



AI powered co-ideation for faster patient impact

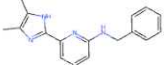
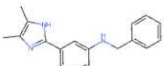
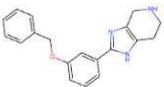
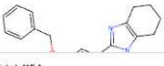


Malaria Libre optimising potency and logD

Molecules Plots

All My molecules Generated molecules

Filters Calculate Properties Predict Columns Share

	Smiles	Generated with AI	3D7 pIC50	LogD
343			6.87	3.37
1			5.77	3.45
2			7.05	2.77 High Novelty
3			5.93	4.75
Total: 1154		Generated: 800	6.63 ± 0.72	3.06 ± 0.72

Draw Generate Upload new data

Property details

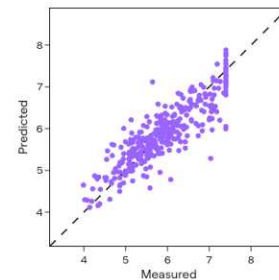
3D7 pIC50

Predicted values ± uncertainty should contain the true value in ~90% of cases.

When sorting for higher or lower 3D7 pIC50 you can expect:
77.1% of the highest predictions to be the true highest values in your dataset.
71.4% of the lowest predictions to be the true lowest values in your dataset.

☐ Add property to all datasets.

Advanced



Comparison between Predicted (y-axis) and Measured (x-axis) values when the measured data was not used for learning. [Read more about this validation](#).

More accurate predictions are closer to the dashed line. Hover over each point for more details.

R-squared: 0.77

Mean error of predictions: 0.30

Model ID: 42386

Molecular features: 2D

Generator **Guided (v2)** ▼Starting molecules: **Auto** ⓘ[+ Add structure filter](#)

▲ LogD



< ▼

3

▲ 3D7 pIC50



> ▼

6.5

☐ Only add molecules that satisfy **all** goals[+ Add goal](#)

To generate more molecules, select a goal threshold that falls within the range of your current data.

Estimated generation time: **7** minutes.

Cancel

Generate

< Malaria Libre optimising potency and logD

Molecules

Plots

All

My molecules

Generated molecules

Draw

Generate

Upload new data

Filters

Calculate

Properties

Predict

Columns

Share

☐

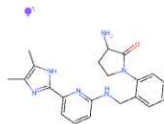
Smiles

Generated with AI

3D7 pIC50

LogD

356



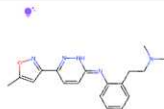
Generated with
'Guided' Model.
Goals: 3D7 pIC50 >
6.5, LogD < 3. Row
343

6.63
High Novelty

2.15
High Novelty



357



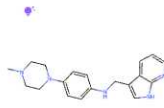
Generated with
'Guided' Model.
Goals: 3D7 pIC50 >
6.5, LogD < 3. Row
343

6.99
High Novelty

2.61
High Novelty



358



Generated with
'Guided' Model.
Goals: 3D7 pIC50 >
6.5, LogD < 3. Row
343

6.90
High Novelty

2.12
High Novelty

Total: 800

Generated: 800

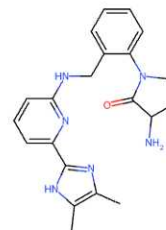
6.94 ± 0.37

2.83 ± 0.48

Molecule Details

Generated

Edit



Generated with AI

3D7 pIC50

LogD

Generated with 'Guided'
Model. Goals: 3D7 pIC50 >
6.5, LogD < 3. Row 343

6.63 (High Novelty)

2.15 (High Novelty)



Compare to similar molecules

See how this molecule compares to similar
molecules from your uploaded dataset

View comparisons →


CAIX Inhibitors

All Molecules

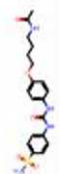
Filters Calculate

Molecules

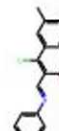
1



2




3



Total: 414

Molecule 1 with CAIX

Target CAIX



Poses ⑦

● pose 1

○ pose 2

○ pose 3

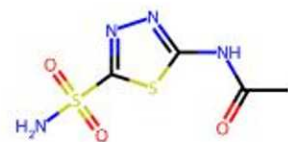
○ pose 4

○ pose 5

MMGBSA ⑦	9.34 ± 12	9.34 ± 12	9.34 ± 12	9.73 ± 18	9.35 ± 23
Property B ⑦	9.67 ± 32	9.34 ± 12	9.34 ± 12	9.73 ± 18	9.35 ± 23

