

Target Name	CCR5 receptor
Target TTD ID	TTDS00326

Target Species	Human
Chemical Type	Substituted 1-(3,3-diphenylpropyl)-piperidinyl amides
Mode of Action	Binder
QSAR Model 1	$\text{pIC}_{50} = -0.863(\pm 0.820)\sigma_{R2_m} + 1.230(\pm 0.355)\sigma_{R2_p} + 0.737(\pm 0.614)\sigma_{R3_p} + 1.179(\pm 0.469)\text{mIR}_{3_p} - 0.356(\pm 0.142)\text{mIR}_{3_p}^2 + 0.791(\pm 0.371)I_{\text{NHCH}_2} - 1.279(\pm 0.670)I_{\text{BRANCH}} - 1.206(\pm 0.666)I_{R4_AS} + 2.986(\pm 0.185)$ <p> $n = 79, R_a^2 = 0.719, R^2 = 0.747, R = 0.865, F = 25.9(\text{df}8, 70), s = 0.455, \text{SDEP} = 0.487, S_{\text{PRESS}} = 0.517, Q^2 = 0.674, \text{PRESS} = 18.706$ </p>
QSAR Model 2	$\text{pIC}_{50} = 3.709(\pm 2.315)\log P_{\text{calcd}} - 0.332(\pm 0.204) \times [\log P_{\text{calcd}}]^2 - 1.752(\pm 1.389)\sigma_{R2_m}^2 + 1.238(\pm 0.331)\sigma_{R2_p} + 0.813(\pm 0.573)\sigma_{R3_p} + 1.391(\pm 0.483)\text{mIR}_{3_p} - 0.415(\pm 0.144)\text{mIR}_{3_p}^2 + 0.764(\pm 0.349)I_{\text{NHCH}_2} - 1.346(\pm 0.625)I_{\text{BRANCH}} - 1.229(\pm 0.623)I_{R4_AS} - 7.287(\pm 6.615)$ <p> $n = 79, R_a^2 = 0.757, R^2 = 0.788, R = 0.888, F = 25.3(\text{df}10, 68), s = 0.423, \text{SDEP} = 0.468, S_{\text{PRESS}} = 0.505, Q^2 = 0.698, \text{PRESS} = 17.344$ </p>
QSAR Model 3	$\text{pIC}_{50} = 4.794(\pm 2.367)\log P_{\text{calcd}} - 0.430(\pm 0.210) \times [\log P_{\text{calcd}}]^2 + 1.013(\pm 0.361)\sigma_{R2_p} + 0.579(\pm 0.397)L_{R2_p} - 0.050(\pm 0.046)L_{R2_p}^2 + 0.840(\pm 0.547)\sigma_{R3_p} + 1.416(\pm 0.459)\text{mIR}_{3_p} - 0.423(\pm 0.138)\text{mIR}_{3_p}^2 + 0.878(\pm 0.329)I_{\text{NHCH}_2} - 1.058(\pm 0.609)I_{\text{BRANCH}} - 1.250(\pm 0.595)I_{R4_AS} - 11.609(\pm 6.770)$ <p> $n = 79, R_a^2 = 0.779, R^2 = 0.810, R = 0.900, F = 25.9(\text{df}11, 67), s = 0.403, \text{SDEP} = 0.462, S_{\text{PRESS}} = 0.501, Q^2 = 0.706, \text{PRESS} = 16.845$ </p>

