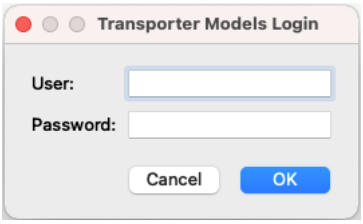
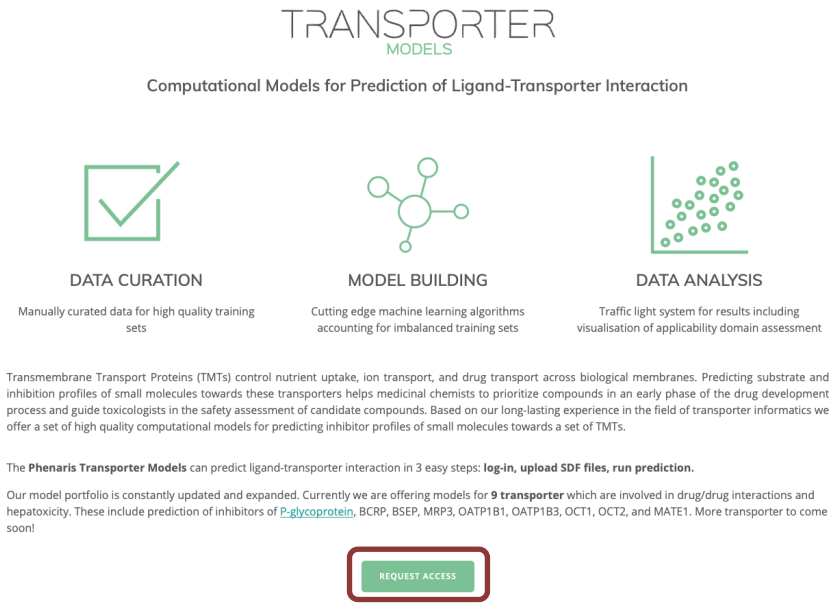
Documentation of the Transporter Models in StarDrop

The Plugin of Phenaris provides classification models which predict inhibitor molecules for transporters considered relevant by FDA, EMA and the Japanese regulatory agency. It is available via **Custom Scripts**. It is possible to predict a single molecule by using the so-called **Single Prediction** as well as a batch upload (**Prediction**) via the StarDrop upload function. When you start the plugin, you are asked to enter your credentials.

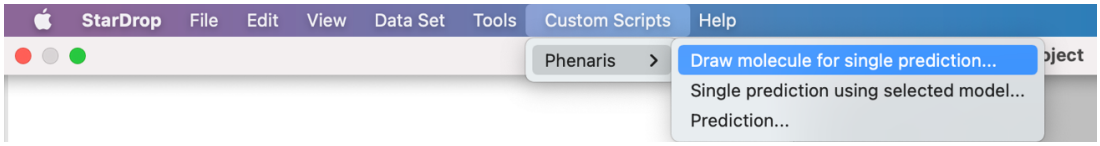


You can request access via our homepage (https://www.phenaris.com/products/transporter-models/).



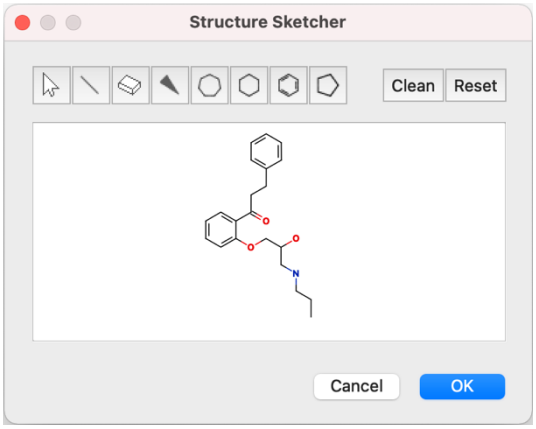
After login you can choose between the following three options:

- **„Draw molecule for single prediction…"**
- **„Single prediction using selected model…"**
- **"Prediction…"**

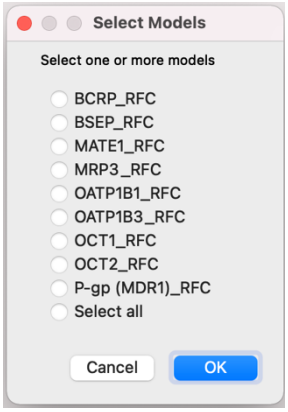


1., „Draw molecule for single prediction…"

- Select ***Custom Scripts > Phenaris > Draw molecule for single prediction…***
- Draw your molecule in the **Structure Sketcher**



- At the moment there are eight classification models of transporters available namely BCRP, BSEP, MATE1, MRP3, OATP1B1, OATP1B3, OCT1, OCT2 and P-gp (MDR1). The models are based on the Random Forest Classifier. You can select one or more transporter models from the following list or select all at once:



- The Output of the prediction provides the classification "yes" and "no" and the prediction score. Further, the applicability domain is given as Boolean result. The results are shown in a newly created dataset called **Single prediction**. If multiple single predictions are made, the newly predicted molecule will be appended to the existing **Single prediction** dataset. If you change the model selection between the different Single Prediction runs the fields without a result obtain the entry "?" which indicates that there is no result available.

	ID	Structure	BSEP_RFC		P-gp (MDR1)_RFC		BSEP - LOF Applicabi.	P-gp (MDR1) - LOF A
1	Stardrop prediction		no	1	yes	0.9	True	True

"Yes" indicates that the compound is predicted as an inhibitor and "no" indicates that the compound is predicted as a non-inhibitor. The prediction score gives the probability if a molecule will inhibit the transporter protein. The score ranges from 0.5 to 1, while a value close to 1 indicate a high probability for the prediction. A value between 0.5 and 0.65 indicate a grey area, where the result has to be taken with caution.
The Applicability Domain defines the chemical space of each model. The algorithm is based on the local outlier factor (LOF) approach, which takes the local density into account. True means the test compound is within the chemical space of the model and is therefore In Domain. False mean that the test compound is Out of Domain and cannot be predicted with the given model.

2., „Single prediction using selected model…"

- You can select a compound from an existing dataset in StarDrop
- Select ***Custom Scripts > Phenaris > Single prediction using selected model…"***
- You can select transporter models for the prediction as mentioned in the section **„Draw molecule for single prediction…"**
- The result is appended to the dataset used for the prediction.
- A more detailed description of the results is mentioned in the section **„Draw molecule for single prediction…"**

3., "Prediction…"

- You first have to upload a file (e.g. SDF) or you can use an existing dataset in StarDrop
- Select ***Custom Scripts > Phenaris > Prediction…***
- You can select transporter models for the prediction as mentioned in the section **„Draw molecule for single prediction…"**
- The result is appended to the dataset used for the prediction.
- A more detailed description of the results is mentioned in the section **„Draw molecule for single prediction…"**