



Delivering high quality
in silico estimates of
human ADME/PK

Strategy used to build confidence in PROSILICO's *in silico* methods for prediction of human clinical ADME/PK

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Early experiences (Years at AstraZeneca: ADME/PK-prediction methodology)

- At CD-selection and FTIM-dose setting:
 - Choice driven by tradition and subjectivism
 - Many opinions & No consensus
- Opinion - *In silico* less accurate than *in vitro*- and animal *in vivo*-data

- Decent *in silico* methods available for some parameters
- Poor for other and secondary parameters
- Common with limited and non-representative test datasets and retrospective fits
(rather than complete cross-validations and true forward-looking predictions)

→ Opportunity to improve

1. Systematic review of prediction methods

- 11 research papers
- Pros and cons highlighted
- Common with cherry-picking and non-reported failures
- No consensus
- Needs and areas of improvement highlighted

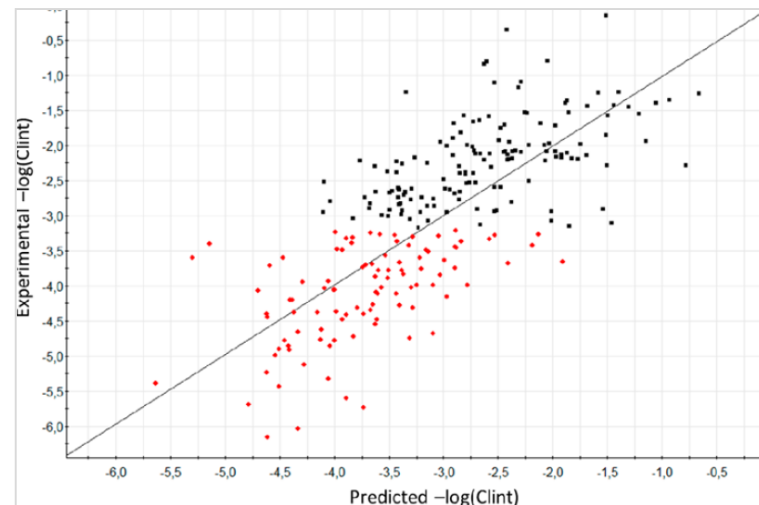
→ Ideas & opportunities

2. Data collection & pilot model building

- Collection/estimation of data for two parameters
- Model building and validation

→ Encouraging results

Better than microsomes
and hepatocytes

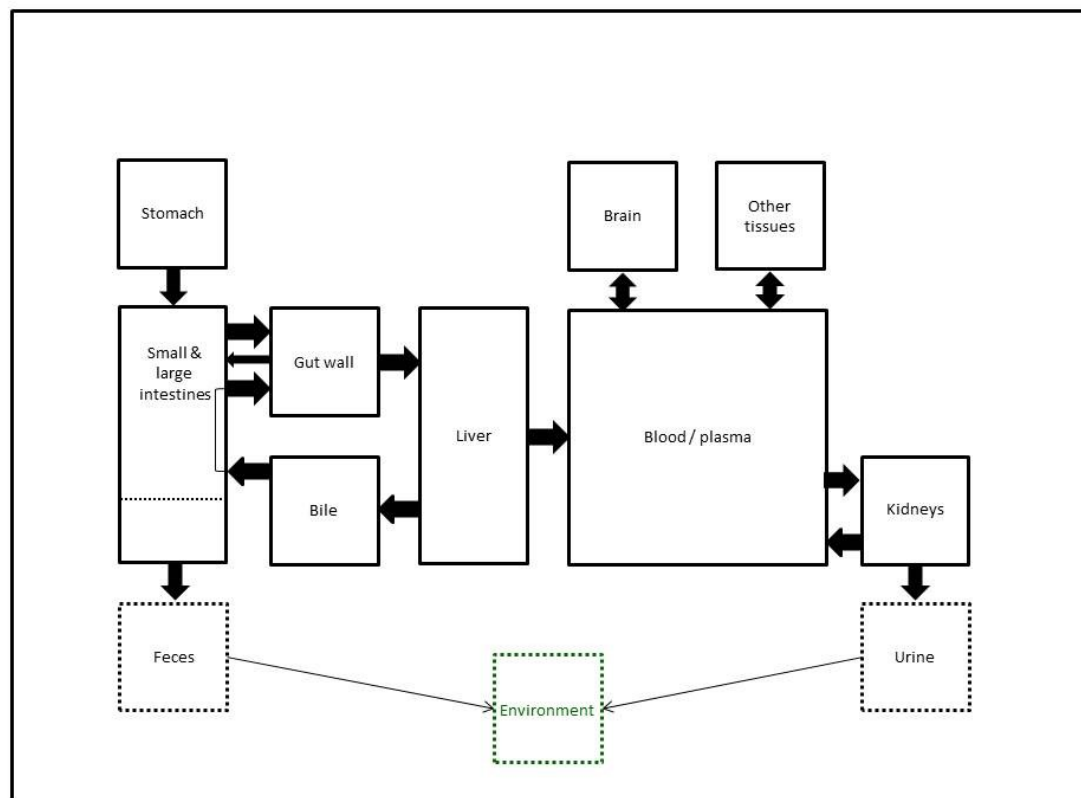
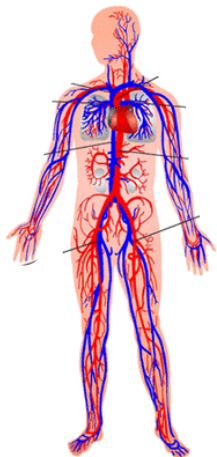


