TEMPUS

Creating more options for your patients

Our collection of offerings uncover unique insights that empower you to customize treatment for individual patients, throughout their cancer journey

PhileKorea
Specialized in Medical & Bio Science since 2000

Welcome to Tempus

Using modern genomic sequencing and state-of-the-art technology, we connect physicians with up-to-date treatment options and relevant insights that can be immediately translated into patient care.

Assay Panels and Specimen Requirements

General Specimen Requirements

- Streck tubes are stable at room temperature for 5 days.
- EDTA tubes are stable at room temperature for 3 days. Friday collection is not ideal unless the specimen is being shipped that day.

xT Solid Tumor + Normal Test

FEATURES

- 648 gene panel focused on actionable mutations by DNA sequencing (500x depth of coverage)
- Tumor + normal match (blood or saliva); Includes 65 incidental germline findings
- MSI status and Tumor Mutational Burden (TMB)
- PD-L1 (22C3, SP142, 28-8 clones) and MMR via IHC stains (optional)
- Full transcriptome by RNA sequencing (including clinically validated identification of relevant fusions, such as NTRK 1, 2 and 3)

SPECIMEN TYPES

- Solid tumor tissue (e.g. lung, colon, breast, pancreas, etc.)
- Normal (blood or saliva)

SPECIMEN REQUIREMENTS

- **Normal:** (2) 8.5ml streck tubes filled with peripheral blood; or saliva from

xT Solid Tumor Only Test

FEATURES

- All of the features listed above without the normal match
- Recommended when unable to obtain matched normal specimen or if the normal specimen cannot be successfully sequenced

SPECIMEN TYPES

- Solid tumor tissue (e.g. lung, colon, breast, pancreas, etc.)

SPECIMEN REQUIREMENTS

- **Normal:** No normal specimen collection

xT Hematologic Test

FEATURES

- All of the features listed above from xT solid tumor + normal test (as indicated by specimen type below)

SPECIMEN TYPES

- **Lymphoma:** Lymph node biopsy or bone marrow aspirate, clot, or biopsy[1]; peripheral blood accepted if sufficient circulating lymphoma involvement in blood
  - Saliva is required if normal match is ordered (no blood accepted for normal)
- **Leukemia:** Peripheral blood or bone marrow aspirate, clot, or biopsy[1]
  - No normal match is accepted
- **Myeloma:** Bone marrow aspirate, clot, or biopsy[1]
  - Saliva is required if normal match is ordered (no blood accepted for normal)

SPECIMEN REQUIREMENTS

- **Lymphoma malignancy:** Lymph node biopsy, peripheral blood, bone marrow aspirate (EDTA tube only), biopsy or clot
- **Lymphoma normal:** Saliva only for normal match, no blood
- **Leukemia malignancy:** Peripheral blood, bone marrow aspirate (EDTA tube only), clot or biopsy[1]
- **Leukemia normal:** No normal match
- **Myeloma malignancy:** Bone marrow aspirate (EDTA tube only), clot or biopsy[1]
- **Myeloma normal:** Saliva only for normal match, no blood

If testing for MDS, then peripheral blood is sufficient (EDTA tube only), but this needs to be explicitly clarified on requisition.

xF Liquid Biopsy Test

FEATURES

- 105 genes cell-free DNA (cfDNA) at 5,000x unique coverage (will be updated soon)
- MSI-H status and median variant allele fraction (mVAF)
- Recommended for lung adenocarcinoma or other solid tumor diagnoses (excluding brain cancers and sarcomas) with insufficient specimen on biopsy

SPECIMEN TYPES

- Peripheral blood for solid tumor only

SPECIMEN REQUIREMENTS

- **Tumor:** (2) 8.5ml streck tubes filled with peripheral blood
- **Normal:** No normal specimen collected

1. If bone or bone marrow biopsy requires decalcification, it must be done in EDTA following formalin fixation. Tissue should then be embedded in paraffin (FFPE).

