CURESPONSE

Curesponse is on a Mission to Improve Cancer Treatment.

ISO 15189 Approved

cResponse™ combines rapid genomic sequencing with a functional test, enabling prioritization of different therapeutic options for patients with metastatic cancer.

The cResponse™ solution

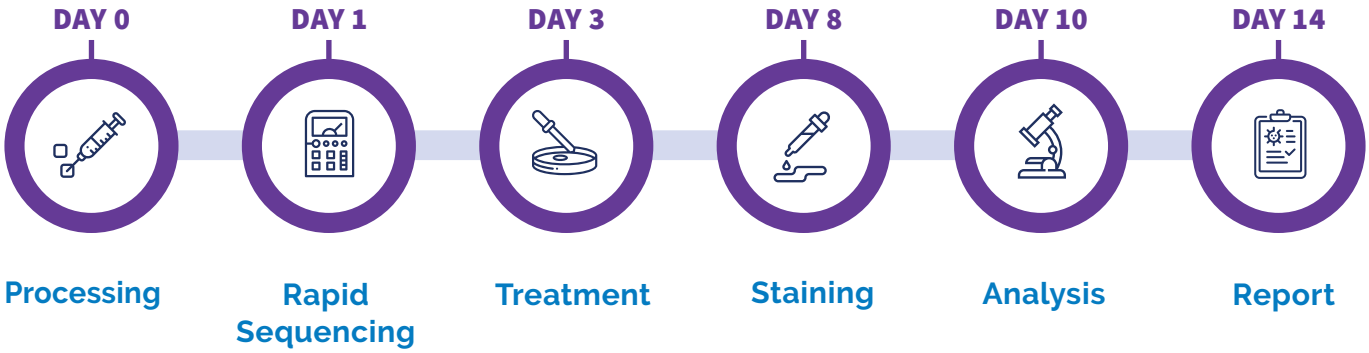
We offer an innovative functional test that in combination with rapid genomic sequencing, could assist your oncologist in prioritizing treatments and selecting the most effective treatment for you.

Background

It is well established that all tumors are different, and each patient will respond differently to anti-cancer drugs. Genomic sequencing provides a map of the genetic profile of your tumor and the potential therapeutic options. The cResponse™ test actually evaluates them on your tumor and assesses their relative effect.

The tumor microenvironment (TME), plays a central role in drug response and in many cases is a major factor in developing resistance of cancer to drugs. The cResponse™ platform preserves the tissue's 3D structure and maintains the TME, enabling assessment of your tumor's response to drugs in laboratory conditions.

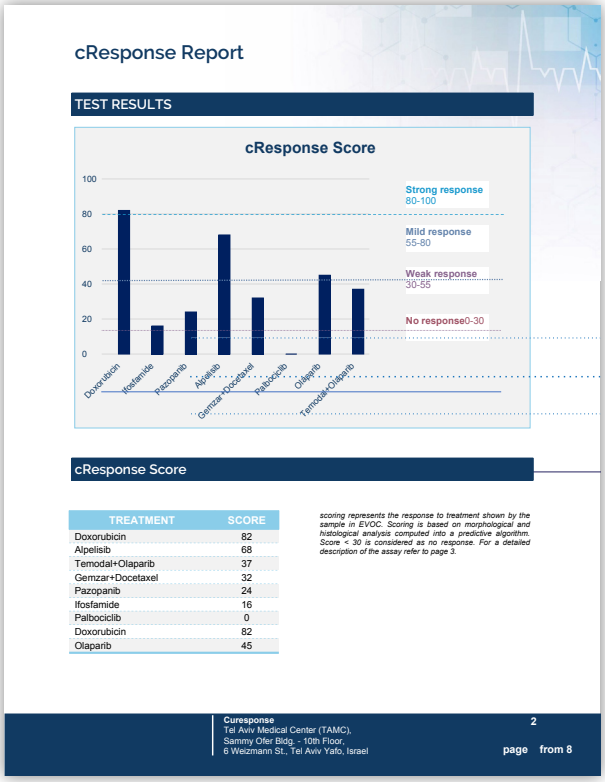
The process



A fresh biopsy arrives at a regional cResponse™ service center. Part of the sample undergoes rapid genomic sequencing to identify tumor-specific genomic alterations that may be targeted by specific anti-cancer drugs. Added to those selected by the physician, they create a panel of therapies to be tested in the system. The biopsy is cut into thick sections which are placed in a proprietary assay culture matrix and tests the cancer's sensitivity to various drugs or novel drug combinations. cResponse's proprietary evaluation system and response algorithm then prioritizes the options according to demonstrated drug efficacy, providing results, usually within two weeks.

