


CERTARA[®]
Pirana PMX Modeling Software

The Premier Workbench for Pharmacometric Workflows





Unify pharmacometric workflows for faster, and more reliable drug development

Pirana is a comprehensive pharmacometrics (PMX) analysis platform that organizes the use of specialized PMX software tools within a unified user experience. Originally designed to work with NONMEM, Perl Speaks NONMEM (PsN), and the R/xpose package, Pirana has expanded its capabilities to include command-line modeling in R via Certara's NLME engine. Additionally, Pirana now offers machine learning-based model selection through an intuitive graphical interface with pyDarwin, and a new Simcyp engine interface to support virtual bioequivalence analyses.

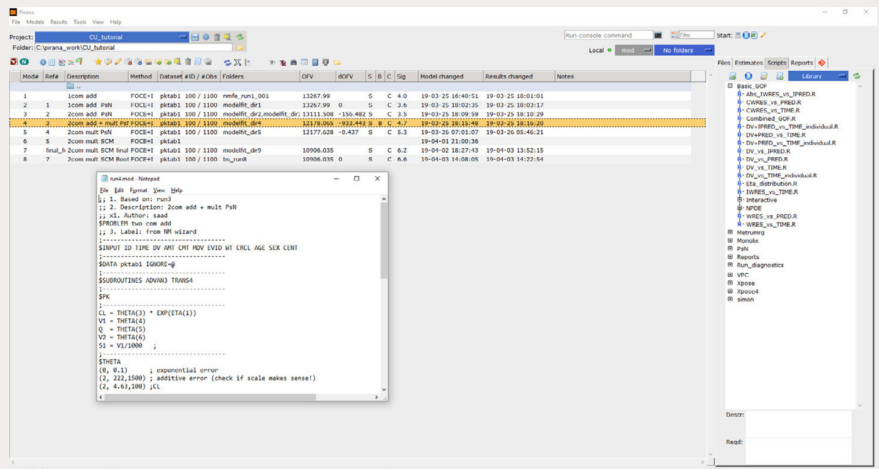
By providing modelers with a structured framework, Pirana enhances the iterative process of PMX model development and evaluation, leading to more organized, efficient, and insightful analysis of pharmacometric data.

Pirana provides modelers a wide range of critical structure, tools and graphics pivotal to validating modeling results for traceability and reproducibility:

- Model templates and wizards
- Library of goodness-of-fit plots (R)
- Model translation tools
- Seamless access to continuously expanding open source toolsets supporting the PMX workflow (diagnostics, simulation, reporting, and more)
- Supported on major operating systems Windows 10, CentOS/ RHEL7&8, Ubuntu 18+, Windows 2019 Server

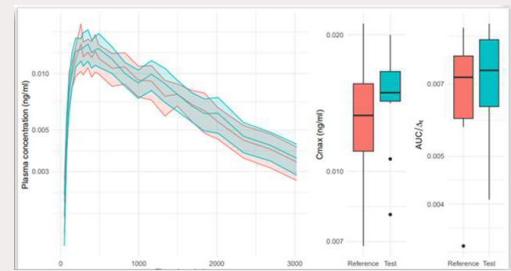
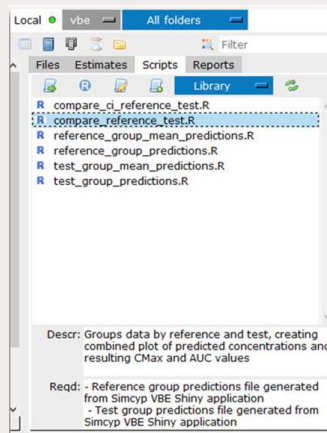
Optimize Pharmacometric Workflows with Pirana

Pirana delivers faster, more efficient modeling and simulation by connecting multiple tools for optimizing a pharmacometrics workflow. A graphical user interface provides an automated folder structure for the storage of analytical results, adding order and traceability to complex analyses.