Primary Test Options

Testing for Solid Tumors

CANCER SITE	PANEL TEST	NORMAL SPECIMEN FROM CLINIC	CANCER SPECIMEN FROM CLINIC	CANCER SPECIMEN
Solid tumor where a biopsy specimen is available	xT **Solid Tumor**	Normal blood or saliva (unless tumor only selected)	–	FFPE resection / biopsy
Solid tumor where a biopsy specimen is not readily available	xF **Liquid Biopsy**	–	Peripheral blood	–

Testing for Hematologic Malignancies

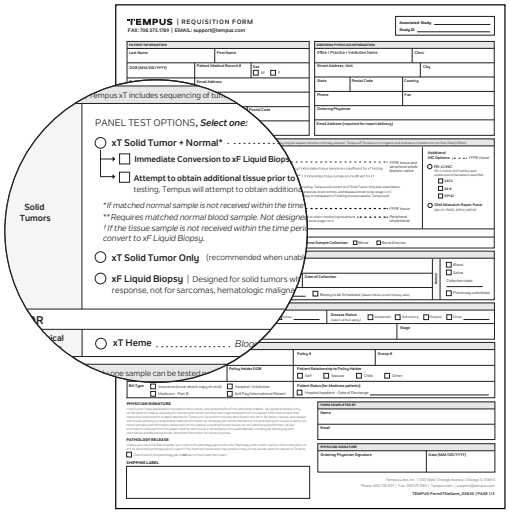
CANCER SITE	PANEL TEST	NORMAL SPECIMEN FROM CLINIC	CANCER SPECIMEN FROM CLINIC		CANCER SPECIMEN
Lymphoma (not in leukemic form)	xT **Solid Tumor**	Normal saliva	–		FFPE resection / biopsy
Leukemia, MDS, MPN	xT **Heme**	–	Peripheral blood or bone marrow aspirate	OR	FFPE bone marrow clot
Multiple myeloma	xT **Heme**	Normal saliva	Bone marrow aspirate	OR	FFPE bone marrow clot

Automatic Conversion to xF Liquid Biopsy

In the event of insufficient tissue quality and/or quantity, the test request can be converted to the xF blood-based biopsy test. Conversion requires the matched normal blood sample.

Select one option on the requisition form if you would like to auto-convert:

- Immediate conversion: if the sample is QNS (Quantity Not Sufficient), convert to xF.
- Attempt to obtain additional tissue: if the sample is QNS, Tempus will ask for more tissue time before converting to xF.



Result Timing and Delivery Method

Reports are delivered in approximately two weeks from the time Tempus has received both the tumor and normal samples (if applicable).

DAY 1	DAYS 3-5	~DAY 14[2]	DAYS 14-21
Sample received	PD-L1 IHC (if applicable)	DNA Sequencing Report[3]	MMR IHC RNA Sequencing/Follow-up Insights*

*Only available in Portal

We will contact care teams about delays to ensure transparency and to offer options.

2. Very small tissue biopsies may require additional lab processing time and/or additional tissue for test completion, resulting in longer testing time
3. Fusion analysis results by RNA Seq will be issued after the DNA Seq Report

Result Report

Ovarian Sample
Patient 109

Diagnosis
High grade serous carcinoma

Accession No.
200001

xT

Date of Birth
08/11/1974

Sex
Female

Physician
Nick Spears

Institution
Chicago Cancer Center

TEMPUS | xT
648 gene panel

Tumor specimen:
Uterus
Collected 04/11/2019
Received 09/26/2019
Tumor Percentage: 40%

Normal specimen:
Blood
Collected 09/22/2019
Received 09/23/2019

Note

This patient has a reportable germline variant in BRCA1 with somatic loss of heterozygosity. Genetic counseling is recommended. For additional detail, please see the Somatic Variant Details and Germline Variant Details sections of this report.

RNA fusion analysis is being performed and any fusions identified will be added to this report as an addendum. RNA expression analysis is being performed and will be reported in the Tempus online portal when complete.

GENOMIC VARIANTS

Somatic - Biologically Relevant | Variant Allele Fraction

TP53	p.R273H Missense variant - LOF	35.1%
BRCA1	Copy number loss	
MAP2K4	Copy number loss	
NF1	Copy number loss	

Germline - Pathogenic / Likely Pathogenic | Clinical Significance

BRCA1	p.S1253fs chr17:41243788	• Pathogenic Hereditary breast and ovarian cancer

IMMUNOTHERAPY MARKERS

Tumor Mutational Burden

3.2 m/MB — 39th percentile

Microsatellite Instability Status

Stable | Equivocal | High

FDA-APPROVED THERAPIES, CURRENT DIAGNOSIS

PARP Inhibitor	**Olaparib or Niraparib or Rucaparib**	BRCA1 p.S1253fs Loss-of-function GERMLINE Consensus, Ovarian Cancer: NCCN
Platinum Agent	**Cisplatin or Carboplatin**	BRCA1 p.S1253fs Loss-of-function GERMLINE Clinical research, Ovarian Cancer: PMID 24240112

