OPEN MEDICINE

withZETA | by Open-Medicine AI

AI Powered Co-Scientist for Conquering Rare Cancers

2026 | Lantern Pharma | Nasdaq: LTRN | Open-Medicine.ai

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withZETA by Open-Medicine AI

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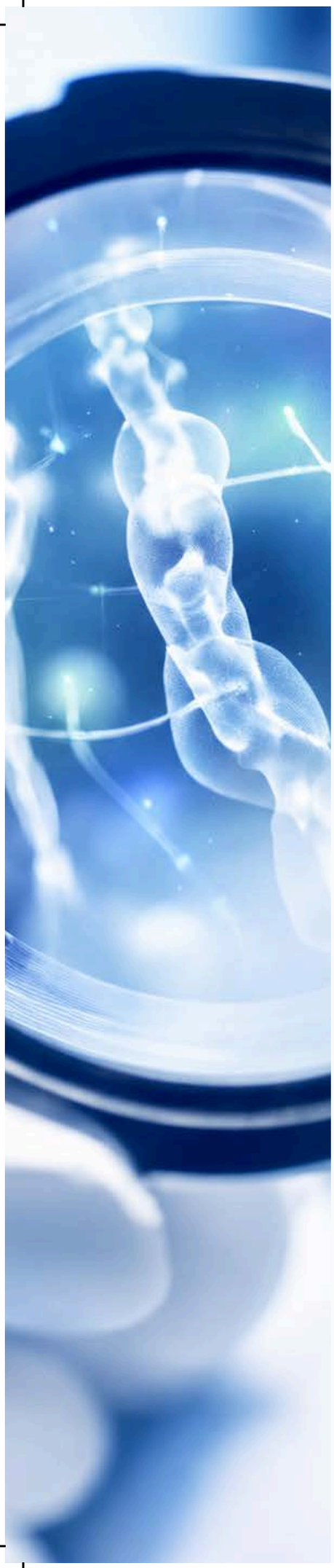
What is withZeta.ai?

AI powered co-scientist for conquering rare cancers.

withZeta is an AI research platform built to accelerate therapeutic development for rare cancers. A rare cancer affects fewer than 15 people per 100,000 annually or fewer than 40,000 people per year in the United States. Collectively rare cancers affect more than 5 million people globally, resulting in over 3 million deaths. These patients face a devastating reality: minimal treatment options not because their diseases are scientifically intractable, but because traditional pharmaceutical economics cannot justify the billion-dollar development costs for small patient populations. withZeta addresses this challenge by making comprehensive rare cancer research accessible to any investigator, anywhere, democratizing expertise and accelerating the path from biological understanding to therapeutic intervention.

Knowledge work is migrating to AI co-scientists, autonomous systems that investigate, reason, and synthesize across the full breadth of scientific evidence. withZeta.ai is that co-scientist: purpose-built for the biology, economics, and urgency of rare cancer drug development, and accessible to any researcher, anywhere.



02

The Rare Cancer Challenge:

Small Populations, Devastating Prognoses, Minimal Treatment Options

Rare cancers account for 27% of all cancer diagnoses. Less than 5% of clinical trials target them.

Drug development costs approximately $1–2 billion regardless of target population size. For common cancers, this investment can generate commercial returns that justify the expense and risk. For rare cancers with small patient populations, these identical development costs cannot be recouped through sales, making investment economically irrational from traditional pharmaceutical perspectives. Limited patient numbers also result in sparse biological and clinical data, fewer disease-relevant models, and significant barriers to recruiting for clinical trials. Yet the burden remains substantial: rare cancers collectively account for approximately **one-quarter of all cancer deaths in the United States.** These scientific, clinical, and economic constraints slow the development of new therapies and leave many patients facing aggressive diseases with few effective treatment options.

The consequences are devastating

Cholangiocarcinoma, with approximately 8,000 US cases annually, sees patients facing median survival of just 12–18 months with minimal targeted therapy options despite clear molecular drivers.

Adrenocortical carcinoma patients have virtually no effective systemic treatments beyond mitotane, which offers minimal response rates.

