

# Supplementary Material

## **Comparative chemometric and QSAR/SAR study of structurally unrelated substrates of a MATE efflux pump VmrA from *V. parahaemolyticus*: prediction of multidrug resistance**

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## Structures retrieved from the Protein Data Bank (PDB)

### 1BWC:

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Bar-On, P., Millard, C. B., Harel, M., Dvir, H., Enz, A., Sussman, J. L., Silman, I. Kinetic and structural studies on the interaction of cholinesterases with the anti-Alzheimer drug rivastigmine. *Biochemistry* 41 (2002) 3555-3564.

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Bar-On, P., Millard, C. B., Harel, M., Dvir, H., Enz, A., Sussman, J. L., Silman, I. Kinetic and structural studies on the interaction of cholinesterases with the anti-Alzheimer drug rivastigmine. *Biochemistry* 41 (2002) 3555-3564.

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Van Den Heuvel, R. H., Van Den Berg, W. A., Rovida, S., Van Berkel, W. J. Laboratory-Evolved Vanillyl-Alcohol Oxidase Produces Natural Vanillin. *J. Biol. Chem.* 279 (2004) 33492-33500.

1W1M:

Van Den Heuvel, R. H., Van Den Berg, W. A., Rovida, S., Van Berkel, W. J. Laboratory-Evolved Vanillyl-Alcohol Oxidase Produces Natural Vanillin. *J. Biol. Chem.* 279 (2004) 33492-33500.

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Hinrichs, W., Kisker, C., Duvel, M., Muller, A., Tovar, K., Hillen, W., Saenger, W. Structure of the Tet repressor-tetracycline complex and regulation of antibiotic resistance. *Science* 264 (1994) 418-420.

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Beaman, T. W., Sugantino, M., Roderick, S. L. Structure of the hexapeptide xenobiotic acetyltransferase from *Pseudomonas aeruginosa*. *Biochemistry* 37 (1998) 6689-6696.

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Gane, P. A. C., Boles, M. O., Bird, A. E. Structure of carfecillin (sodium salt). *Acta Cryst.* B38 (1982) 929-932.

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McMahon, J. A., Zaworotko, M. J., Remenar, J. F. Polymorphism in butylated hydroxy anisole (BHA). *Chem. Commun.* (2004) 278-279.

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Subramanian, E., Trotter, J., Bugg, C. E. Crystal structure of ethidium bromide. *J. Cryst. Mol. Struct.* 1 (1971) 3-15.

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Stezowski, J. J. Chemical-structural properties of tetracycline derivatives. 1. Molecular structure and conformation of the free base derivatives. *J. Amer. Chem. Soc.* 98 (1976) 6012-6018.

