CYTOCAST DIGITAL TWIN Platform™

Reveal the risks. Understand mechanisms. Advance the best.

AI- and simulation-powered platform integrating systems biology, machine learning, and high-performance computing to predict clinically relevant side effects early in drug development with interpretable, mechanism-linked outputs.

>7,700	15	>1,000	0.70
proteins modeled	tissue types	MedDRA PT side effects	median accuracy, Gold-tier*

How the platform works

The Cytocast platform **predicts clinically relevant side effects through a multi-layer modeling pipeline**. Starting from compound structure (SMILES string), AI models identify potential on- and off-target interactions.

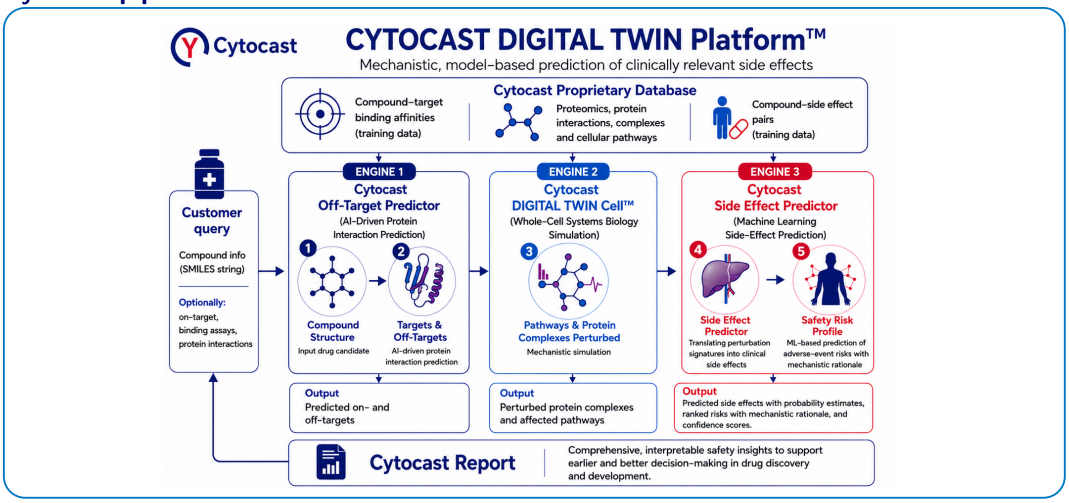
Perturbations propagate through protein complexes[1] and signaling pathways using the CYTOCAST DIGITAL TWIN Cell™ simulation, after which system perturbations are mapped to clinical phenotypes using machine learning models. This mechanistic chain works in both directions: it supports not only prediction of side effects, but also mechanistic interpretation at pathway and off-target level.[2]

Core output

Interpretable safety reports linking predicted adverse-event risks to molecular interactions, perturbed protein complexes, affected pathways, and confidence-ranked side-effect profiles.

The scalable architecture of the platform supports secure integration into pharmaceutical R&D workflows.

Cytocast pipeline



Where Cytocast fits in R&D

DISCOVERY / VIRTUAL SCREENING
Cytocast Screener™
High-throughput triage of hundreds to thousands of compounds during early discovery.

→

LEAD OPTIMIZATION
Cytocast Optimizer™
Comparative safety reasoning to guide compound optimization and series prioritization.

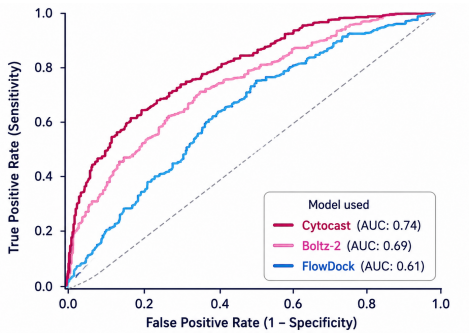
→

CANDIDATE NOMINATION
Cytocast Nominator™
Mechanistic safety reports supporting preclinical development and preparation for first-in-human clinical studies.

Validation and predictive performance

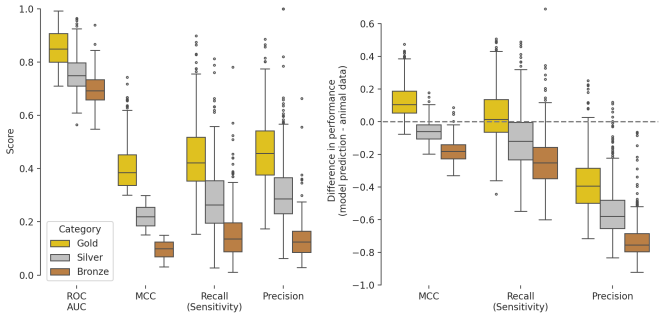
Cytocast validation evaluates: **(i)** compound–protein interaction prediction, **(ii)** clinically observed side-effect ranking, and **(iii)** translational performance relative to animal-to-human toxicity benchmarks. *Gold-tier metrics represent the current decision-grade operating range.

Off-target prediction benchmarking (ROC)



ROC benchmarking shows Cytocast achieving the highest discriminative performance, with an **AUC of 0.74** compared with **0.69 for Boltz-2** and **0.61 for FlowDock**.

Performance relative to animal-to-human translation



Cytocast Gold-tier predictions outperform published animal-to-human toxicity benchmarks (*Clark & Steger-Hartmann, 2018*), demonstrating **improved predictive performance and enhanced detection of clinically relevant safety risks**.

Side-effect prediction performance

- **567 predicted side-effect categories**, stratified into Gold, Silver and Bronze reliability tiers, with **113 clinically relevant side effects in the Gold tier**.
- Most reliable predictions: median balanced accuracy ∼**0.70** (IQR **0.68–0.76**), median specificity ∼**0.85**, and median sensitivity ∼**0.58**.

Interpretability

- Predictions are linked to **targets, off-targets, complexes, and pathways**, supporting hypothesis generation and mechanistically grounded safety assessment.

Platform Coverage

- **7,700+ proteins modeled**
- **15 tissue types simulated**
- Predicts **1,000+ MedDRA PT side effects**, compared with approximately **283** commonly assessed in animal toxicology.

Rare-event prediction robustness

- **Rare-event prediction:** balanced accuracy around **0.70** across major organ systems, accounting for class imbalance inherent in rare-event side-effect prediction.

Platform strengths

- **Mechanistically grounded** prediction rather than chemistry-only similarity.
- **Whole-cell, multi-tissue simulation** for system-level biological context.
- **Transparent reliability** via tiered prediction stratification.
- **High-confidence predictions** provide decision-relevant insight into safety risks.
- Enables **large-scale safety assessment** across compound portfolios **at a fraction of the time and cost of traditional animal studies**.
- **Continuous improvement** with documented performance gains.
- **Clinically framed output** using observed side effects.
- Designed to **support earlier go/no-go and prioritization decisions**.
- **Aligned with model-informed drug development frameworks (FDA/EMA MIDD)**.

Relevant publications

1. Computational tools to predict context-specific protein complexes. *Current Opinion in Systems Biology*.
2. Digital twin approaches for interpretable side effect prediction in drug discovery. *Drug Discovery Today*.

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