Patients with **MGMT-unmethylated glioblastoma** face resistance to standard temozolomide chemotherapy with no additional approved options.

Across 438 distinct rare cancer types characterized in Zeta's knowledge base, this pattern repeats: **small populations, devastating prognoses, and minimal treatment options.**

03

Multiple Agents & Tools **Working in Concert**

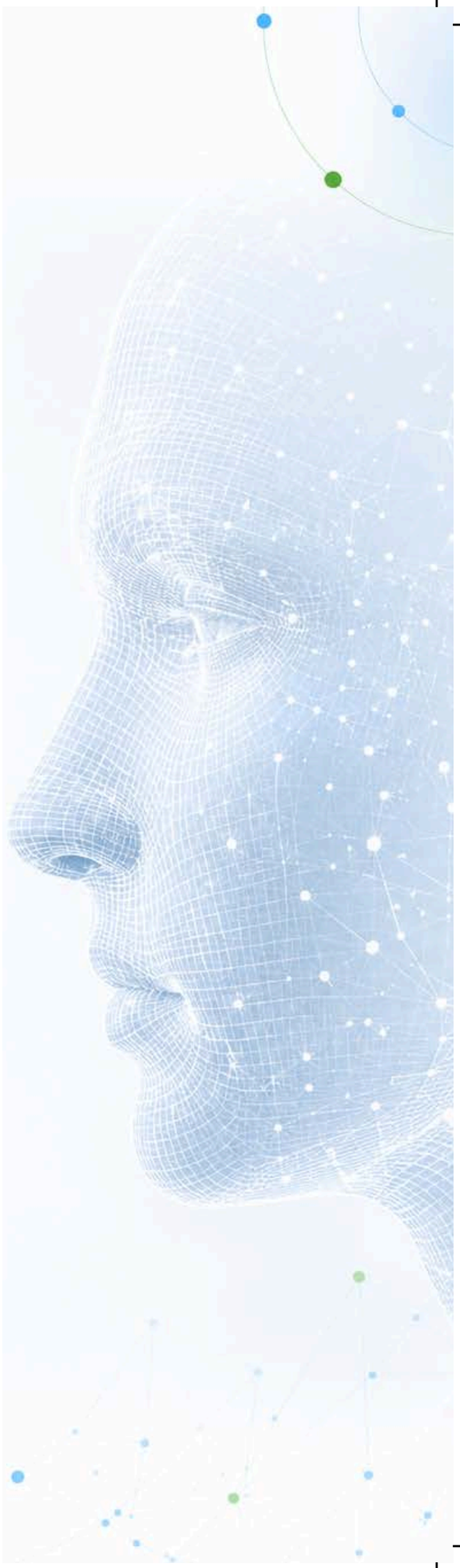
withZeta.ai is built on a multi-agentic architecture - a network of specialized AI agents, each equipped with purpose-built tools, that collaborate autonomously to accomplish what no single model could achieve alone. Each agent operates with a defined role and curated toolkit: one searches PubMed and retrieves peer-reviewed literature in real time; another queries clinical trials registries and regulatory databases; a third applies molecular pathway analysis and biomarker reasoning. These aren't static lookups; agents actively decide which tools to invoke, in what sequence, and how to interpret findings before passing insights forward through the workflow.

A coordinating orchestration layer directs the agents, synthesizes outputs, identifies gaps, and dynamically adapts the research strategy as new evidence emerges - mirroring how expert scientists actually work.

Critically, withZeta doesn't summarize what's already known - it generates net-new scientific knowledge. By reasoning across disparate data sources and surfacing non-obvious connections, withZeta functions as a genuine contributor to the scientific record. Every conclusion is traceable, every inference grounded, and every output built to meet the rigorous standards of drug development.

Today, withZeta.ai's agents draw on 34 specialized tools spanning curated rare cancer datasets, clinical trial intelligence, chemical and biomedical literature, and molecular profiling and design capabilities.

