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Cancer Hope
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# Comprehensive Tumour Investigation. More Knowledge. Better Treatment.

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ENCYCLOPEDIC TUMOUR ANALYSIS

**ABSOLUTE IMPACT**
**ABSOLUTE SCIENCE**
**ABSOLUTE COMMON SENSE**

DATAR CANCER GENETICS
UNITED KINGDOM | GERMANY | INDIA

## About exacta

Every human being is different and unique, similarly every person's cancer is unique.
Therefore, cancer should ideally be treated with a personalised strategy. Conventional 'Standard of Care' approaches do not take into consideration the molecular-genetic architecture of a particular patient's tumour. Consequently, patients could suffer due to failed therapies or aggressive relapse. It is imperative that the molecular architecture of the tumour is studied comprehensively before deciding on the treatment plan. The therapy can thus be tailored to the individual patient and their disease. This significantly increases the likelihood of successful treatment.

**exacta is a comprehensive analysis of molecular-genetic characteristics of solid tumours based on the results of several clinical studies.**

exacta helps to reveal clinically relevant **driver mutations and pathways.** This is ensured by the use of a variety of biomarkers and the analysis of **20,800 genes** in the tumour.
exacta identifies the most effective **chemotherapeutic agents** and **targeted therapies**.
exacta enables a **highly sophisticated treatment strategy** beyond conventional perspective, even for difficult to treat or late stage cancers.

## exacta is particularly recommended for cancer patients where ...

... first-line therapy has failed.

... cancer has relapsed.

... cancer is high-grade / metastatic.

... challenging cancers such as stomach, oesophagus, pancreas, gall bladder, GIST etc. have been newly diagnosed.

... the risk of therapy failure is high.

## exacta Methodology

| | |
|---|---|
| Targeted genes | Tissue DNA and ctDNA:<br>SNVs, CNVs, gene amplifications, mutational burden, germline mutations |
| Immunocytochemical analysis | CTC:<br>mTOR, VEGFR1, VEGFR2, EGFR, VEGFA |
| mRNA sequencing | Tissue or exosomes: Signalling pathways, transcriptome (disease-related, therapy-relevant and resistance patterns) |
| Pharmacogenetics | Genotyping, including for CYP450, transporter proteins for assessment of drug toxicity and efficacy |
| Chemoresistance profile | CTC: Patented in vitro cell based assay on living cells to assess the effectiveness of chemotherapeutic agents |
| Immunohistochemistry | Tissue:<br>PDL1, AR and if applicable, ER/ PR /HER2 |

ctDNA: Circulating Tumour DNA
TMB: Tumour Mutational Burden
SNVs: Single Nucleotide Variations
CTC: Circulating Tumour Cells
CNVs: Copy Number Variations

## exacta Advantages

### Most Optimal Targeted Therapy Selection:

- exacta identifies possible molecular targets and cell cycle pathways to find the most appropriate molecular therapy for targeted treatment.
- All relevant biomarkers for targeted therapy selection, including mutations, deletions, gene rearrangements, gene amplifications /expression, are analysed.

### Most Optimal Cytotoxic Therapy Selection:

- Cytotoxic drug response /resistance of cancer genome, based on DNA and gene expression.
- Analysis of the effectiveness of chemotherapeutic agents and, upon request, other active substances on living tumour cells.

### Assessment of adverse drug reactions:

- Selection of therapy with least side effects based on pharmacogenetics.

## Comprehensive exacta

| Parameters and Methods of Analysis | exacta |
|---|---|
| Tumour DNA analysis | 511 genes (tissue biopsy)<br>411 genes (liquid biopsy) |
| Mutations and gene amplifications | ✓ |
| Fusion / rearrangements | 51 genes (tissue biopsy)<br>12 genes (liquid biopsy) |
| Tumour gene expression | approx. 20.800 genes |
| Cellular pathways as per KEGG | ✓ |
| Chemoresistance profile<br>(Chemotherapeutic agents + complementary substances) | up to 70 substances |
| Liquid biopsy cell free DNA (cfDNA) | ✓ |
| ICC immunocytochemistry (mTOR, VEGFR, EGFR, etc.) | ✓ |
| Microsatellite instability (MSI / MMR) | ✓ (tissue biopsy / liquid biopsy) |
| Tumour mutational burden (TMB) | ✓ |
| Relevant IHC, PD-L1, AR etc. | ✓ (tissue biopsy) |
| Circulating tumour cells (CTCs) | ✓ |
| Pharmacogenetics | ✓ |
| Limit of detection (MAF) | 0,1% (cfTNA) |
| Sensitivity at 0,1% MAF (cfTNA) | 97,06% |
| Positive predictive value | 100% |

