Combining Ensemble Learning with a Fragment-Based Topological Approach to Generate New Molecular Diversity in Drug Discovery: In Silico Design of Hsp90 Inhibitors

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b _t	N _{Total} (b _t)	N _{Active} (b _t)	N _{Inactive} (b _t)	$[Sn(\%)]b_t$	$[Sp(\%)]b_t$	Series
Hsp90a	486	252	234	85.32%	75.21%	Training Set
Hsp90β	288	121	167	80.17%	92.81%	Training Set
Hsp90a	161	83	78	89.16%	76.92%	Test Set
Hsp90β	94	38	56	78.95%	87.50%	Test Set

Table S1. Local measures of the statistical quality and performance of the mt-QSAR-EL model.

The symbols in this table have the following meanings:

 \mathbf{b}_t refers to the biological target (Hsp90 isoform). Therefore, Hsp90 α is the heat shock protein 90 alpha, while Hsp90 β is the heat shock protein 90 beta.

 $N_{Total}(b_t)$ – total number of molecules depending on the target.

 $N_{\text{Active}}(\mathbf{b}_t)$ – number of active molecules depending on the target.

 $N_{\text{Inactive}}(\mathbf{b}_t)$ – number of inactive molecules depending on the target.

 $[Sn(\%)]b_t$ – Local sensitivity expressed as the percentage of molecules correctly classified as active depending on the target.

 $[Sp(\%)]b_t$ – Local specificity expressed as the percentage of molecules correctly classified as inactive depending on the target.