FDA-APPROVED THERAPIES, OTHER INDICATIONS

Combination (Platinum Agent + PARP Inhibitor)	**Cisplatin + Olaparib**	BRCA1 p.S1253fs Loss-of-function GERMLINE Clinical research, Ovarian Cancer: PMID 24827126

We were unable to determine whether treatments on this report were previously prescribed for this patient.

xT Validation

The Tempus xT next generation sequencing assay is designed to detect actionable oncologic targets by sequencing tumor samples with matched normal saliva or blood samples, when available. The fourth version of the xT assay (v4) covers 648 genes spanning ~3.6 Mb of genomic space. From DNA sequencing, somatic and incidentally detected germline single nucleotide variants (SNVs), insertions and deletions (indels), copy number variants (CNVs) and translocations in 22 genes are detected, along with two promoter regions (PMS2 and TERT) and 239 sites to determine microsatellite instability status. From RNA-seq, gene fusions (translocations) are detected in an unbiased and comprehensive manner, which allows association with fusion targeting FDA-approved therapies and investigational therapies in clinical trials. Tumor mutational burden (TMB) and Microsatellite Instability (MSI) status are reported. Whole transcriptome RNA expression counts are analytically validated. Some viral sequences, such as HPV and EBV, may be reported as a diagnostic or prognostic insight when deemed appropriate by our Pathologists.

CAP/CLIA validation of the Tempus xT panel in both the Chicago and RTP locations focused on actionableoncologic variants. The assay requires specimens with a tumor content of 20% post macrodissection (minimum 30% for MSI status). For solid tumors, an FFPE tumor sample is sequenced along with a matched normal blood or saliva sample (when available). For circulating hematologic malignancies, a blood or bone marrow sample is sequenced. Clinical sequencing is performed to 500x depth of coverage for tumor specimens and 150x for normal specimens. Performance specifications are listed in Table 1 below. These results establish high sensitivity and specificity for the Tempus xT (v4) assay.

The xT assay is used across a diverse set of clinical settings including leading academic centers, NCI designated cancer centers, hospital networks, and community hospitals.

PERFORMANCE SPECIFICATIONS

Variant Class	Limit of Detection	Sensitivity (%)	Specificity (%)
Single Nucleotide Variants (SNVs)	5% VAF	>96.8	>99.9
Insertions and Deletions	5% VAF	91.4	>99.9
Copy Number Alterations (TN)	Gain—30% tumor purity; loss—40% tumor purity; gain—8 copies; loss—0 copies	>92.0	>99.3
Rearrangements/Fusions*	30% tumor purity	>91.7	>99.9
Microsatellites Instability Status	30% tumor purity	>95.2	>99.9

*Utilizing both DNA and RNA sequencing

xF Validation

The non-invasive Tempus xF liquid biopsy assay detects cell-free DNA (cfDNA) in blood specimens of advanced solid tumor patients. The assay is capable of detecting mutations in two variant classes in ~105 genes, including: Single Nucleotide Variants (SNVs) and insertions and deletions (indels), as well as Copy Number Amplifications (CNAs) in 6 genes, Copy Number Deletions (CNDs) in 2 genes*, and gene rearrangements (translocations) in 7 genes spanning ~0.3 Mb of genomic space. The assay spans clinically relevant coding exons for 24 genes and covers recurrent hotspot mutations in 70 genes. Insertions and deletions will be reported down to the lower limit of detection (LLOD) in clinically relevant regions in 97 genes (list available upon request). Microsatellite Instability High(MSI-H) status is also reported when detected. The panel is designed to provide clinical decision support for patients with solid tumors and is focused on the identification of oncologic, including resistance, mutations.

CAP/CLIA validation of the Tempus xF panel focused on the detection of actionable oncologic and resistance variants in blood plasma. The assay requires two 8.5 mL Streck tubes of peripheral blood. Clinical sequencing is performed to ~20,000x coverage (at least 5,000x deduplicated reads). Performance specifications are listed in Table 1 below. These results establish, as shown in the table, high sensitivity and specificity for the Tempus xF assay.