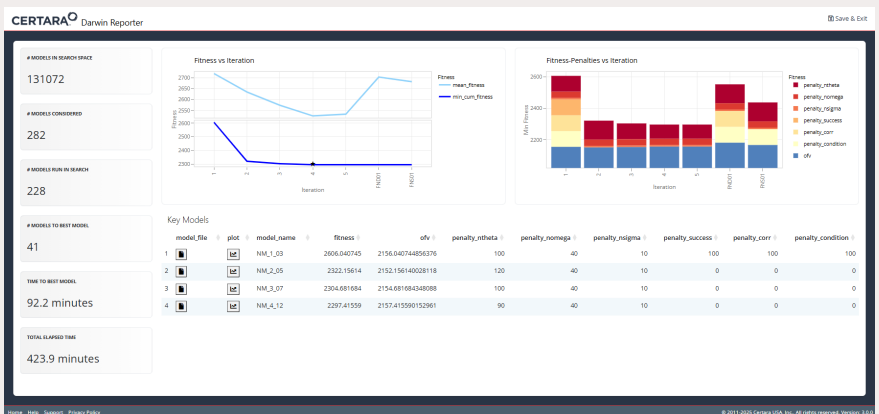
New capabilities: Virtual Bioequivalence with Simcyp Integration

Integration with Simcyp™ Simulator Engine for performing simulation based virtual bioequivalence analyses for long acting injectables via extensible R based workflows. Project is shareable, reproducible, and self-contained within a single *.vbe file.



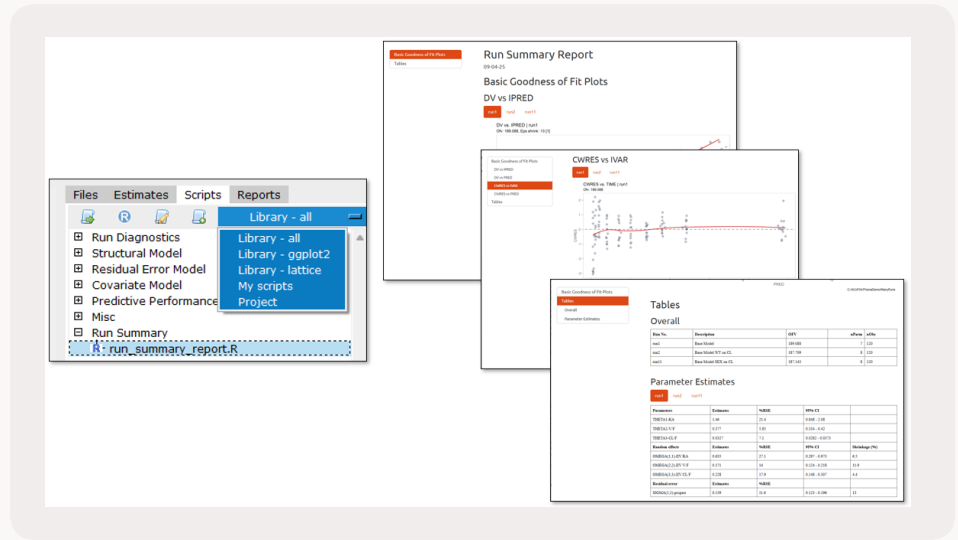
Machine Learning Based Automated Model Selection

The Darwin Model Search feature in Pirana provides a streamlined user interface to pyDarwin, a cutting edge opensource Python package collaboratively developed under a grant funded by FDA that implements a number of machine learning algorithms for automated pharmacometrics (PMX) model selection. The best model selected by a Darwin search is fully compatible with the existing suite of Pirana tools for PMX workflow management.



