Target Name	Choline kinase
Target TTD ID	TTDR00805

Target Species	Human
Chemical Type	Biscationic dibromides
Mode of Action	Inhibitor
Activity Type	*ex* vivo inhibitory potency
QSAR Model 1	$p(IC_{50})_{ex\ vivo} = 4.08\ (\pm 0.08) - 0.84\ (\pm 0.17)\ \sigma_P$ n=5, r=0.943, s = 0.160, $F_{1,3}$ = 24.3 (significance at $\alpha < 0.025$)
QSAR Model 2	$p(IC_{50})_{ex\ vivo} = 4.22\ (\pm 0.30) + 0.19\ (\pm 2.15)\ \sigma_I$ $n = 5, r = 0.052, s = 0.482, F_{1,3} = 0.008$ (no significance)
QSAR Model 3	$p(IC_{50})_{ex\ vivo} = 3.92\ (\pm 0.00) - 0.92\ (\pm 0.06)\ \sigma_R$ $n = 5, r = 0.994, s = 0.052, F_{1,3} = 250\ (\alpha < 0.001)$
QSAR Model 4	$p(IC_{50})_{ex\ vivo} = 19.35\ (\pm 1.20) - 0.24\ (\pm 0.04)\ \delta CH_2N^+$ $n = 9, r = 0.978, F_{1,7} = 152, s = 0.097\ (\alpha < 0.001)$
QSAR Model 5	$p(IC_{50})_{ex\ vivo} = -3.82\ (\pm 1.74) - 13.4\ (\pm 2.81)$ (N^1 charge) $n = 10, r = -0.860, s = 0.220, F_{1,8} = 22.8, \alpha < 0.005$
QSAR Model 6	$p(IC_{50})_{ex\ vivo} = 5.33\ (\pm 0.17) + 0.02\ (\pm 0.00)\ E_{LUMO}$ $n = 10, r = 0.878, s = 0.207, F_{1,8} = 26.8, \alpha < 0.001$
QSAR Model 7	$p(IC_{50})_{ex\ vivo} = 8.83\ (\pm 0.85) + 0.01\ (\pm 0.00)\ E_{HOMO}$ $n = 10, r = 0.874, s = 0.210, F_{1,8} = 5.81, \alpha < 0.001$
Molecular	Access the following web-servers to compute molecular descriptors: **MoDel** and **e-dragon**

Descriptor	n is the number of compounds, r is the correlation coefficient, s is the standard deviation, and data within parentheses are standard errors of estimate. F is the F ratio between the variances of observed and calculated activities. σ_p is a descriptor of the overall electronic effect of R_4.
Reference	QSAR as a Tool for the Development of Potent Antiproliferative Agents by Inhibition of Choline Kinase. *Current Computer-Aided Drug Design*, 2007, 3, 297-313

Target Species	Human
Chemical Type	Biscationic dibromides
Mode of Action	Inhibitor
Activity Type	Antiproliferative activity against HT-29 Cell Line
QSAR Model 1	$p(IC_{50})_{HT\text{-}29} = 1.35 + 1.48\ (\pm 0.17)\ p(IC_{50})_{ex\ vivo} + 0.25\ (\pm 0.05)\ \sum f$ $n = 7, r = 0.987, s = 0.123, F_{2,4} = 75.4\ (\alpha < 0.001)$
QSAR Model 2	$p(IC_{50})_{HT\text{-}29} = 29.68 - 3.90\ (\pm 0.22)\ \delta^{*}CH_2N^{+} + 0.33\ (\pm 0.04)\ \sum f$ $n = 8, r = 0.996, s = 0.098, F_{2,5} = 311\ (\alpha < 0.001)$ Where $\delta^{*}CH_2N^{+} = 0.1 \times \delta CH_2N^{+}$
QSAR Model 3	$p(IC_{50})_{HT\text{-}29} = 7.32\ (\pm 0.21) + 4.42\times10^{-2}\ (\pm 4.39 \times 10^{-3})\ E_{LUMO}$ $n = 9, r = 0.967, s = 0.270, F_{1,7} = 102, \alpha < 0.001$
QSAR Model 4	$p(IC_{50})_{HT\text{-}29} = 5.36 - 0.96\ (\pm 0.10)\ \sigma_R^{+} + 0.35\ (\pm 0.04)\ \log P$ $n = 37, r = 0.907, s = 0.309, F_{2,34} = 78.6, \alpha < 0.001$
QSAR Model 5	$p(IC_{50})_{HT\text{-}29} = 5.36 - 1.31\ (\pm 0.13)\ \sigma_R + 0.35\ (\pm 0.04)\ \log P$ $n = 37, r = 0.910, s = 0.304, F_{2,34} = 81.7, \alpha < 0.001$
QSAR Model 6	$p(IC_{50})_{HT\text{-}29} = 5.58 - 0.91(\pm 0.31)\ (\log P)^2 + 0.34\ (\pm 0.16)\ \log P - 1.04(\pm 0.18)\ \sigma_R$ $n = 14, r = 0.934, s = 0.238, F_{3,10} = 23.8, \alpha < 0.001$
QSAR Model 7	$p(IC_{50})_{HT\text{-}29} = -2.66 - 0.03\ (\pm 0.00)\ MR_8^2 + 0.10\ (\pm 0.02)\ \log P + 1.05\ (\pm 0.31)\ \pi_{linker} - 3.73\ (\pm 0.71)\ \sigma_R$

	$n = 40, r = 0.920, s = 0.223, F_{4,35} = 47.9, \alpha < 0.001$
QSAR Model 8	$p(IC_{50})_{\text{HT-29 experimental}} = -0.35 + 1.05\ (\pm 0.08)\ p(IC_{50})_{\text{HT-29 theoretical}}$ $n = 40, r = 0.916, s = 0.220, F_{1,38} = 199, \alpha < 0.001$
Molecular Descriptor	Access the following web-servers to compute molecular descriptors: **MoDel** and **e-dragon** $\sum f$ is the sum of the Rekker hydrophobic fragmental constants for R_4. *n* is the number of compounds, *r* is the correlation coefficient, s is the standard deviation, and data within parentheses are standard errors of estimate. *F* is the *F* ratio between the variances of observed and calculated activities. σ_p is a descriptor of the overall electronic effect of R_4. *n* is the number of compounds, *r* is the correlation coefficient, s is the standard deviation, and data within parentheses are standard errors of estimate. *F* is the *F* ratio between the variances of observed and calculated activities. σ_p is a descriptor of the overall electronic effect of R_4. σ_P: Hammett constant for *para* substitution; σ_P^+: electronic parameter for resonance effect; σ_R: Hammett constant for *para* substitution; σ_R^+: electronic parameter defined for systems where a + charge is delocalised between the substituent and the reaction center *via* "through resonance". Linker= clog *P*R4 – clog *P*H; R: Electronic parameter for resonance effects. *n* is the number of compounds, *r* is the correlation coefficient, s is the standard deviation, and data within parentheses are standard errors of estimate. *F* is the *F* ratio between the variances of observed and calculated activities. σ_p is a descriptor of the overall electronic effect of R_4. σ_P: Hammett constant for *para* substitution; σ_P^+: electronic parameter for resonance effect; σ_R: Hammett constant for *para* substitution; σ_R^+: electronic parameter defined for systems where a + charge is delocalised between the substituent and the reaction center *via* "through resonance".
Reference	QSAR as a Tool for the Development of Potent Antiproliferative Agents by Inhibition of Choline Kinase. *Current Computer-Aided Drug Design*, 2007, 3, 297-313