This is what sets withZeta apart:
not retrieving and repackaging information, but advancing scientific understanding in ways that accelerate the path from hypothesis to clinical use.



04 Foundational Knowledge

The power of withZeta's research capabilities rests fundamentally on meticulously curated knowledge bases that organize the fragmented landscape of rare cancer data into a unified ontology.

Rare cancer research spans hundreds of distinct disease entities, each with unique molecular drivers, treatment responses, and clinical presentations scattered across disparate literature sources and disconnected databases. Lantern Pharma's decade-long curation effort has systematically structured this heterogenous data by mapping synonymous disease names, linking molecular biomarkers to therapeutic responses, connecting cell line models to clinical indications, and building hierarchical relationships between cancer subtypes. This structured ontology serves as the semantic foundation upon which withZeta grounds its investigations, enabling the AI to reason about complex relationships, identifying relevant evidence across naming variations, and synthesize insights that would otherwise remain invisible. The insights provided by this foundation mean that the promise of a cure and an eventual cure itself no longer need to struggle to navigate the terminological chaos and data fragmentation that characterize rare cancer research.

Rare Cancer Knowledge Base

Curated database linking rare cancer types to therapeutic compounds, biomarkers, and clinical research

438	292	8,746
Cancer types	Biomarkers	Total Records

Cancer Drug Database

Comprehensive cancer drug database with FDA approval status, clinical trial data, and molecular targets

532	564	1,096
FDA Approved	Standard of Care	Total Records

Clinical Trial Database

Self-hosted index of all registered clinical studies from ClinicalTrials.gov via AACT

563K	25,391	4.6%
Total Trials	Rare Cancer Trials	Rare Cancer %

Rare Cancers Library

Comprehensive document library with research papers, clinical guidelines, and treatment protocols

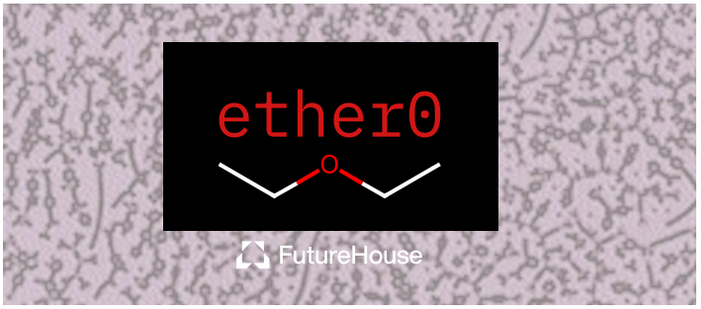
204K	45,955	1.3M
Total Papers	Full Text Available	Vector Chunks

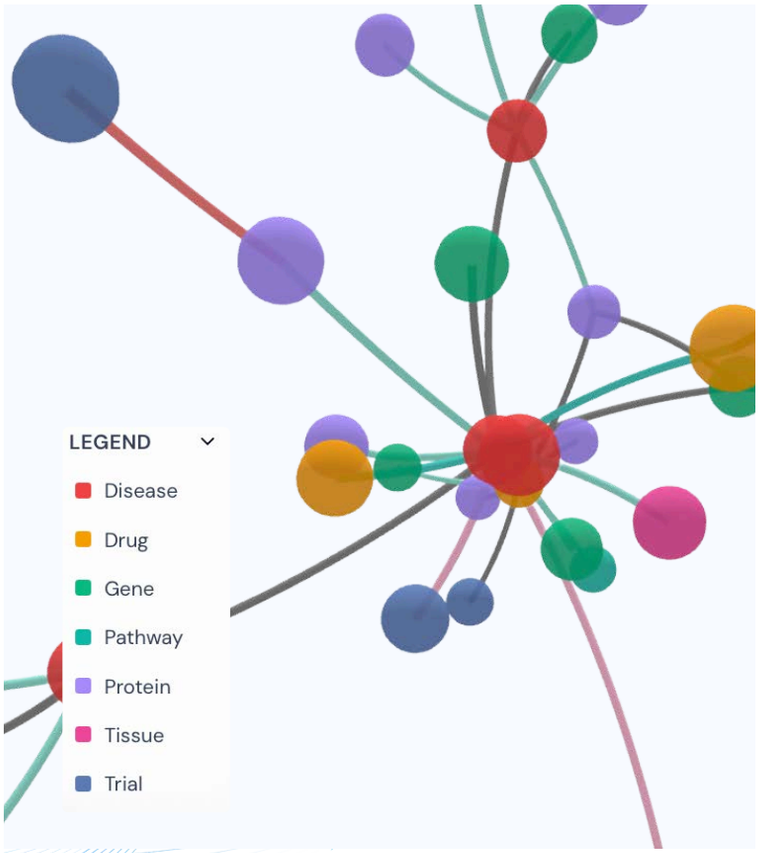
For researchers developing **therapies targeting the central nervous system,**

