# Indication Profile Generation Instructions

## Purpose

Create structured indication profiles in JSON format for drug MOA (mechanism of action) matching and indication selection. These profiles enable systematic comparison of indications based on clinical precedent, disease biology, and strategic opportunity.

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## What You'll Create

A comprehensive JSON file containing:

- Disease biology and immune landscape

- Clinical precedent for each MOA class (with detailed outcomes and lessons)

- Development pipeline by MOA

- Unmet needs framed as MOA requirements

- MOA compatibility assessments

- Strategic insights for indication selection

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## Input Materials

You should have:

1. \*\*Reference document\*\* (Word doc, PDF, or memo) about the indication

2. \*\*Clinical trial data\*\* for drugs tested in this indication

3. \*\*Biology/immunology literature\*\* about the disease

4. \*\*Pipeline/competitive intelligence\*\* (if available)

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## Template Structure

```json

{

"metadata": {

"indication\_name": "Disease Name",

"indication\_code": "ICD-10 code",

"subtypes": [...],

"data\_version": "YYYY-MM-DD",

"data\_sources": "Where data came from"

},

"disease\_biology": {

"pathophysiology": {...},

"immune\_landscape": {

"tumor\_microenvironment": {...},

"cytokine\_environment": {...},

"immune\_receptors": [...]

},

"tumor\_antigens": [...],

"biological\_features\_for\_moa\_matching": [...]

},

"moa\_landscape": {

"moa\_category": [

{

"name": "MOA Class Name",

"biological\_rationale": {...},

"clinical\_precedent": {

"precedent\_drug": [

{

"drug\_name": "Drug",

"specific\_moa": "Detailed MOA",

"clinical\_evidence": {...},

"lessons\_learned": {...},

"similarity\_matching\_tags": [...]

}

]

},

"moa\_compatibility\_score": {...}

}

]

},

"current\_treatment\_landscape": {...},

"development\_pipeline": {...},

"unmet\_needs": [...],

"biomarkers": {...},

"combination\_rationale": [...]

}

**Step-by-Step Instructions**

**STEP 1: Provide Your Source Material**

**Say to Claude:**

I need to create an indication profile for [INDICATION NAME].

I have a reference document that contains information about:

- Disease biology and immunology

- Clinical trials and drug development

- Treatment landscape

- Unmet needs

Here is my reference document:

[PASTE YOUR DOCUMENT]

Please help me create a comprehensive indication profile in JSON format

optimized for MOA matching and indication selection.

**STEP 2: Specify Key Requirements**

**Critical sections to emphasize:**

1. **MOA Landscape** (Most Important)
   * For EACH MOA class tested in this indication
   * List specific drugs with detailed MOAs
   * Clinical trial results (efficacy numbers, safety)
   * **Lessons learned** (why it succeeded or failed)
   * **MOA tags** for computational matching
2. **Disease Biology**
   * Immune landscape (hot/cold/mixed tumors)
   * Key immune cells and checkpoints
   * Tumor antigens (for bispecifics/ADCs)
   * Cytokine environment
3. **Unmet Needs**
   * Frame as **MOA requirements** (not just gaps)
   * Link to suitable MOA classes
   * Prioritize by severity
4. **Precedent Lessons**
   * Extract strategic insights from failures
   * Identify what differentiates successful drugs
   * Note class-wide patterns (e.g., "TIGIT failures in NSCLC")
5. **STEP 3: Request Specific MOA Categories**
6. **Say to Claude:**

Focus on these MOA categories:

- Checkpoint inhibitors (PD-1/PD-L1, CTLA-4, next-gen)

- Bispecific antibodies (T-cell engagers, dual pathway)

- Antibody-drug conjugates (ADCs)

- Cytokine therapies (IL-2, IL-12, etc)

- Cell therapies (CAR-T, TIL)

- Cancer vaccines

- [Any other relevant categories]

For EACH category, I need:

1. All drugs tested (approved + pipeline)

2. Detailed MOA descriptions

3. Clinical trial outcomes with numbers

4. Lessons learned (success factors + failure reasons)

5. MOA tags for matching

**STEP 4: Ensure MOA Tags Are Included**

**MOA tags are critical for matching.** Each precedent drug should have tags like:

"similarity\_matching\_tags": [

"IL-2\_pathway",

"CD25\_binding",

"T\_cell\_activation",

"NK\_cell\_activation",

"Treg\_activation",

"systemic\_cytokine",

"approved"

]

Say to claude:

For each precedent drug, include detailed MOA tags covering:

- Pathway/target (e.g., IL-2\_pathway, PD-1\_targeting)

- Mechanism details (e.g., CD25\_binding, CD25\_abolished)

- Cell types affected (e.g., T\_cell\_activation, NK\_activation)

- Selectivity (e.g., Treg\_sparing, Treg\_activation)

- Delivery (e.g., systemic, tumor\_targeted, pegylated)

- Stage (e.g., approved, Phase\_III, FAILED)

**STEP 5: Request Strategic Assessments**

**Say to Claude:**

For each MOA category, provide:

1. MOA Compatibility Score:

- Biological fit (1-10): Does disease biology support this MOA?

- Clinical validation (1-10): Strength of precedent evidence?

- Unmet need match (1-10): Does MOA address gaps?

- Overall assessment: Narrative recommendation

2. Strategic Insights:

- What's working vs failing in this MOA class?

- Key learnings from precedent (especially failures)?

- Patient selection requirements?

- Competitive landscape?

**STEP 6: Specify Output Format**

**Say to Claude:**

Output the complete indication profile as:

1. Valid JSON (I will save this as a .json file)

2. Use the structure from the template

3. Include ALL sections (don't skip any)

4. Be comprehensive - include all available data

5. Use proper JSON formatting (quoted keys, proper nesting)

Example:

I need to create an indication profile for NON-SMALL CELL LUNG CANCER (NSCLC).

PURPOSE: This profile will be used for MOA-based indication selection.

I want to match drug candidates against clinical precedent in NSCLC to

determine if NSCLC is a good indication for specific MOAs.

SOURCE MATERIAL:

[Paste your lung cancer memo/document here]

REQUIREMENTS:

1. DISEASE BIOLOGY section:

- Immune landscape (hot/cold tumors, TILs, checkpoints)

- Tumor antigens (TROP2, HER3, etc with expression frequencies)

- Key pathways (PD-1/PD-L1, EGFR, KRAS, TME)

- Features relevant for MOA matching

2. MOA LANDSCAPE section (CRITICAL):

For each MOA class (checkpoint inhibitors, ADCs, bispecifics, etc):

a) List ALL precedent drugs tested

b) For EACH drug include:

- Drug name

- Specific MOA (detailed description)

- Clinical evidence (Phase, ORR, PFS, OS with numbers)

- Lessons learned (why succeeded or failed)

- MOA tags (for computational matching)

c) Overall MOA compatibility score for NSCLC

3. UNMET NEEDS section:

- Frame needs as MOA requirements

- Link to suitable MOA classes

- Prioritize (Critical/High/Medium)

4. PIPELINE section:

- Current development by MOA class and phase

- Competitive threats

5. STRATEGIC INSIGHTS:

- What MOAs are succeeding vs failing?

- Key learnings (e.g., TIGIT failures)

- Recommendations

OUTPUT: Complete JSON file following the template structure.

Please start by confirming you understand the requirements, then create

the comprehensive NSCLC indication profile.