Original Article

Designing of Thiazolidin-4-one Pharmacophore using QSAR Studies for Anti-HIV Activity

Trupti Sameer Chitre*, Shital Manoj Patil, Anagha Govindrao Sujalegaonkar, Kalyani Dhirendra Asgaonkar

Department of Pharmaceutical Chemistry, All India Shri Shivaji Memorial Society's College of Pharmacy, Kennedy Road, Near R.T.O., Pune, Maharashtra, INDIA.

ABSTRACT

Background and Aim: In an effort of drug development in the area of HIV, present work deals with development of 2D and 3D QSAR of thiazolidinone derivatives against HIV-RT activity as a powerful method for elucidation the relationships between structure and activity. **Materials and Methods:** 2D QSAR and 3D QSAR were performed using MLR and SA kNN method respectively. Models which had higher predictability were generated as indicated from their statistical parameters. **Results and Discussion:** Best models generated showed correlation coefficient r^2 = 0.9256 and q^2 = 0.8623 for 2D QSAR and q^2 = 0.8444 for 3D QSAR. The models indicated the requirement of electro topological, electrostatic and steric descriptors which would significantly contribute to HIV-RT inhibitory activity. Further a few compounds were designed using the outcome of QSAR studies.

Key words: Non-nucleoside Reverse Transcriptase, Human Immunodeficiency Virus-1, QSAR, Thiazolidin-4-one, Combilib.

INTRODUCTION

Development of newer molecules against HIV drug resistant strains is the need of the hour due to rapid emergence of drug resistance strains which are limiting the performance of existing drugs in treatment of HIV.[1] Non-nucleoside reverse transcriptase inhibitors (NNRTIs) have played a significant role in management of HIV infection especially with excellent potency of second generation NNRTIs against wild and various mutant strains of HIV-1. They also provide diversity in chemical structures providing a wider opportunity for drug development.[2-4] Thiazolidin-4-one derivatives have gained importance for drug development because of its wide array of biological activities, including Anti tubercular and Anti-HIV.[5] Several thiazolidin-4-one derivatives have been studied and have shown promising activity at micromolar concentrations against reverse transcriptase with less cytotoxicity.[1,6-9] Quantitative structure activity relationship (QSAR) is an important chemometric method of analysis for rational drug design of new anti-HIV drugs. It reveals the relationship between chemical structures and their biological activity. In continuation of our efforts in computational studies QSAR studies were carried out to predict the desired properties of compounds for a series of thiazolidinone derivatives.[10,11]

In the present study we have performed 2D QSAR with multiple linear regression (MLR) and 3D QSAR using simulated annealing k Nearest Neighbor (SA kNN) method.[12-16] Compounds were designed using Combilib tool and were screened with Lipinski filter to study their drug like pharmacokinetics.

RESULTS AND DISCUSSION

2D QSAR study

The results of unicolumn statistics indicated that the test set molecules were within the activity range of the training set. The mean

Submission Date: 09-10-2019;
Revision Date: 27-02-2020;
Accepted Date: 03-02-2021

DOI: 10.5530/ijper.55.2.97

Correspondence:
Dr. Trupti S Chitre
Department of Pharmaceutical Chemistry, All India Shri Shivaji Memorial Society's College of Pharmacy, Kennedy Road, Near R.T.O., Pune-411001, Maharashtra, INDIA.
Phone: +91 9860993381
E-mail: chitretrupti@rediffmail.com

www.ijper.org

and standard deviation values were compared for training and test sets. Mean in test set was found to be higher than mean in training set where as standard deviation was higher in training set (Table 1). The mean values indicated presence of relatively more active molecules in test set as compared to inactive ones in training set.