NGS: Next-Generation Sequencing
IHC: Immunohistochemistry
cfDNA: Cell Free DNA

cfTNA: Cell Free Total Nucleic Acid
MAF: Mutant allele frequency
MMR: DNA mismatch repair

KEGG: Kyoto Encyclopedia of Genes and Genomes

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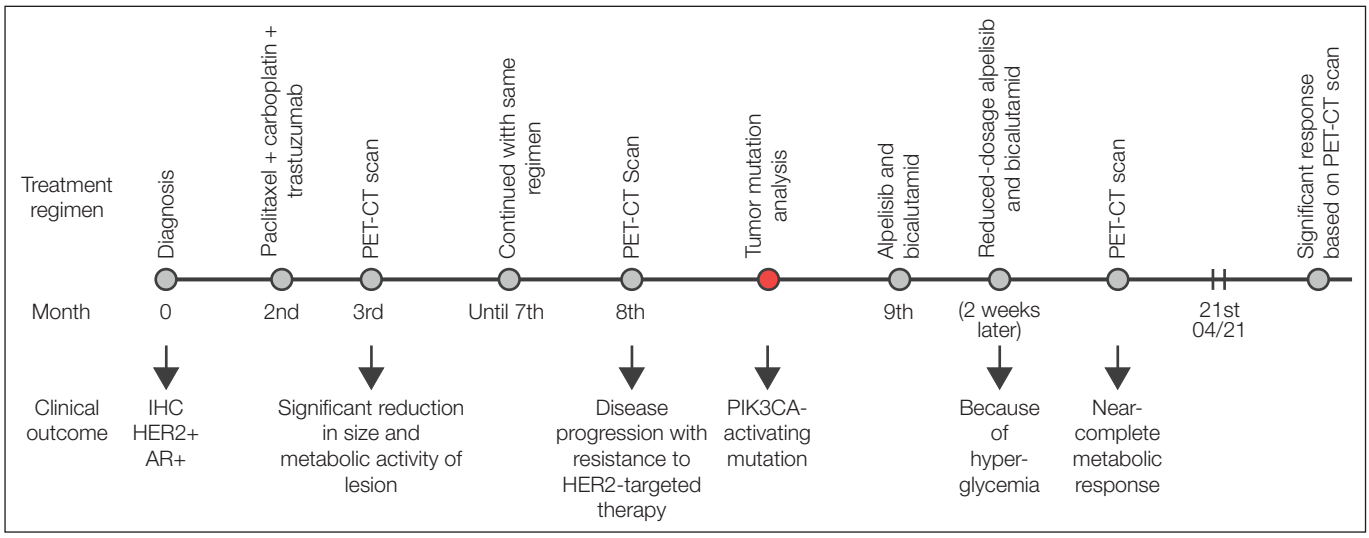
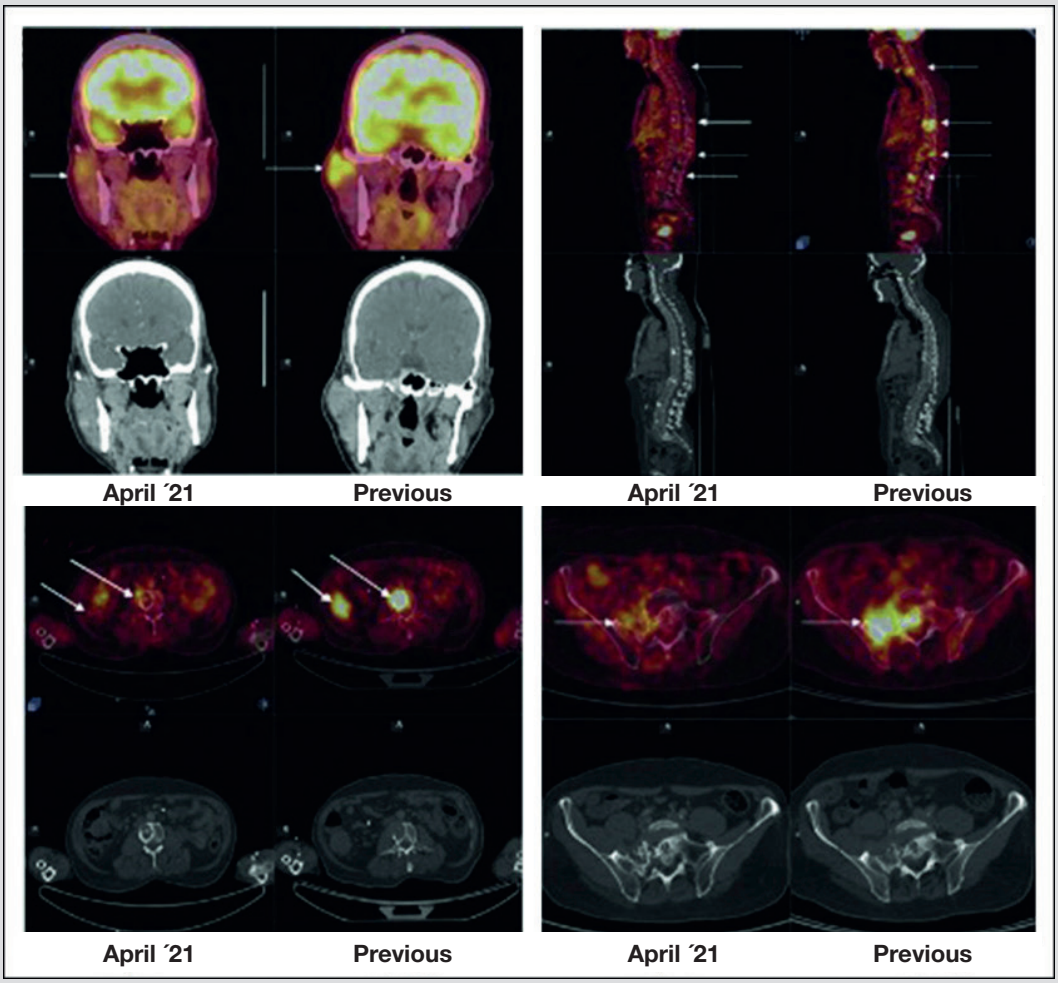
## Case Study I

