

# MCP Server Integration Test Report

**Patient ID: PAT001-OVC-2025**  
**Sarah Elizabeth Anderson**

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This report documents the comprehensive multi-modal analysis performed using Model Context Protocol (MCP) servers for a patient with high-grade serous ovarian carcinoma. Five integrated tests were conducted spanning clinical genomics, multi-omics, spatial transcriptomics, imaging analysis, and integrated clinical recommendations.

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# TEST 1: Clinical Data and Genomic Analysis

## Test Objective:

Retrieve and analyze clinical data for patient PAT001-OVC-2025, including demographics, genetic mutations, lab results (CA-125 trends), and comparison with TCGA-OV cohort data to determine molecular subtype and prognosis.

## MCP Servers Used:

| Server       | Purpose                 | Key Functions  |
|--------------|-------------------------|--|
| mcp-mockepic | Clinical data retrieval | Patient demographics, lab results, genetic history       |
| mcp-tcga     | TCGA comparison         | Expression data, mutation frequencies, survival analysis |
| mcp-fgbio    | Genomic analysis        | Variant parsing, reference genome access                 |

## Key Results:

### Clinical Findings:

- Patient: Sarah Elizabeth Anderson, 58 years old
- BRCA1 pathogenic germline mutation confirmed
- CA-125 trajectory: 1456 → 22 → 389 → 289 U/mL (platinum resistance pattern)

### Genomic Alterations:

- TP53 R175H (hotspot mutation)
- PIK3CA E545K (activating mutation)
- PTEN loss of heterozygosity
- Copy number: MYC, CCNE1, AKT2 amplifications

### TCGA Classification:

- Molecular subtype: C1 (Immunoreactive) or C2 (Differentiated)
- Poor prognosis with Stage IV + platinum resistance
- Median OS ~48.5 months for BRCA1+ patients

# TEST 2: Multi-Omics Resistance Analysis

## Test Objective:

Analyze platinum resistance mechanisms in PDX models using integrated multi-omics data (RNA-seq, proteomics, phosphoproteomics) and perform Stouffer's meta-analysis to identify consistently dysregulated pathways across all modalities.

## MCP Servers Used:

| Server         | Purpose              | Key Functions  |
|----------------|----------------------|--|
| mcp-multiomics | Data integration     | Integrate RNA/protein/phospho data, Stouffer's meta-analysis |
| mcp-multiomics | Statistical analysis | HALLA associations, FDR correction, pathway analysis         |

## Key Results:

### Sample Analysis:

- 15 PDX samples analyzed (7 resistant, 8 sensitive)
- All 3 modalities successfully integrated

### Stouffer's Meta-Analysis Results (Z-scores):

- PIK3CA: Z = 12.537 (p < 1e-15) - Upregulated
- AKT1: Z = 13.413 (p < 1e-15) - Upregulated
- MTOR: Z = 13.293 (p < 1e-15) - Upregulated
- PTEN: Z = -13.684 (p < 1e-15) - Downregulated
- ABCB1: Z = 14.219 (p < 1e-15) - Upregulated (6.6-fold)
- BCL2L1: Z = 12.744 (p < 1e-15) - Upregulated

### Pathway Analysis:

- PI3K/AKT/mTOR pathway: ACTIVATED in resistant samples
- All 6 genes passed FDR correction ( $\alpha = 0.05$ )
- 100% consistency across RNA, protein, and phospho modalities

# TEST 3: Spatial Transcriptomics Analysis

## Test Objective:

Analyze spatial gene expression patterns to understand tissue architecture, proliferation zones, resistance marker distribution, and immune cell localization. Determine tumor microenvironment classification (hot vs cold) and implications for immunotherapy.

## MCP Servers Used:

| Server           | Purpose          | Key Functions  |
|------------------|------------------|--|
| mcp-spatialtools | Spatial analysis | QC filtering, region segmentation, expression mapping        |
| mcp-spatialtools | Statistics       | Spatial autocorrelation (Moran's I), differential expression |

## Key Results:

### Spatial Structure:

- 900 spots across 6 regions analyzed
- Regions: tumor\_core (69), tumor\_proliferative (124), tumor\_interface (112), stroma\_immune (212), stroma (180), necrotic\_hypoxic (203)

### Expression Patterns:

- Proliferation (MKI67/PCNA): Highest in tumor\_proliferative region
- Resistance markers (PIK3CA/AKT1/ABCB1): Concentrated in tumor regions
- Immune cells (CD3D/CD8A/CD68): Localized to stroma\_immune region

### Key Findings:

- Immune exclusion confirmed: 6.0x higher immune cells in stroma vs tumor
- Tumor microenvironment: Immunologically COLD
- Spatial heterogeneity in resistance markers confirmed (CV 7-9%)
- Immunotherapy efficacy: LIMITED expected due to immune exclusion

# TEST 4: Histology and Imaging Analysis

## Test Objective:

Analyze histology (H&E;) and immunofluorescence images to assess tissue morphology, CD8+ T cell infiltration, Ki67 proliferation index, and multiplex IF for TP53/Ki67 co-expression. Validate molecular findings through imaging biomarkers.