withZeta offers sophisticated molecular analysis capabilities. Its blood-brain barrier prediction system, powered by PredictBBB.ai, achieves 94.1% accuracy in evaluating whether drug candidates can penetrate the CNS, a critical consideration for treating brain cancers. Beyond permeability prediction, the platform delivers multi-dimensional molecular analysis—including structural, physicochemical, surface, and topology insights—enabling deeper understanding of drug behavior. It calculates comprehensive molecular properties and drug-likeness assessments, helping researchers optimize compounds before expensive synthesis and testing.

For truly **novel therapeutic development,**

withZeta integrates ether0,— AI-Powered Chemical Reasoning (by FutureHouse). An advanced AI reasoning model that thinks through complex chemistry problems step-by-step. ether0 explores drug design opportunities by generating hypotheses, evaluating molecular structures, and proposing novel therapeutic candidates — identifying promising scaffolds and optimizing drug-like properties for rare cancer targets.





With every conversation, withZeta builds a **living knowledge graph**

With every conversation, withZeta builds a living knowledge graph, evolving in real time as the platform connects concepts, compounds, and clinical insights across your session. This dynamic semantic network organizes your research dialogue into nodes (diseases, drugs, genes, proteins, pathways, and clinical trials) and edges (relationships between them, such as "TREATS," "TARGETS," "ASSOCIATED_WITH," or "INHIBITS"). The graph builds incrementally: after each response, withZeta's extraction system identifies new entities, links them to existing knowledge using a medical research ontology, and updates relationships as new evidence emerges. Each node contains structured summaries and metadata, while edges capture specific facts with citation context and temporal validity. You can visualize the graph in an interactive 3D network view, search entities, filter by type, and export the structure for use in other tools — turning linear conversation into a navigable semantic map that surfaces patterns and research gaps invisible in text alone.

05 Multiple Research Modes

When you ask withZeta a research question, it follows a recursive investigation pattern that mirrors how scientists actually conduct research. The system enters a cycle: it analyzes what information is needed, calls relevant research tools (searching PubMed, querying clinical trials, analyzing molecular pathways), receives and interprets the results, thinks about what those findings mean and what gaps remain, then decides whether to investigate deeper or synthesize a final answer.

When a question calls for deeper investigation, withZeta autonomously broadens its search-selecting additional tools, following relevant leads, and connecting evidence across databases. Each recursion round builds on previous findings: early rounds might search broadly across diseases and treatments, middle rounds might dive deep into specific molecular mechanisms discovered, and later rounds might cross-reference clinical trial eligibility against identified biomarkers. The recursion continues until withZeta reaches an emergent base case, which is the moment when it determines that sufficient evidence has been gathered to answer your question comprehensively. This isn't a fixed number of searches; rather, the AI autonomously decides when investigation is complete based on evidence quality and coverage, just as an expert researcher knows when they've read enough papers to draw sound conclusions.

withZeta offers **three research modes** that you can switch between at any time based on needs.