3. Extensive collection, quality-checking & stratification of data

Restrictions / challenges

- ~1500 marketed drugs
- Common with data gaps
- Many erratic/questionable data in reports
- Difficult to stratify data according to mechanisms

4. Creation of new algorithms and PBPK-model



5. Model building, validation and selection

- Applied different *in silico* methods (incl. machine learning)
Directly from molecular structure to human *in vivo*
Cross-validation = True, forward-looking predictions
- Developed and validated models for >50 parameters

The Prediction Platform

A collection of fully validated human ADME/PK-models

Oral F & $t_{1/2}$

Fabs & k_a

considering efflux & low solubility
colon uptake (ER-potential)
BCS-classing

DDIs & food interaction

CL_{int} & CL_H

Also for metabolically
stable cmpds

Renal & biliary CL

Total CL & V_{ss}

F_{gut}

AUC, C_{max} , t_{max}

BBB uptake & CNS-exposure

Eye, skin & lung uptake

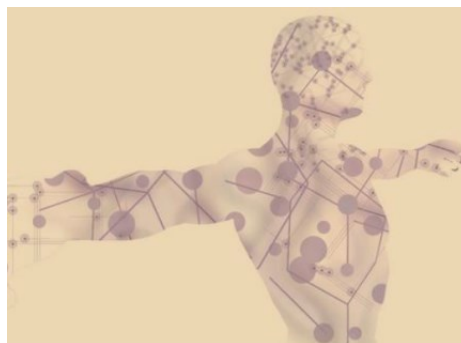
Metabolite PK & exp.

Prodrug PK

CYPID & -inhibition

f_u in plasma, blood & brain

Environmental excretion



6. Competitor evaluation

- Some good models
- Often lack of validation results
 - in particular for secondary parameters such as exposure, clearance & $t_{1/2}$
 - often partial validation (with limited and favourable test sets)
- More common with simulations (rather than predictions)
- Poor prediction accuracy when testing software

7. Confidence building I-III (internal & external)

- I. Complete cross-validations
=true, forward-looking predictions
- II. Predictions for new drugs on the market (2012-18)
- III. Early customer predictions & experiences
Including 3 FTIM-studies

8. Confidence building IV

IV. External blind validations by small to major international pharmaceutical companies

>150 non-marketed compounds with clinical PK-data

9. Confidence building V

V. Application of conformal prediction methodology

- Assigns confidence measurements in predictions that are both based on the training data and the test objects
- Takes into account strangeness of a new compound vs training data
- Smaller prediction intervals produced for “easier” compounds
- Each prediction comes with an estimate and confidence interval
E.g. 31% (15%; 54%) and 31% (7%; 84%)

