
	<b>QMRF identifier (JRC Inventory):</b> To be entered by JRC <b>QMRF Title:</b> Insubria QSAR PaDEL-Descriptor model for prediction of Pharmaceuticals Aquatic Toxicity Index (ATI) <b>Keywords:</b> QSARINS; PaDEL-Descriptor; GA-OLS; ATI; Pharmaceuticals; INSUBRIA <b>Printing Date:</b> Jan 25, 2017	
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## 1. QSAR identifier

### 1.1. QSAR identifier (title):

Insubria QSAR PaDEL-Descriptor model for prediction of Pharmaceuticals Aquatic Toxicity Index (ATI)  
 Keywords: QSARINS; PaDEL-Descriptor; GA-OLS; ATI; Pharmaceuticals; INSUBRIA

### 1.2. Other related models:

A. Sangion, P. Gramatica, Hazard of pharmaceuticals for aquatic environment: Prioritization by structural approaches and prediction of ecotoxicity, Environ. Int. 95 (2016) 131–143. doi: 10.1016/j.envint.2016.08.008 [1]

### 1.3. Software coding the model:

[1] PaDEL-Descriptor A software to calculate molecular descriptors and fingerprints, version 2.21 [2] Yap Chun Wei, phayapc@nus.edu.sg <http://padel.nus.edu.sg/software/padeldescriptor/index.html>

[2] QSARINS Software for the development, analysis and validation of QSAR MLR models, version 2.2.1 [3,4] Prof. Paola Gramatica, paola.gramatica@uninsubria.it <http://www.qsar.it/>

## 2. General information

### 2.1. Date of QMRF:

19/01/2017

### 2.2. QMRF author(s) and contact details:

[1] Alessandro Sangion Insubria University, Department of Theoretical and Applied Sciences (DiSTA), via J.H. Dunant 3, 21100 Varese (Italy) +390332421439 alessandro.sangion@uninsubria.it <http://www.qsar.it/>

[2] Paola Gramatica Insubria University, Department of Theoretical and Applied Sciences (DiSTA), via J.H. Dunant 3, 21100 Varese (Italy) +390332421573 paola.gramatica@uninsubria.it <http://www.qsar.it/>

### 2.3. Date of QMRF update(s):

### 2.4. QMRF update(s):

### 2.5. Model developer(s) and contact details:

[1] Paola Gramatica Insubria University, Department of Theoretical and Applied Sciences (DiSTA), via J.H. Dunant 3, 21100 Varese (Italy) +390332421573 paola.gramatica@uninsubria.it <http://www.qsar.it/>

[2] Alessandro Sangion Insubria University, Department of Theoretical and Applied Sciences (DiSTA), via J.H. Dunant 3, 21100 Varese (Italy) +390332421439 alessandro.sangion@uninsubria.it <http://www.qsar.it/>

## 2.6.Date of model development and/or publication:

Developed and Published in 2016.

## 2.7.Reference(s) to main scientific papers and/or software package:

[1]A.Sangion, P. Gramatica, Hazard of pharmaceuticals for aquatic environment: Prioritization by structural approaches and prediction of ecotoxicity, Environ. Int. 95 (2016) 131–143 doi:10.1016/j.envint.2016.08.008

[2]C.W. Yap, PaDEL-Descriptor: An open source software to calculate molecular descriptors and fingerprints., JComput Chem. 32 (2011) 1466–1474. doi:10.1002/jcc.21707

[3]P. Gramatica, N. Chirico, E. Papa, S. Cassani, S. Kovarich, QSARINS: A new software for the development, analysis and validation of QSAR MLR models, J Comput Chem. 34 (2013) 2121–2132 doi:10.1002/jcc.23361.

[4]P. Gramatica, S. Cassani, N. Chirico, QSARINS-Chem: Insubria Datasets and New QSAR/QSPR Models for Environmental Pollutants in QSARINS, J.Comput.Chem. 35 (2014) 1036–1044. doi:10.1002/jcc.23576.

## 2.8.Availability of information about the model:

Non-proprietary. Defined algorithm, available in QSARINS [3,4]. Training and prediction sets are available in the Supporting Information of the related paper [1], in the attached sdf files of this QMRF (section 9) and in the QSARINS-Chem database [4].

