Therapeutic Targets Database



QSAR Model

Target Name	MAO-A
Target TTD ID	TTDS00289

Target Species	Human
Chemical Type	Propargyl (clorgyline analogues)
Mode of Action	Inhibitor
QSAR Model 1	$i-MAO-A = -1.32\chi_1(C_{sat}) - 2.56\chi_2(Het) + 0.46\alpha_0(Het) + 1.69\alpha_1(Het) + 1.16MR_1 + 1.21 + 7.12MR_2(C_{unsat}) - 1.71MR_0(Het) - 2.95 \cdot \log P_0 - 5.6 \cdot \log P_2(C_{unsat}) \lambda = 0.36 F = 273.93 p < 0.01$
Molecular Descriptor	Access the following web-servers to compute molecular descriptors: MoDel and e-dragon ${}^{k}\chi(G)$: molecular or group electro-negativities; ${}^{k}MR(G)$: refractivities; ${}^{k}\alpha(G)$: polarizabilities; $\log^{k}P$: logarithms of water/ <i>n</i> -octanol partition coefficients; <i>G</i> : atoms included in a specific group; i-MAO-A: MAO-A inhibitory activity score; <i>W</i> : Wilk's λ statistic; <i>F</i> : the Fisher ratio; <i>p</i> : the <i>p</i> -level.
Reference	A QSAR Model for in Silico Screening of MAO-A Inhibitors. Prediction, Synthesis, and Biological Assay of Novel Coumarins. <i>J. Med. Chem.</i> 2006, 49, 1149-1156

Target Species	Human
Chemical Type	Benzamide (moclobemide analogues)
Mode of Action	Inhibitor

QSAR Model 1	$i-MAO-A = -1.32\chi_1(C_{sat}) - 2.56\chi_2(Het) + 0.46\alpha_0(Het) + 1.69\alpha_1(Het) + 1.16MR_1 + 1.21$ $+ 7.12MR_2(C_{unsat}) - 1.71MR_0(Het) - 2.95 \cdot \log P_0 - 5.6 \cdot \log P_2(C_{unsat})$ $\lambda = 0.36 F = 273.93 p < 0.01$
Molecular Descriptor	Access the following web-servers to compute molecular descriptors: MoDel and e-dragon ${}^{k}\chi(G)$: molecular or group electro-negativities; ${}^{k}MR(G)$: refractivities; ${}^{k}\alpha(G)$: polarizabilities; $\log^{k}P$: logarithms of water/ <i>n</i> -octanol partition coefficients; <i>G</i> : atoms included in a specific group; i-MAO-A: MAO-A inhibitory activity score; <i>W</i> : Wilk's λ statistic; <i>F</i> : the Fisher ratio; <i>p</i> : the <i>p</i> -level.
Reference	A QSAR Model for in Silico Screening of MAO-A Inhibitors. Prediction, Synthesis, and Biological Assay of Novel Coumarins. <i>J. Med. Chem.</i> 2006, 49, 1149-1156

Target Species	Human
Chemical Type	Phenylethylamines
Mode of Action	Inhibitor
QSAR Model 1	$i-MAO-A = -1.32\chi_1(C_{sat}) - 2.56\chi_2(Het) + 0.46\alpha_0(Het) + 1.69\alpha_1(Het) + 1.16MR_1 + 1.21 + 7.12MR_2(C_{unsat}) - 1.71MR_0(Het) - 2.95 \cdot \log P_0 - 5.6 \cdot \log P_2(C_{unsat}) \lambda = 0.36 F = 273.93 p < 0.01$
Molecular Descriptor	Access the following web-servers to compute molecular descriptors: MoDel and e-dragon ${}^{k}\chi(G)$: molecular or group electro-negativities; ${}^{k}MR(G)$: refractivities; ${}^{k}\alpha(G)$: polarizabilities; $\log^{k}P$: logarithms of water/ <i>n</i> -octanol partition coefficients; <i>G</i> : atoms included in a specific group; i-MAO-A: MAO-A inhibitory activity score; <i>W</i> : Wilk's λ statistic; <i>F</i> : the Fisher ratio; <i>p</i> : the <i>p</i> -level.
Reference	A QSAR Model for in Silico Screening of MAO-A Inhibitors. Prediction, Synthesis, and Biological Assay of Novel Coumarins. <i>J. Med. Chem.</i> 2006, 49, 1149-1156

Target	Human
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Species	
Chemical Type	Indoles
Mode of Action	Inhibitor
QSAR Model 1	$i-MAO-A = -1.32\chi_1(C_{sat}) - 2.56\chi_2(Het) + 0.46\alpha_0(Het) + 1.69\alpha_1(Het) + 1.16MR_1 + 1.21$ $+ 7.12MR_2(C_{unsat}) - 1.71MR_0(Het) - 2.95 \cdot \log P_0 - 5.6 \cdot \log P_2(C_{unsat})$ $\lambda = 0.36 F = 273.93 p < 0.01$
Molecular Descriptor	Access the following web-servers to compute molecular descriptors: MoDel and e-dragon ${}^{k}\chi(G)$: molecular or group electro-negativities; ${}^{k}MR(G)$: refractivities; ${}^{k}\alpha(G)$: polarizabilities; $\log^{k}P$: logarithms of water/ <i>n</i> -octanol partition coefficients; <i>G</i> : atoms included in a specific group; i-MAO-A: MAO-A inhibitory activity score; <i>W</i> : Wilk's λ statistic; <i>F</i> : the Fisher ratio; <i>p</i> : the <i>p</i> -level.
Reference	A QSAR Model for in Silico Screening of MAO-A Inhibitors. Prediction, Synthesis, and Biological Assay of Novel Coumarins. <i>J. Med. Chem.</i> 2006, 49, 1149-1156