Explorer mode

- Provides fast, conversational research for iterative dialogue and quick insights
- Ideal for brainstorming, initial exploration, and targeted questions
- Efficient focused searches (–4 investigation rounds, 3 parallel tools) optimized for speed rather than comprehensive depth

Investigator mode

- Conducts systematic, deep research across multiple evidence streams
- Uses up to 10 investigation rounds with 6 parallel tools for comprehensive multi/database validation and evidence synthesis

Reporter mode

- Synthesizes research conversations into structured, comprehensive reports
- Best used after completing your investigation to transform dialogue into formal documentation

06 Co-scientists with Diverse Roles

Co-scientist Personas

withZeta.ai now offers six co-scientist personas - five focused on chemistry, trials, and clinical context, and one, ZetaOmics™, focused on computational biology itself. Each co-scientist tunes withZeta's system prompt, tool selection priorities, and communication style. For example, the Medicinal Chemist emphasizes cheminformatics tools and SAR language, while the Clinical Trialist prioritizes trial databases and regulatory context.

General Research Scientist

Broad oncology research expertise

This scientist researches across domains. The default co-scientist for general purpose rare cancer research, literature review, and exploratory investigation.

Medicinal Chemist

Drug design and molecular optimization

Specialized in de novo drug design, scaffold optimization, SAR analysis, ADMET prediction, and molecular property evaluation. Prioritizes cheminformatics tools and AI-driven molecular design.

Clinical Trial Strategist

Trial design and protocol strategy

Expert in clinical trial protocol development, endpoint selection, eligibility criteria design, regulatory strategy, and trial landscape analysis. Prioritizes clinical trials databases and regulatory knowledge.

Clinical Oncologist

Treatment landscape and clinical context

Specialized in treatment landscape analysis, standard of care evaluation, biomarker-guided therapy selection, and patient stratification strategies. Focuses on translating molecular findings into clinical context.

Biomarker and Translational Scientist

Biomarker discovery and translational research

Expert in biomarker discovery and validation, companion diagnostic development, translational research pipelines, and genotype-phenotype correlation analysis. Bridges molecular findings to clinical application.

ZetaOmics™ Computational Biologist

Multi-omics bioinformatics and biostatistics

Specialized in cohort building, differential expression, pathway enrichment, survival analysis, and drug-response correlation across real biological data. Encodes the judgment of a tenured bioinformatician to keep scientific rigor the default.

**These personas are intended for research support purposes only and are not designed for clinical decision-making.*

07 ZetaOmics™ – The Computational Biologist

Meet ZetaOmics™ – an autonomous **Computational Biologist** that designs experiments, builds rigorous cohorts, and delivers publication-quality multi-omic analysis in minutes. Purpose-built for the rare and pediatric cancers that have long been underserved — and powerful across every cancer type.

500K+	9	14	100.0%
Cancer samples	Data sources	Intelligent tools	Every cancer type

Intelligence in every tool not just automation

Most agentic tools wrap a language model around off-the-shelf software and will happily run a confounded cohort or the wrong statistical test — handing back a confident answer only an expert would recognize as wrong.

ZetaOmics™ takes the opposite approach: domain judgment is embedded in all fourteen tools. When an analysis is flawed, it is designed to **recognize the flaw, decline to run it, and explain how to fix the experimental design.**

Rigor by default —

Batch-effect safeguards, effect sizes, confidence intervals, power, and false discovery rate — enforced automatically, with a queryable audit trail on every run.

"For decades, the deepest bottleneck in drug discovery hasn't been data; it has been judgment… With ZetaOmics, we've worked to encode that judgment into an autonomous agent and make rigor the default—so any researcher, anywhere, can run analysis at a level once reserved for the world's best-resourced labs."
-Panna Sharma

ZetaOmics™ in Action

The difference between orchestrating tools and encoding judgment is easiest to see in practice. Three examples:

01

Accurate Discovery, Protein-Validated

Finding a drug vulnerability in a rare, hard-to-treat cancer

Ask — Are there drug vulnerabilities in KRAS-mutant lung cancer, and are they real at the protein level?

Description — ZetaOmics builds batch-safe cohorts, enforces true loss-of-function variant calls, checks statistical power, and validates hits at the protein level via RNA-protein concordance.