## 2.9.Availability of another QMRF for exactly the same model:

No other information available

## 3.Defining the endpoint - OECD Principle 1

### 3.1.Species:

*Pseudokirchneriella subcapitata*, *Daphnia magna*, *Pimephales promelas*,  
*Oncorhynchus mykiss*

### 3.2.Endpoint:

[1]3.Ecotoxic effects 3.2.Short-term toxicity to algae (inhibition of the exponential growth rate)

[2]3.Ecotoxic effects 3.1.Short-term toxicity to Daphnia (immobilisation)

[3]3.Ecotoxic effects 3.3.Acute toxicity to fish (lethality)

### 3.3.Comment on endpoint:

The Aquatic Toxicity Index (ATI) is a trend of cumulative acute aquatic toxicity and condenses the toxicity of a Pharmaceutical in algae, Daphnia and fish. This endpoint represents the overall aquatic toxicity in an aquatic scenario.

It is derived by Principal Component Analysis (PCA) from experimental and reliable predicted acute toxicity in *Pseudokirchneriella subcapitata*, *Daphnia magna*, *Pimephales promelas* and *Oncorhynchus mykiss* for a set of 706 Pharmaceuticals. PC1, which provides alone the largest part (62.18%) of the total information, is a new macrovariable that was defined ATI. This index ranks the compounds according to their cumulative overall aquatic toxicity in an aquatic scenario for standardized aquatic species.

### 3.4.Endpoint units:

The original median lethal concentrations for *Pseudokirchneriella subcapitata*, *Daphnia magna*, *Pimephales promelas* and *Oncorhynchus mykiss* were reported as the minus logarithm of the molar concentration:  $-\log(\text{mmol/l})$ . These data were combined by Principal Component Analysis and the final endpoint, ATI (PC1 values), is thus a-dimensional.

### 3.5.Dependent variable:

ATI (PC1 values)

### 3.6.Experimental protocol:

The whole training set includes 706 organic compounds; experimental values were taken from ECOTOX online database [5] while the rest of the dataset was composed of reliable predicted data (interpolated predictions, within the Applicability Domain of the models) from the QSAR models developed in the same publication [1].

### 3.7.Endpoint data quality and variability:

The experimental data were specifically filtered for the species, defined time of exposure, endpoints and measured effects, trying to ensure the highest degree of homogeneity in experimental measures. If different and multiple values were found for a specific chemical, the minimum LC/EC50 value was taken and modelled, considering the "worst case scenario" (i.e. the most toxic value). Once these experimental values were selected and filtered, the data were additionally carefully checked, removing the duplicates and measures reported as "nominal concentration". Predicted data were reliable, being interpolated predictions within the Applicability Domain of the QSAR models.

## 4.Defining the algorithm - OECD Principle 2

### 4.1.Type of model:

QSAR - Multiple linear regression model (OLS - Ordinary Least Square)

### 4.2.Explicit algorithm:

ATI Random split

MLR-OLS method. Model developed on a training set of 495 compounds

ATI Ordered Response split

MLR-OLS method. Model developed on a training set of 472 compounds

ATI Structural Similarity split

MLR-OLS method. Model developed on a training set of 472 compounds.

ATI Full Model

MLR-OLS method. Model developed on 706 compounds.

Random split equation:  $ATI = -1.82 + 0.61CrippenLogP + 0.07SaaCH - 0.05SHBint2$

Ordered Response split equation:  $ATI = -1.93 + 0.62CrippenLogP + 0.08SaaCH - 0.05SHBint2$

Structural Similarity split equation:  $ATI = -1.91 + 0.64CrippenLogP + 0.07SaaCH - 0.05SHBint2$

Full model equation:  $ATI = -1.87 + 0.62CrippenLogKow + 0.07SaaCH - 0.05SHBint2$

#### 4.3.Descriptors in the model:

[1]CrippenLogP Crippen's LogP

[2]SaaCH Sum of atom-type E-State: :CH:

[3]SHBint2 Sum of E-State descriptors of strength for potential hydrogen bonds of path length 2

#### 4.4.Descriptor selection:

A total of 1444 molecular descriptors of differing types (0D, 1D, 2D) were calculated by PaDEL-Descriptor 2.21 [2]. Constant and semi-constant values and descriptors found to be correlated pairwise were excluded in a pre-reduction step (one of any two descriptors with a correlation greater than 0.98 was removed to reduce redundant information), and a final set of 612 molecular descriptors were used as input variables for variable subset selection. All the possible combinations of two descriptors were investigated by the all-subset procedure, then, the Genetic Algorithm (GAVSS) was applied to explore new combinations with additional descriptors using Q2LOO (leave one out) as fitness function to be optimized during the variable selection procedure.