Target Species	Human
Chemical Type	Coumarins
Mode of Action	Inhibitor
QSAR Model 1	$i-MAO-A = -1.32\chi_1(C_{sat}) - 2.56\chi_2(Het) + 0.46\alpha_0(Het) + 1.69\alpha_1(Het) + 1.16MR_1 + 1.21$ $+ 7.12MR_2(C_{unsat}) - 1.71MR_0(Het) - 2.95 \cdot \log P_0 - 5.6 \cdot \log P_2(C_{unsat})$ $\lambda = 0.36 F = 273.93 p < 0.01$
Molecular Descriptor	Access the following web-servers to compute molecular descriptors: <u>MoDel</u> and <u>e-dragon</u> ${}^{k}\chi(G)$: molecular or group electro-negativities; ${}^{k}MR(G)$: refractivities; ${}^{k}\alpha(G)$: polarizabilities; $\log^{k}P$: logarithms of water/ <i>n</i> -octanol partition coefficients; <i>G</i> : atoms included in a specific group; i-MAO-A:

	MAO-A inhibitory activity score; W: Wilk's λ statistic; F: the Fisher ratio; p: the p-level.
Reference	A QSAR Model for in Silico Screening of MAO-A Inhibitors. Prediction, Synthesis, and Biological
	Assay of Novel Coumarins. J. Med. Chem. 2006, 49, 1149-1156

Target Species	Human
Chemical Type	Thioxanthenes
Mode of Action	Inhibitor
QSAR Model 1	$i-MAO-A = -1.32\chi_1(C_{sat}) - 2.56\chi_2(Het) + 0.46\alpha_0(Het) + 1.69\alpha_1(Het) + 1.16MR_1 + 1.21$ $+ 7.12MR_2(C_{unsat}) - 1.71MR_0(Het) - 2.95 \cdot \log P_0 - 5.6 \cdot \log P_2(C_{unsat})$ $\lambda = 0.36 F = 273.93 p < 0.01$
Molecular Descriptor	Access the following web-servers to compute molecular descriptors: MoDel and e-dragon ${}^{k}\chi(G)$: molecular or group electro-negativities; ${}^{k}MR(G)$: refractivities; ${}^{k}\alpha(G)$: polarizabilities; $\log^{k}P$: logarithms of water/ <i>n</i> -octanol partition coefficients; <i>G</i> : atoms included in a specific group; i-MAO-A: MAO-A inhibitory activity score; <i>W</i> : Wilk's λ statistic; <i>F</i> : the Fisher ratio; <i>p</i> : the <i>p</i> -level.
Reference	A QSAR Model for in Silico Screening of MAO-A Inhibitors. Prediction, Synthesis, and Biological Assay of Novel Coumarins. <i>J. Med. Chem.</i> 2006, 49, 1149-1156

Target Species	Human
Chemical Type	Oxadiazolidone (toloxatone analogues)
Mode of Action	Inhibitor

QSAR Model 1	$i-MAO-A = -1.32\chi_1(C_{sat}) - 2.56\chi_2(Het) + 0.46\alpha_0(Het) + 1.69\alpha_1(Het) + 1.16MR_1 + 1.21 + 7.12MR_2(C_{unsat}) - 1.71MR_0(Het) - 2.95 \cdot \log P_0 - 5.6 \cdot \log P_2(C_{unsat}) \lambda = 0.36 F = 273.93 p < 0.01$
Molecular Descriptor	Access the following web-servers to compute molecular descriptors: MoDel and e-dragon ${}^{k}\chi(G)$: molecular or group electro-negativities; ${}^{k}MR(G)$: refractivities; ${}^{k}\alpha(G)$: polarizabilities; $\log^{k}P$: logarithms of water/ <i>n</i> -octanol partition coefficients; <i>G</i> : atoms included in a specific group; i-MAO-A: MAO-A inhibitory activity score; <i>W</i> : Wilk's λ statistic; <i>F</i> : the Fisher ratio; <i>p</i> : the <i>p</i> -level.
Reference	A QSAR Model for in Silico Screening of MAO-A Inhibitors. Prediction, Synthesis, and Biological Assay of Novel Coumarins. <i>J. Med. Chem.</i> 2006, 49, 1149-1156

Target Species	Human
Chemical Type	Diazoheterocyclic derivatives
Mode of Action	Inhibitor
QSAR Model 1	$i-MAO-A = -1.32\chi_1(C_{sat}) - 2.56\chi_2(Het) + 0.46\alpha_0(Het) + 1.69\alpha_1(Het) + 1.16MR_1 + 1.21 + 7.12MR_2(C_{unsat}) - 1.71MR_0(Het) - 2.95 \cdot \log P_0 - 5.6 \cdot \log P_2(C_{unsat}) \lambda = 0.36 F = 273.93 p < 0.01$
Molecular Descriptor	Access the following web-servers to compute molecular descriptors: MoDel and e-dragon ${}^{k}\chi(G)$: molecular or group electro-negativities; ${}^{k}MR(G)$: refractivities; ${}^{k}\alpha(G)$: polarizabilities; $\log^{k}P$: logarithms of water/ <i>n</i> -octanol partition coefficients; <i>G</i> : atoms included in a specific group; i-MAO-A: MAO-A inhibitory activity score; <i>W</i> : Wilk's λ statistic; <i>F</i> : the Fisher ratio; <i>p</i> : the <i>p</i> -level.
Reference	A QSAR Model for in Silico Screening of MAO-A Inhibitors. Prediction, Synthesis, and Biological Assay of Novel Coumarins. <i>J. Med. Chem.</i> 2006, 49, 1149-1156