## MCP Servers Used:

| Server            | Purpose           | Key Functions  |
|-------------------|-------------------|--|
| mcp-openimagedata | Image management  | Fetch histology images, extract morphological features |
| mcp-deepcell      | Cell segmentation | Nuclear segmentation, cell state classification        |

## Key Results:

### H&E; Analysis:

- Tumor cellularity: 75%
- Necrotic regions: 18% of tissue
- High-grade nuclear atypia consistent with HGSOC

### Immunofluorescence:

- CD8+ T cells: 12.5 cells/mm² (LOW infiltration)
- Spatial pattern: 75% at periphery, 25% intratumoral (immune exclusion)
- Ki67 proliferation index: 50% (HIGH)

### Multiplex IF (TP53/Ki67/DAPI):

- Total cells segmented: 650
- TP53+: 70% (mutant p53 accumulation)
- Ki67+: 50% (high proliferation)
- TP53+/Ki67+ double positive: 45.1%
- Correlation: 90% of TP53+ cells are proliferating

# TEST 5: Integrated Analysis & Clinical Recommendations

## Test Objective:

Synthesize findings from all previous tests to identify primary resistance mechanisms, assess multi-modal data consistency, provide targeted therapy recommendations, and develop a comprehensive monitoring strategy with realistic prognostic estimates.

## MCP Servers Used:

Integration of results from all previous MCP servers - no new data loading required. Synthesis performed using findings from mcp-mockepic, mcp-tcga, mcp-multiomics, mcp-spatialtools, mcp-openimagedata, and mcp-deepcell.

## Key Results:

### Primary Resistance Mechanisms (Ranked):

1. PI3K/AKT/mTOR pathway hyperactivation (HIGH evidence - all modalities)
2. Drug efflux via ABCB1/MDR1 (HIGH evidence - 6.6-fold increase)
3. Immune exclusion/Cold TME (HIGH evidence - spatial + imaging)
4. Anti-apoptotic signaling BCL2L1 (MEDIUM evidence)

### Treatment Recommendations:

1. PARP + PI3K inhibitor (Olaparib + Alpelisib) - Expected RR: 40-45%
2. mTOR inhibitor + chemotherapy - Expected RR: 30-35%
3. MDR1 inhibitor + platinum rechallenge - Expected RR: 20-25%

### Immunotherapy Strategy:

- Monotherapy NOT recommended (cold TME, immune exclusion)
- Combination approaches required to overcome exclusion
- Expected monotherapy response: <10%

### Prognosis with Optimal Therapy:

- Median PFS: 6-8 months
- Median OS: 16-20 months
- Without targeted therapy: OS 8-12 months

# MCP Server Usage Summary

| MCP Server        | Tests Used | Primary Functions       | Data Types                      |
|-------------------|------------|-------------------------|---------------------------------|
| mcp-mockepic      | Test 1     | Clinical data retrieval | Demographics, labs, medications |
| mcp-tcga          | Test 1, 5  | TCGA comparison         | Expression, mutations, survival |
| mcp-fgbio         | Test 1     | Genomic processing      | FASTQ, VCF, annotations         |
| mcp-multiomics    | Test 2, 5  | Multi-omics integration | RNA, protein, phospho           |
| mcp-spatialtools  | Test 3, 5  | Spatial analysis        | Spatial coordinates, expression |
| mcp-openimagedata | Test 4, 5  | Histology images        | H&E, IF images                  |
| mcp-deepcell      | Test 4, 5  | Cell segmentation       | Multiplex IF, phenotypes        |
| mcp-pubmed        | Available  | Literature search       | Publications, full text         |
| mcp-huggingface   | Available  | AI models               | Genomic language models         |
| mcp-seqera        | Available  | Pipeline execution      | Nextflow workflows              |

## Workflow Integration:

**Data Flow Through MCP Servers:**

1. Clinical data (mockepic) → Patient context and history
2. Genomic comparison (tcga) → Molecular subtyping and prognosis
3. Multi-omics (multiomics) → Resistance mechanism identification
4. Spatial analysis (spatialtools) → Tissue architecture and heterogeneity
5. Imaging (openimagedata/deepcell) → Morphological validation
6. Integration → Comprehensive clinical recommendations

**Key Advantages of MCP Architecture:**

- Modular design allows independent server updates
- Standardized interfaces enable seamless data exchange
- AI-driven orchestration through conversational interface
- Reproducible workflows across different patients
- Scalable to additional data modalities

End of Report