logP Plugin

Introduction

The log$P$ Plugin calculates the octanol/water partition coefficient, which is used in QSAR analysis and rational drug design as a measure of molecular hydrophobicity. The calculation method is based on the publication of Viswanadhan et al. The log$P$ of a molecule is composed of the increment of its atoms. However, the algorithm described in the paper was modified at several points:

1. Many atomic types were redefined to accommodate electron delocalization and contributions of ionic forms were added.
2. The log$P$ of zwitterions are calculated from their log$D$ value at their isoelectric point.
3. The effect of hydrogen bonds on the log$P$ is considered if there is a chance to form a six membered ring between suitable donor and acceptor atoms.
4. New atom types were introduced especially for sulfur, carbon, nitrogen and metal atoms.

To find details on log$P$ calculation, see the following page.

The result of the calculation appears in a new window, either in a MarvinView (for a 2D view) window or in a MarvinSpace (for a 3D view) window.
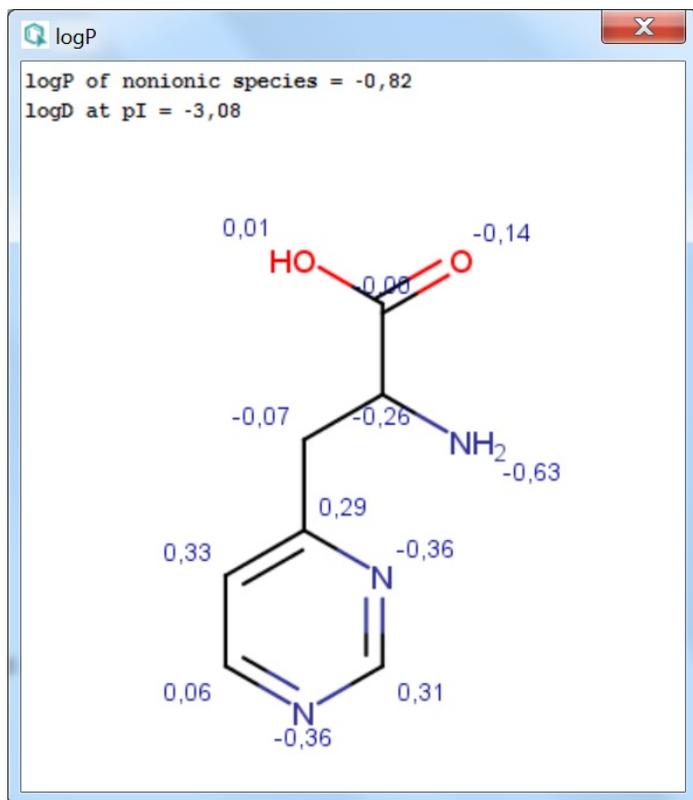
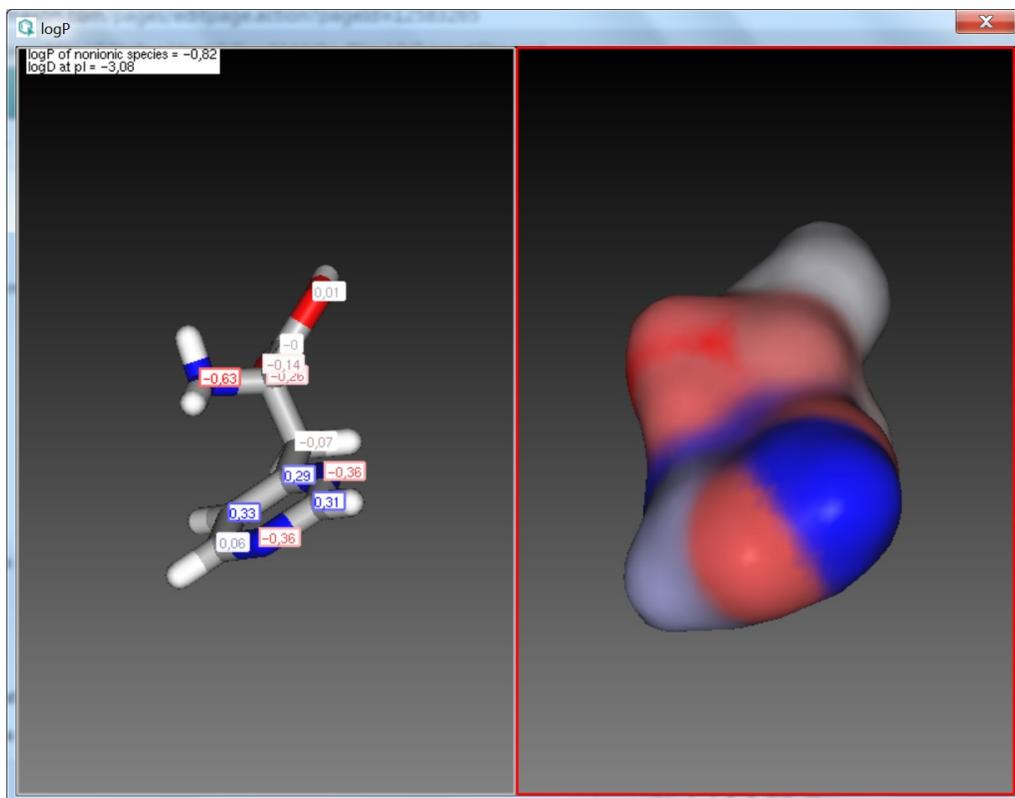Fig. 1 Log*P* result window with atomic increments displayed in MarvinView