#### 4.5.Algorithm and descriptor generation:

Multiple linear regression (Ordinary Least Square method) was applied to generate the model. Molecular descriptors were generated by PaDEL-Descriptor software 2.21. The input files for descriptor calculation contain information on atom and bond types, connectivity, partial charges and atomic spatial coordinates, relative to the minimum energy conformation of the molecule, and were firstly obtained by the semi empirical AM1 method using the package HYPERCHEM 7.03 [6]. Then, these files were converted by

OpenBabel 2.3.2 [7] into MDL-MOL format and used as input for the calculation of descriptors in PaDEL-Descriptor. Any user can re-derives the model calculating the molecular descriptors by PaDEL-Descriptor 2.21 software (included in QSARINS 2.2.1) and applying the given equation (automatically done by QSARINS 2.2.1).

#### 4.6.Software name and version for descriptor generation:

PaDEL-Descriptor

A software to calculate molecular descriptors and fingerprints, version 2.21  
Yap Chun Wei, Department of Pharmacy, National University of Singapore  
<http://padel.nus.edu.sg/software/padeldescriptor/index.html>

## HYPERCHEM

Software for molecular drawing and conformational energy optimization, ver. 7.03, 2002

Hypercube, Inc., 1115 NW 4th Street, Gainesville, Florida 32601, USA, 2002  
<http://www.hyper.com/>

## OpenBabel

Open Babel: The Open Source Chemistry Toolbox. Used for conversion between HYPERCHEM files (hin) and MDL-MOL files, version 2.3.2, 2012.  
[http://openbabel.org/wiki/Main\\_Page](http://openbabel.org/wiki/Main_Page)

### 4.7.Chemicals/Descriptors ratio:

Random split equation:  $495/3=165$

Ordered Response split equation:  $472/3=157.33$

Structural Similarity split equation:  $472/3=157.33$

Full model equation:  $706/3=235.33$

## 5.Defining the applicability domain - OECD Principle 3

### 5.1.Description of the applicability domain of the model:

The applicability domain of the model was verified by the leverage approach and fixed thresholds has been used to define both structural and response outliers (see section 5.4). The plot of standardized residuals versus leverages (hat diagonals), i.e. the Williams plot, verified the presence of response outliers (i.e. compounds with cross-validated standardized residuals greater than 2.5 standard deviation units) and chemicals very structurally influential in determining model parameters (i.e. compounds with a leverage value ( $h$ ) greater than  $3p'/n$  ( $h^*$ ), where  $p'$  is the number of model variables plus one, and  $n$  is the number of the objects used to calculate the model). For new compounds without experimental data, leverage can be used as a quantitative measure for evaluating the degree of extrapolation: for compounds with a high leverage value ( $h > h^*$ ), that are structural outliers, predictions should be considered less reliable. In QSARINS the Insubria graph allows to identify for which new chemicals the predictions are inter- or extrapolated by the model.

Response and descriptor space:

Range of experimental ATI values: -4.68 / 4.2

Range of descriptor values: CrippenLogP: -1.47 / 6.27; SHBint2: -0.29 / 36.78; SaaCH: 0 / 36.07

### 5.2.Method used to assess the applicability domain:

As it has been stated in section 5.1, the structural applicability domain of the model was assessed by the leverage approach, providing a cut-off hat value ( $h^*=0.017$ ). HAT values are calculated as the diagonal elements of the HAT matrix:  $H = X(X^T X)^{-1} X^T$ . The response

applicability domain can be verified by the standardized residuals in cross-validation; chemicals with a standardized residual greater than 2.5 standard deviation units were considered outliers.

### 5.3. Software name and version for applicability domain assessment:

QSARINS

Software for the development, analysis and validation of QSAR MLR models, version 2.2.1

Prof. Paola Gramatica; [paola.gramatica@uninsubria.it](mailto:paola.gramatica@uninsubria.it)

