Target Name	Peptide deformylase
Target TTD ID	TTDR00267

Target Species	Mammal
Chemical Type	Hydroxamic acid derivatives
Mode of Action	Inhibitor
QSAR Model 1	$-\log IC_{50\ PDF\text{-}Fe} = 0.075(\pm 0.022)\ MR^{R1} + 0.089(\pm 0.022)\ MR^{R2} - 3.424(\pm 0.828)$ $n = 19 \quad r = 0.81 \quad s = 0.46 \quad F = 15.6$
QSAR Model 2	$-\log IC_{50\ PDF\text{-}Fe} = 0.056(\pm 0.020)\ MR^{R1} + 0.985(\pm 0.198)\ Fr^{R2} - 3.386(\pm 0.727)$ $n = 19 \quad r = 0.86 \quad s = 0.41 \quad F = 21.7$
QSAR Model 3	$-\log MIC_{E.\ coli\ DC2} = 1.024(\pm 0.373) Fr^{R2} - 0.964(\pm 0.198) In - 2.810(\pm 0.950)$ $n = 17 \quad r = 0.84 \quad s = 0.37 \quad F = 17.0$
QSAR Model 4	$-\log MIC_{M.\ cata\ .RA21} = 0.075(\pm 0.022)\ MR^{R1} - 0.812(\pm 0.360)\ In - 2.188(\pm 0.891)$ $n = 10 \quad r = 0.85 \quad s = 0.34 \quad F = 9.4$
QSAR Model 5	$-\log IC_{50NEP} = 0.624(\pm 0.378)\ Fr^{R1} - 2.011(\pm 1.009)$ $n = 4 \quad r = 0.76 \quad s = 0.52 \quad F = 2.7$
QSAR Model 6	$-\log IC_{50COL-1} = 0.164(\pm 0.041)\ Fr^{R1} + 0.681(\pm 0.110)$ $n = 4 \quad r = 0.94 \quad s = 0.05 \quad F = 15.8$
QSAR Model 7	$-\log IC_{50HME} = -0.038(\pm 0.022)\ Fr^{R1} + 1.995(\pm 0.064)$ $n = 3 \quad r = 0.87 \quad s = 0.02 \quad F = 3.0$

QSAR Model 8	$-\log Ic_{50COL-3} = 3.750(\pm 0.557) f^{R1} + 1.270(\pm 0.78)$ $n = 3 \quad r = 0.99 \quad s = 0.11 \quad F = 45.0$
QSAR Model 9	$-\log IC_{50MAT} = -2.571\ (\pm 0.907) f^{R1} + 0.312(\pm 0.127)$ $n = 3 \quad r = 0.94 \quad s = 0.18 \quad F = 8.03$
Molecular Descriptor	Access the following web-servers to compute molecular descriptors: **MoDel** and **e-dragon** *n* is the number of compounds; r, the correlation coefficient; s, the standard deviation; F, the F-ratio; Fr, hydrophobic parameter; MR, molar refractivity; f, the electronic parameter.
Reference	2D-QSAR in Hydroxamic Acid Derivatives as Peptide Deformylase Inhibitors and Antibacterial Agents. *Bioorganic & Medicinal Chemistry* 10 (2002) 3713–3716