# Full Test Prompt Documentation

## MCP Server Integration Test Suite

Documentation Generated: December 09, 2025

## EXECUTIVE SUMMARY

This document contains the complete prompts and instructions used to generate the comprehensive multi-modal analysis report for patient PAT001-OVC-2025 with high-grade serous ovarian carcinoma. The test suite demonstrates the integration of Model Context Protocol (MCP) servers for clinical genomics, multi-omics analysis, spatial transcriptomics, imaging analysis, and integrated clinical recommendations.

## TEST STRUCTURE OVERVIEW

The complete analysis consisted of 5 integrated tests, each building upon previous results: **TEST 1: Clinical Data and Genomic Analysis** - Retrieve patient demographics and clinical history - Analyze genomic mutations and copy number alterations - Compare with TCGA-OV cohort for molecular subtyping **TEST 2: Multi-Omics Resistance Analysis** - Integrate RNA-seq, proteomics, and phosphoproteomics data - Perform Stouffer's meta-analysis across modalities - Identify resistance pathways and drug targets **TEST 3: Spatial Transcriptomics Analysis** - Analyze 900 spatial spots across 6 tissue regions - Map resistance markers and immune cell distribution - Determine tumor microenvironment classification **TEST 4: Histology and Imaging Analysis** - Analyze H&E; morphology and tumor cellularity - Quantify CD8+ T cell infiltration patterns - Assess Ki67 proliferation and TP53/Ki67 co-expression **TEST 5: Integrated Analysis & Clinical Recommendations** - Synthesize findings from all previous tests - Rank resistance mechanisms by evidence strength - Provide targeted therapy recommendations - Develop monitoring strategy and prognostic estimates

# COMPLETE TEST 5 PROMPT

## (Integration Test - As Provided)

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TEST 5: Integrated Analysis & Clinical Recommendations
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Patient ID: PAT001-OVC-2025

■■ NOTE: Run this test AFTER completing Tests 1-4

This test synthesizes findings from all previous tests - NO new data loading required.

## Integration & Clinical Recommendations

Based on the findings from Tests 1-4, please synthesize a comprehensive clinical report.

### Reference Results from Previous Tests:

**TEST 1 - Clinical & Genomic:**
- Patient: Sarah Anderson, 58yo, BRCA1 germline mutation
- CA-125 trajectory: 1456 → 22 → 389 → 289 U/mL (platinum resistance)
- Somatic mutations: TP53 R175H, PIK3CA E545K, PTEN LOH
- TCGA subtype: C1/C2 (poor prognosis with Stage IV + resistance)

**TEST 2 - Multi-Omics:**
- PI3K/AKT pathway: ACTIVATED across RNA/Protein/Phospho
- Key genes dysregulated: PIK3CA, AKT1, MTOR (up); PTEN (down)
- Drug resistance: ABCB1 upregulated (MDR1 efflux pump)
- Anti-apoptotic: BCL2L1 upregulated

**TEST 3 - Spatial Transcriptomics:**
- 900 spots across 6 regions
- Resistance markers: Concentrated in tumor regions (heterogeneous)
- Immune cells: EXCLUDED from tumor (located in stroma_immune region)
- Tumor microenvironment: Immunologically "COLD"

**TEST 4 - Imaging:**
- High proliferation (Ki67 ~45-55%)
- Low CD8+ infiltration (~5-15 cells/mm²)
- TP53-mutant cells are highly proliferative
- Immune exclusion phenotype confirmed

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## Analysis Questions:

### 1. PRIMARY RESISTANCE MECHANISMS (Rank by Evidence Strength)

Based on ALL modalities (genomics, multi-omics, spatial, imaging), identify the 2-3 main mechanisms driving p

For each mechanism, provide:
- **Mechanism name**
- **Supporting evidence** (which tests/modalities show this?)
- **Strength of evidence** (High/Medium/Low)
- **Therapeutic implications**

Expected top mechanisms:
1. PI3K/AKT/mTOR pathway activation
2. Drug efflux (ABCB1/MDR1)
3. Anti-apoptotic signaling (BCL2L1)
4. TP53 loss of function

### 2. MULTI-MODAL CONSISTENCY

Which molecular alterations appear consistently across multiple data types?

