



# Report



Prediction and Applicability Domain analysis for models:

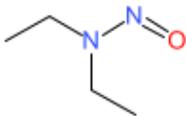
Henry's Law model (OPERA) 1.0.1

Core version: 1.3.14



## 1. Prediction Summary

Prediction for compound Molecule 0 -

 <p>The image shows the chemical structure of N,N-diethylnitrosamine, which consists of a central nitrogen atom bonded to two ethyl groups and a nitroso group (N=O).</p>	<p>Prediction:  Reliability:   </p> <p>Prediction is -4.9375 log atm-m<sup>3</sup>/mole, but the result may be not reliable. A check of the information given in the following section should be done, paying particular attention to the following issues:</p> <ul style="list-style-type: none"><li>- similar molecules found in the training set have experimental values that disagree with the predicted value</li><li>- the maximum error in prediction of similar molecules found in the training set has a moderate value, considering the experimental variability</li><li>- a prominent number of atom centered fragments of the compound have not been found in the compounds of the training set or are rare fragments (2 unknown fragments found)</li></ul>
--	--

Compound: Molecule 0

Compound SMILES: O=NN(CC)CC

Experimental value: -

Predicted Henry's law [log atm-m<sup>3</sup>/mole]: -4.9375

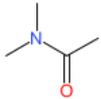
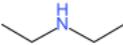
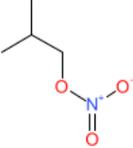
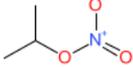
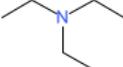
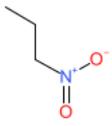
Reliability: The predicted compound is outside the Applicability Domain of the model

Remarks:

none

### 3.1 Applicability Domain: Similar Compounds, with Predicted and Experimental Values



	<p>Compound #1</p> <p>CAS: 127-19-5 Dataset id:239 (Training Set) SMILES: O=C(N(C)C)C Similarity: 0.803 Experimental value : -7.883 Predicted value : -7.118</p>
	<p>Compound #2</p> <p>CAS: 109-89-7 Dataset id:188 (Training Set) SMILES: N(CC)CC Similarity: 0.761 Experimental value : -4.593 Predicted value : -5.048</p>
	<p>Compound #3</p> <p>CAS: 543-29-3 Dataset id:287 (Training Set) SMILES: O=[N+](O-)OCC(C)C Similarity: 0.76 Experimental value : -2.648 Predicted value : -2.786</p>
	<p>Compound #4</p> <p>CAS: 1712-64-7 Dataset id:334 (Training Set) SMILES: O=[N+](O-)OC(C)C Similarity: 0.755 Experimental value : -2.793 Predicted value : -2.785</p>
	<p>Compound #5</p> <p>CAS: 121-44-8 Dataset id:220 (Training Set) SMILES: N(CC)(CC)CC Similarity: 0.754 Experimental value : -3.827 Predicted value : -3.979</p>
	<p>Compound #6</p> <p>CAS: 108-03-2 Dataset id:157 (Training Set) SMILES: O=[N+](O-)CCC Similarity: 0.75 Experimental value : -4.06 Predicted value : -4.576</p>

## 3.2 Applicability Domain: Measured Applicability Domain Scores



Global AD Index

AD index = 0.309

Explanation: The predicted compound is outside the Applicability Domain of the model.



Similar molecules with known experimental value

Similarity index = 0.773

Explanation: Strongly similar compounds with known experimental value in the training set have been ..



Accuracy of prediction for similar molecules

Accuracy index = 0.452

Explanation: Accuracy of prediction for similar molecules found in the training set is good..



Concordance for similar molecules

Concordance index = 1.86

Explanation: similar molecules found in the training set have experimental values that disagree with the predicted value..



Maximum error of prediction among similar molecules

Max error index = 0.765

Explanation: the maximum error in prediction of similar molecules found in the training set has a moderate value, considering the experimental variability..



Atom Centered Fragments similarity check

ACF index = 0.4

Explanation: a prominent number of atom centered fragments of the compound have not been found in the compounds of the training set or are rare fragments (2 unknown fragments found)..

Symbols explanation:



The feature has a good assessment, model is reliable regarding this aspect.



The feature has a non optimal assessment, this aspect should be reviewed by an expert.



The feature has a bad assessment, model is not reliable regarding this aspect.

## 4.1 Reasoning: Relevant Chemical Fragments and Moieties

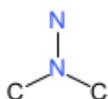


(Molecule 0) Reasoning on rare and missing Atom Centered Fragments .

The following Atom Centered Fragments have been found in the molecule, but they are not found or rarely found in the model's training set:



Fragment defined by the SMILES: NN=O  
The fragment has never been found in the model's training set



Fragment defined by the SMILES: CN(C)N  
The fragment has never been found in the model's training set