Molecule 1

Hide 3D target binding Edit



pIC50 8.03 (± 0.825)

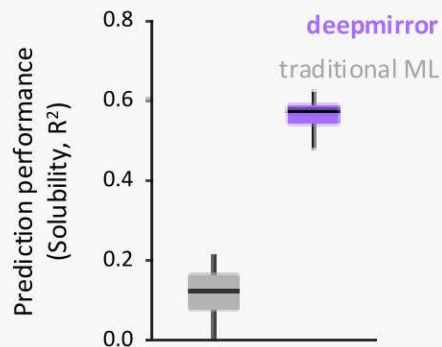
hERG (pIC50) 5.01 (± 1.56)

CYP3A4 Inhibition (pIC50) 4.98 (± 0.27)

deepmirror engine

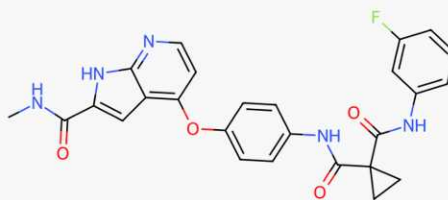
Foundation Models for Molecular Properties

Step up performance in potency, ADMET, and more



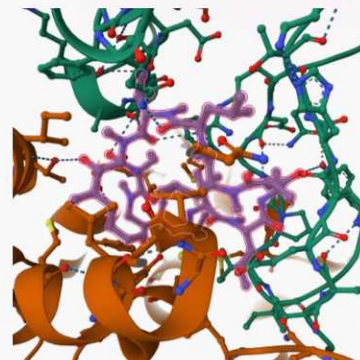
Generative AI Tailored to Medicinal Chemistry