10. Confidence building VI-IX

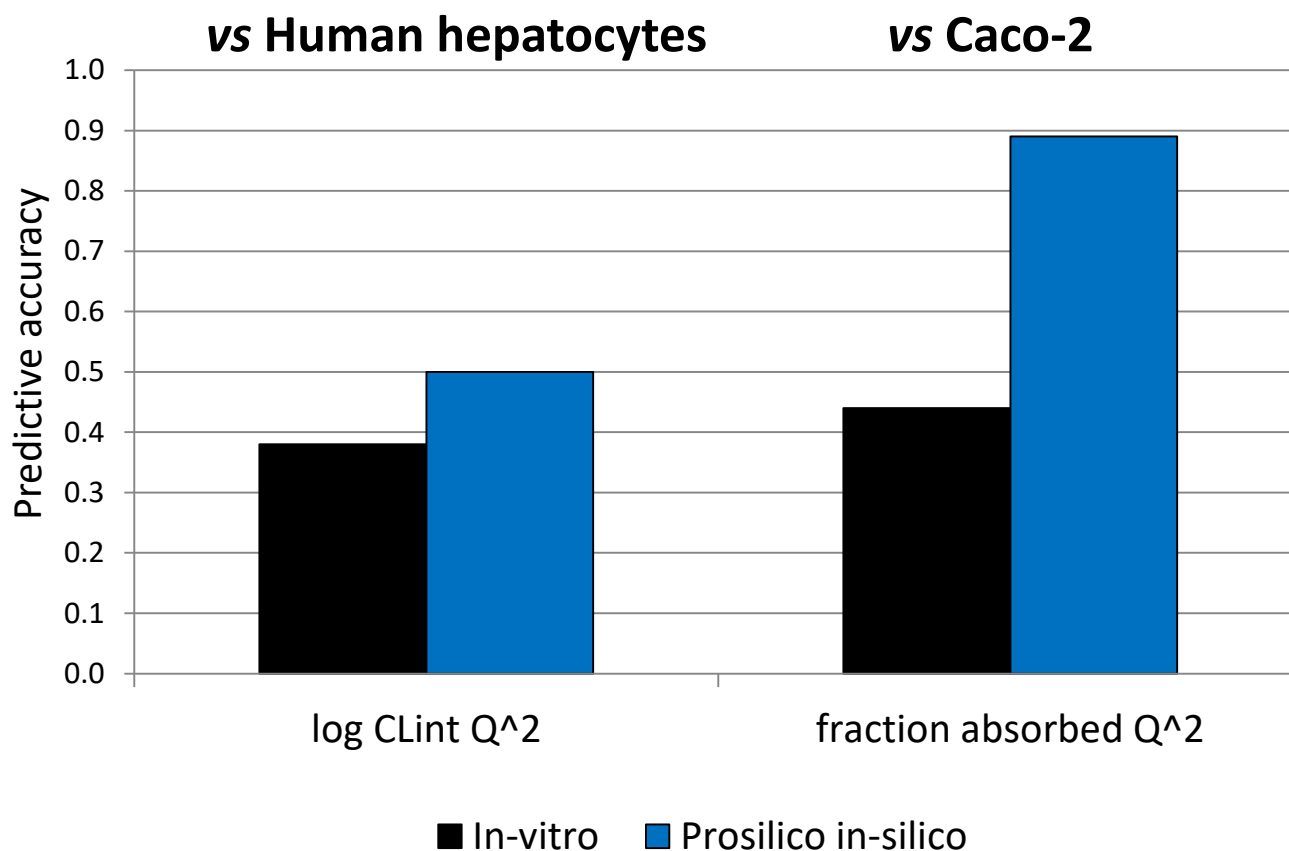
VI. Satisfied customers and positive reviews