Impact — A vulnerability that a specialist team might spend weeks qualifying is surfaced, statistically defended, and protein-validated in one session.

02

Guardrails That Prevent False Discovery

Refusing a comparison that would have produced a false discovery

Ask — Compare gene expression between these two glioblastoma cohorts I've assembled.

Description — ZetaOmics detects that the cohorts mix incompatible quantification pipelines, declines to run the naive comparison, and auto-matches pipeline consistent controls instead.

Impact — The single largest source of false discoveries in multi cohort studies is caught automatically.

03

Actionable Signals in Sparse Data

Prioritizing a druggable biomarker in a pediatric cancer with sparse data

Ask — What are the most promising druggable targets in this rare pediatric tumor?

Description — With no validated prognostic panel available, ZetaOmics pivots automatically to a plasma-led path and surfaces circulating biomarker candidates as an actionable shortlist.

Impact — For exactly the populations the field tends to abandon, ZetaOmics turns data scarcity into a defensible starting point.

Inside the computational biologist : 14 tools, one conversation

Ask anything. withZeta.ai orchestrates the right tools, data, and methods -so you get trusted answers, faster and with full provenance.

01 Discovery
Ask in plain English; it routes only to the datasets that hold the modality you need.

02 Gene Intelligence
Genome to proteome in one query, across Ensembl, UniProt, OMIM, and Orphanet.

03 Batch Guardian
Profiles cohorts for hidden confounders and mixed pipelines before anything runs.

04 Cohort Builder
Turns plain-language filters into analysis-ready groups with diagnostic feedback.

05 Expression
Auto-selects the right normalization and validates RNA against protein evidence.

06 Mutations
Consequence-aware stratification; true loss-of-function vs. benign missense.

07 Drug Response
Reports effect size, confidence intervals, power, and FDR — not just p-values.

08 Differential Expression
Ask in plain English; it routes only to the datasets that hold the modality you need.

09 Survival
Covariate-adjusted Cox modeling with hazard ratios and PH diagnostics.

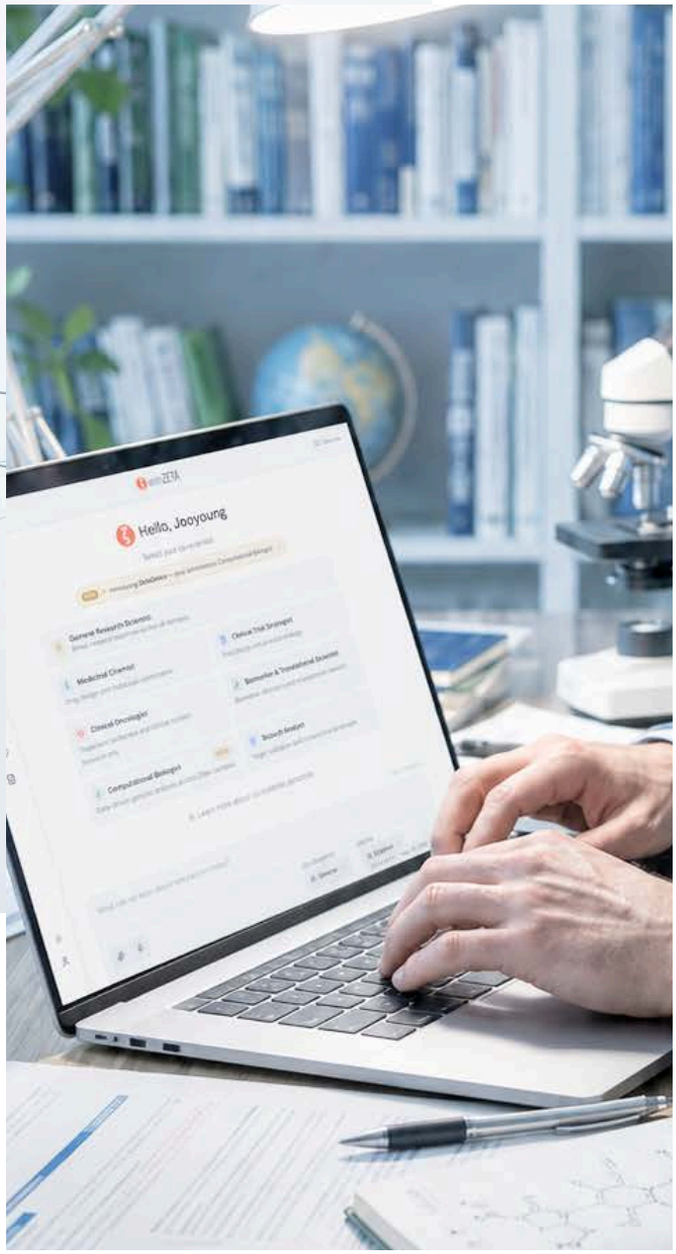
10 Stratification
Split cohorts by expression, signatures, metadata, or drug/CRISPR response.