# Advanced salivary duct carcinoma, 64-year-old male patient




## Result of the recommended therapy




Sheth H. et al. Excellent Response With Alpelisib and Bicalutamide for Advanced Salivary Duct Carcinoma With PIK3CA Mutation and High Androgen Receptor Expression-A Case Report. JCO Precis Oncol. 2021 May 3;5:PO.20.00436. doi: 10.1200/PO.20.00436.

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## Case Study II

# Stage IV Triple negative breast cancer
# 22-year-old female patient

### Clinical History

| | |
|---|---|
| Aug '16 | **Diagnosis: TNBC** |
| Aug – Jan '16 | Cyclophosphamide + Doxorubicin + Docetaxel |
| Nov '16 | Left Mastectomy |
| Feb – Mar '17 | Radiotherapy |
| May – Jun '17 | Methotrexate + Cyclophosphamide |
| Jun – Jul '17 | Everolimus |
| Jul '17 | **PET-CT: Progression** |
| Jul '17 | exacta |

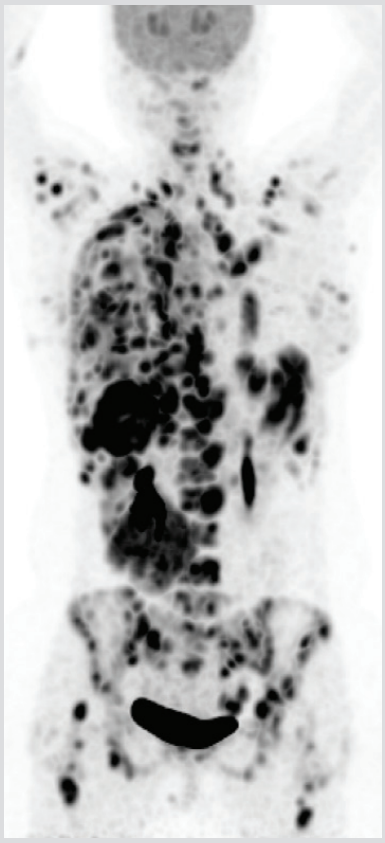
### Results from exacta

| Gene / Pathway / Analysis | Medications based on the respective analysis |
|---|---|
| PDGFRA, KIT, KDR | Axitinib |
| Chemosensitivity | Carboplatin Gemcitabine |