The report

Upon conclusion of the test and analysis, we will provide a comprehensive report, summarizing the genomic information found in our rapid 57-gene panel, the different drugs we tested and the effect of each tested drug on the tumor sample as assessed in our platform.



cResponse Report

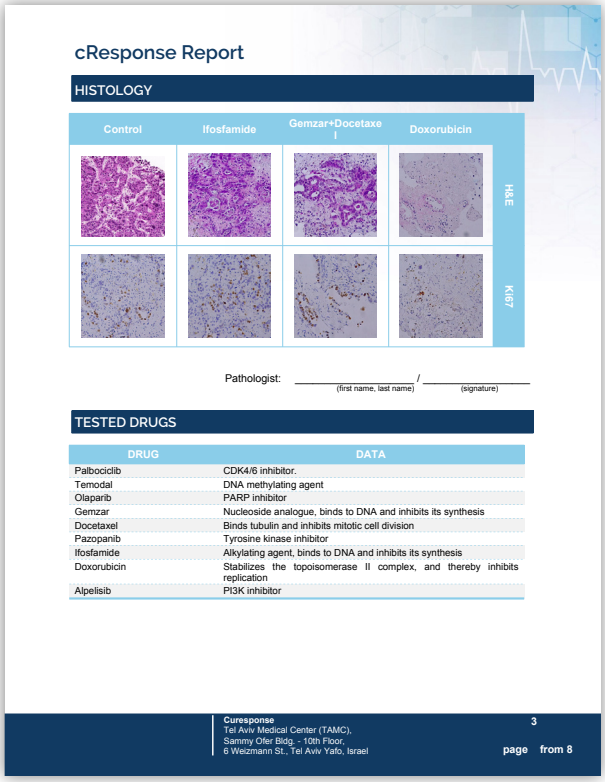
TEST RESULTS

cResponse Score

cResponse Score

TREATMENT	SCORE
Doxorubicin	82
Alpelisib	68
Temodal+Olaparib	37
Gemzar+Docetaxel	32
Pazopanib	24
Ifosfamide	16
Palbociclib	0
Doxorubicin	82
Olaparib	45

scoring represents the response to treatment shown by the sample in EVOC. Scoring is based on morphological and histological analysis computed into a predictive algorithm. Score < 30 is considered as no response. For a detailed description of the assay refer to page 3.



cResponse Report

HISTOLOGY

Pathologist: _____ / _____
(first name, last name) (signature)