11 Protein Triage
Ranks druggable, tumor-restricted targets - pivots to plasma biomarkers when data is sparse.

12 Analysis Sandbox
Describe a bespoke test in plain language; it generates and runs sandboxed code.

13 Visualization
Thirteen publication-quality presets rendered so figures always match the numbers.

14 Investigation Memory
Stores, versions, and traces every result so multi-step workflows never rebuild.



08

Who Uses withZeta.ai?

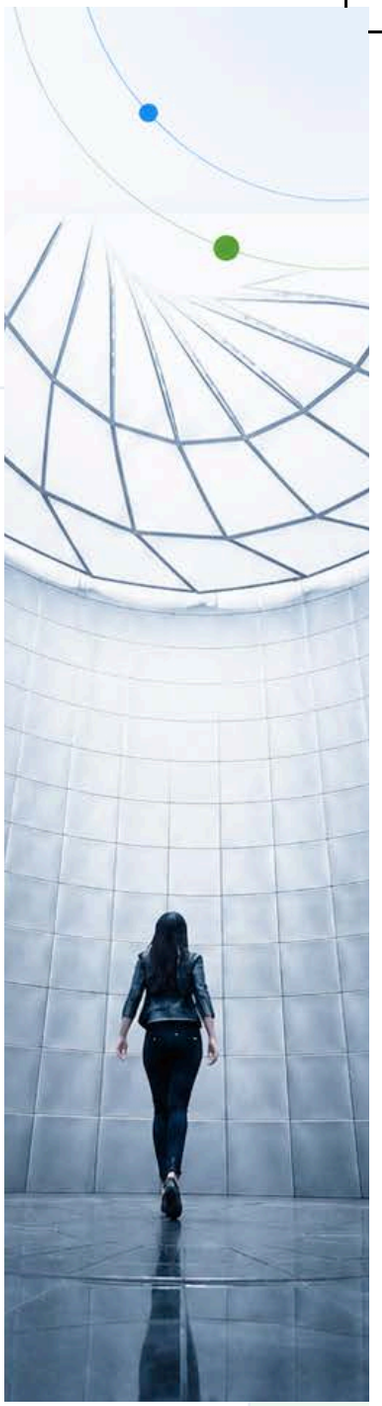
withZeta serves oncology researchers, drug discovery scientists, and clinical trial designers working to advance therapeutic options for rare cancer patients. Academic investigators use withZeta to accelerate systematic literature reviews that would traditionally take weeks to compile manually, synthesizing evidence across PubMed, clinical trials databases, and curated rare cancer knowledge in hours rather than days. Pharmaceutical R&D teams leverage the platform to evaluate rare cancer development opportunities, assessing biological plausibility and competitive landscapes before committing resources to expensive preclinical programs. Clinical trial designers use withZeta to identify appropriate patient populations and develop molecularly-informed eligibility criteria, while drug discovery scientists explore repurposing opportunities by identifying existing approved drugs that might address rare cancer indications through shared molecular mechanisms.