VII. Visibility (marketing, publishing, conference attendance, social media)

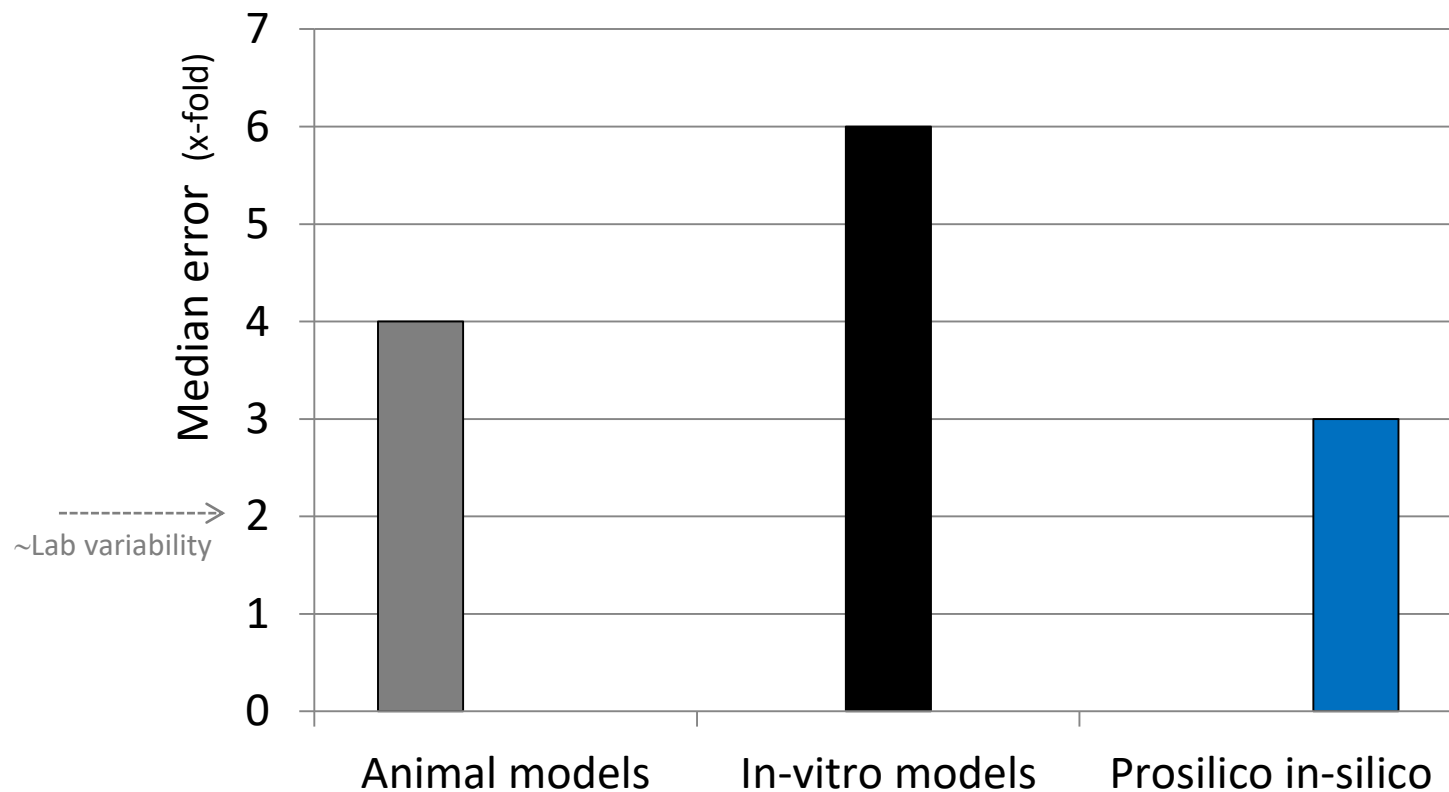
VIII. Customers among major companies

IX. Benchmarking (successful)

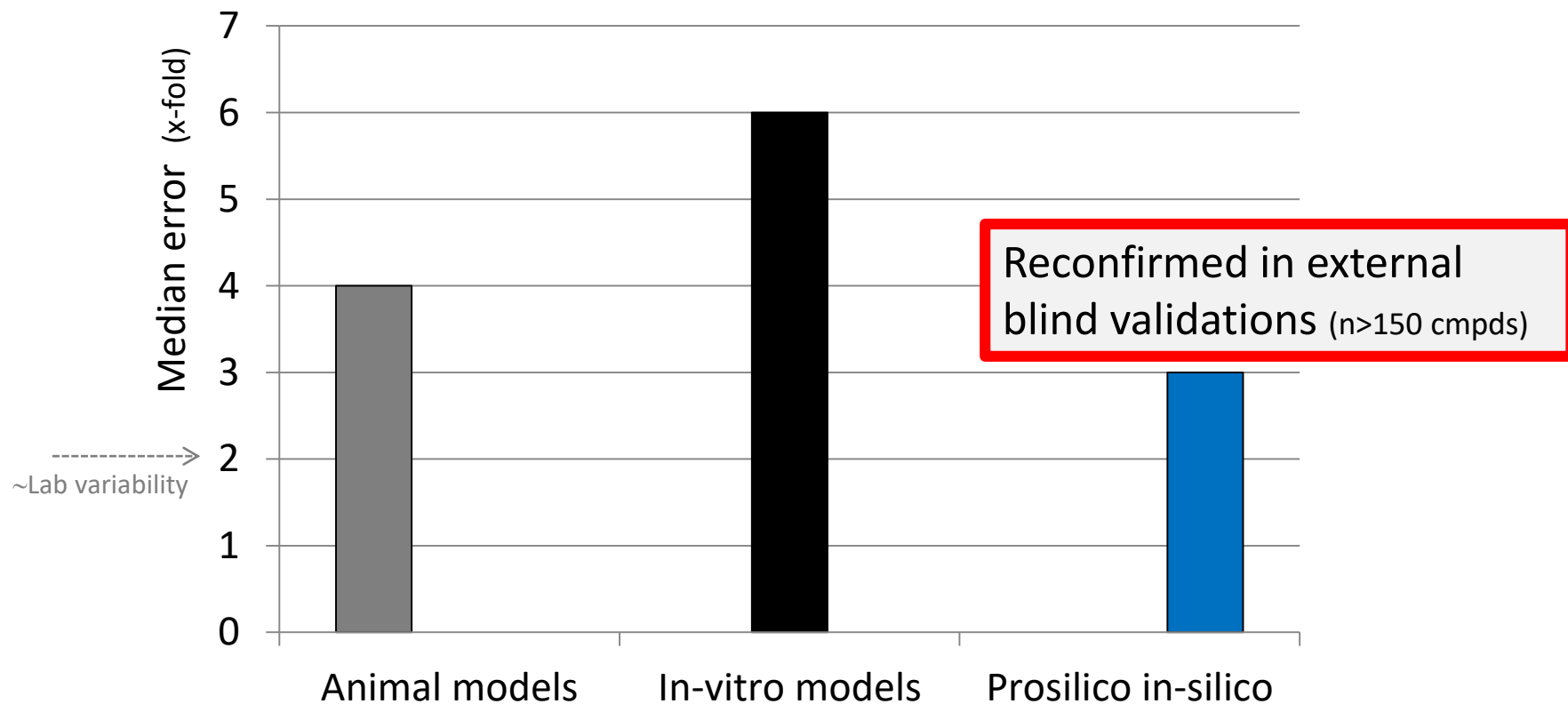
PERFORMANCE - BENCHMARKING



Prediction of exposure after oral dosing (AUC_{po})



Prediction of exposure after oral dosing (AUC_{po})



11. Authority (MPA) views and guidelines

- **No quality standards/limits** for human clinical ADME/PK and dose predictions
"Different from case to case"!
- Apparently, **accepts poor methods**