Design novel, viable molecules that address multiple design goal



Protein-Ligand Structure Predictions

Accurate AlphaFold3-style predictions for biomolecular complexes



autoML for chemistry

**User
Dataset.**

**Build the
best model**

**Make
predictions**

autoML for chemistry

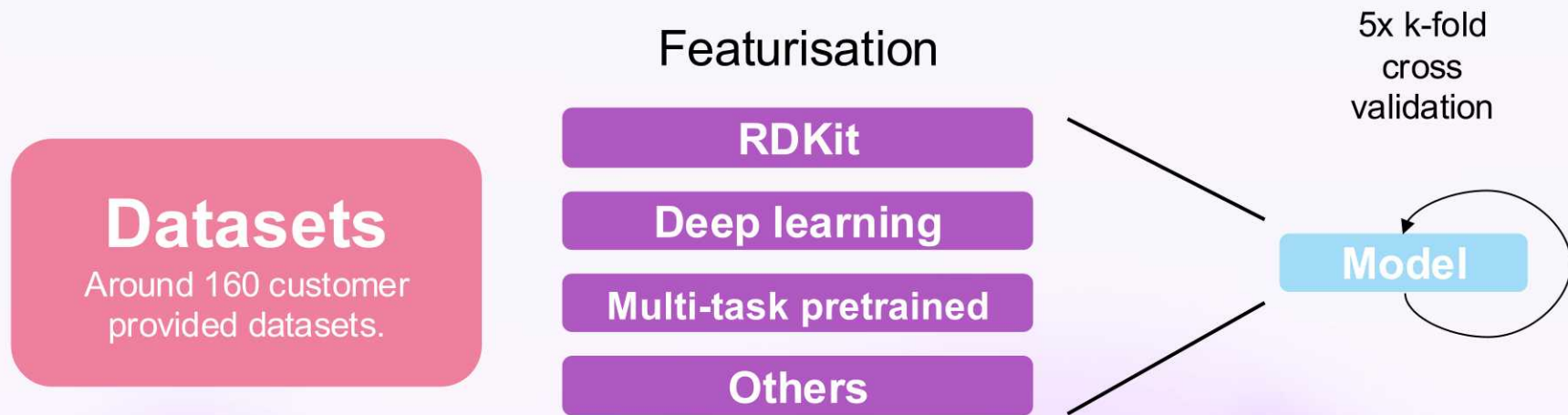


Expert

Graph

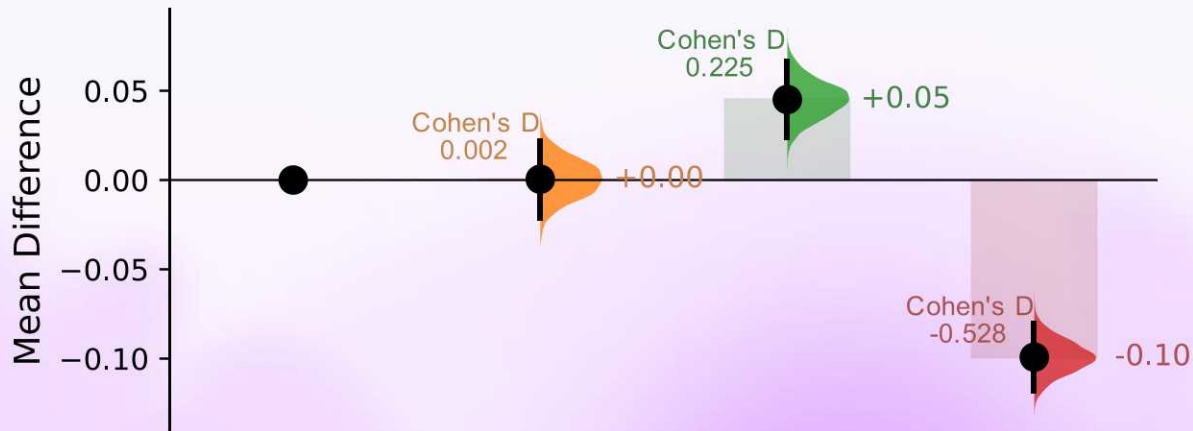
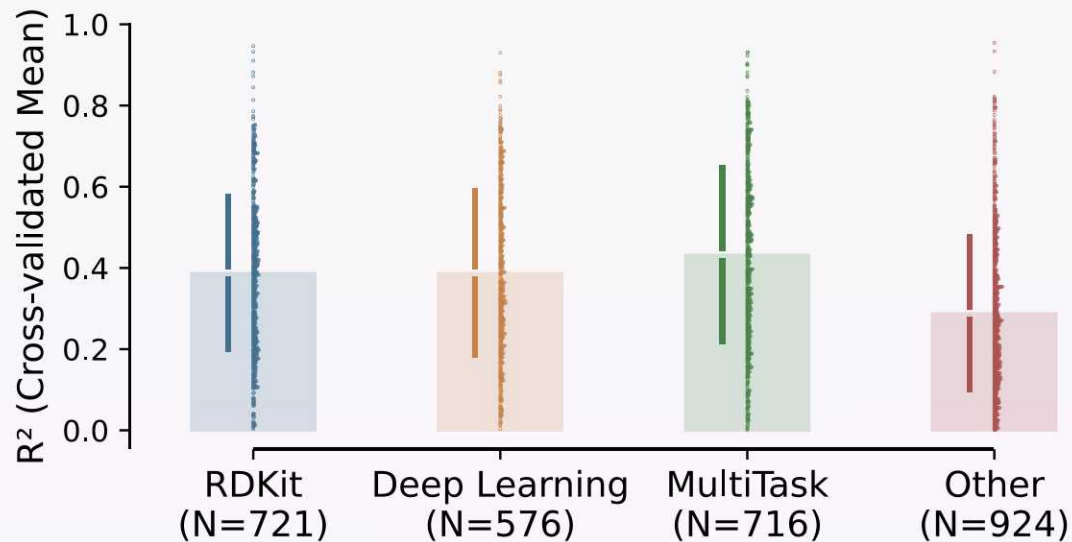
Text

