

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