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# A structure–activity relationship survey of histone deacetylase (HDAC) inhibitors

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**Background and Aims:** Histone deacetylase inhibitors have gained a great attention, recently, for the treatment of many malignant diseases, especially cancers. So design of newly inhibitors is of great importance in pharmaceutical industries and labs. As synthesis is money and time consuming process, it would be better if one can estimate compound's property or activity before synthesis beginning. On the other hand, computational methods have been used variously to predict activity or properties of designed molecules.
**Methods:** Here, we elaborated a novel ranked-base ant system to generate a QSAR model for predicting histone deacetylase inhibition activity. The data set had 320 molecules and the obtained model was validated by predicting inhibition of 80 compounds as external set.
**Results and Conclusions:** Developed model has high prediction power characterized by R2 (train and all) values 0.75 and 0.75 respectively and RMSE value of 0.51 for the external test set. The following equation was acquired for describing HDAC inhibition activity:
Log IC"50"=-0.08 SP20-0.07piPC09-78.42HATS8v+0.04ALogP+0.61nR06+4.71 ntraining=313; ntest=80; R2training=0.75; Q2LOO=0.75; Q2EXT=0.87; R2predicted=0.78; R2all=0.75; AAEall=0.43; RMSEall=0.52; RMSEtrain=0.52; RMSEtest=0.52; F=1207.58; AAREall =0.29; AAREtrain=0.33; AAREtest=0.28 RQK function parameters: ΔK=0.016; ΔQ=0.006; RP=0.24; RN= 0.19 The results show that the acquired model is capable of predicting HDAC inhibition activity with good accuracy.

**Keywords:** Histone deacetylase; Cancer; Structure Activity Relationships (SAR); Rank-based system