Create a cross-reference table:

| Feature | Genomics | Multi-Omics | Spatial | Imaging | Consistent? |
|---------|----------|-------------|---------|---------|-------------|
| TP53 mutation/loss | TP53 R175H | ? | ? | TP53+ cells | Yes/No |
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| PI3K/AKT activation | PIK3CA E545K | PIK3CA/AKT1 up | ? | ? | Yes/No |
| High proliferation | ? | ? | MKI67 high | Ki67 high | Yes/No |
| Immune exclusion | ? | ? | CD8 in stroma | CD8 at periphery | Yes/No |

### 3. THERAPEUTIC RECOMMENDATIONS

Based on the integrated data, provide:

**A. Targeted Therapy Recommendations (Top 3):**

For each recommendation:
- **Drug/class**
- **Molecular target**
- **Supporting evidence** (from which tests?)
- **Expected efficacy** (High/Medium/Low)
- **FDA approval status** for HGSOC

Expected recommendations should include:
- PI3K/AKT/mTOR inhibitors (e.g., alpelisib + olaparib)
- MDR1 inhibitors or chemotherapy modifications
- BCL2L1 inhibitors (if available)
- PARP inhibitors (BRCA1 mutation)

**B. Immunotherapy Consideration:**

- Should checkpoint inhibitors be considered? (Yes/No)
- Why or why not? (Cite spatial and imaging evidence)
- Expected response rate based on immune phenotype
- Could combination with other agents overcome exclusion?

**C. Clinical Trial Opportunities:**

For BRCA1-mutant, platinum-resistant, Stage IV HGSOC with:
- PI3K/AKT pathway activation
- Immune exclusion phenotype
- High proliferation

Suggest trial types:
- PARP + PI3K/AKT inhibitor combinations
- Novel immunotherapy combinations
- BRCA-targeted therapies

### 4. BIOMARKERS FOR MONITORING

**A. Molecular Biomarkers:**
- Which genes/proteins should be tracked for treatment response?
- How often should they be monitored?
- What change indicates resistance?

**B. Imaging Biomarkers:**
- Which imaging features predict resistance?
- Can spatial transcriptomics track treatment response?
- Should Ki67 or immune infiltration be monitored?

**C. Clinical Biomarkers:**
- CA-125 trends (what trajectory indicates response vs resistance?)
- RECIST criteria
- Circulating tumor DNA

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## Output Format:

Please provide a **concise 1-2 page clinical report** with:

### Executive Summary (3-4 sentences)
Brief overview of patient case and key findings

### Section 1: Resistance Mechanisms
**Ranked by evidence strength:**
1. [Mechanism] - Evidence: [tests], Strength: [High/Medium/Low]
2. [Mechanism] - Evidence: [tests], Strength: [High/Medium/Low]
3. [Mechanism] - Evidence: [tests], Strength: [High/Medium/Low]

### Section 2: Multi-Modal Consistency
Table showing which findings are consistent across modalities

### Section 3: Treatment Recommendations
**A. Targeted Therapies (Ranked by expected efficacy):**
1. [Drug/class] - Target: [gene/pathway], Evidence: [tests]
2. [Drug/class] - Target: [gene/pathway], Evidence: [tests]
3. [Drug/class] - Target: [gene/pathway], Evidence: [tests]

**B. Immunotherapy:**
- Recommendation: Yes/No
- Rationale: [cite immune exclusion evidence]
- Combination strategies: [if applicable]

**C. Clinical Trials:**
- Trial type 1: [description]
- Trial type 2: [description]

### Section 4: Monitoring Strategy
**Molecular:** [genes/proteins to track]
**Imaging:** [features to monitor]
**Clinical:** [CA-125, RECIST, ctDNA]

### Section 5: Prognosis
Based on TCGA data and integrated findings, expected outcomes with:
- Standard platinum re-challenge: [expected response]
- Recommended targeted therapies: [expected response]
- Novel immunotherapy: [expected response]

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## Validation Checkpoints:

■ Synthesized: Findings from all 4 previous tests
■ Resistance mechanisms: Identified and ranked by evidence
■ Multi-modal consistency: Confirmed across genomics/multi-omics/spatial/imaging
■ Targeted therapies: Prioritized based on molecular evidence
■ Immunotherapy: Recommendation based on immune phenotype (COLD)
■ Monitoring strategy: Molecular, imaging, and clinical biomarkers defined
■ Prognosis: Realistic expectations based on TCGA cohort data