autoML for chemistry

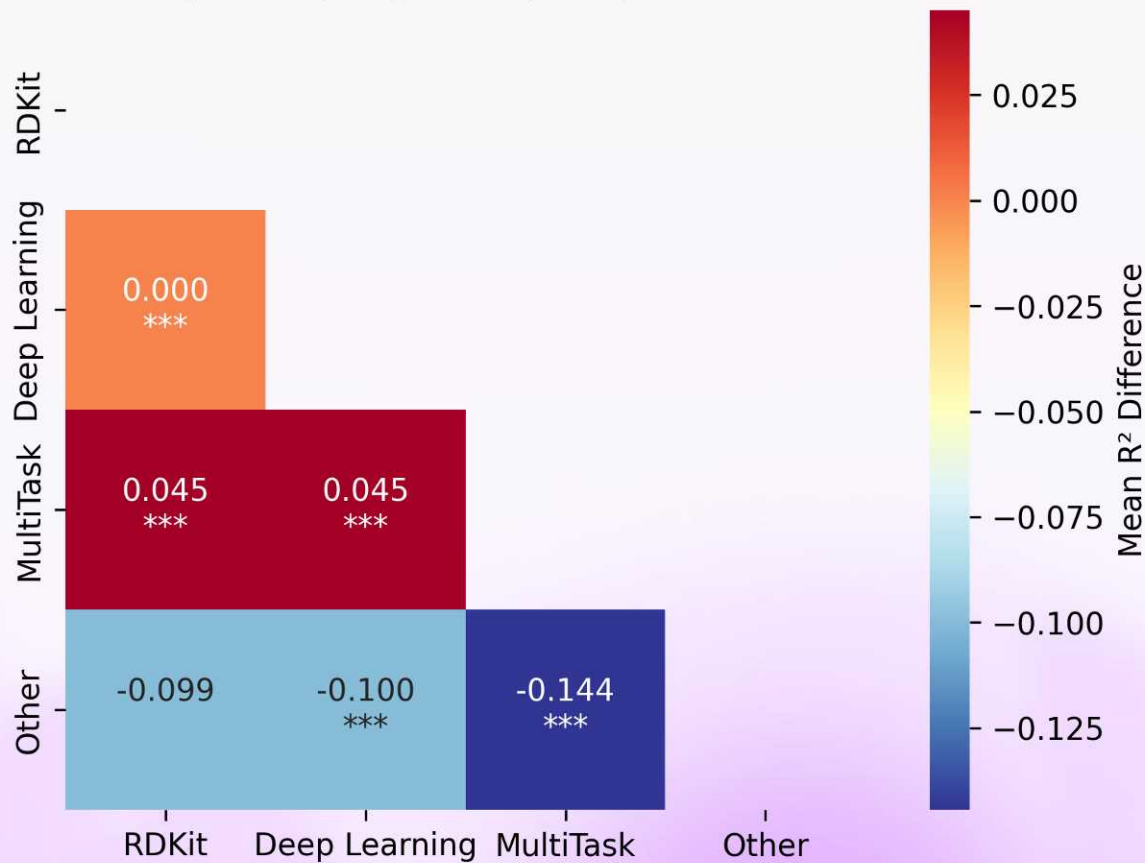


autoML for chemistry

- RDKit-based models (e.g., Morgan, RDKit2D)
- Deep Learning-based models (e.g., ChemBERTa, Mol2Vec)
- Multi-task pretrained models (trained on large portions of ChEMBL / private data)
- Other (e.g., Pharmacophore-based models)



R^2 (Cross-validated Mean)
 Holm-Bonferroni correction
 * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$



Lessons Learned from our autoML Pipeline:

1. Classical fingerprints (RDKit-based) are a very strong baseline and are often comparable to deep learning models.
2. Multi-task pretrained models consistently deliver strong results, validating their practical effectiveness.

Thank you for listening



Viplov
Backend



Max
CEO



Cecilia
PM & UI



Andrea
Sales



Shannon
Frontend



Janosch
AI Research



Ryan
CTO

Reach out for more: ryan@deepmirror.ai



cerevance



and more...