Various 2D QSAR models were developed using SA-MLR method and the best 2D QSAR model had four contributing descriptors including constant. The equation obtained is as given below (Equation 1):

pEC_{50} = - 0.139 T_N_N_7- 0.037 Polar SurfaceArea Excluding P and S + 0.759 SsssNE-index + 0.395T_N_O_4 (Equation 1)

The values obtained for *r2* and q^2 were 0.925 and 0.862 respectively, predicted r^2 was 0.758 and r^2m of 0.725. A brief idea about the physicochemical parameters influencing biological activity was obtained through the generated descriptors. The 2D descriptor such as electro topological state indices for number of Nitrogen atoms connected with three single bonds (SsssNE-index) contributed positively and T_N_O_4 the count of number of nitrogen atoms (single double or triple bonded) separated from any oxygen atom (single or double bonded) by 4 bond distance in a molecule contributed positively towards activity. The negatively contributing descriptors include Polar Surface Area (Excluding P and S) signified reduced and total polar surface area excluding sulphur. Similarly another negatively contributing descriptor, T_N_N_7, suggested that the separation of nitrogen atom (single double or triple bonded) by 7 bonds distance with another nitrogen atom may not show good activity (Table 2).

3D QSAR study

3D QSAR models were generated using the SA-kNN method and the best model resulted in q^2 of 0.844 and pred r^2 of 0.900, r^2m of 0.798. The 3D data points generated were, E_933 (-0.354,-0.325), E_555 (-10.000,-10.000) and S_774 (-0.326,-0.311) (Figure 1). The generated negative values in electrostatic as well as steric parameters indicated the requirement of more electronegative substituent and less sterically groups as the preferred substituent for increase in activity (Table 2).

Combilib: More than 120 molecules were generated using Combilib tool of V-Life software that follows the Lipinski's rule. Only 30 most active molecules on the basis of their predicted activity from QSAR and Lipinski screen score (Table 3).

Table 1: Uni-Column statistics of compounds.

	Column name	Average (mean)	Max*	Min*	Std Dev	Sum
Training set	pEC_{50}	-1.03706	1.6989	-2.0617	0.6927	-11.6145
Test set	pEC_{50}	-0.17898	1	-1.2391	0.6367	-14.4307

Table 2: Results of 2D and 3D QSAR for thiazolidinone derivatives.

Sr. No.	Statistical Parameter	2D QSAR SA-MLR	3D QSAR SA kNN
1	r^2	0.9256	-
2	q^2	0.8623	0.8444
3	Pred_r^2	0.7585	0.9001
4	r^2 se	0.3615	-
5	F-Test	52.8947	-
6.	q^2 se	0.4919	0.4350
7.	Pred_r^2se	0.4919	0.4077
8.	best _ ran r^2	0.42388	-
9.	best_ ranq^2	-0.05907	-
10.	Z score_ ran r^2	6.22534	-
11.	Z score _ranq^2	6.02746	-
12.	N	25	25
13	K Nearest Neighbour	-	2
14	Contributing Descriptors	Positively Contributing SsssNE-index T_N_O_4 Negatively Contributing T_N_N_7 Polar Surface Area Excluding P and S	Electrostatics parameter E_933(-0.3549,-0.3252) E_555(-10.0000,-10.0000) steric parameter S_774(-0.3261,-0.3115)

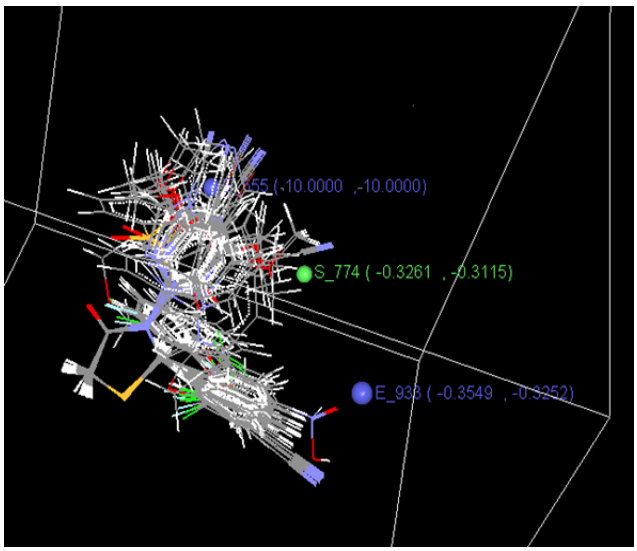
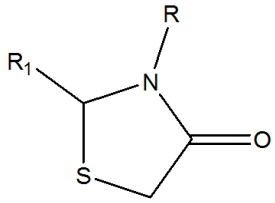


Figure 1: Molecular rectangular grid around the superimposed molecular units of thiazolidinone series of compounds.