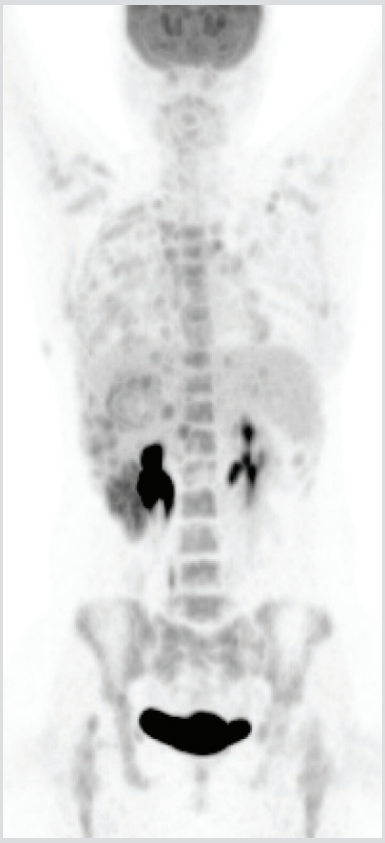
## Success of the recommended therapy

**before**

Cancer had progressed following 5 lines of therapy.



day 0



**after**

Administration of exacta: recommended therapy led to regression of cancer.

day 34

# Comparison chart exacta / exacta Basic

| No. | Features | exacta Tissue and blood based | exacta Blood based | exacta Basic Tissue and blood based | exacta Basic Blood based |
|---|---|---|---|---|---|
| 1) | Analysed genes | 511 genes | 411 genes | 511 genes | 411 genes |
| 2) | Gene rearrangements / InDels | 51 genes | 12 genes | 51 genes | 12 genes |
| 3) | Gene amplifications | 354 genes | 409 genes | 354 genes | 409 genes |
| 4) | Chemoresistance profile of cytotoxic drugs | up to 70 substances | up to 70 substances | up to 70 substances | up to 70 substances |
| 5) | mTOR, EGFR, VEGFR1, VEGFA, VEGFR2 expression analysis through ICC | ✓ | ✓ | ✓ | ✓ |
| 6) | Gene expression: ca 20.800 genes | ✓(tissue) | ✓(exosomal) | × | × |
| 7) | Tumour mutation burden (TMB) | ✓(TMB) | ✓(blood TMB) | ✓(TMB) | ✓(blood TMB) |
| 8) | Microsatellite instability/ MMR gene analysis | ✓(MSI/MMR) | Germline sequencing of MMR genes | × | × |
| 9) | IHC analysis | ✓ | × | × | × |
| | AR, PD-L1 28-8 and 22C3 IHC analysis (for all solid tumours) | ✓ | × | × | × |
| | HER2 IHC analysis (breast, endometrium, esophagus, stomach, colon, gall bladder) | ✓ | × | × | × |
| | ER, PR IHC analysis (breast, ovaries, endometrium) | ✓ | × | × | × |
| 10) | Number of circulating tumour cells | ✓ | ✓ | ✓ | ✓ |
| 11) | Blood-based HMAF | ✓ | ✓ | × | ✓ |
| 12) | Pharmacogenetics | ✓ | ✓ | × | × |
| 13) | Simultaneous analysis of tissue DNA and cellfree DNA | ✓ | × | × | × |
| 14) | Sectoral BRCA1/2 gene sequencing | ✓ | × | ✓ | × |
| 15) | BRCA1/2 MLPA analysis (breast, ovaries, pancreas, prostate) | ✓ | ✓ | × | × |
| 16) | Complementary substances | Based on RNA, optional chemosensitivity | Based on RNA, optional chemosensitivity | Optional | Optional |

HMAF: Highest mutant allele frequency MLPA: Multiplex ligation-dependent probe amplification

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## FAQs

### Can a patient's exacta result be used for another patient with the same diagnosis?

Just as every patient is unique, so is every cancer. No two patients' cancers are alike. Even two similar patients (e.g. age, gender, height, lifestyle) with the same type of cancer will have different molecular tumour profiles. Hence, each patient should perform an individual exacta test.