With >1,000 to ~1,000,000-fold maximum prediction errors
- **Uncertain if accepts performance of our methods**

12. Confidence building X-XI

X. Let customers make predictions and evaluations themselves – build software

XI. Transparency with results, limitations and strenghts

Human Clinical ADME/PK-Studio

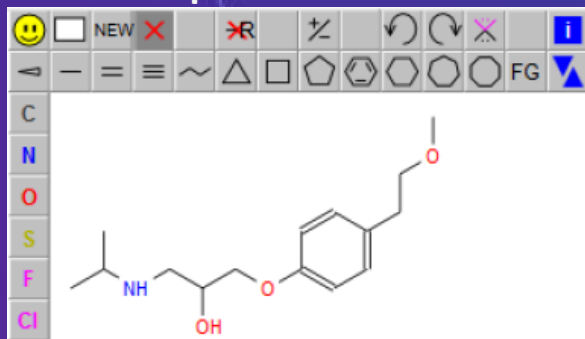
Web-based or intranet installation

Design, Predict & Optimize ADME/PK with Confidence

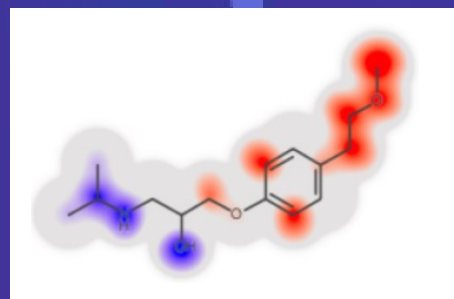
Higher accuracy and broader range than lab methods