METHODS AND MATERIALS

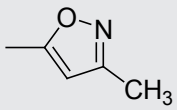
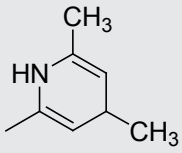
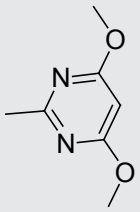
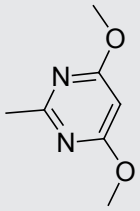
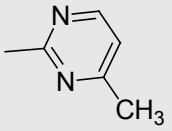
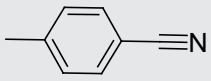
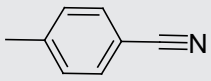
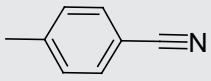
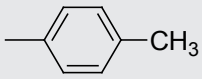
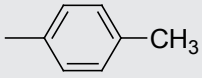
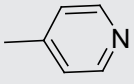
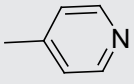
Database and biological activity: Considering the structural and biological activity diversity a data set of thirty thiazolidin-4-one derivatives having the same parent skeleton and reported as HIV-1 NNRTIs was selected for the QSAR study.[17]

The QSAR studies were performed using V-Life Molecular Design Suite (MDS), version 4.4. The reported EC_{50} values were converted into pEC_{50} [pEC_{50}= -log (EC_{50})]. (Table 4).

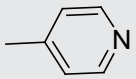
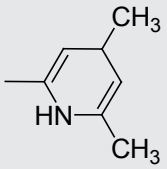
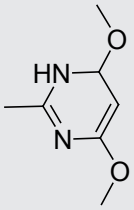
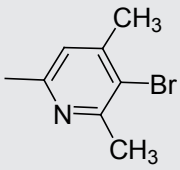
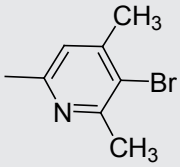
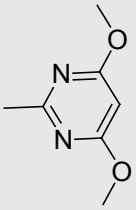
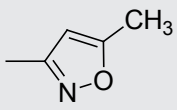
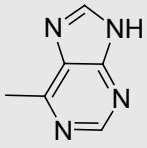
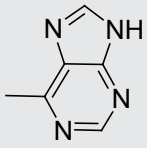
Table 3: Result of Combilib study with predicted activity.

Comp. No	R	R_1	Lipinski Screen Result	Lipinski Screen Score	Predicted Activity (pEC_{50})
	4-chlorophenyl	3-chlorophenyl	ADRX	4	-1.92327
	2,3-dihydroxyphenyl	3-ethoxy-4-hydroxyphenyl	ADRWS	5	-1.94622
	4-bromophenyl	3-hydroxy phenyl	ADRXW	5	-1.95089
	2,3-dihydroxyphenyl	4-chlorophenyl	ADRWS	5	-1.94538
	2,4-dihydroxyphenyl	4-hydroxy-3-methoxyphenyl	ADRWS	5	-1.92488
	4-chlorophenyl	3,4-dimethoxyphenyl	ADRXS	5	-1.94956
	4-chlorophenyl	2,3-dichlorophenyl	ADRXWS	6	-1.92312
	4-chlorophenyl	2,4-dimethoxyphenyl	ADRXWS	6	-1.94751
	2,3-dihydroxyphenyl	3-chlorophenyl	ADRWS	5	-1.93219
	2,3-dihydroxyphenyl	3-ethoxy-4-hydroxyphenyl	ADRWS	5	-1.94871
	2,3-dichlorophenyl	3-hydroxy phenyl	ADXWS	5	-1.9489
	2,3-dibromophenyl	4-chlorophenyl	ADRWS	5	-1.92069
	2,3-dichlorophenyl	4-fluorophenyl	ADRXWS	6	-1.92314
	3-hydroxyphenyl	4-hydroxy-3-methoxyphenyl	ARXWS	5	-1.92348
	2-chlorophenyl	3,4-dimethoxyphenyl	ADWS	4	-1.9418
	2,3-dichlorophenyl	4-hydroxyphenyl	ADRXWS	6	-1.92277
	2,3-dichlorophenyl	2,3-dichlorophenyl	ADRXWS	6	-1.94761
	2,3-dichlorophenyl	3,4-dimethoxyphenyl	ADRXWS	6	-1.92458
	2,3-dichlorophenyl	2,4-dimethoxyphenyl	ADRXWS	6	-1.92223
	4-fluorophenyl	3-chlorophenyl	ADRWS	5	-1.95433
	2,3-dibromophenyl	3-ethoxy-4-hydroxyphenyl	ADRXW	5	-1.95059
	3-hydroxyphenyl	3-hydroxy phenyl	ADRXS	5	-1.92246
	4-fluorophenyl	4-bromophenyl	ADXWS	5	-1.92262
	3,4-dihydroxyphenyl	4-chlorophenyl	ARXWS	5	-1.94344
	2-fluorophenyl	4-fluorophenyl	ADRXWS	6	-1.94395
	2,3-dimethoxyphenyl	4-hydroxy-3-methoxyphenyl	ADRWS	5	-1.92345
	4-fluorophenyl	3,4-dimethoxyphenyl	ADXWS	5	-1.9232
	4-fluorophenyl	4-hydroxyphenyl	ADRXWS	6	-1.92259
	4-fluorophenyl	2,3-dichlorophenyl	ADRXWS	6	-1.94854
	4-fluorophenyl	3,4-dimethoxyphenyl	ADRXWS	6	-1.92382

