Target Name	Adenosine A_1 receptor
Target TTD ID	TTDS00186

Target Species	Human
Chemical Type	Adenosine analogues
Mode of Action	Agonist
QSAR Model 1	$\log(A_1K_i) = -1.33(\pm 0.23) \cdot \log k' + 0.43(\pm 0.03) \cdot (\log k')^2 + 0.99(\pm 0.25)$ $N = 8$ $S = 0.18$ $R^2 = 0.99$ $F = 128.21$ $p < 0.0001$
Molecular Descriptor	Access the following web-servers to compute molecular descriptors: **MoDel** and **e-dragon** Log K': lipophilicity; N is the number of compounds included in the analysis, S is the root mean square error, R2 is the square of the correlation coefficient, F relates the variance of the null hypothesis to the correlation variance, p is the probability that a random set of data would yield a higher F value, and terms are given ± their standard errors.
Reference	Quantitative Structure Activity Relationships as Useful Tools for the Design of New Adenosine Receptor Ligands. 1. Agonist. *Current Medicinal Chemistry*, 2006, 13, 2253-2266

Target Species	Human
Chemical Type	Adenosine analogues
Mode of Action	Agonist
Activity	Adenosine derivatives with affinity for A_1 adenosine receptors

Type	
QSAR Model 1	$\log(K_i) = 23.886 - 8.143 \cdot (H8v) - 45.062 \cdot (REIG) - 10.686 \cdot (R2u^+) + 91.678 \cdot (R7u^+) - 11.937 \cdot (R5v) + 29425 \cdot (R1v^+)$ $N = 32\ S = 0.383\ R^2 = 0.773\ F = 14.188\ p < 10^{-5}\ S_{CV\text{-}LOO} = 0.501\ q^2_{LOO} = 0.664$
Molecular Descriptor	Access the following web-servers to compute molecular descriptors: **MoDel** and **e-dragon** Topological: MSD, CIC1, VRA1, MPC09, piPC09, T(N..S) Galvez Topological Charges indexes: GGI2, GGI3, GGI8, GGI9, GGI10, JGI5 Randic Molecular Profiles: DP01, SP03, SP04, SP07, SP12, SP13 Geometrical: W3D, AGDD, DDI, ADDD, MAXDP, FDI WHIM: E3u, P2m, G3m, L2s, E2s, Gu GETAWAY: H8v, REIG, R2u+, R7u+, R5v, R1v+ The REIG descriptor is defined as the first eigenvalue of the influence/distance matrix of the magnitude in question.
Reference	Quantitative Structure Activity Relationships as Useful Tools for the Design of New Adenosine Receptor Ligands. 1. Agonist. *Current Medicinal Chemistry*, 2006, 13, 2253-2266

Target Species	Human
Chemical Type	Arylpiperazines
Mode of Action	Binder
QSAR Model 1	aff. = 7.61 - 0.56 “Hbond acceptor” + 0.18 “Rotlbonds” + 1.15 “CHI-V-12_PC” LOF=0.21; R^2=0.86; F=70.85; Q^2=0.82
QSAR Model 2	aff. = 7.78 + 1.33 “CHI-V-13_PC” - 0.57 “Hbond acceptor” + 0.19 “Rotlbonds” LOF=0.21; R^2=0.85; F=70.74; Q^2=0.82

QSAR Model 3	aff. = 9.25 + 0.16 “Rotlbonds” - 0.38 “Shadow-nu” - 0.62 “Hbond acceptor” + 1.47 “CHI-V-13_PC” LOF=0.22; R^2=0.88; F=64.52; Q^2=0.84
QSAR Model 4	aff. = 9.73 - 0.59 “Hbond acceptor” + 0.21 “Rotlbonds” + 1.78 “CHI-V-14_PC” - 0.09 “Shadow-Xlength” LOF=0.22; R^2=0.88; F=64.37; Q^2=0.84
QSAR Model 5	aff. = 7.38 + 0.18 “Rotlbonds” - 0.54 “Hbond acceptor” + 1.01 “CHI-V-11_PC” LOF=0.22; R^2=0.85; F=69.55; Q^2=0.82
QSAR Model 6	aff. = 9.46 - 0.63 “Hbond acceptor” + 1.71 “CHI-V-14_PC” + 0.17 “Rotlbonds” - 0.41 “Shadow-nu” LOF=0.22; R^2=0.88; F=63.92; Q^2=0.84
QSAR Model 7	aff. = 9.42 - 0.08 “Shadow-Xlength” - 0.58 “Hbond acceptor” + 1.52 “CHI-V-13_PC” + 0.19 “Rotlbonds” LOF=0.22; R^2=0.88; F=63.82; Q^2=0.84
QSAR Model 8	aff. = 7.85 - 0.57 “Hbond acceptor” + 1.52 “CHI-V-14_PC” + 0.20 “Rotlbonds” LOF=0.22; R^2=0.85; F=68.10; Q^2=0.82
QSAR Model 9	aff. = 7.17 - 0.54 “Hbond acceptor” + 0.18 “Rotlbonds” + 0.91 “CHI-V-10_PC” LOF=0.22; R^2=0.85; F=67.58; Q^2=0.81
QSAR Model 10	aff. = 8.90 + 1.26 “CHI-V-12_PC” + 0.16 “Rotlbonds” - 0.34 “Shadow-nu” - 0.60 “Hbond acceptor” LOF=0.23; R^2=0.88; F=61.85; Q^2=0.83
QSAR Model 11	$-\log K_i = 7.61 - 0.56\ (\pm 0.08)$ “Hbond acceptor” $+\ 0.18\ (\pm 0.02)$ “Rotlbonds” $+ 1.15\ (\pm 0.13)$ “CHI-V-12_PC”
Molecular Descriptor	Access the following web-servers to compute molecular descriptors: **MoDel** and **e-dragon** The term aff. represents -log Ki where Ki is the affinity of compounds toward R1-AR, expressed in M concentrations. R^2, LOF, F, and Q^2 are the coefficient of determination, the lack-of-fit value, the value from F test, and the cross-validated coefficient of determination, respectively. Descriptors, such as Rotlbonds (RB), Hbond acceptor (HBA), and a variable belonging to the CHI family. Both RB and CHI relate to the size of the molecules and CHI accounts for the connectivity of ligand structures.