Guaranteed confidence limits

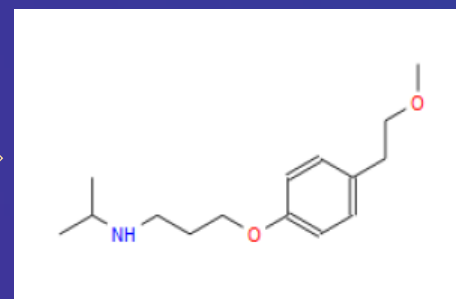
Sketch or paste structure



Guidance

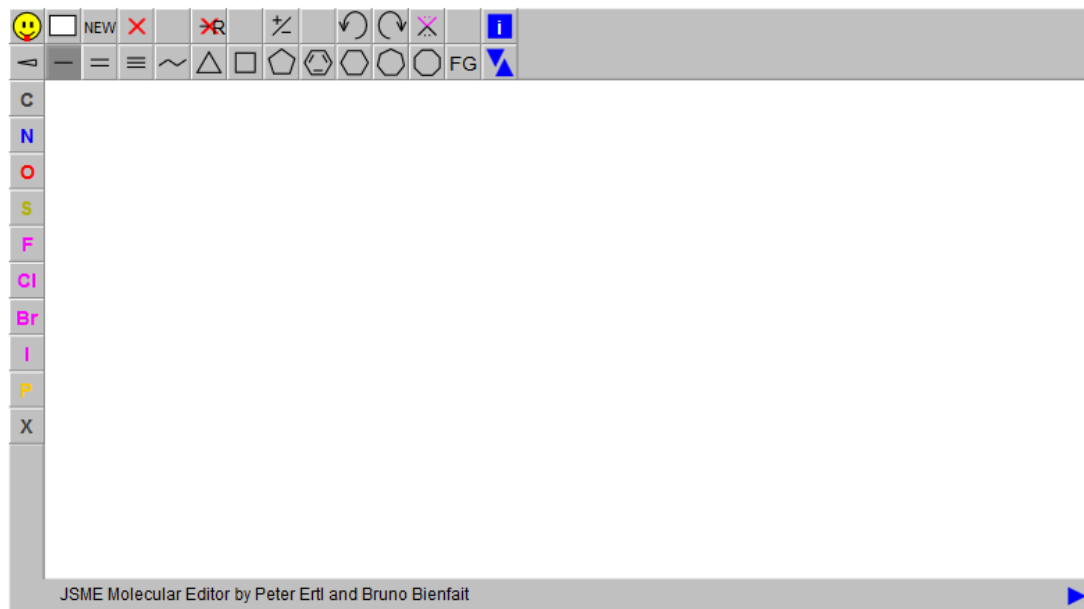


Optimize



Human Clinical ADME/PK-Studio

Prosilico



About

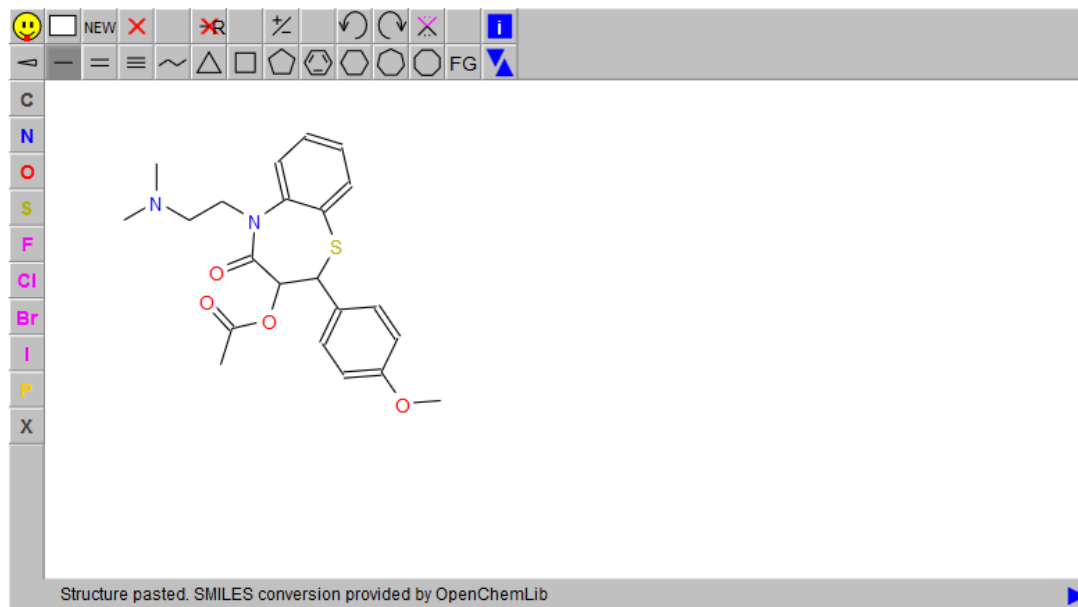
PROSILICO's studio for prediction and optimization of human *in-vivo* ADME/PK.

[Read more...](#)

[Clear JSME editor](#)

Human Clinical ADME/PK-Studio

Prosilico



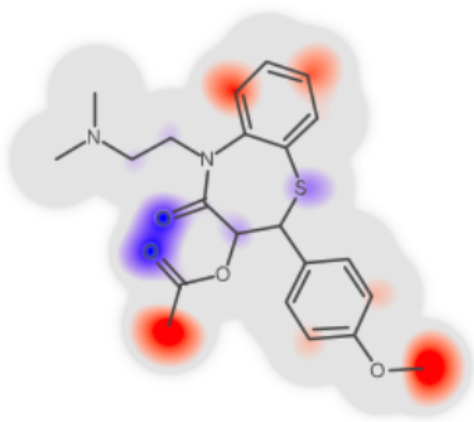
About

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fabs ▾



Absorption

fabs 100% (86%, 100%)

fdiss 100% (77%, 100%)

