Target Name	PPAR-γ
Target TTD ID	TTDS00338

Target Species	Human
Chemical Type	23 compounds of PPAR-γ agonist
Mode of Action	Agonist
QSAR Model 1	$-\log EC_{50} = 0.3656(\pm 0.0890) - 0.0004(\pm 0.0002)HF \ -0.0144(\pm 0.0004)DIP\text{-}X + 0.0006(\pm 0.0001)Jurs\_TASA$ $N = 18,\ q^2 = 0.530,\ r^2 = 0.718,\ r = 0.848,\ s = 0.036,\ \ F\text{-test} = 11.908$
QSAR Model 2	$-\log EC_{50} = 0.4758(\pm 0.0752) - 0.0133(\pm 0.0045)DIP\text{-}X + 0.0091(\pm 0.0051)DIP\text{-}Z + 0.0005(\pm 0.0001)Jurs\_TASA$ $N = 18,\ q^2 = 0.551,\ r^2 = 0.737,\ r = 0.858,\ s = 0.035,\ \ F\text{-test} = 13.065$
QSAR Model 3	$-\log EC_{50} = 0.4098(\pm 0.108) + 0.0137(\pm 0.009) \times DIP\text{-}Y + 0.0002(\pm 0.0000) \times Jurs\_RNCS + 0.0029(\pm 0.0007) \times MR$ $N = 18,\ q^2 = 0.442,\ r^2 = 0.676,\ r = 0.823,\ s = 0.039,\ \ F\text{-test} = 9.762$
QSAR Model 4	$-\log EC_{50} = 0.9879(\pm 0.0642) - 0.0026(\pm 0.0007) \times Jurs\_WNSA3 - 2.7977(\pm 0.6845) \times Jurs\_RNCG$ $N = 18,\ q^2 = 0.462,\ r^2 = 0.649,\ r = 0.806,\ s = 0.039,\ F\text{-test} = 13.906$
QSAR Model 5	$-\log EC_{50} = 0.8659(\pm 0.1041) + 0.0295(\pm 0.0109) \times HBA \ -2.0895(\pm 0.7906)Jurs\_RNCG$ $N = 18,\ q^2 = 0.401,\ r^2 = 0.570,\ r = 0.755,\ s = 0.043,\ \ F\text{-test} = 9.937$
Molecular Descriptor	Access the following web-servers to compute molecular descriptors: **MoDel** and **e-dragon** N is number of compounds, q^2 is leave one out cross-validated r^2, r^2 is coefficient of determination, r is correlation coefficient, s is standard error and F-test is F-value for Fischer's test of significance. The equations contain DIP-Y, MR. The dipole moment (DIP) descriptor is a 3D electronic descriptor that indicates the strength and orientation behavior of a molecule in an electrostatic field. The molar refractivity (MR) is the molar volume corrected by the refractive index. It represents size and polarizability of a fragment or molecule. Molar refractivity is given by

	$$MR = \left(\frac{(n^2-1)}{(n^2+2)}\right)\frac{(MW)}{d}$$ where n is the refractive index, MW is the molecular weight, and d is the compound density. Heat of formation (Hf) represents the chemical stability and reactivity of the molecules. Jurs_RNCS is calculated as relative negative charge surface area mapped over the solvent-accessible surface area of individual atoms. These surface area descriptors are important as they may indicate the factors influencing the binding of a ligand to its target.
Reference	QSAR analysis of PPAR-g agonists as anti-diabetic agents. *European Journal of Medicinal Chemistry* 43 (2008) 73e80

Target Species	Human
Target Location	Liver and peripheral tissues
Chemical Type	Thiazolidine-2,4-dione (TZD)
Mode of Action	Agonist
QSAR Model 1	$-\log EC_{50} = 0.3656(\pm 0.0890) - 0.0004(\pm 0.0002)HF \ -0.0144(\pm 0.0004)DIP\text{-}X + 0.0006(\pm 0.0001)Jurs\_TASA$ $N = 18,\ q^2 = 0.530,\ r^2 = 0.718,\ r = 0.848,\ s = 0.036,\ F\text{-test} = 11.908$
QSAR Model 2	$-\log EC_{50} = 0.4758(\pm 0.0752) - 0.0133(\pm 0.0045)DIP\text{-}X + 0.0091(\pm 0.0051)DIP\text{-}Z + 0.0005(\pm 0.0001)Jurs\_TASA$ $N = 18,\ q^2 = 0.551,\ r^2 = 0.737,\ r = 0.858,\ s = 0.035,\ F\text{-test} = 13.065$
QSAR Model 3	$-\log EC_{50} = 0.4098(\pm 0.108) + 0.0137(\pm 0.009) \times DIP\text{-}Y + 0.0002(\pm 0.0000) \times Jurs\_RNCS + 0.0029(\pm 0.0007) \times MR$ $N = 18,\ q^2 = 0.442,\ r^2 = 0.676,\ r = 0.823,\ s = 0.039,\ F\text{-test} = 9.762$