Fig. 2 Log*P* result window with atomic increments displayed in MarvinSpace

Options

General Options

Different general options can be set in the *logP Options* window:

Method

This option defines the method for calculating logP. These can be:

- **Consensus**: this method uses a consensus model built on the ChemAxon and Klopman et al. models and the PhysProp database.
- **ChemAxon**: this method is based on ChemAxon's own logP model, which is based on the VG method (derived from Viswanadhan et al.). Read more about it here.

- **User defined:** if a training set of structures and corresponding experimental log$P$ values is available, it can be used as a database for log$P$ calculations. See the manual page on creating such training sets.

ⓘ **The relation of ChemAxon's logP method to the AlogP and ClogP methods**

The Consensus logP method is a unique, in-house developed logP model based on the methods listed above. Comparison-wise, our Consensus logP method is similar (but not identical) to the ClogP method, while our ChemAxon logP method is similar (but not identical) to the AlogP method.

Other options

These options are for refining the logP calculation.

- **Training ID:** if the **User defined** method is selected, this dropdown list becomes active. All created training sets are listed here. Choose the one to apply for the calculation.
- **Electrolyte concentration**
    - **Cl⁻ concentration:** can be set between 0.1 and 0.25 mol/L.
    - **Na⁺ K⁺ concentration:** can be set between 0.1 and 0.25 mol/L.
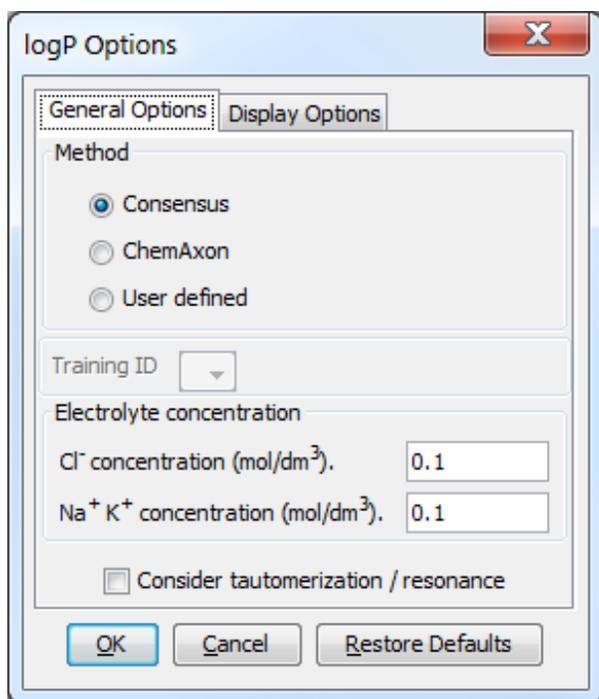- **Consider tautomerization/resonance:** the log$P$ of the major tautomer will be calcutated if enabled.