Distribution

fu 18.0% (4.29%, 51.7%)

Vss 4.1 (1.9, 8.9) L/kg

Metabolism

CLint 1778 (277, 11402)
mL/min

Secondary Parameters

CLH 263 mL/min

t_{1/2} 13 h

Long Half-life

F 82 %

High Bioavailability

Indications

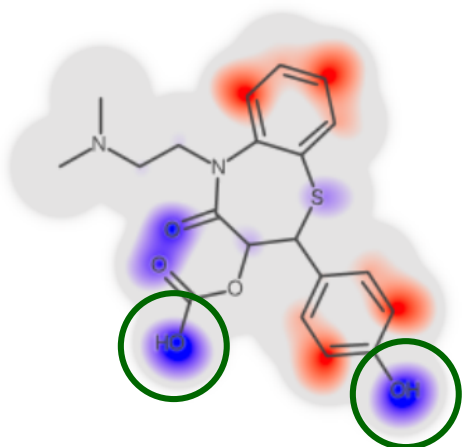
⚠ Renal and/or biliary clearance could contribute significantly to total clearance and produce a lower t_{1/2} than estimated based on hepatic clearance only.

⚠ Potential for significant influence of efflux on fabs and F (if efflux occurs)

Contact Prosilico for additional prediction of renal and biliary excretion.

Contact Prosilico for additional predictions of efflux (MDR1, BCRP, MRP2) and its role.

fabs ▾



Absorption

fabs 87% (73%, 100%)

fdiss 100% (76%, 100%)

Distribution

fu 26.8% (6.54%, 65.7%)

Vss 2.1 (0.84, 5.1) L/kg

Metabolism

CLint 1694 (257, 11143)
mL/min

Secondary Parameters

CLH 349 mL/min

t_{1/2} 5 h

Medium Half-life

F 67 %

High Bioavailability

Indications

⚠ Renal and/or biliary clearance could contribute significantly to total clearance and produce a lower $t_{1/2}$ than estimated based on hepatic clearance only.

⚠ Potential for significant influence of efflux on fabs and F (if efflux occurs)

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Contact Prosilico for additional predictions of efflux (MDR1, BCRP, MRP2) and its role.