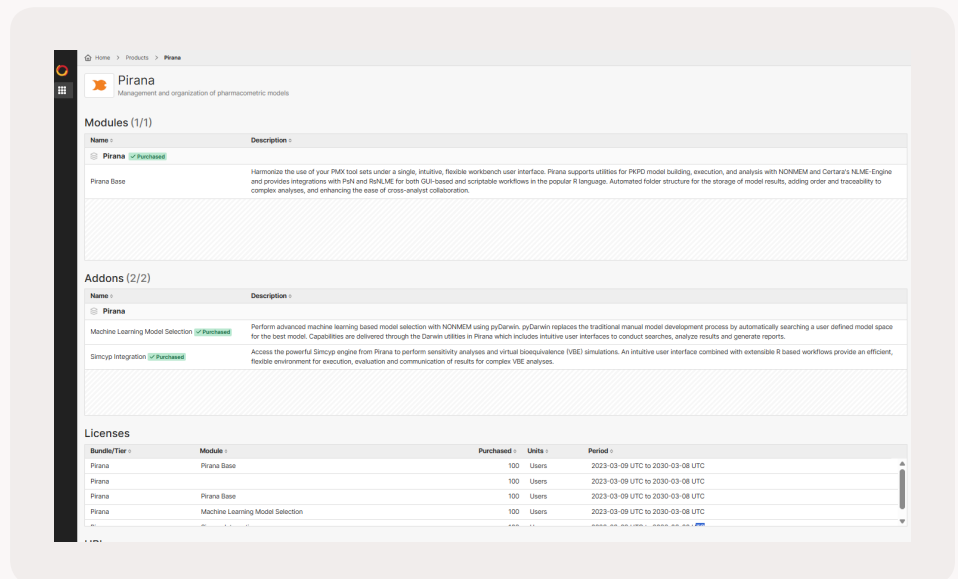
Enhanced Model Script Library

New interactive scripts and multi-model summary scripts have been added to further enrich the comprehensive library of built-in R scripts for model post-processing.



Simplified License Management through Integration with Certara Admin

Unified Certara ID enables users to use single credentials to request and access Certara software and live product catalog and enables IT administrators to manage and configure all Certara software in a centralized interface.



Unify pharmacometric workflows for faster, and more reliable drug development

3,500+

Pirana users

120+

Organizations worldwide use Pirana

440+

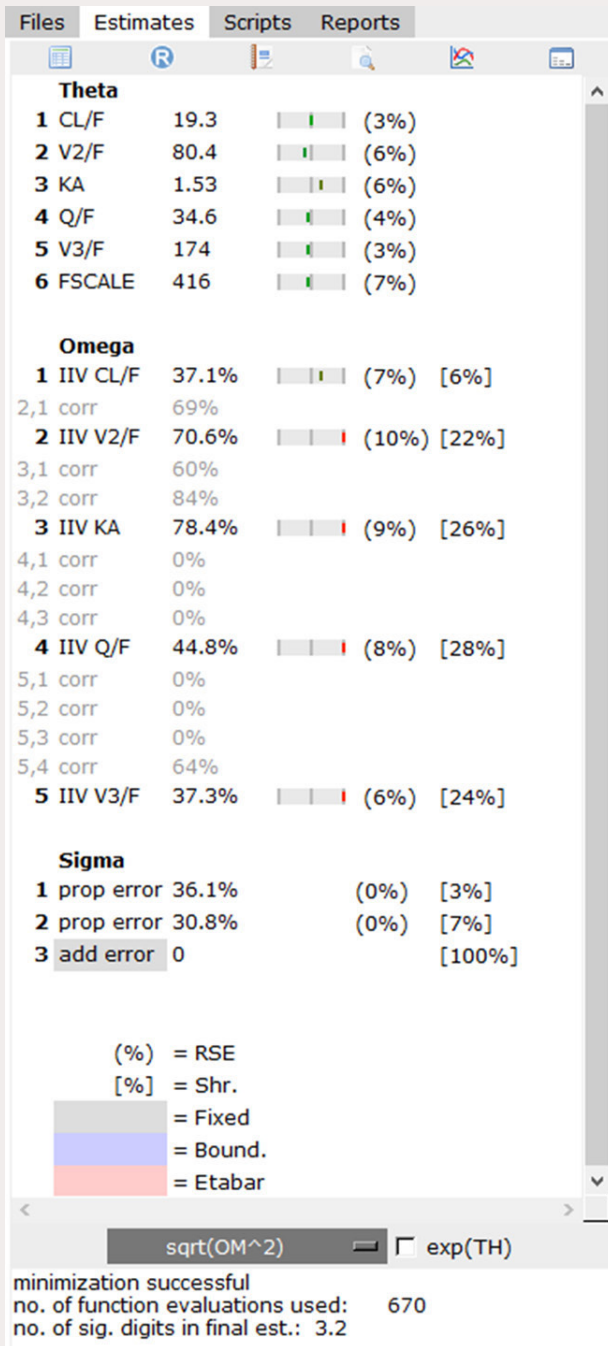
Scientific citations

Pirana Graphical User Interface

The Pirana modeling workbench provides a flexible and intuitive graphical user interface for the management of pharmacometric workflows using NONMEM, NLME and other analysis software.