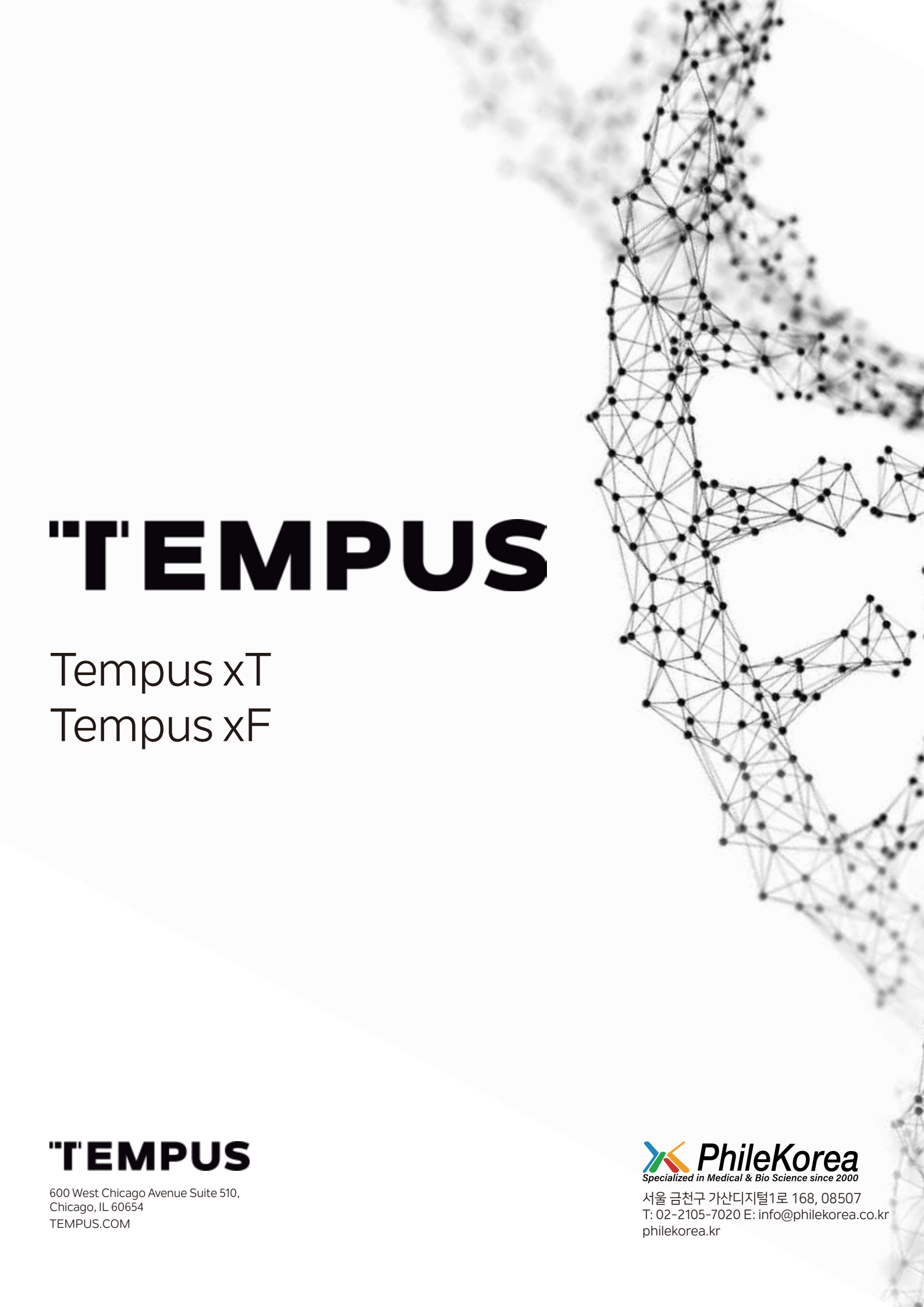
Not intended for:

- Hematologic malignancies
- Early stage (stage I/II) cancers
- Primary CNS malignancies

PERFORMANCE SPECIFICATIONS

Variant Class	Variant Allele Fraction (VAF) (%)	Sensitivity (%)	Specificity (%)
Single Nucleotide Variants (SNVs)	>0.50	>99.9	>99.9
	0.50	>99.9	>99.9
	0.25	97.0	>99.9
	0.10	70.4	>99.9
Insertions and Deletions	>0.50	98.8	>99.9
	0.50	96.0	>99.9
	0.25	81.0	>99.9
Copy Number Amplifications (CNAs)	>0.50	>99.9	>99.3
	0.50	>99.9	
Rearrangements/Fusions	>0.50	97.4	>99.9
	0.50	70.8	
Microsatellites Instability Status	>0.50	N/A	>99.9

*BRCA1 and BRCA2 copy number loss are reported when detecte



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Tempus xT
Tempus xF

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