Barrier uptake models

- applicable for tox./risk-evaluations



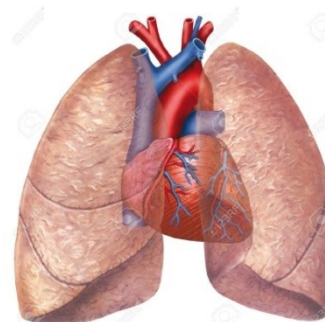
$$Q^2 = 0.8$$



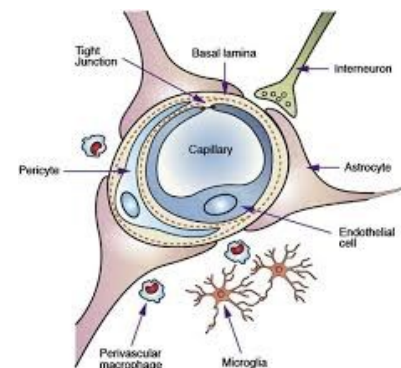
$$Q^2 = 0.8$$



$$Q^2 = 0.5$$



$$Q^2 = 0.5$$



$$Q^2 = 0.5$$



Summary - Confidence building

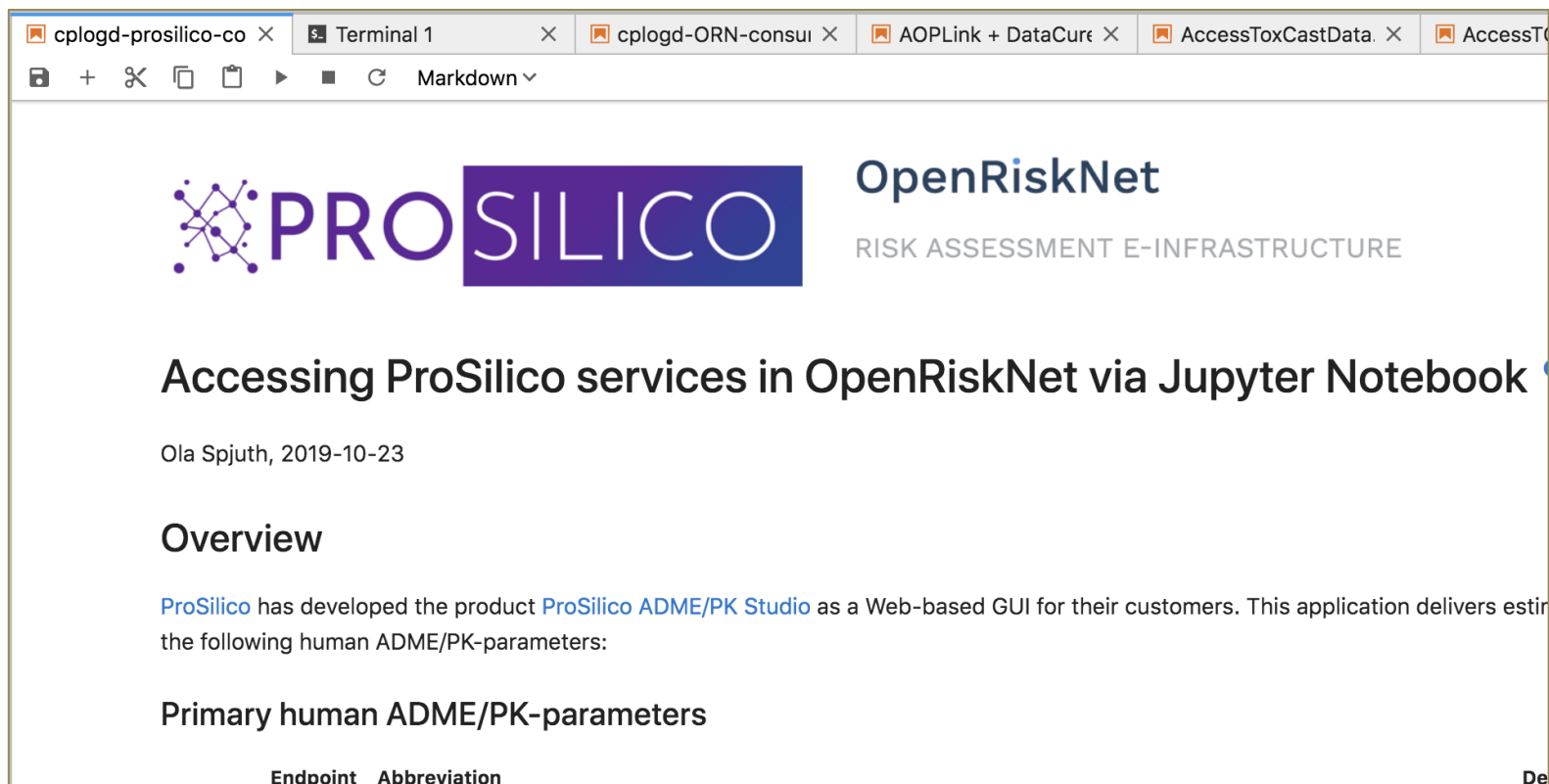
- I. Cross-validations / only true forward predictions
- II. Predictions for new drugs
- III. Customer predictions & experiences
- IV. External blind validations
- V. Conformal prediction methodology
- VI. Satisfied customers and positive reviews
- VII. Visibility
- VIII. Major pharma customers
- IX. Successful benchmarking
- X. Software (customers can make predictions and evaluations themselves)
- XI. Transparency

Integration of ProSilico into OpenRiskNet

- Publish models under ORN APIs
 - 5 primary endpoints (CPSign models)
 - 3 secondary endpoints
- Run ProSilico services on ORN production cluster
- Incorporate Authentication and Authorization using KeyCloak for ProSilico ORN services
 - Support custom license for ProSilico service
 - ProSilico allowed to authorize specific users with expiry date

Demo: Accessing ProSilico as OpenRiskNet services via Jupyter Notebook

<https://github.com/OpenRiskNet/notebooks/blob/master/prosilico/prosilico-orn.ipynb>



The screenshot shows a Jupyter Notebook interface with several tabs open: 'cplogd-prosilico-co', 'Terminal 1', 'cplogd-ORN-consui', 'AOPLink + DataCur', 'AccessToxCastData', and 'AccessTo'. The notebook content displays the ProSilico logo and the OpenRiskNet logo with the tagline 'RISK ASSESSMENT E-INFRASTRUCTURE'. The title of the notebook is 'Accessing ProSilico services in OpenRiskNet via Jupyter Notebook'. Below the title, it says 'Ola Spjuth, 2019-10-23'. The section 'Overview' is visible, followed by a paragraph stating that ProSilico has developed the product 'ProSilico ADME/PK Studio' as a Web-based GUI for their customers. This application delivers estimates of the following human ADME/PK-parameters:

Primary human ADME/PK-parameters

Endpoint	Abbreviation	De
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