Pirana provides functionality for model management, model execution, output generation, and interpretation of results:

- Models can be read from a folder or created in Pirana
- Analyses are automatically managed through an intuitive graphical interface
- Post-processing work can be performed on models executed in Pirana



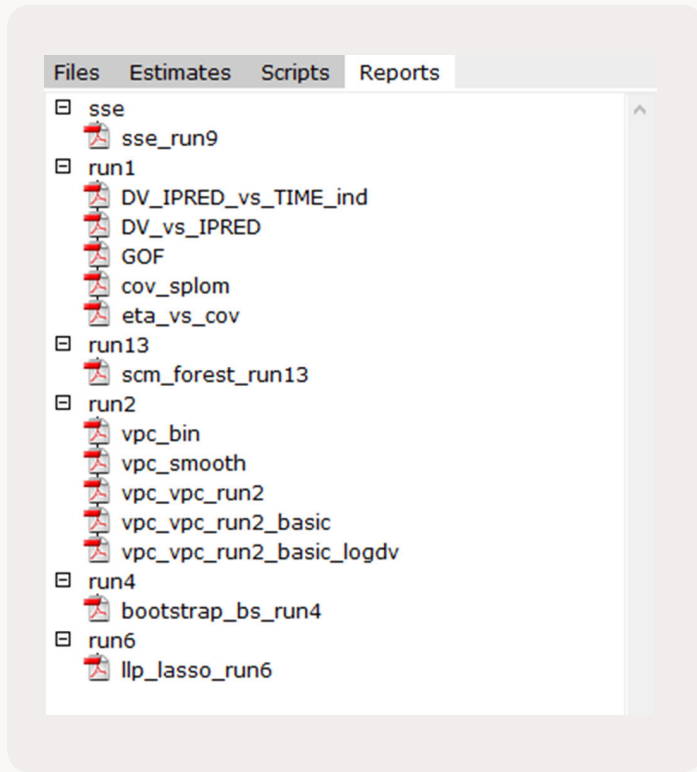
Pirana provides modelers a wide range of critical structure, tools and graphics pivotal to validating modeling results for traceability and reproducibility:

- The Estimates tab contains model results displaying summaries of estimated model parameters
- A library of scripts provides options to run, generate plots and analyses, create, review or modify R code and run additional scripts by other integrated software, e.g., PsN, Xpose, or Certara.R packages
- Basic summaries of results and reports and generated plots of the scripts in html, PDF, Word, and LaTeX format can be easily accessed from the Results tab
- Rmarkdown reporting capability can be accessed through modelResults and VPCResults R shiny interfaces