Common research workflows include:

Rare cancer characterization	Analyzing biomarkers, molecular drivers, and epidemiology for understudied diseases	**CNS drug optimization**	Evaluating blood-brain barrier penetration for brain cancer therapeutics
Drug discovery	Identifying therapeutic candidates based on mechanism-of-action alignment	**Clinical trial matching**	Finding relevant trials for patients with specific molecular profiles
Combination therapy exploration	Identifying synergistic treatment approaches through complementary mechanism analysis	**Multi-omic cohort analysis**	Building rigorous, batch-safe cohorts & running publication ready bioinformatics

Researchers also use withZeta to generate comprehensive knowledge graphs that visualize complex disease-drug-gene relationships, making it easier to identify research gaps and promising development pathways that might not be apparent from literature review alone.

09 Future Directions



Enterprise Features

- Team workspaces with shared knowledge graphs, collaborative annotation, and full session history
- Role-based access controls and audit trails built for regulated pharmaceutical and clinical environments
- API access and custom integrations with internal R&D platforms and proprietary data systems
- White-label deployment for pharma, CRO, and academic medical center partners

Social Features

- Shared research environments where teams can co-author, annotate, and distribute findings
- Credentialed researcher profiles linking institutional affiliations and published work
- Multi-user investigation sessions enabling real-time collaborative discovery
- Personalized feeds highlighting relevant breakthroughs across rare and precision oncology

Tool Enhancements

- Specialized AI agents supporting computational biology, medicinal chemistry, and clinical development workflows
- Expanded ZetaOmics™ analysis tools for genomic, transcriptomic, and pathway-level interpretation
- Advanced molecular design capabilities supporting drug optimization, property evaluation, and novel molecule generation
- Enhanced evidence synthesis tools connecting literature, biomarkers, drugs, trials, and research findings across investigations

Biology Models

- Broader data modality support spanning proteomics, transcriptomics, and real-world clinical evidence
- Integrated IP landscape analysis to inform patent decisions
- Integration of Lantern's proprietary pathway and mechanism knowledge base to accelerate mechanistic insights
- Expanded connectivity to external research platforms, databases, and institutional data systems

Other

- Mobile-optimized interface for research access across devices and settings
- Structured onboarding and educational resources for investigators new to AI-assisted drug discovery
- Regulatory strategy assistance tools supporting IND preparation, Orphan Drug, and Breakthrough Therapy designation framing

"Multi-agentic AI isn't the next step in drug development — it's a fundamental reset of what's possible. ***withZeta.ai*** *represents our conviction that the greatest breakthroughs in medicine will come from the intersection of human expertise and autonomous scientific intelligence."*

– Panna Sharma

Ask a question.
Get a complete investigation.

Traditional Research

8–12 hours

per investigation

1 Manual Literature Mining — 3–4 hours
Search PubMed for rare cancer papers, sift through abstracts one by one, no connections between entities

2 Clinical Trial Hunting — 2-3 hours
Navigate Clinical Trials, gov filters, decode eligibility criteria, manually match patient biomarkers

3 Drug-Target Mapping — 2-3 hours
Cross-reference FDA labels, ORPHANET disease data, and molecular databases separately

4 Evidence Synthesis — 2-4 hours
Compile fragmented findings from disparate sources, manually identify therapeutic opportunities

Manual, fragmented, time-intensive.

Research with Zeta

5–10 minutes

comprehensive synthesis

1 Natural Language Query — Instant
Ask your research question in plain English about rare cancer therapies, biomarkers, or trials

2 Autonomous Multi-Source Search — Seconds
Zeta simultaneously queries rare cancer databases, clinical trials, literature, and drug data

3 Recursive Investigation — Minutes
AI analyzes initial findings, decides which leads warrant deeper investigation, executes follow-up searches

4 Synthesized Insights — Complete
Citation-backed analysis with drug candidates, trial matches, biomarker correlations, and knowledge graphs

Autonomous, connected, insight-driven.

OPEN MEDICINE

Rare cancer patients can't wait 50 years for the next 50 years of progress.
With **withZeta by Open-Medicine AI**, they won't have to.

Open-Medicine.ai

withZeta.ai