Life Sciences MCP Platform

Grounded AI for Drug Discovery

From researcher question to connected knowledge graph in seconds

The Problem: LLMs Hallucinate Biomedical Knowledge

The status quo is broken:

No Authoritative Access

LLMs rely on stale training data or hallucinate drug-target interactions

Identifier Fragmentation

BRCA1 = HGNC:1100 = P38398 = ENSG00000012048 = 672

Manual Integration

Days/weeks per database; code breaks when APIs change

Cognitive Overload

Scientists become integration engineers instead of researchers

"When asked about drug-target interactions, LLMs either hallucinate or rely on stale training data."
Researchers spend 60-80% of their time on data wrangling

The Solution: Platform Engineering for Biomedical AI

12 Authoritative APIs in Unified MCP Interface

- **Fuzzy-to-Fact Protocol:** Natural language to canonical identifiers

- **Cross-reference graph:** Automatic multi-hop traversal between databases

- **Token budgeting:** slim=True reduces 115+ tokens to 20 tokens per entity

- **Recovery hints:** Error envelopes guide agent self-correction

- **Consistent patterns:** Same schema across all 12 servers

TIER 1: MCP NODES (Verified Entities)
12 FastMCP servers with canonical CURIEs + cross-references

TIER 2: CURL EDGES (Relationship Discovery)
Platform skills for bulk traversal without protocol overhead

TIER 3: GRAPHITI (Research Memory)
Persist validated findings as structured episodes

Quantitative Evidence: Structured APIs Outperform Retrieval

Benchmark Results from 2025 Research

Study	Baseline	With APIs	Improvement
BTE-RAG (GPT-4o mini)	51%	75.8%	+24.8 pp
BTE-RAG (GPT-4o)	69.8%	78.6%	+8.8 pp
RAG Systematic Review	1.0x	1.35x	+35% odds

Key insight: Canonical CURIEs, typed entities, and evidence scores are what benchmarks prove works.

Sources: Xu et al. (2025) "BTE-RAG" bioRxiv; Wang et al. (2025) "RAG in Biomedicine" JAMIA

Value Pillar 1: Rapid API Scaffolding

/scaffold-fastmcp Generates:

Client
Async httpx client with rate limiting

Server
FastMCP server with tool stubs

Models
Pydantic models with CURIE validation

Tests
Integration test scaffolding

Platform Statistics

MCP Servers	**12**
Total Tests	**600+**
Client LOC	**8,200**
Server LOC	**2,200**

Adding Reactome = 1-2 hours (vs. weeks of custom integration)

Value Pillar 2: Deterministic Nodes, Agentic Edges

The Intentional Separation

MCP SERVERS	PLATFORM SKILLS	GRAPHITI MEMORY
12 FastMCP endpoints for verified node retrieval with canonical CURIEs	curl-based workflows for agentic edge discovery without protocol overhead	JSON episodes to persist validated research findings

Why separate?

MCP carries JSON-RPC protocol overhead (~100ms/call). For bulk edge discovery (10-50 calls/workflow), direct curl is more efficient. Agents choose the right tool for the job.

lifesciences-genomics

lifesciences-proteomics

lifesciences-pharmacology

lifesciences-clinical

The Fuzzy-to-Fact Protocol

Solving the Identifier Problem

PHASE 1 (FUZZY)

```
"BRCA1" -> Ranked candidates
HGNC:1100 (score: 1.0)
HGNC:1101 (score: 0.8)
```

PHASE 2 (STRICT)

```
"HGNC:1100" -> Complete record
ensembl: ENSG00000012048
uniprot: ["P38398"]
entrez: "672"
```

Why This Matters

1 **Prevents hallucination** - Forces entity resolution before retrieval

2 **Enables self-healing** - Error envelopes include recovery hints

3 **Enables graph traversal** - Cross-references link across databases

```
{"error": {"code": "UNRESOLVED_ENTITY",
"recovery_hint": "Use search_genes()
first to resolve to HGNC CURIE"}}
```

Value Pillar 3: Embracing Our Gaps

Honest Positioning: What We're Not (Yet)

Gene Ontology Keys
Missing go_process, go_function, go_component

Confidence Calibration
No STRING-style benchmarking against gold standards

Phenotype Integration
No HPO support for phenotype-to-gene queries

DrugMechDB Validation
Gold standard benchmark not yet integrated

Our Philosophy

1. Document prior art first (sections 1-6 of research docs)

2. Then articulate unique contributions (section 7)

3. Alignment with standards is a **strength**, not a limitation

"Embracing alignment with standards like TRAPI, Biolink, and the Fuzzy-to-Fact pattern means the work builds on proven foundations rather than reinventing them."

Industry Standards Alignment

Standing on Proven Foundations

Standard	Compliance	Notes
TRAPI	85%	Intentional deviations for 60% token reduction
Biolink Model	80%	22-key cross-reference registry
W3C CURIE	Full	Bioregistry-validated prefixes
BioThings Explorer	Aligned	Federated API query patterns

Collaborations

NCATS Translator
TRAPI standard alignment

Bioregistry
Canonical CURIE prefixes

ELIXIR
European life sciences data

Cross-reference registry covers 10/15 major Biolink categories with documented gaps

Novel Contributions

What We Add to the Field

Token Budgeting

Recovery Hints

Fuzzy-to-Fact Protocol

Quality Metrics

CQ Classification

Impact

5-15x context efficiency for batch operations

Autonomous multi-step workflows

Teachable and enforceable patterns

Quantifiable graph quality scores

Systematic capability validation

Key insight: Node retrieval (MCP) separated from edge discovery (curl) for protocol efficiency

Demo: Synthetic Lethality Target Discovery (ARID1A)

"Show me synthetic lethal partners for ARID1A in ovarian cancer"

1. `hgnc_search_genes("ARID1A") -> HGNC:11110`

2. `get_gene("HGNC:11110") -> cross_references.ensembl_gene`

3. `string_get_interactions(...) -> EZH2 (0.999), SMARCC1 (0.997)`

4. `chembl_search_compounds("EZH2 inhibitor") -> Tazemetostat`

5. `clinicaltrials_search_trials("Tazemetostat ARID1A") -> NCT03348631`

TIME TO INSIGHT	BEFORE	MANUAL API CALLS	ID RECONCILIATION
Seconds	**1 Week**	**0**	**Automatic**

Join Us in Building Grounded Biomedical AI

For Researchers

Use the platform for drug discovery workflows. Test the 15 competency questions in our catalog.

For Bioinformaticians

Contribute API wrappers via /scaffold-fastmcp. Help close the Gene Ontology and HPO gaps.

For AI Engineers

Build agents using MCP tools + platform skills. Explore Fuzzy-to-Fact for other domains.

For Standards Bodies

Help us align with TRAPI, Biolink, DrugMechDB. Validate our cross-reference registry.

Canonical identifiers. Structured responses. Grounded AI.

REPOSITORY
lifesciences-research

DOCUMENTATION
docs/platform-engineering-rationale.md

SPECIFICATION
docs/adr/accepted/adr-001-v1.4.md