<p>QSAR Model 4</p>	$\text{pIC}_{50} = -2.008\sigma_{R2_m}^2 + 0.461\sigma_{R2_p} + 0.786\sigma_{R2_p}^2 - 0.201\pi_{R2_p} - 0.071\text{mr}_{R3_p}^2 + 0.890\sigma_{R3_p} + 0.163B5_{R3_p} + 0.032B5_{R3_p}^2 - 0.007L_{R3_p}^2 + 0.666I_{\text{NHCH}_2} - 1.237I_{\text{BRANCH}} - 0.504I_{R2_2S} - 1.448I_{R4_4S} + 3.006$ <p>$n = 79, R_a^2 = 0.757, R^2 = 0.797, R = 0.893, F = 98.5, \text{SDEP} = 0.437, S_{\text{PRESS}} = 0.448, Q^2 = 0.737, \text{PRESS} = 15.068$</p>
<p>QSAR Model 5</p>	$\text{pIC}_{50} = -0.156(\pm 0.086)fs1 + 0.158(\pm 0.086)fs2 + 0.141(\pm 0.086)fs3 + 0.559(\pm 0.086)fs4 - 0.157(\pm 0.086)fs5 - 0.154(\pm 0.086)fs6 + 0.170(\pm 0.086)fs8 - 0.157(\pm 0.086)fs9 + 0.234(\pm 0.086)fs10 - 0.207(\pm 0.086)fs12 + 0.132(\pm 0.086)fs14 - 0.121(\pm 0.086)fs18 + 3.651(\pm 0.086)$ <p>$n = 79, R_a^2 = 0.804, R^2 = 0.834, R = 0.913, F = 27.6(\text{df} 12, 66), s = 0.380, \text{SDEP} = 0.408, S_{\text{PRESS}} = 0.447, Q^2 = 0.770, \text{PRESS} = 13.174$</p>
<p>Molecular Descriptor</p>	<p>Access the following web-servers to compute molecular descriptors: MoDel and e-dragon</p> <p>I_{CH_2}: Indicator variable having value 1 if methylene group is present at X position, value 0 otherwise.</p> <p>I_{NH}: Indicator variable having value 1 if NH group is present at X position, value 0 otherwise</p> <p>I_{NHCH_2}: Indicator variable having value 1 if NH-CH₂ group is present at X position, value 0 otherwise</p> <p>I_{BRANCH}: Indicator variable having value 1 if branching is present at X position, value 0 otherwise</p> <p>I_{ETHYL}: Indicator variable having value 1 if ethyl group is present at R¹-position, value 0 otherwise</p> <p>I_{ALLYL}: Indicator variable having value 1 if allyl group is present at R¹-position, value 0 otherwise</p> <p>$I_{\text{C-PRO}}$: Indicator variable having value 1 if c-propyl group is present at R¹-position, value 0 otherwise</p> <p>I_{R2_2S}: Indicator variable having value 1 if any substituent is present at 2nd position at R², 0 otherwise</p> <p>I_{R4_3S}: Indicator variable having value 1 if any substituent is present at 3rd position at R⁴, 0 otherwise</p> <p>I_{R4_4S}: Indicator variable having value 1 if any substituent is present at 4th position at R⁴, 0 otherwise</p> <p>Lipophilicity (π), electronic (Hammett σ), and steric (molar refractivity mr and STERIMOL L, B1, and B5). Hydrophobic whole molecular descriptor (partition coefficient $\log P_{\text{calcd}}$). Molar refractivity of R³ substituents (mr_{R3_p}). The STERIMOL parameter (L) of the para-substituents at R3-position. Lipophilic substituent constant (π_{R2_p}) of the para-substituents at the R²-position. Molar refractivity (mr), length (L) and width (B5) of para-substituents at R³. Molar refractivity (mr), length (L) and width (B5) of para-substituents at R². Lipophilicity (π), electronic (Hammett σ) parameters, and width (B5) of para-substituents at R². The</p>

	electronic (Hammett σ) parameters of the para-substituents at R ³ . NHCH ₂ substituents at X, para-substituents at R ⁴ -position.
Reference	Comparative QSAR modeling of CCR5 receptor binding affinity of substituted 1-(3,3-diphenylpropyl)-piperidinyl amides and ureas. <i>Bioorganic & Medicinal Chemistry Letters</i> 16 (2006) 4467–4474

Target Species	Human
Chemical Type	Substituted 1-(3,3-diphenylpropyl)-piperidinyl ureas
Mode of Action	Binder
QSAR Model 1	$\text{pIC}_{50} = -0.863(\pm 0.820)\sigma_{\text{R}2\text{-m}} + 1.230(\pm 0.355)\sigma_{\text{R}2\text{-p}} + 0.737(\pm 0.614)\sigma_{\text{R}3\text{-p}} + 1.179(\pm 0.469)\text{mI}_{\text{R}3\text{-p}}$ $- 0.356(\pm 0.142)\text{mI}_{\text{R}3\text{-p}}^2 + 0.791(\pm 0.371)I_{\text{NHCH}_2} - 1.279(\pm 0.670)I_{\text{BRANCH}} - 1.206(\pm 0.666)I_{\text{R}4\text{-AS}}$ $+ 2.986(\pm 0.185)$ <p>$n = 79$, $R_a^2 = 0.719$, $R^2 = 0.747$, $R = 0.865$, $F = 25.9(\text{df}8, 70)$, $s = 0.455$, SDEP = 0.487, $S_{\text{PRESS}} = 0.517$, $Q^2 = 0.674$, PRESS = 18.706</p>
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