QSAR Model 4	$-\log EC_{50} = 0.9879(\pm 0.0642) - 0.0026(\pm 0.0007) \times \text{Jurs\_WNSA3} - 2.7977(\pm 0.6845) \times \text{Jurs\_RNCG}$ $N = 18,\ q^2 = 0.462,\ r^2 = 0.649,\ r = 0.806,\ s = 0.039,\ F\text{-test} = 13.906$
QSAR Model 5	$-\log EC_{50} = 0.8659(\pm 0.1041) + 0.0295(\pm 0.0109) \times \text{HBA} - 2.0895(\pm 0.7906) \text{Jurs\_RNCG}$ $N = 18,\ q^2 = 0.401,\ r^2 = 0.570,\ r = 0.755,\ s = 0.043,\ F\text{-test} = 9.937$
Molecular Descriptor	Access the following web-servers to compute molecular descriptors: **MoDel** and **e-dragon** N is the number of compounds; q^2, leave one out cross-validated r^2; r^2, coefficient of determination; r, correlation coefficient; s, standard error; F-test, F value for Fischer's test of significance; HF, heat of formation and Jurs_TASA, total hydrophobic surface area. The equations contain DIP-X, DIP-Y, DIP-Z, MR, HF and various Jurs descriptors. The dipole moment (DIP) descriptor is a 3D electronic descriptor that indicates the strength and orientation behavior of a molecule in an electrostatic field. The molar refractivity (MR) is the molar volume corrected by the refractive index. It represents size and polarizability of a fragment or molecule. Molar refractivity is given by: $$MR = \left(\frac{(n^2-1)}{(n^2+2)}\right)\frac{(MW)}{d}$$ where n is the refractive index, MW is the molecular weight, and d is the compound density. Heat of formation (H_f) represents the chemical stability and reactivity of the molecules. Jurs_RNCS is calculated as relative negative charge surface area mapped over the solvent-accessible surface area of individual atoms, Jurs_TASA is calculated as total hydrophobic surface area while Jurs_RNCG is relative negative charge i.e. most negative charge/total negative charge. These surface area descriptors are important as they may indicate the factors influencing the binding of a ligand to its target.
Reference	QSAR analysis of PPAR- γ agonists as anti-diabetic agents. *European Journal of Medicinal Chemistry* 43 (2008) 73-80

Target Species	Human
Target	Liver and peripheral tissues

Location	
Chemical Type	Glitazones
Mode of Action	Agonist
QSAR Model 1	$-\log EC_{50} = 0.3656(\pm 0.0890) - 0.0004(\pm 0.0002)\text{HF} \ -0.0144(\pm 0.0004)\text{DIP-X} + 0.0006(\pm 0.0001)\text{Jurs\_TASA}$ $N = 18,\ q^2 = 0.530,\ r^2 = 0.718,\ r = 0.848,\ s = 0.036,\ F\text{-test} = 11.908$
QSAR Model 2	$-\log EC_{50} = 0.4758(\pm 0.0752) - 0.0133(\pm 0.0045)\text{DIP-X} + 0.0091(\pm 0.0051)\text{DIP-Z} + 0.0005(\pm 0.0001)\text{Jurs\_TASA}$ $N = 18,\ q^2 = 0.551,\ r^2 = 0.737,\ r = 0.858,\ s = 0.035,\ F\text{-test} = 13.065$
QSAR Model 3	$-\log EC_{50} = 0.4098(\pm 0.108) + 0.0137(\pm 0.009) \times \text{DIP-Y} + 0.0002(\pm 0.0000) \times \text{Jurs\_RNCS} + 0.0029(\pm 0.0007) \times \text{MR}$ $N = 18,\ q^2 = 0.442,\ r^2 = 0.676,\ r = 0.823,\ s = 0.039,\ F\text{-test} = 9.762$
QSAR Model 4	$-\log EC_{50} = 0.9879(\pm 0.0642) - 0.0026(\pm 0.0007) \times \text{Jurs\_WNSA3} - 2.7977(\pm 0.6845) \times \text{Jurs\_RNCG}$ $N = 18,\ q^2 = 0.462,\ r^2 = 0.649,\ r = 0.806,\ s = 0.039,\ F\text{-test} = 13.906$
QSAR Model 5	$-\log EC_{50} = 0.8659(\pm 0.1041) + 0.0295(\pm 0.0109) \times \text{HBA} \ -2.0895(\pm 0.7906) \text{Jurs\_RNCG}$ $N = 18,\ q^2 = 0.401,\ r^2 = 0.570,\ r = 0.755,\ s = 0.043,\ F\text{-test} = 9.937$
Molecular Descriptor	Access the following web-servers to compute molecular descriptors: **MoDel** and **e-dragon** N is the number of compounds; q^2, leave one out cross-validated r^2; r^2, coefficient of determination; r, correlation coefficient; s, standard error; F-test, F value for Fischer's test of significance; HF, heat of formation and Jurs_TASA, total hydrophobic surface area. The equations contain DIP-X, DIP-Y, DIP-Z, MR, HF and various Jurs descriptors. The dipole moment (DIP) descriptor is a 3D electronic descriptor that indicates the strength and orientation behavior of a molecule in an electrostatic field. The molar refractivity (MR) is the molar volume

