

Target Name	Thymidine kinase
Target TTD ID	TTDR00500

Target Species	Herpes simplex virus (HSV)
Chemical Type	N <sup>2</sup> -phenylguanines
Mode of Action	Inhibitor
QSAR Model 1	$\log(1/C_{HSV1\ TK}) = 0.594(\pm 0.229)\pi_m - 0.414(\pm 0.200) \times \pi_p + 1.048(\pm 0.746)\sigma_m$ $+ 2.381(\pm 0.871)\mathfrak{R}_p + 5.077(\pm 0.244)$ <p><math>n = 34; r = 0.897; s = 0.399; F = 29.767; Q^2 = 0.741; s_{PRESS} = 0.459</math></p>
QSAR Model 2	$\log(1/C_{HSV2\ TK}) = 0.424(\pm 0.239)\pi_m - 0.496(\pm 0.221) \times \pi_p + 2.055(\pm 0.771)\sigma_n$ $+ 1.468(\pm 0.898)\mathfrak{R}_p + 5.238(\pm 0.253)$ <p><math>n = 33; r = 0.896; s = 0.410; F = 28.431; Q^2 = 0.736; s_{PRESS} = 0.474</math></p>
QSAR Model 3	$\log(1/C_{HSV1\ TK}) = 1.28(\pm 0.77)\pi_{3,4} - 2.22(\pm 1.17) \times \log(\beta \cdot 10^{\pi_{3,4}} + 1) + 3.20(\pm 0.86)$ $- 1.42(\pm 0.82)\mathcal{F} + 1.79(\pm 0.59) \times B_{1-3}$ <p><math>n = 30; r = 0.831; s = 0.530; F = 10.74; \pi_o = 0.53; \log\beta = -0.401</math></p>
QSAR Model 4	$\log(1/C_{HSV1\ TK}) = 0.486(\pm 0.160)\pi_m + 8.201 \times (\pm 3.000)F_2^{(e)} - 6.180(\pm 4.230)$ <p><math>n = 13; r = 0.953; s = 0.209; F_{(2,10)} = 49.057; Q^2 = 0.805; s_{PRESS} = 0.303</math></p>
QSAR Model 5	$\log(1/C_{HSV2\ TK}) = 0.292(\pm 0.096)\pi_m - 0.205 \times (\pm 0.030)F_1^{(n)} - 0.922(\pm 0.370)B_{1m}$ $+ 2.067(\pm 0.570)$ <p><math>n = 13; r = 0.988; s = 0.117; F_{(3,9)} = 120.946; Q^2 = 0.952; s_{PRESS} = 0.166</math></p>
Molecular	Access the following web-servers to compute molecular descriptors: <a href="#">MoDel</a> and <a href="#">e-dragon</a>

<b>Descriptor</b>	<p><math>C_{\text{HSV1 TK}}</math> and <math>C_{\text{HSV2 TK}}</math> are the PHG molar concentrations that provide 50% of HSV1 TK and HSV2 TK inhibition, respectively; <math>\pi</math> is the Hansch lipophilic substituent constant; <math>\sigma</math> is the Hammett electronic substituent constant; <math>\mathcal{R}</math> is the Swain-Lupton resonance parameter; subscripts m and p stand for meta and para positions of the phenyl ring of the PHG derivative molecule, respectively; n is the number of compounds included in the models; r is the correlation coefficient; s is the overall standard deviation; F is the Fischer variance ratio; Q is the cross validation correlation coefficient; and <math>S_{\text{PRESS}}</math> is the cross validation standard deviation. The numbers in parentheses are the 95% confidence interval of the respective regression coefficients; <math>\pi_{3,4}</math> is the sum of the <math>\pi</math> constant of the substituents attached to meta and para positions of the phenyl ring of PHG derivatives, <math>\beta</math> is the bilinear constant, <math>B_{1-3}</math> is the Sterimol parameter <math>B_1</math>, which is a measure of the width of the substituent, on the meta position, <math>\mathfrak{F}</math> is the Swain-Lupton field substituent parameter, and <math>\pi_o</math> is the optimum <math>\pi_{3,4}</math> value. The atomic frontier electron density <math>F_n^{(e)}</math> is a property that denotes the electron density in the HOMO of a given atom in a molecule.</p>
<b>Reference</b>	<p>QSAR and molecular graphics analysis of N<sup>2</sup>-phenylguanines as inhibitors of herpes simplex virus thymidine kinases. <i>Journal of Molecular Graphics and Modelling</i> 18, 33–41, 2000</p>