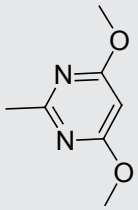
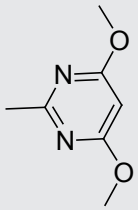
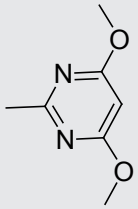
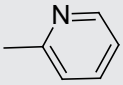
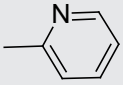
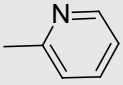
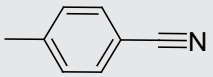
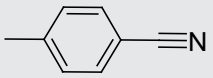
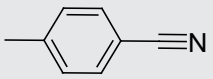
Table 4: Structure and NNRT inhibition data (EC50 in μM) of selected series of compounds along with pEC_{50} values.[17]

Compound	R1	R2	R3	X	Ar	EC_{50} (μM)	pEC_{50}
1	-H	-H	-CN	-		88.74	-1.94812
2	-H	-H	-CN	-		40.43	-1.606
3	-H	-H	-CN	-		68.02	-1.83264
4	-H	-H	-CN	-		115.28	-2.06175
5	-H	-H	-CN	-		85.70	-1.93298
6	-H	-H	-CN	-		67.82	-1.83136
7	-H	-H	-CN	-		53.60	-1.72916
8	-Cl	-Cl	-H	-		20.52	-1.31218
9	-Cl	-Cl	-H	-SO2NH		29.40	-1.46835
10	-Cl	-F	-H	-SO2NH		63.11	-1.8001
11	-Cl	-Cl	-H	-CONH		36.66	-1.56419
12	-H	-H	-H	-CONH		15.68	-1.19535

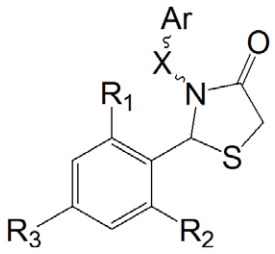
Continued...

13	-Me	-Me	-H	-CONH		29.38	-1.46805
14	-Cl	-NO2	-H	-		0.02	1.69897
15*	-Cl	-NO2	-H	-		0.10	1
16	-F	-F	-H	-		0.35	0.455932
17*	-OMe	-OMe	-H	-		2.22	-0.34635
18	-OMe	-OMe	-H	-		3.17	-0.50106
19*	-OMe	-OMe	-H	-		11.33	-1.05423
20	-Cl	-Cl	-H	-		11.82	-1.07262
21	-F	-F	-H	-		36.33	-1.56027

Continued...

