

Target Name	CYP2A5
Target TTD ID	TTDR01445

Target Species	Rat
Chemical Type	Naphthalene and non-naphthalene derivatives
Mode of Action	Inhibitor
QSAR Model 1	$\text{pIC}_{50(2A5)} = 2.682(\pm 0.858) - 0.316(\pm 0.134)\text{Sr} + 0.728(\pm 0.105)\text{Shadow_Xlength}$ $- 7.569(\pm 0.915)\text{FPSA}_2 - 0.067(\pm 0.010)\text{WNSA}_1$ $- 2.497(\pm 0.619)\text{RNCG} - 0.141(\pm 0.030)\text{PNSA}_3$ $n_{\text{Training}} = 31, \text{LOF} = 0.253, R^2 = 0.796, R_a^2 = 0.745, F = 15.64(\text{df } 6, 24), Q^2 = 0.686,$ $\text{PRESS} = 4.533, n_{\text{Test}} = 11, R_{\text{pred}}^2 = 0.707, r^2 = 0.734, r_0^2 = 0.732, r_m^2 = 0.701$
QSAR Model 2	$\text{pIC}_{50(2A5)} = 2.225 - 0.780\text{RNCG} + 0.647\text{Shadow_Xlength} - 0.0003\text{Apol} - 0.439\text{Sr}$ $- 0.005\text{PMI} + 0.014\text{RPCS} + 3.131\text{FNSA}_1 - 51.603\text{FPSA}_3$ $n_{\text{Training}} = 31, \text{LSE} = 0.091, R^2 = 0.779, R_a^2 = 0.726, F = 22.88(\text{df } 4, 26), Q^2 = 0.575,$ $\text{PRESS} = 6.140, n_{\text{Test}} = 11, R_{\text{pred}}^2 = 0.615, r^2 = 0.679, r_0^2 = 0.639, r_m^2 = 0.543$
QSAR Model 3	$\text{pIC}_{50(2A5)} = 2.989(\pm 0.727) + 0.334(\pm 0.071)\text{pIC}_{50(2A6)} + 0.422(\pm 0.076)\text{Shadow_Xlength}$ $- 0.367(\pm 0.118)\text{Sr} - 43.219(\pm 8.814)\text{FPSA}_3 - 0.058(\pm 0.014)\text{Molref}$ $+ 0.236(\pm 0.095) \text{A log P98}$ $n_{\text{Training}} = 29, \text{LOF} = 0.128, R^2 = 0.898, R_a^2 = 0.870,$ $F = 32.36(\text{df } 6, 22), Q^2 = 0.814, \text{PRESS} = 2.321,$ $n_{\text{Test}} = 10, R_{\text{pred}}^2 = 0.914, r^2 = 0.905, r_0^2 = 0.904, r_m^2 = 0.876$

<p>QSAR Model 4</p>	$pIC_{50(2A5)} = -1.994 + 0.427pIC_{50(2A6)} + 0.166Shadow_Zlength + 3.850FNSA_1$ $+ 0.394Shadow_Xlength + 0.012PNSA_2 - 0.355Sr$ <p>$n_{Training} = 29, LSE = 0.061, R^2 = 0.859, R_a^2 = 0.794,$</p> <p>$F = 36.67(df\ 4, 24), Q^2 = 0.746, PRESS = 3.168,$</p> <p>$n_{Test} = 10, R_{pred}^2 = 0.902, r^2 = 0.903, r_2^0 = 0.881, r_m^2 = 0.769$</p>
<p>Molecular Descriptor</p>	<p>Access the following web-servers to compute molecular descriptors: MoDel and e-dragon</p> <p>Type of descriptor-Descriptor name: Definition</p> <p>Electronic-Apol: Sum of atomic polarizabilities; Dipole: Dipole moment; HOMO: Highest occupied molecular orbital energy; LUMO: Lowest unoccupied molecular orbital energy; Sr Superdelocalizability</p> <p>Shape-DIFFV: The difference between the volume of the individual molecule and the volume of the shape reference compound; COSV The common volume between each individual molecule and the molecule selected as the reference compound; Fo: The common overlap steric volume descriptor (COSV, see above) divided by the volume of the individual molecule; NCOSV: The difference between the volume of the individual molecule and the common overlap steric volume (COSV); ShapeRMS: Root mean square (RMS) deviation between the individual molecule and the shape reference compound; SRVolume: The volume of the shape reference compound</p> <p>Spatial-RadOfGyration: ; Density: The ratio of molecular weight to molecular volume; PMI-mag: It calculates the principal moments of inertia about the principal axes of a molecule; Vm: Molecular volume inside the contact surface; Area: van der Waals area of a molecule; Jurs descriptors: These are calculated by mapping atomic partial charges on solvent-accessible surface areas of individual atoms; Shadow indices: This set of geometric descriptors helps to characterize the shape of the molecules</p> <p>Thermodynamic-AlogP: Log of the partition coefficient; Molref: Molar refractivity; AlogP98: Log of partition coefficient</p>
<p>Reference</p>	<p>Exploring QSAR and QAAR for inhibitors of cytochrome P450 2A6 and 2A5 enzymes using GFA and G/PLS techniques. <i>European Journal of Medicinal Chemistry</i> 44 (2009) 1941–1951</p>