Supplementary material

Metal and metal oxide nanoparticle toxicity: Moving towards a more holistic structure-activity approach

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S1. Descriptor selection

The absolute value of the Pearson correlation coefficient is presented in Figure S1, below.



Figure S1. Pearson correlation coefficient for the initial descriptor set.

Following the results of Figure S1, the descriptors with an intercorrelation above 0.95 are deemed to be intercorrelated, and only one of the intercorrelated descriptors is kept. Following this procedure, the descriptors that are omitted are presented below, in Table S1.

Descriptor removed	Intercorrelation with		
A_MSM	E_MSM		
M MSM			
Ne_MSM			
AW_M			
M_M			
Ne_M			
E_M			
A_NM	_		
Ne_NM	E_NM		
M_NM			
IP_NM			
X_NM			
VWR_NM			
E_SM	-		
A_SM	_		
Ne_SM	_		
M_SM	SM IP		
IP_SM			
X_SM			
VWR_SM			
N_SM			
A_SM	_		
Ne_SM	E_M		
M_SM			
X_M	IP_M		
N_M	M_IP		
Eg	Dhio		
Ec	DUIU		
Z	HE		

Table S1. List of eliminated descriptors from the intercorrelation analysis

S2. Optimal descriptor combination

Based on the descriptor selection procedure, the four most relevant descriptors (Dbio, HE, IP_M, E_MSM) were tested in different combinations. Models were built using different descriptor combinations, and the respective model accuracy was estimated. The results towards the most populous individual cell line dataset (A549 cells) are presented in Table S2

Dbio	HE	E_MSM	IP_M	Accuracy	
Single descriptor models					
\checkmark	×	×	×	88.2	
×	\checkmark	×	×	85.3	
×	×	\checkmark	×	91.2	
×	×	×	\checkmark	88.2	
Two descriptor models					
\checkmark	\checkmark	×	×	94.1	
\checkmark	×	\checkmark	×	82.4	
\checkmark	×	×	\checkmark	82.4	
×	\checkmark	\checkmark	×	85.3	
×	\checkmark	×	\checkmark	91.2	
×	×	\checkmark	\checkmark	88.2	
Three descriptor models					
\checkmark	\checkmark	\checkmark	×	88.2	
\checkmark	\checkmark	×	\checkmark	94.1	
\checkmark	×	\checkmark	\checkmark	85.3	
×	\checkmark	\checkmark	\checkmark	85.3	
Four descriptor models					
\checkmark	\checkmark	\checkmark	\checkmark	88.2	

Table S2. Model accuracy with the different descriptor combinations towards the A549 dataset

Results of Table S2 show that the optimal model accuracy is obtained using the Dbio-HE and the Dbio-HE-IP_M descriptor sets. Since the addition of IP_M does not increase the model accuracy, the set of Dbio-HE descriptors is selected as the optimal model.