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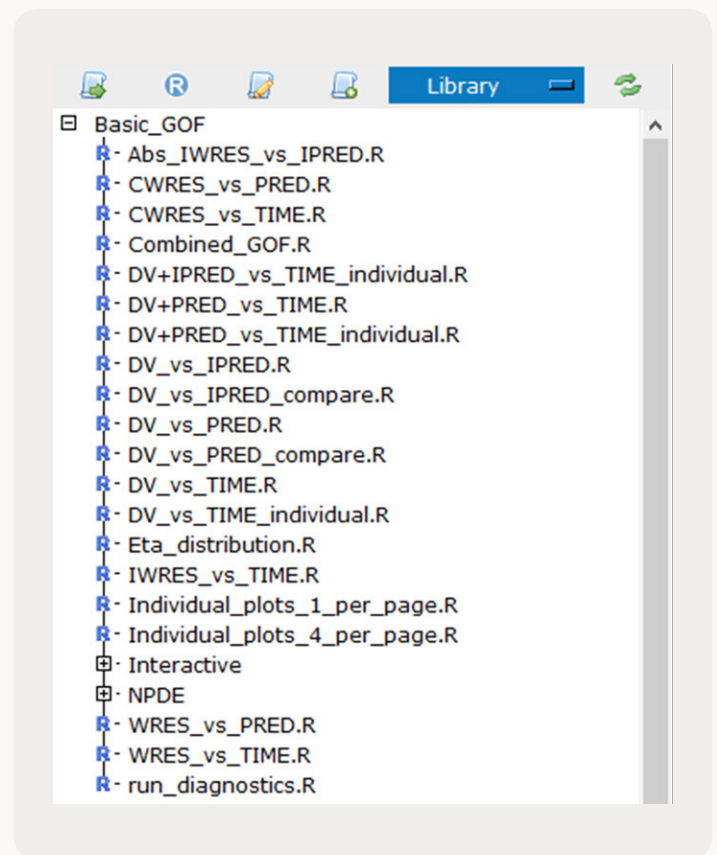
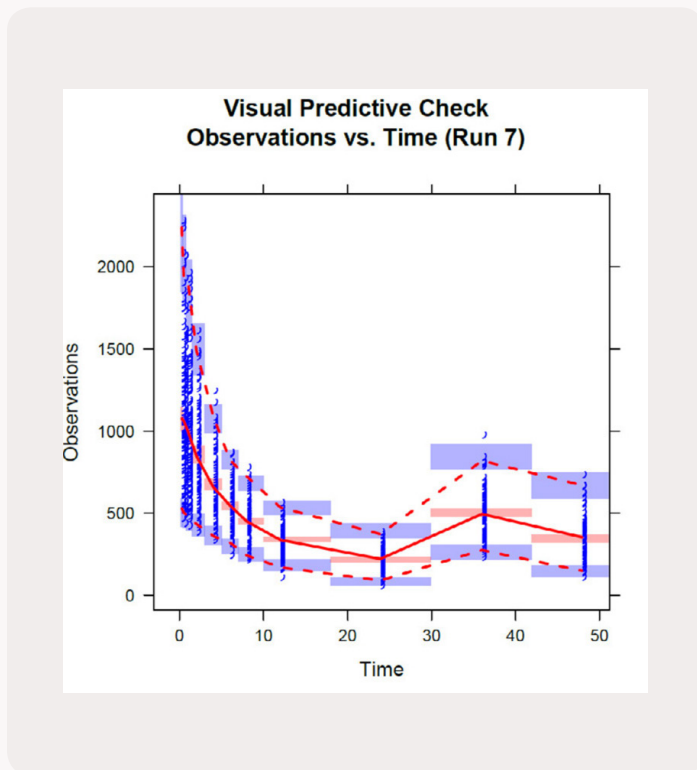
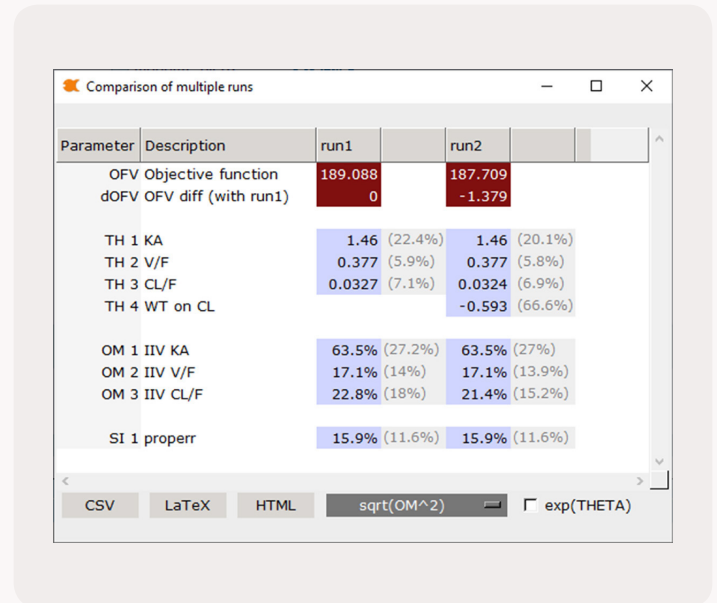
Data Visualization

Pirana provides a quick and easy graphical interface to R plotting tools and supports the generation of plots in R using PSN and Xpose or custom user scripts.



