found and
- the available treatment options derived from them.

In addition to the approval status, a traffic light color system allows at-a-glance predictions of efficacy and potential side effects. ^{6,9} The biomarkers are assigned to levels IA-IV according to the validated scoring system of the joint Association for Molecular Pathology (AMP), American Society of Clinical Oncology (ASCO), and College of American Pathologists (CAP) guideline, with an additional supplemental MH Guide proprietary classification.⁸

Figure 3: All important information for the therapy decision at a glance with the MH Guide report.

Potential impact	Treatment	Drug approval	Biomarker	VAF	Biomarker score
Effective	Osimertinib	Approved	EGFR p.T790M (SNV)	29.39%	AMP Tier I A 7 Clinically Approved
			EGFR p.E746_A750del (del)	29.59%	AMP Tier I A 7 Clinically Approved
Ineffective	Gefitinib	Approved	EGFR p.T790M (SNV)	29.39%	AMP Tier I B 6 Clinical
Ineffective	Afatinib	Approved	EGFR p.T790M (SNV)	29.39%	AMP Tier I B 6 Clinical
Ineffective	Erlotinib	Approved	EGFR p.T790M (SNV)	29.39%	AMP Tier I B 6 Clinical
Ineffective	Daacomitinib	Approved	EGFR p.T790M (SNV)	29.39%	AMP Tier I B 6 Clinical

MH Guide provides information on suitable clinical studies near the patient's home

In addition to identifying potentially effective treatment options, MH Guide allows you to find appropriate clinical trials for your patients and filter individually by proximity of the trial site to the patient's residence (Fig. 4). Based on the analyzed molecular genetic tumor profile, relevant and recruiting phase I-IV clinical trials deposited in the WHO or NIH database are displayed.^{5,6,10} Likewise, the user will find the following important information about the studies in a clear manner:

- Study title including identification number
- Inclusion criteria
- Phase of the study
- Active substance
- Location and distance of the study

Figure 4: MH Guide provides comprehensive information on suitable, recruiting clinical studies..

Clinical trials							
Review and select potentially suitable clinical trials for the report							
12 in total (12 reported)							
Trial	Biomarker eligibility criteria	Phase of trial	Eligibility	Drugs	Diseases	City	Report
NCT03374017: A Study of the Efficacy and Safety of Abiraterone Plus Enzalutamide Versus Enzalutamide Plus Placebo in Patients With Early Relapsing Recurrent Triple-Negative Breast Cancer	-	Phase 3	Age: 18, Gender: Both	Capecitabine; Carboplatin	Breast Neoplasms	Frankfurt (3 km)	<input checked="" type="checkbox"/>
NCT03369137: A Randomized, Open-Label, Multi-center Phase IV Study Evaluating Palbocicb Plus Endocrine Treatment Versus a Chemotherapy-based Treatment Strategy in Patients With Hormone Receptor Positive / HER2 Negative Breast Cancer in a Real-World Setting (SBC 93 - PADMA Study).	-	Phase 4	Age: 18, Gender: Both	Capecitabine	Breast Neoplasms	Frankfurt am Main (9 km)	<input checked="" type="checkbox"/>
NCT03901339: Study of IMMU-132 in HR+HER2- MBC (TROPIC-02)	Inclusion: ERBB2 protein expression: no expression ESR1 prot...	Phase 3	Age: 18, Gender: Both	Capecitabine	Breast Neoplasms	Frankfurt (9 km)	<input checked="" type="checkbox"/>
NCT02516819: Phase 1 Trial of MSC2480484A, an Inhibitor of a DNA-dependent Protein Kinase, in Combination With Radiotherapy	-	Phase 1	Age: 18, Gender: Both	Cisplatin	Neoplasms; Solid tumor	Mainz (27 km)	<input checked="" type="checkbox"/>

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