Reference	A Genetic-Function-Approximation-Based QSAR Model for the Affinity of Arylpiperazines toward α1 Adrenoceptors. *J. Chem. Inf. Model*. 2006, 46, 1466-1478

Target Species	Rat
Target Location	Brain
Chemical Type	8-substituted xanthines
Mode of Action	Antagonist
QSAR Model 1	$pK_i(A_1) = 0.69 (\pm 0.16)\pi_8 - 1.43 (\pm 0.29)7CH_3 + 0.77 (\pm 0.18)\pi_1 + 4.46 (\pm 0.32)$ $n = 37; r = 0.78; s^2 = 0.68; F = 17.61.$
QSAR Model 2	$pK_i(A_1) = 0.64 (\pm 0.14)\pi_8 - 1.75 (\pm 0.27)7CH_3 + 1.49 (\pm 0.26)13DPR + 4.90 (\pm 0.24)$ $n = 37; r = 0.84; s^2 = 0.53; F = 25.42.$
QSAR Model 3	$pK_i(A_1) = 0.65 (\pm 0.13)\pi_8 - 1.81 (\pm 0.25)7CH_3 + 1.43 (\pm 0.25)13DPR + 4.97 (\pm 0.23)$ $n = 36; r = 0.86; s^2 = 0.47; F = 29.34.$
QSAR Model 4	$pK_i(A_1) = 0.57 (\pm 0.11)\pi_8 - 2.06 (\pm 0.21)7CH_3 + 1.54 (\pm 0.20)13DPR - 59.21 (\pm 12.30)q_1 - 17.02 (\pm 4.56)$ $n = 37; r = 0.91; s^2 = 0.32; F = 37.66.$
Molecular Descriptor	Access the following web-servers to compute molecular descriptors: **MoDel** and **e-dragon** A_1 adenosine receptor binding affinity was measured by inhibition of [3H]-N6-phenylisopropyladenosine in rat brain membranes and by inhibition of N6-R-PIA-elicited inhibition of adenylate cyclase in rat fat cell membranes. In our MO calculations, we routinely examined: the net atomic charges; the energies of the highest occupied and lowest unoccupied molecular orbitals, the HOMO and LUMO, respectively; the dipole moments; and the donor and acceptor superdelocalizabilities. 1) set of π-constants for the substituents: π_1, π_3, π_7, π_8, which describe the hydrophobicity of the

	substituents at the l-, 3-, 7- and 8-positions, respectively; 2) the set of σ-constants for the substituent R^8: σ_m, σ_p, σ*, which describe the mesomeric and inductive effect of the R^8; 3) the molecular refractivity of the substituent R^8, MR^8, which describes the volume of R^8; 4) the set of quantum chemical indices discussed above; and 5) the indicator variables 13DPR and 7CH, which account for the presence or absence of a certain group in a certain position. The indicator variable 13DPR has value 1 when propyl groups are attached to both N^1 and N^3 and value 0 when they are absent. The indicator variable $7CH_3$ has value 1 when a methyl group is present at the 7-position and value 0 when a hydrogen is present. These indicator variables quantify the effect of a substituent on the biological activity that cannot be attributed to the physicochemical properties considered.
Reference	QSAR studies of S-substituted xanthenes as adenosine receptor antagonists. *Euv JMed Chem* (1994) 29,133-138