22	-Cl	-Cl	-H	-		0.07	1.154902
23*	-Cl	-F	-H	-		0.18	0.744727
24	-F	-F	-H	-		0.25	0.60206
25	-Cl	-Cl	-H	-		0.99	0.004365
26	-Cl	-F	-H	-		2.10	-0.32222
27*	-F	-F	-H	-		17.34	-1.23905
28	-Cl	-Cl	-H	-		30.30	-1.48144
29	-Cl	-F	-H	-		33.55	-1.52569
30	-F	-F	-H	-		42.58	-1.62921

* Test set Compounds.
pEC_{50} [pEC_{50} = -log (EC_{50})]



Building and optimizing the compounds

The molecules which are selected as a target for this study were constructed by V-life MDS software with standard bond lengths and bond angles. Conformational search analysis was done by Montecarlo method. Through optimization process parameters such as bond energy, angle energy, torsion energy and electrostatic energy are computed. The optimized molecules have much lesser total energy than the unoptimized molecules indicating that the most stable conformer has been selected for further study. For initial optimization we used Merck Molecular Force Field (MMFF) method with energy gradient of 0.001 kcal/mol Å.[9,10,17,18]

Selection of training and test sets

Based on biological activities of different 30 thiazolidinone derivatives the entire data set was split into training set (25 compounds)and the test set (5 compounds) using sphere exclusion method with dissimilarity value of 5.0. The predictive ability of the models was validated using Test set.[18]

Descriptors and model generation for 2D QSAR

Physicochemical descriptors like distance based Topological, Polar Surface Area, electro topological and alignment independent descriptors were selected. Correlation matrix was used to select the principle descriptors which influenced the anti-HIV activity (dependent variable) of the analogues the most were considered for further study. Descriptors that several 2D models using Simulated Annealing - multiple linear regression (SA-MLR) were generated and the best model was selected on the basis of statistical parameters such as r^2 (square of correlation coefficient, q^2 (cross validated r), pred_r^2 and variation of the descriptors. High regression values are indicators of the high predictive ability of the model. Multiple regression estimates the values of the regression coefficients by applying least squares curve fitting method.[18]

Descriptors and model generation for 3D QSAR

Various 3D QSAR models were generated using SA kNN method. The parameters were set to maximum temperature as 100, minimum temperature as 0.01, Iteration at given temperature as 5, temperature was decreased by 10, Seed as 0 and Perturbation Limit as 1. The optimized molecules were suitably aligned on a common substructure (Figure 2) of the data base as it is assumed that they have the same mechanism of action. For obtaining descriptors, 3D grid spacing with an interval of 2 in x, y and z directions was created to accommodate the aligned molecules. The descriptors were used as independent variables and the pEC_{50} activity value was used as a dependent variable. Force field properties such as steric, hydrophobic and electrostatic interaction energies were computed at the lattice points of the grid. Model that satisfied all the statistical parameters like q^2, pred r^2, error of estimate (*SEE*), Fischer ratio value (*F*) was finalized.

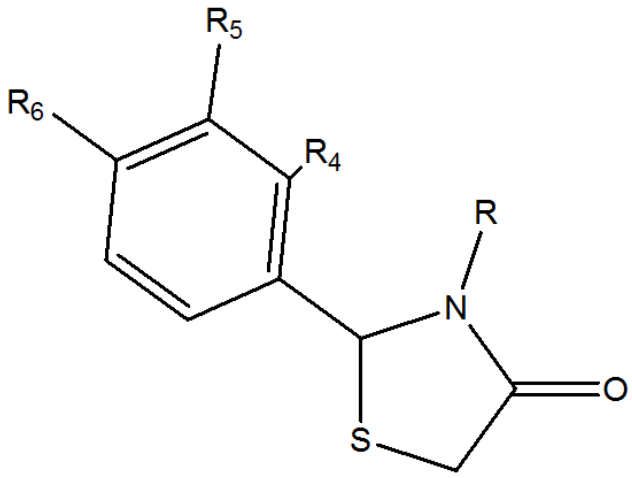


Figure 2: Common substructure used for 3D QSAR.

