Target Name	Adenosine A$_{2A}$ receptor
Target TTD ID	TTDS00187

Target Species	Human
Chemical Type	Adenosine analogues
Mode of Action	Agonist
QSAR Model 1	$\log(A_2K_i) = -0.50(\pm 0.31) \cdot \log k' + 0.19(\pm 0.06) \cdot (\log k')2 + 3.05(\pm 0.34)$ $N = 8\ S = 0.25\ R^2 = 0.92\ F = 28.87\ p < 0.0018$
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 $\pm$ 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

QSAR Model 1	$\log(K_i) = 1.038\text{-}54.677 \cdot (R6u+) + 1.793 \cdot HGM - 23.814\,(R5e+)$ $+15.137 \cdot (HATS3u) - 14.396 \cdot (R1v+)$ $N = 29\ \ S = 0.375\ \ R^2 = 0.778\ \ F = 16.149\ \ p < 10^{-5}\ \ q^2_{LOO} = 0.681\ \ S_{CV\text{-}LOO} = 0.464$
QSAR Model 2	$\log(K_i) = 0.001\text{-}0.371 \cdot {}^1\Omega R6u+ + 0.604 \cdot {}^2\Omega HGM -$ $0.307 \cdot {}^3\Omega R5e+ + 0.392 \cdot {}^4\Omega HATS3u - 0.280 \cdot 5\Omega R1v+$ $N = 28\ \ S = 0.331\ \ R^2 = 0.831\ \ F = 21.658\ \ p < 10^{-5}\ \ q^2_{LOO} = 0.793\ \ S_{CV\text{-}LOO} = 0.362$
QSAR Model 3	$\text{-}\log(K_i) = 0.22 \pm 0.07 \cdot {}^1\Omega RDF075p - 0.11 \cdot {}^2\Omega RDF135m -$ $0.10 \cdot {}^3\Omega RDF130v + 0.18 \cdot {}^4\Omega RDF100m - 0.15 \cdot {}^5\Omega RDF140m$ $N = 28\ \ S = 0.299\ \ R^2 = 0.849\ \ F = 24.812\ \ p < 10^{-5}\ \ q^2\,(LOO) = 0.786\ \ S_{LOO} = 0.368$ $q^2\,(LGO) = 0.749\ \ S_{LGO} = 0.407$
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	Rat
Target Location	Brain

Chemical Type	8-substituted xanthines
Mode of Action	Antagonist
QSAR Model 1	$pK_i (A_2) = 0.66 (\pm 0.14)\pi_8 + 0.48 (\pm 0.16)\pi_1 - 0.57 (\pm 0.25)7CH_3 + 4.34 (\pm 0.28)$ $n = 38; r = 0.71; s^2 = 0.52; F = 11.78.$
QSAR Model 2	$pK_i (A_2) = 0.57 (\pm 0.13) \pi_8 - 0.46 (\pm 0.17)\pi_1 - 3.42 (\pm 1.75)\sigma_{m8} + 4.37 (\pm 0.27)$ $n = 25; r = 0.81; s^2 = 0.40; F = 13.27.$
QSAR Model 3	$pK_i (A_2) = 0.49 (\pm 0.11)\pi_8 + 0.40 (\pm 0.14)\pi_1 - 4.88 (\pm 1.44)\sigma_{m8} + 4.42 (\pm 0.22)$ $n = 24; r = 0.87; s^2 = 0.25; F = 20.50.$
QSAR Model 4	$pK_i (A_2) = 0.64 (\pm 0.12)\pi_8 - 0.59 (\pm 0.22)7CH_3 + 0.48 (\pm 0.14)\pi_1 + 57.87 (\pm 19.60)S_8^N - 8.07 (\pm 4.21)$ $n = 38; r = 0.78; s^2 = 0.43; F = 13.02.$
QSAR Model 5	$pK_i (A_2) = 0.66 (\pm 0.11)\pi_8 - 0.47 (\pm 0.21)7CH_3 + 0.41 (\pm 0.13)\pi_1$ $\qquad + 61.57 (\pm 17.88)S_8^N + 45.39 (\pm 16.15)q_3 + 5.90 (\pm 3.19)$ $n = 38; r = 0.83; s^2 = 0.35; F = 14.17.$
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: $\pi_1, \pi_3, \pi_7, \pi_8$, 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: $\sigma_m, \sigma_p, \sigma^*$, 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