<http://www.qsar.it/>

### 5.4. Limits of applicability:

Random split model domain: Outlier for response (standardised residual > 2.5 std unit): 000058-27-5, 000060-32-2, 000070-26-8, 000101-20-2, 000103-90-2, 000117-10-2, 000120-97-8, 000777-11-7, 002016-88-8, 004342-03-4, 013035-61-5, 058001-44-8, 060643-86-9, 079617-96-2; Outlier for structure ( $\hat{h} > 0.024$ ): 093390-81-9, 023593-75-1, 000054-47-7, 000114-86-3, 000050-06-6, 000692-13-7, 000509-86-4, 000057-44-3, 056211-40-6, 000077-02-1, 000077-26-9, 000057-67-0, 000077-28-1, 000115-44-6, 000076-73-3, 000057-43-2, 000076-74-4, 000125-40-6, 000500-92-5; Ordered response split model domain: Outlier for response (standardised residual > 2.5 std unit): 000057-44-3, 000058-27-5, 000060-32-2, 000070-26-8, 000101-20-2, 000103-90-2, 000117-10-2, 000120-97-8, 000777-11-7, 002016-88-8, 004342-03-4, 013035-61-5, 058001-44-8, 060643-86-9, 079617-96-2; Outlier for structure ( $\hat{h} > 0.0254$ ): 000050-06-6, 000054-47-7, 000057-43-2, 000057-44-3, 000057-67-0, 000076-73-3, 000076-74-4, 000077-02-1, 000077-26-9, 000077-28-1, 000101-20-2, 000114-86-3, 000115-44-6, 000125-40-6, 000302-79-4, 000500-92-5, 000509-86-4, 000692-13-7, 002016-88-8, 004759-48-2, 023593-75-1, 056211-40-6, 093390-81-9; Structural Similarity split model domain: Outlier for response (standardised residual > 2.5 std unit): 000058-27-5, 000060-32-2, 000103-90-2, 000117-10-2, 000120-97-8, 000777-11-7, 002016-88-8, 004342-03-4, 013035-61-5, 060643-86-9; Outlier for structure ( $\hat{h} > 0.0254$ ): 000050-06-6, 000054-47-7, 000057-43-2, 000057-44-3, 000057-67-0, 000057-96-5, 000076-73-3, 000076-74-4, 000077-02-1, 000077-26-9, 000077-28-1, 000114-86-3, 000115-44-6, 000125-40-6, 000509-86-4, 000692-13-7, 023593-75-1, 056211-40-6, 093390-81-9.; Full model domain: Outlier for response (standardised residual > 2.5 std unit): 000058-27-5, 000060-32-2, 000101-20-2, 000103-90-2, 000117-10-2, 000120-97-8, 000777-11-7, 002016-88-8, 004342-03-4, 013035-61-5, 060643-86-9, 079617-96-2; Outlier for structure ( $\hat{h} > 0.017$ ): 000050-06-6, 000054-47-7, 000057-43-2, 000057-44-3, 000057-67-0, 000076-73-3, 000076-74-4, 000077-02-1, 000077-26-9, 000077-28-1, 000114-86-3, 000115-44-6, 000125-40-6, 000509-86-4, 000692-13-7, 023593-75-1, 056211-40-6, 093390-81-9.

## 6.Internal validation - OECD Principle 4

### 6.1.Availability of the training set:

Yes

### 6.2.Available information for the training set:

CAS RN:Yes

Chemical Name:No

Smiles:Yes

Formula:No

INChI:No

MOL file:Yes

### 6.3.Data for each descriptor variable for the training set:

All

### 6.4.Data for the dependent variable for the training set:

All

### 6.5.Other information about the training set:

To verify the predictive capability of the proposed models, the whole dataset (n=706) was split, before model development, into training sets used for model development and prediction sets used later for external validation. Three different splitting techniques were applied: Random (n training= 495), by ordered response (n training= 472) and by structural similarity (n training= 472). In the Random splitting chemicals are randomly assigned to the training set. In the Ordered response splitting chemicals have been ordered according to their increasing toxicity and one out of every three chemicals has been assigned to the prediction set (always including the most and the least toxic compound in the training set, i.e. the lowest and the highest ATI values). This splitting guarantees that the training set covers the entire range of the modeled response. In the structural similarity splitting, training and prediction set are structurally balanced, being the splitting based on the structural similarity analysis (performed with Principal Component Analysis of the molecular descriptors).

### 6.6.Pre-processing of data before modelling:

The original median lethal concentrations for *Pseudokirchneriella subcapitata*, *Daphnia magna*, *Pimephales promela* and *Oncorhynchus mykiss* were reported as the minus logarithm of the molar concentration:  $-\log(\text{mmol/l})$ . This data were combined by Principal Component Analysis and the final endpoint, ATI (PC1 values), is thus a-dimensional.