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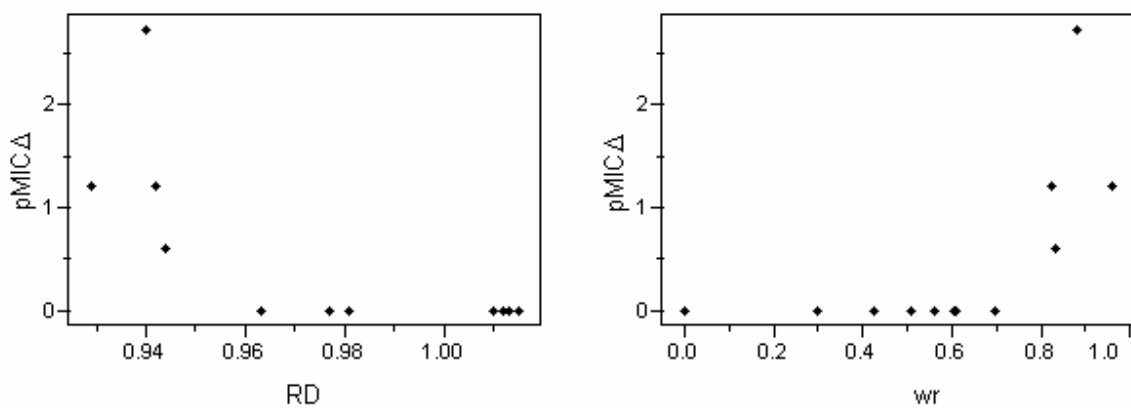
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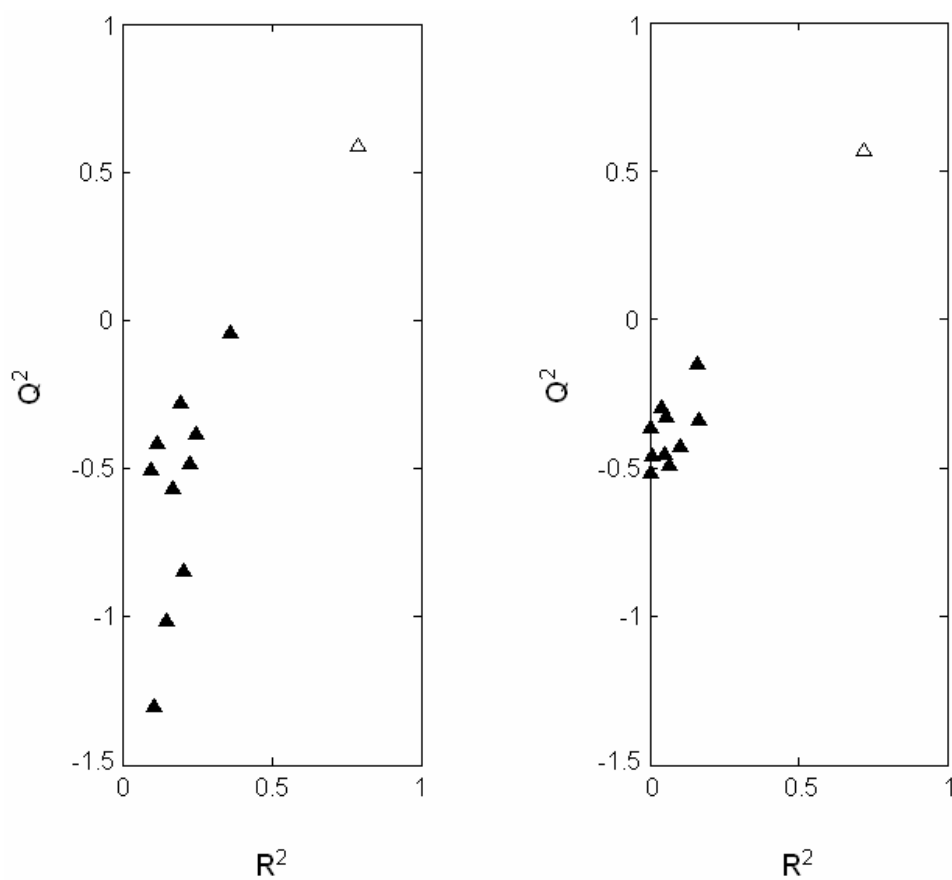
XAYGEJ:

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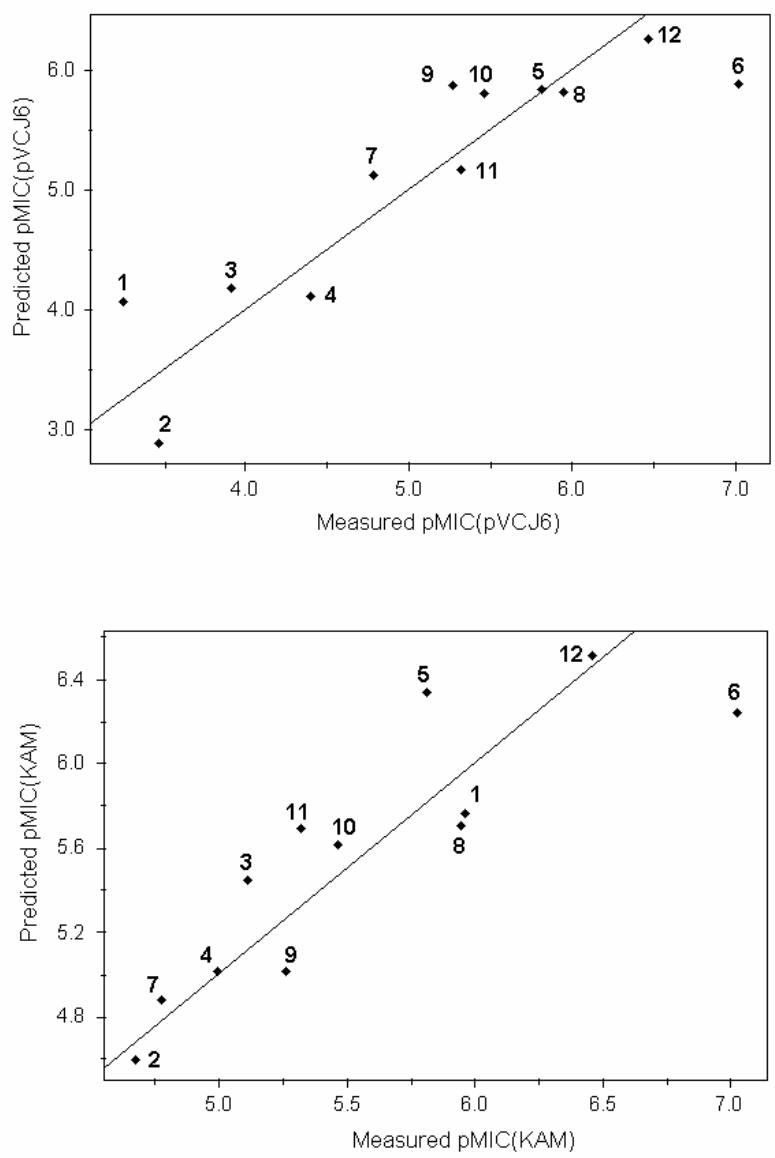