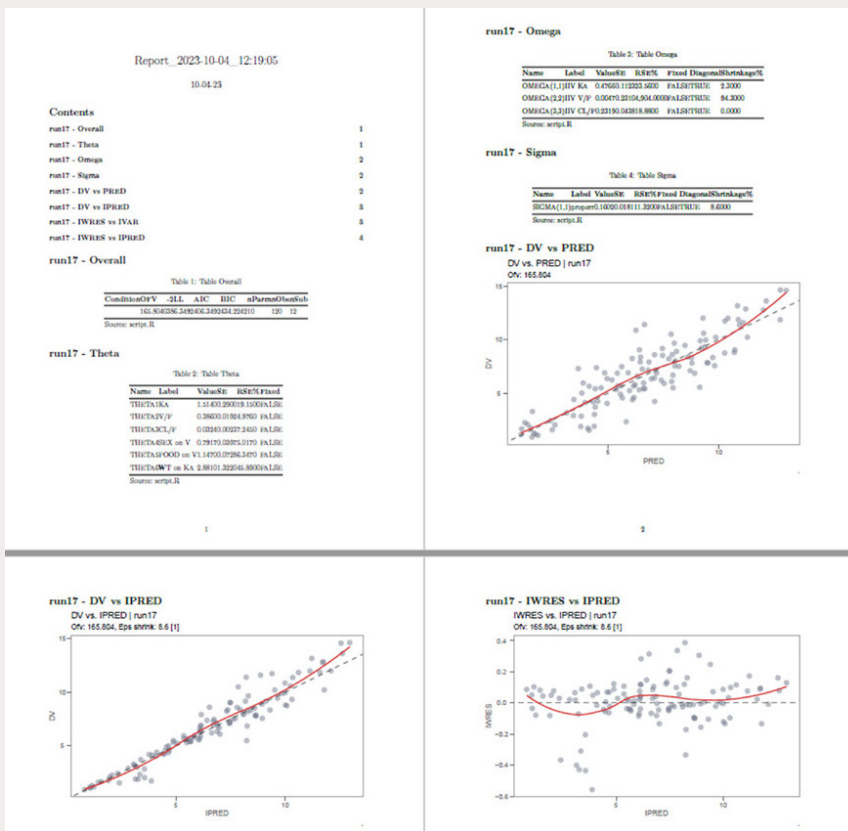
Compare model diagnostics

Pirana provides faster, easier model evaluation and side-by-side model diagnostics to aid in the model development process.



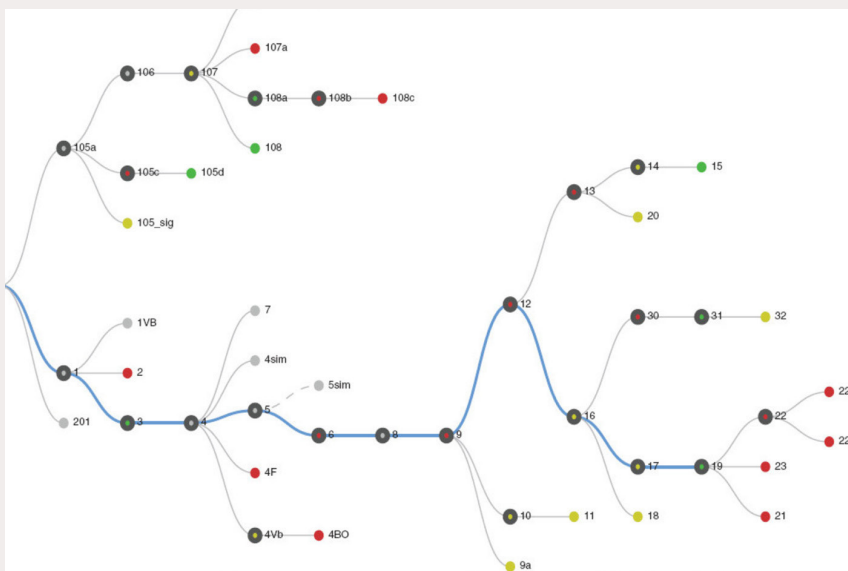
Report and summarize model results

Pirana's powerful reporting tools provide options to run reports in various formats, including Word, html, plain text, LaTeX, and Excel. Launch the companion modelResultsUI shiny application to access interactive diagnostics with Rmarkdown reporting capability.



Visualize the model decision tree

The Visual Run Record in Pirana documents the model development process through a unique interactive visualization. A summary of the model selection thought process displays how models were evaluated, and how/ why the final model was chosen.



Interface with most pharmacometric software

Pirana provides interfaces to a range of software tools used in pharmacometric modeling including NONMEM®, PsN, Xpose, R Software (including R Studio), RsNLME, pyDarwin and Simcyp unleashing a concert of functionality for efficient and organized pharmacometric analyses.



Learn more: certara.com/Pirana



About Certara

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