### Why is it important to start treatment immediately?

Cancer can be very aggressive and may evolve rapidly; the tumour profile can change dramatically over time. If there is a long enough delay, the cancer may gain resistance to treatments and re-analysis may be required. With exacta, therapy can be adapted quickly.

### What kind of drugs will be recommended to the patient?

Only drugs that have been approved by the FDA will be recommended. exacta will distinguish in its report clearly between on-/off-label drugs based on the individual cancer disease. Complementary substances can be tested as an additional option.

### Are there any follow-up molecular tests to assess the result of recommended therapy?

Molecular tests like our cancertrack analysis allow the oncologists to monitor the therapy in real time. In addition, the test provides insights into genetic changes of the original tumour in order to adapt the therapy.

## Publications


1. Schaffrin-Nabe D., Josten-Nabe A. et al. (2025) 'Real-World Applications of Comprehensive Tumor Profiling for Personalized Cancer Therapy in Metastatic Patients', J Oncol Res Ther, 10:10289. doi: 10.29011/2574-710X.10289.
2. Patil D., Akolkar D. et al. (2022) 'Multi-analyte liquid biopsies for molecular pathway guided personalized treatment selection in advanced refractory cancers: A clinical utility pilot study', Front Oncol, 12:972322. doi: 10.3389/fonc.2022.972322.
3. Schaffrin-Nabe D., Schuster S. et al. (2022) 'Case Report: Extensive Tumor Profiling in Primary Neuroendocrine Breast Cancer Cases as a Role Model for Personalized Treatment in Rare and Aggressive Cancer Types', Front Med (Lausanne), 9:841441. doi: 10.3389/fmed.2022.841441.
4. Crook T., Patil D. et al. (2021) 'Angiogenesis Inhibitors in Personalized Combination Regimens for the Treatment of Advanced Refractory Cancers', Frontiers in Molecular Medicine, 1, p. 749283. doi: 10.3389/fmmed.2021.749283.
5. Akolkar D.B., Patil D. et al. (2021) 'Concordancy of Immunocytochemistry Profiling of Circulating Tumor Cells with Immunohistochemistry for Analysis of Therapeutically Relevant Biomarkers', Journal of Clinical Oncology 39, no. 15_suppl (May 20, 2021) 3047-3047. doi: 10.1200/JCO.2021.39.15_suppl.3047.
6. Sheth H., Kumar P. et al. (2021) 'Excellent Response With Alpelisib and Bicalutamide for Advanced Salivary Duct Carcinoma With PIK3CA Mutation and High Androgen Receptor Expression—A Case Report', JCO Precision Oncology, (5), pp. 744–750. doi: 10.1200/PO.20.00436.
7. Crook T., Patil D. et al. (2021) 'Improved Treatment Outcomes by Using Patient Specific Drug Combinations in Mammalian Target of Rapamycin Activated Advanced Metastatic Cancers', Frontiers in Pharmacology, 12, p. 631135. doi: 10.3389/fphar.2021.631135.
8. Crook T., Gaya A. et al. (2021) 'Clinical utility of circulating tumor-associated cells to predict and monitor chemo-response in solid tumors', Cancer Chemotherapy and Pharmacology, 87(2), pp. 197–205. doi: 10.1007/s00280-020-04189-8.
9. Limaye S., Kumar P. et al. (2020) 'A case report of androgen receptor inhibitor therapy in recurrent high-grade serous ovarian cancer', Oncotarget, 1(46), pp. 4358–4363. doi: 10.18632/oncotarget.27809.
10. Nagarkar R., Patil D. et al. (2019) 'Encyclopedic Tumor Analysis for Guiding Treatment of Advanced, Broadly Refractory Cancers: Results from The RESILIENT Trial', Oncotarget, 10(54), pp. 5605-5621. doi: 10.18632/oncotarget.27188.
11. Crook T., Vaid A. et al. (2019) 'mTOR Inhibitors in Combination Regimens Guided by Encyclopedic Tumour Analysis Show Superior Outcomes Compared to Monotherapy in Refractory Cancers', Annals of Oncology, 30 (Supplement_7), vii32. doi: 10.1093/annonc/mdz413.115.
12. Ranade A., Patil D. et al. (2019) 'Adaptive, Iterative, Long-Term Personalized Therapy Management in a Case of Stage IV Refractory NSCLC', Journal of Personalized Medicine, 9(3), p. 34. doi: 10.3390/jpm9030034.



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