Models validation

Internal and external statistical validation metrics were computed to estimate predictive ability of developed models. Cross validation of generated models was performed using the leave-one-out (LOO) method. It is also indicative of the robustness of the model. Models were assessed for internal validation based on correlation coefficient r^2, cross-validated correlation coefficient (q^2) and external validation by pred_r^2 and more reliable parameter r^2m.[4,17,19-21]

Design of new molecules containing the thiazolidin-4-one structure

Taking into consideration topological, physicochemical, electrostatic, steric descriptors generated from 2D and 3D QSAR studies new molecules were designed for anti-HIV activity. Combilib tool of V life MDS was used to design the molecules. Designed derivatives were subjected to Lipinski filter to detect their drug likeness. There were six parameters on which these molecules were evaluated such as Number of hydrogen bond acceptor (A) (<10), Number of hydrogen bond donor (B) (<5), Number of rotatable bond (R) (<10), Xlog P (X) (<5), Molecular weight (W) (<500 g/ mol), Polar surface area (S) is (<140 Å).[18]

CONCLUSION

In this study 30 derivatives of thiazolidinone were studied using 2D and 3D QSAR for pharmacophore optimization for anti-HIV activity. Best models generated showed correlation coefficient *r2*= 0.9256 and q^2 =0.8623 for 2D QSAR and q^2 =0.8444 for 3D QSAR. Results of 2D QSAR indicated the importance of thiazolidinone ring and presence of hydroxyl, ethoxy substituted aryl ring on nitrogen atom and 2nd position of thiazolidinone pharmacophore. 3D QSAR studies revealed that presence of more electronegative substituent such as haloaryl ring at 2nd position of thiazolidinone ring would result in increased activity. Similarly substitution of haloaryl ring and sterically less bulky groups on the nitrogen atom of thiazolidinone ring would be preferred for enhanced anti-HIV activity.

Thus a library of thiazolidinone derivatives was designed based on QSAR results and screened for drug likeness by passing them through Lipinski filter. Molecules with best Lipinski score and higher predicted activity can be subjected to molecular docking studies and best fit molecules can be further synthesized and tested for bioactivity.

ACKNOWLEDGEMENT

Authors are thankful to Dr. A R Madgulkar, Principal AISSMS college of Pharmacy, Pune for providing necessary research facilities and support. We are thankful to BCUD, Savitribai Phule Pune University for providing the financial support (14PHM000172).

CONFLICT OF INTEREST

The authors declare no conflicts of interest.

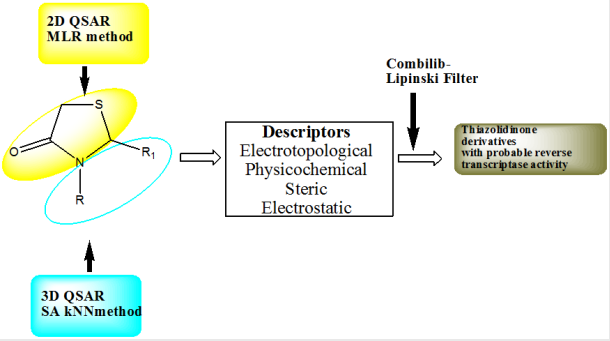
ABBREVIATIONS

AIDS: Acquired immunodeficiency syndrome; **HIV:** Human immunodeficiency virus; **NRTIs/ NTRIs:** Nucleoside/nucleotide reverse transcriptase inhibitors; **NNRTIs:** Non-nucleoside reverse transcriptase inhibitors; **RT:** Reverse transcriptase; **QSAR:** Quantitative structure activity relationship; **MLR:** Multiple linear regression; **SA-kNN:** Simulated annealing k nearest neighbor.