### 6.7.Statistics for goodness-of-fit:

Random split:

$R^2 = 0.81$ ; RMSE= 0.68

Ordered Response split:

$R^2 = 0.83$ ; RMSE= 0.67

Structural Similarity split:

$R^2 = 0.81$ ; RMSE= 0.69

Full model

$R^2$ : 0.81; RMSE: 0.68

**6.8. Robustness - Statistics obtained by leave-one-out cross-validation:**

Random split:

$$Q^2_{loo}=0.81$$

Ordered Response split:

$$Q^2_{loo}=0.82$$

Structural Similarity split:

$$Q^2_{loo}=0.81$$

Full model  $Q^2_{loo}$ : 0.81

**6.9. Robustness - Statistics obtained by leave-many-out cross-validation:**

Random split:

$$Q^2_{LMO30\%}=0.81$$

Ordered Response split:

$$Q^2_{LMO30\%}=0.82$$

Structural Similarity split:

$$Q^2_{LMO30\%}=0.81$$

Full model:  $Q^2_{LMO30\%}=0.81$

**6.10. Robustness - Statistics obtained by Y-scrambling:**

Random split:

$$R^2_{Yscr}=0.01$$

Ordered Response split:

$$R^2_{Yscr}=0.01$$

Structural Similarity split:

$$R^2_{Yscr}=0.01$$

Full model:  $R^2_{Yscr}=0.004$

**6.11. Robustness - Statistics obtained by bootstrap:**

No information available (since only  $Q^2_{LMO}$  was calculated)

**6.12. Robustness - Statistics obtained by other methods:**

Random split:

$$RMSE_{CV}= 0.69; CCC_{CV}= 0.90$$

Ordered Response split:

$$RMSE_{CV}= 0.67; CCC_{CV}=0.90$$

Structural Similarity split:

$$RMSE_{CV}= 0.7; CCC_{CV}=0.9$$

Full model  $RMSE_{CV}=0.69; CCC_{CV}=0.9$

**7. External validation - OECD Principle 4**

**7.1. Availability of the external validation set:**

Yes

**7.2. Available information for the external validation set:**

CAS RN: Yes

Chemical Name: No

Smiles:Yes  
Formula:No  
INChI:No  
MOL file:Yes

### 7.3.Data for each descriptor variable for the external validation set:

All

### 7.4.Data for the dependent variable for the external validation set:

All

### 7.5.Other information about the external validation set:

As said in section 6.5, to verify the predictive capability of the proposed models, the dataset (n=706) was split, before model development, into a training set used for model development and a prediction set used later for external validation.

### 7.6.Experimental design of test set:

As said in section 6.5, in the Random splitting chemicals are randomly assigned to the training set.

In the case of split by Ordered response model, chemicals were ordered according to their increasing activity, and one out of every three chemicals was put in the prediction set (always including the most and the least active compounds in the training set).

The splitting based on structural similarity, allowed the selection of a structurally meaningful training set and an equally representative prediction set. The selection is based on Principal Component Analysis that is able to project chemicals in the multivariate descriptors space. This method ensures that both sets are homogeneously distributed within the entire area of the descriptors space.

### 7.7.Predictivity - Statistics obtained by external validation:

Random split model:

$Q^2_{\text{extF1}} [8] = 0.81$ ;  $Q^2_{\text{extF2}} [9] = 0.81$ ;  $Q^2_{\text{extF3}} [10] = 0.81$ ;  $\text{CCC}_{\text{ext}} [11] = 0.89$ ;  $\text{RMSE} = 0.69$

Ordered response split model:

$Q^2_{\text{extF1}} = 0.79$ ;  $Q^2_{\text{extF2}} = 0.79$ ;  $Q^2_{\text{extF3}} = 0.8$ ;  $\text{CCC}_{\text{ext}} = 0.89$ ;  $\text{RMSE} = 0.72$

Structural Similarity split model:

$Q^2_{\text{extF1}} = 0.81$ ;  $Q^2_{\text{extF2}} = 0.81$ ;  $Q^2_{\text{extF3}} = 0.82$ ;  $\text{CCC}_{\text{ext}} = 0.90$ ;  $\text{RMSE} = 0.67$

The high values of external  $Q^2$  and concordance correlation coefficient-CCC (threshold for accepting the external  $Q^2_{\text{F1-F2-F3}}$  is 0.70, threshold for CCC is 0.85,[11, 12]), show that the proposed model is predictive, when applied to chemicals never seen during the model development (prediction sets)[13].

### 7.8.Predictivity - Assessment of the external validation set:

The splitting methodology based on similarity analysis, by ordered response and random allowed for the selection of meaningful training sets and representative prediction sets.