	corrected by the refractive index. It represents size and polarizability of a fragment or molecule. Molar refractivity is given by: $$MR = (\frac{(n^2-1)}{(n^2+2)})\frac{(MW)}{d}$$ where n is the refractive index, MW is the molecular weight, and d is the compound density. Heat of formation (H_f) represents the chemical stability and reactivity of the molecules. Jurs_RNCS is calculated as relative negative charge surface area mapped over the solvent-accessible surface area of individual atoms, Jurs_TASA is calculated as total hydrophobic surface area while Jurs_RNCG is relative negative charge i.e. most negative charge/total negative charge. These surface area descriptors are important as they may indicate the factors influencing the binding of a ligand to its target.
Reference	QSAR analysis of PPAR- γ agonists as anti-diabetic agents. *European Journal of Medicinal Chemistry* 43 (2008) 73-80

Target Species	Human
Chemical Type	Indole-based derivatives
Mode of Action	Agonist
QSAR Model 1	$\mathrm{p}EC_{50} = 0.61(\pm 0.05)\ \mathrm{p}Ki + 0.010\ (\pm 0.002)\ MW - 0.006(\pm 0.001)\ \mathrm{npSASA} + 1.19\ (\pm 0.24)\ E_{\mathrm{LUMO}} + 1.99(\pm 0.24)$ $n = 75,\ r^2 = 0.84,\ s = 0.45,\ F = 97.57$
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; x, hydrophobic parameter; MW, molecular weight and npSASA, non-polar solvent accessible surface area; Lipophilicity (logP and logD7.4), molecular weight (MW), hydrogen bond acceptors and donor sites (HBA and HBD), rotatable bonds (RB), topological polar surface area (TPSA); number of rings (nRings); The number of halogens (nHal); The number of oxygen (nO), the number of aromatic rings (nArC6) and the number of hydrogen bond acceptor sites (HA). Flexibility (nRB), Solvent accessible

	surface area (SASA) and non polar SASA (SASA-np).
Reference	A QSAR Study on Indole-Based PPAR-γ Agonists in Respect to Receptor Binding and Gene Transactivation Data. *QSAR Comb. Sci*. 28, 2009, No. 8, 802 – 805

Target Species	Human
Chemical Type	2-Alkoxydihydrocinnamates
Mode of Action	PPAR-α/γ dual agonist
QSAR Model 1	pEC_{50}= [-0.811(± 0.353)] +σ_p [1.637(± 1.064)] +I_2 [0.949(± 0.412)] n=12, r=0.896, r^2 =0.803, SEE=0.290, F=18.338, Q^2= 0.705, SPRESS=0.354, SDEP=0.307
QSAR Model 2	pEC_{50}= [-0.363(± 0.221)] +D1 [-0.349 (± 0.137)] +D3 [- 0.160(± 0.138)] n=13, r=0.914, r^2=0.835, SEE=0.272, F=25.336, Q^2= 0.755, SPRESS=0.331, SDEP=0.291
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; SEE, standard error of estimation; Q^2, cross-validated squared correlation coefficient; SPRESS, predictive residual sum of square; SDEP, standard error of predictivity; F, F-ratio; D1, dipole moment of X-axis and D3, dipole moment of Z-axis; σ_p, Harmett's constant. structural indicator variable I_1 expresses 1 for presence of two carbon spacer between biphenyloxy and the central ring, I2 expresses 1 for presence of methyl and ethyl group at R2 and 0 for its absence. hydrophobic (π), steric (molar refractivity or MR) hydrogen acceptor (HA), hydrogen Donor (HD) and electronic (field effect or $\mathcal{F}$, resonance effect or $\mathcal{R}$ and Hammett's constant or σ_p); Logarithmic partition coefficient (LogP); Connolly accessible area (CAA), Connolly molecular area (CMA), Connolly solvent excluded volume (CSEV), exact mass (EM), molecular weight (MW), principal moment of inertia X-axis (PMIX); Electronic energy (EE), highest occupied molecular orbital energy (HOMO), lowest unoccupied molecular orbital energy (LUMO), dipole moment of X-axis (D1),

	dipole moment of Y-axis (D2), dipole moment of Z-axis (D3), resultant dipole (D4), repulsion energy (RE), VDW-1, 4-energy (E14), Non-1, 4-VDW energy (EV) and total energy (TE)
Reference	Quantitative Structure Activity Analysis of 2-Alkoxydihydrocinnamates as PPAR α/γ Dual Agonist. *Medicinal Chemistry*, 2008, *4*, 273-277