## MCP SERVER CONTEXT

**Available MCP Servers for the Analysis:** 1. **mcp-pubmed** - Biomedical literature search and retrieval • Search PubMed articles • Retrieve full text from PMC • Convert between PMIDs, PMCIDs, DOIs 2. **mcp-fgbio** - Genomic data processing and QC • Fetch reference genomes • Validate FASTQ files • Extract UMIs • Query gene annotations 3. **mcp-huggingface** - Genomic foundation models and AI • Load genomic language models • Predict cell types • Generate sequence embeddings 4. **mcp-seqera** - Nextflow pipeline execution • Launch nf-core pipelines • Monitor workflow status • List available pipelines 5. **mcp-mockepic** - Mock clinical/EHR data • Query patient records • Link spatial to clinical data • Search ICD-10 diagnoses 6. **mcp-deepcell** - Deep learning cell segmentation • Segment cells from microscopy • Classify cell states/phenotypes • Nuclear/membrane segmentation 7. **mcp-openimagedata** - Histology and imaging • Fetch histology images • Register images to spatial coordinates • Extract morphological features 8. **mcp-tcga** - TCGA cancer genomics database • Query TCGA cohorts • Fetch gene expression data • Compare to TCGA cohorts • Get survival data 9. **mcp-spatialtools** - Spatial transcriptomics • QC filtering of spatial barcodes • Split data by regions • Calculate spatial autocorrelation • Differential expression 10. **mcp-multiomics** - Multi-omics integration • Integrate RNA/protein/phospho data • HAllA association testing • Stouffer's meta-analysis • Multi-omics PCA

## TEST EXECUTION INSTRUCTIONS

**How the Tests Were Executed:** 1. **Sequential Execution:** Tests 1-4 were run in order, with each test building on previous results. 2. **Data Generation:** Since this was a demonstration, mock data files were created to simulate: • Clinical records (demographics, labs, medications) • Multi-omics data (RNA-seq, proteomics, phosphoproteomics) • Spatial transcriptomics (900 spots, 6 regions) • Imaging data (H&E;, immunofluorescence) 3. **MCP Server Calls:** Each test utilized specific MCP servers through function calls: • Data retrieval functions (query, fetch, get) • Analysis functions (integrate, segment, calculate) • Comparison functions (compare to TCGA) 4. **Result Integration:** Test 5 synthesized all findings without new data loading, creating: • Ranked resistance mechanisms • Multi-modal consistency table • Treatment recommendations • Monitoring strategy • Prognostic estimates 5. **Output Generation:** Multiple formats were created: • Technical PDF report (14 pages) • Patient-friendly HTML summary • One-page visual PDF • Medication guide • Visual infographic **Key Design Principles:** • **Modularity:** Each MCP server handles specific data types/analyses • **Interoperability:** Standardized interfaces enable data exchange • **Reproducibility:** Same workflow can be applied to different patients • **Scalability:** Additional MCP servers can be added as needed • **Interpretability:** Results translated from technical to patient-friendly **Validation Approach:** Each test included validation checkpoints to ensure: • Data loaded correctly • Expected patterns were found • Results were consistent across modalities • Clinical recommendations were evidence-based • Patient materials were accessible and accurate

## ADDITIONAL CONTEXT

**Patient Context Provided:** Patient ID: PAT001-OVC-2025 Name: Sarah Elizabeth Anderson Age: 58 years Diagnosis: Stage IV High-Grade Serous Ovarian Carcinoma (HGSOC) Key Finding: BRCA1 germline mutation with platinum resistance **Clinical Question:** How can we integrate multi-modal data (genomics, transcriptomics, proteomics, spatial, and imaging) to: 1. Understand resistance mechanisms 2. Identify therapeutic targets 3. Make evidence-based treatment recommendations 4. Develop a monitoring strategy 5. Provide realistic prognostic estimates **Expected Outcomes:** The analysis was expected to reveal: • Multiple resistance mechanisms working together • PI3K/AKT pathway as a key driver • Immune exclusion limiting immunotherapy efficacy • PARP + PI3K inhibitor combination as optimal therapy • Need for combination strategies to overcome resistance **Demonstration Purpose:** This comprehensive test suite demonstrates: • The power of MCP architecture for complex bioinformatics workflows • AI-driven orchestration through conversational interfaces • Integration of diverse data modalities • Translation of technical findings to clinical recommendations • Generation of patient-friendly educational materials **Real-World Application:** In clinical practice, this workflow would: • Use actual patient data from EHR systems • Access real TCGA database queries • Process actual sequencing and imaging files • Connect to clinical trial databases • Generate reports for medical records • Provide decision support for oncologists

## DOCUMENT INFORMATION

**Document Type:** Test Prompt Documentation **Purpose:** Complete documentation of prompts used for MCP server integration tests **Patient ID:** PAT001-OVC-2025 (Demonstration) **Generated:** December 09, 2025 at 23:17:26 **Total Tests:** 5 integrated tests **MCP Servers Used:** 10 servers **Output Files Generated:** 8 documents (PDFs, HTML, PNG) **Version Information:** • Test Suite Version: 1.0 • MCP Protocol Version: Current • Documentation Version: 1.0 **Disclaimer:** This documentation represents a demonstration of MCP server capabilities using simulated patient data. In production use, actual patient data would be processed through secure, HIPAA-compliant systems with appropriate consent and data governance protocols. **End of Document**