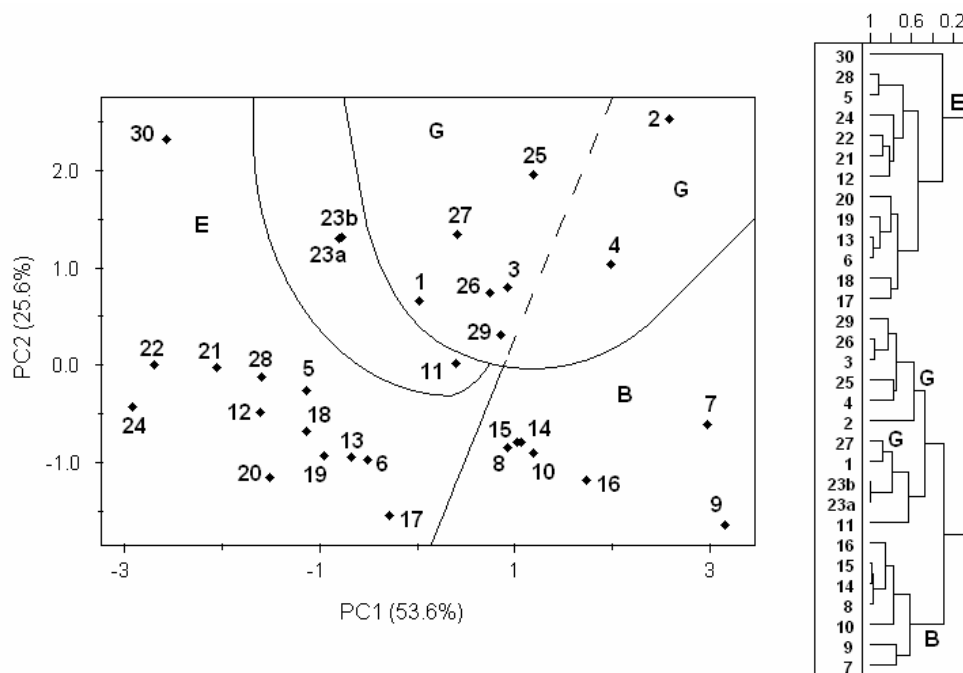
**Figure A.** Examples of representative pMIC $\Delta$ -descriptor relations regarding VmrA resistance to heteroaromatics **1-4**.



**Figure B.** Results of the Y-randomization tests. Left: testing the PLS model for pMIC(pVCJ6). Right: testing the PCR model for pMIC(KAM). The plots for the other two models are similar. Ten random shuffles of the Y-vectors were performed, as was recommended by Wold and Eriksson [25] and as it has become a practise in QSAR studies.  $Q^2$  is from leave-one-out crossvalidation.



**Figure C.** PLS plots for biological activities pMIC(KAM) and pMIC(pVJC6).



**Figure D.** PCA scores plot (left) and HCA dendrogram of samples with complete linkage (right) related to the efflux power of the strain KAM32 of *E. coli* with respect to the training+prediction set **1-30**.

### Comments for Figure D

Previous exploratory analysis for the prediction set (Fig. 3 top, in the text) could not recognize clearly the agents to which VmrA would be resistant: two groups of more elongated (E) and more branched (B) agents were observed. In the present analysis for the training+prediction data set relative to KAM32 (Figure D), this E-B discrimination may also be perceived, but more detailed clustering is visible. Well-defined regions of agents, assigned as G in the previous analysis (Fig. 5 left, in the text), is situated at the right top corner of the PC1-PC2 scores space. **11**, **23a** and **23b** are close to this group. Other two groups are more branched (**7-10**, **14-16**) and more linear (**5**, **6**, **12**, **13**,

17-22, 24, 28, 30) agents to which VmrA is sensitive. This clustering is clearly shown in the corresponding HCA dendrogram (Fig. C right). It is clear that the PCA-HCA analysis related to the both *E. coli* strains can provide correct VmrA resistance/sensitivity assignments for diverse agents.