Training and prediction sets were balanced according to both structure

and response and the predictivity was assessed even on random training and prediction set. In particular:

Random split model:

-response range of ATI values: training [-4.68 / 4.17] prediction [-4.08 / 4.2]

-descriptor range:

CrippenLogP: training [-1.36 / 6.27] prediction [-1.47 / 6.03]

SHBint2: training [-0.29 / 36.78] prediction [0 / 30.02]

SaaCH: training [0 / 36.07] prediction [0 / 21.08]

Ordered response split model:

-response range of ATI values: training [-4.68 / 4.2] prediction [-4.17 / 4.02]

-descriptor range:

CrippenLogP: training [-1.47 / 6.27] prediction [-1.36 / 6.18]

SHBint2: training [-0.29 / 36.78] prediction [0 / 28.76]

SaaCH: training [0 / 36.07] prediction [0 / 23.06]

Structural Similarity split model: -response range of ATI values: training [-4.68 / 4.19] prediction [-4.32 / 4.17]

-descriptor range:

CrippenLogP: training [-1.47 / 6.27] prediction [-1.25 / 6.18]

SHBint2: training [-0.29 / 36.78] prediction [0 / 30.02]

SaaCH: training [0 / 23.06] prediction [0 / 36.07]

The applicability domain of the model on the prediction set has been verified by the Williams plot

#### **7.9. Comments on the external validation of the model:**

no other information available

### **8. Providing a mechanistic interpretation - OECD Principle 5**

#### **8.1. Mechanistic basis of the model:**

The model was developed by statistical approach. No mechanistic basis for this biological activity was set a priori, but a mechanistic interpretation of molecular descriptors was provided a posteriori (see 8.2).

#### **8.2. A priori or a posteriori mechanistic interpretation:**

CrippenLogKow (std coefficient: 0.63) is the most important descriptor in predicting the overall toxicity of chemicals in this aquatic scenario. It has, as expected, a positive sign in the equation, thus a positive influence increasing the cumulative toxicity trend. This confirms the well-known relevance of lipophilicity in increasing toxicity. The second descriptor is SaaCH (std coefficient: 0.28) that encodes for the sum of the E-States of the CH groups bounded to two aromatic atoms. This descriptor increases with the overall aromatic character of the studied compounds and has a positive influence in the model equation. The last descriptor is SHBint2 (std coefficient: -0.22) that codifies for the sum of the E-State of strength for potential hydrogen bonds. This descriptor

accounts for the potential to establish hydrogen bonds and increases with the presence of electronegative atoms. It has a negative sign in the model equation, so structural features described by this descriptor have a negative influence in the overall aquatic toxicity. The most hydrophilic compounds are the less toxic [1]

### 8.3. Other information about the mechanistic interpretation:

no other information available

## 9. Miscellaneous information

### 9.1. Comments:

To predict ATI for new Pharmaceuticals without experimental data, it is suggested to apply the equation of the Full Model, developed on all the available chemicals (N Training=706).

Full model equation:  $ATI = -1.87 + 0.62CrippenLogKow + 0.07SaaCH - 0.05SHBint2$

N Training set= 706;  $R^2 = 0.81$ ;  $Q^2_{LOO} = 0.81$ ;  $Q^2_{LMO30\%} = 0.81$ ;  $CCC_{CV} = 0.9$ ;  $RMSE = 0.68$ ;  $RMSE_{CV} = 0.69$ .

End-point, descriptors and splitting status for each chemical are reported in the supporting information.

### 9.2. Bibliography:

- [1] A. Sangion, P. Gramatica, Hazard of pharmaceuticals for aquatic environment: Prioritization by structural approaches and prediction of ecotoxicity, *Environ. Int.* 95 (2016) 131–143. doi:10.1016/j.envint.2016.08.008
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- [6] Hypercube, inc, HyperChem(TM), Hypercube, Inc., 1115 NW 4th Street, Gainesville, Florida 32601, USA, 2002 <http://www.hyper.com/>
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- [8] L.M. Shi, H. Fang, W.D. Tong, J. Wu, R. Perkins, R.M. Blair, W.S. Branham, S.L. Dial, C.I. Moland, D.M. Sheehan, QSAR models using a large diverse set of estrogens, *J. Chem. Inf. Comput. Sci.* 41 (2001) 186–195.

doi:10.1021/ci000066d.

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### **9.3.Supporting information:**

Training set(s)Test set(s)Supporting information

## **10.Summary (JRC Inventory)**

### **10.1.QMRF number:**

To be entered by JRC

### **10.2.Publication date:**

To be entered by JRC

### **10.3.Keywords:**

To be entered by JRC

### **10.4.Comments:**

To be entered by JRC