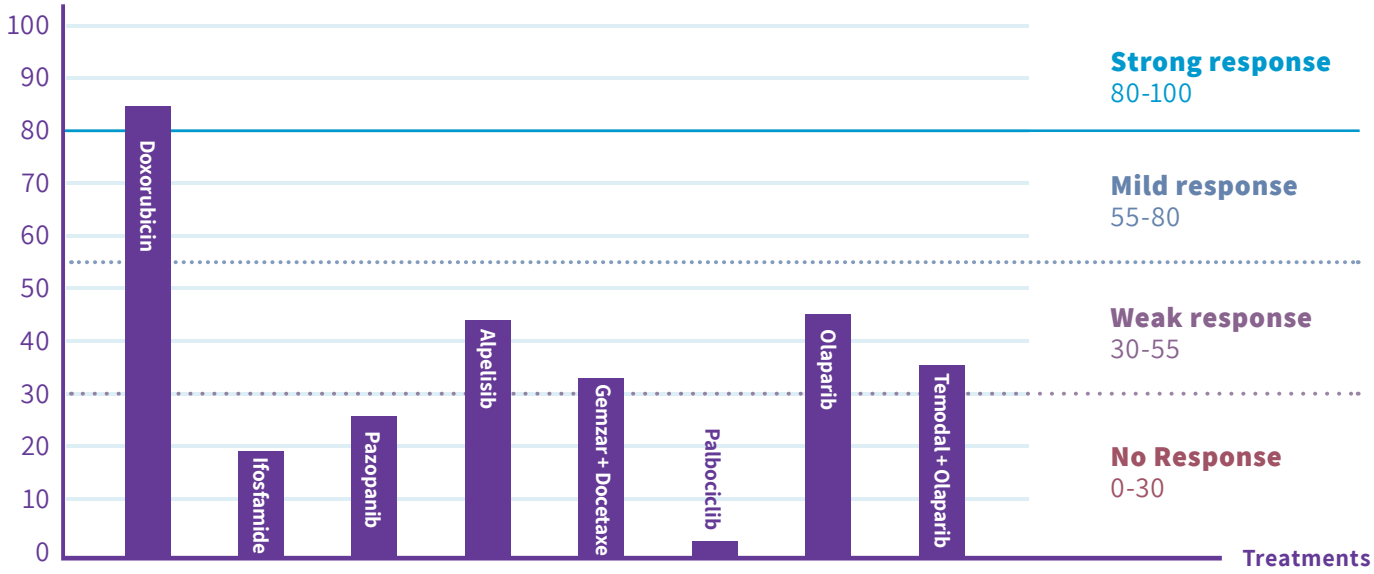
TESTED DRUGS

DRUG	DATA
Palbociclib	CDK4/6 inhibitor.
Temodal	DNA methylating agent
Olaparib	PARP inhibitor
Gemzar	Nucleoside analogue, binds to DNA and inhibits its synthesis
Docetaxel	Binds tubulin and inhibits mitotic cell division
Pazopanib	Tyrosine kinase inhibitor
Ifosfamide	Alkylating agent, binds to DNA and inhibits its synthesis
Doxorubicin	Stabilizes the topoisomerase II complex, and thereby inhibits replication
Alpelisib	PI3K inhibitor

The cResponse™ test is using a proprietary algorithm, where each drug is assigned a score of 0-100, with 100 reflecting a strong response to therapy in our assay and 0 reflects no response. The highest scoring drugs represent the most potent treatment option as tested in our proprietary assay and may indicate higher chances of clinical effect.

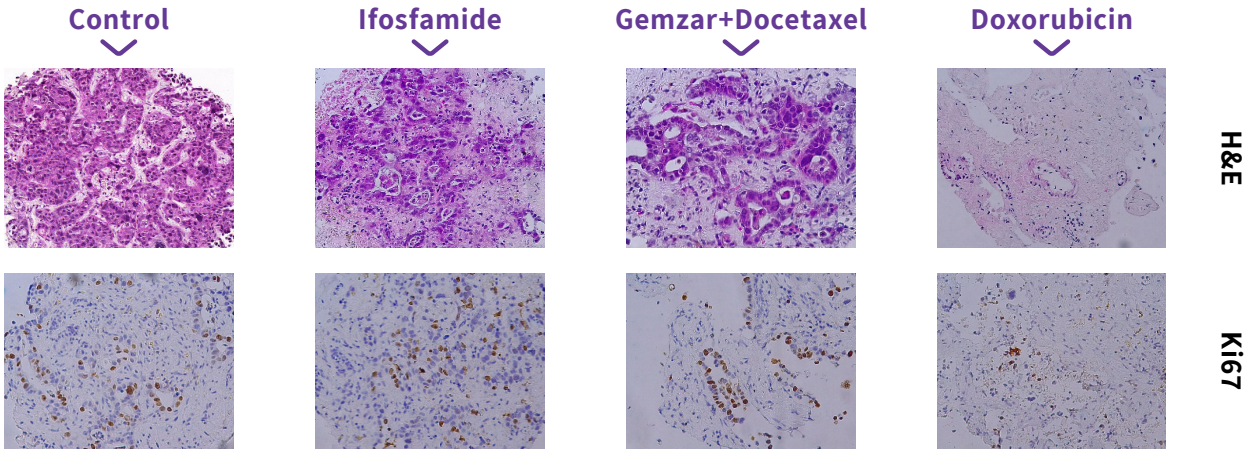
Drug response chart

cResponse™ Score



Images of the cancer tissue are also included in the report, demonstrating tissue morphology, viability and replication.

Images of the cancer tissue under different treatments



A list of the genes tested in our panel

286 amplicons covering hotspots of 57 actionable genes

ABL1, AKT1, ALK, APC, ATM, BRAF, CDH1, CDKN2A, CSF1R, CTNNB1, DDR2, DNMT3A, EGFR, ERBB2, ERBB4, EZH2, FBXW7, FGFR1, FGFR2, FGFR3, FLT3, FOXL2, GNA11, GNAQ, GNAS, HNF1A, HRAS, IDH1, IDH2, JAK2, JAK3, KDR, KIT, KRAS, MAP2K1, MET, MLH1, MPL, MSH6, NOTCH1, NMP1, NRAS, PDGFRA, PIK3CA, PTEN, PTPN11, RB1, RET, SMAD4, SMARCB1, SMO, SRC, STK11, TP53 (Whole CDS coverage), TSC1, TSC2, VHL.

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