Fig. 3 log*P* Options window with the General Options panel

Display Options

Different display options can be set in the *logP Options* window:

- **Decimal places**: setting the number of decimal places for the precision of the result value.
- **Show value**: sets which logP values be displayed in the result window. It can be:
    - **Increments**: calculates and shows the increments for atoms one-by-one.
    - **log*P***: shows just the value of the log*P*.
- **Display in MarvinSpace:** the result window opens as 3D MarvinSpace viewer. If unchecked, the results will be shown in a 2D MarvinView panel.
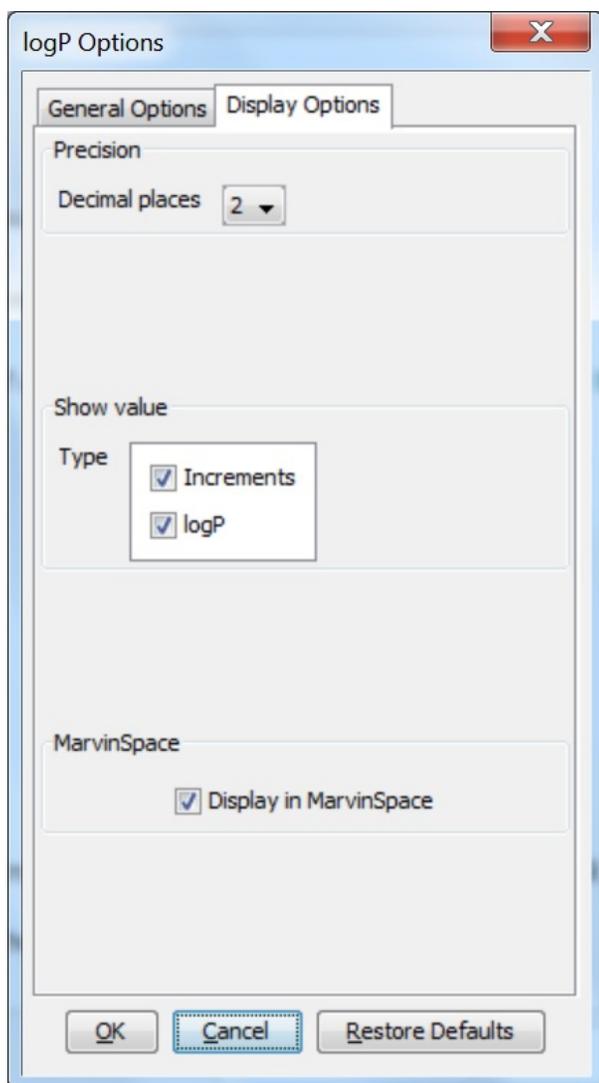
Fig. 4 log*P* Options window with the Display Options panel

References

1. Viswanadhan, V. N.; Ghose, A. K.; Revankar, G. R.; Robins, R. K., *J. Chem. Inf. Comput. Sci.*, **1989**, *29*, 163-172; doi
2. Klopman, G.; Li, Ju-Yun.; Wang, S.; Dimayuga, M.: *J.Chem.Inf.Comput.Sci.*, **1994**, *34*, 752; doi
3. PHYSPROP© database
4. Csizmadia, F; Tsantili-Kakoulidou, A.; Pander, I.; Darvas, F., *J. Pharm. Sci.*, **1997**, *86*, 865-871; doi