REFERENCES

1. Suryawanshi R, Jadhav S, Makwana N, Desai D, Chaturbhuj D, Sonawani A, *et al*. Evaluation of 4-thiazolidinone derivatives as potential reverse transcriptase inhibitors against HIV-1 drug resistant strains. Bioorg Chem. 2017;71:211-8.
2. Esposito F, Tramontano E. Current drugs targeting HIV-1 integrase and reverse transcriptase-associated ribonuclease H activity: Single and dual active site inhibitors. Antivir Chem and Chemother. 2014;23(4):129-44.
3. Esposito F, Corona A, Tramontano E. HIV-1 Reverse Transcriptase Still Remains a New Drug Target: Structure, Function, Classical Inhibitors and New Inhibitors with Innovative Mechanisms of Actions. Molecul Biol Internat. 2012; 2012:1-23.
4. Pawar V, Lokwani D, Bhandari S, Mitra D, Sabde S, Bothara K, *et al*. Design of potential reverse transcriptase inhibitor containing Isatin nucleus using molecular modeling studies. Bioorg Medi Chem. 2010;18(9):3198-211.
5. Tripathi AC, Gupta SJ, Fatima GN, Sonar PK, Saraf SK. 4-Thiazolidinones: The advances continue. Euro J of Medi Chem. 2014;72:52-77.
6. Gu SX, Lu HH, Liu GY, Ju XL, Zhu YY. Advances in diarylpyrimidines and related analogues as HIV-1 nonnucleoside reverse transcriptase inhibitors. Euro J of Medi Chem. 2018;158:371-92.
7. Manjala S, Kaura R, Bhatia AR, Kumara K, Singh V, Kaurab R, *et al*. Synthetic and medicinal perspective of thiazolidinones: A review. Bioorg Chem. 2017;75:406-23.
8. Jain AK, Vaidya A, Ravichandran V, Kashaw SK, Agrawal RK. Recent developments and biological activities of thiazolidinone derivatives: A review. Bioorg and Medi Chem. 2012;20(11):3378-95.
9. Krishna SM, Padmalatha Y, Ravindranath LK. Tetrazole as a Core unit Biological evaluation Agent. Internat J of Medi and Pharm Resear. 2015;3:1004-10.
10. Chitre TS, Asgaonkar KD, Patil SM, Kumar S, Khedkar VM, Garud DR. QSAR, docking studies of 1,3-thiazinan-3-yl isonicotinamide derivatives for antitubercular activity. Computat Biol and Chem. 2017;68:211-8.
11. Chitre TS, Bothara KG, Bhandari SV, Jalnapurkar RR, Kathiravan MK. Pharmacophore Optimization and Design of Competitive Inhibitors of Thymidine Monophosphate Kinase through Molecular Modeling Studies. Chem Biol and Drug Design. 2011;78(5):826-34.
12. Barzegara A, Mousavi SJ, Hamidi H, Sadeghi M. 2D-QSAR study of fullerene nanostructure derivatives as potent HIV-1 protease inhibitors. Physica E: Low-dimension Syst and Nanostruct. 2017;93:324-31.
13. Murugesan V, Tiwari VS, Saxena R, Tripathi R, Paranjape R, Kulkarni S, *et al*. Lead optimization at C-2 and N-3 positions of thiazolidin-4 -ones as HIV-1 non- nucleoside reverse transcriptase inhibitors. Bioorg and Medi Chem. 2011;19:6919-26.
14. Tong J, Wu Y, Bai M, Zhan PJ. 3D-QSAR and molecular docking studies on HIV protease inhibitors. Molecul Struct. 2017;1129:17-22.
15. Ravichandran V, Prashantha KBR, Sankar S, Agrawal RK. Predicting anti-HIV activity of 1, 3, 4-thiazolidinone derivatives: 3D-QSAR approach. Euro J of Medi Chem. 2009;44(3):1180-7.
16. Tong J, Leim S, Qin S, Wang YJ. QSAR studies of TIBO derivatives as HIV-1 reverse transcriptase inhibitors using HQSAR, CoMFA and CoMSIA. Molecul Struct. 2018;1168:56-64.
17. Murugesan V, Makwana N, Suryawanshi R, Saxena R, Tripathi R, Paranjape R, *et al*. Rational design and synthesis of novel thiazolidin-4-ones as non-nucleoside HIV-1 reverse transcriptase inhibitors. Bioorg and Medi Chem. 2014;22(12):3159-70.
18. V life Software Instruction manual version 4.4. 2018.
19. Lokwani D, Bhandari S, Pujari R, Shastri P, Shelke G, Pawar VJ. Use of Quantitative Structure–Activity Relationship (QSAR) and ADMET prediction studies as screening methods for design of benzyl urea derivatives for anti-cancer activity. Enz Inhibi and Medi Chem. 2010;26(3):1-13.
20. Veerasamy R, Rajak H, Jain A, Sivadasan S, Varghese CP, Agrawal RK. Validation of QSAR Models - Strategies and Importance. Internation J of Drug Design and Discov. 2011;2(3):511-9.

PICTORIAL ABSTRACT



SUMMARY

2D and 3D QSAR studies were carried on a data set of 30 different thiazolidinone derivatives showing anti-HIV activity. Different models were generated using MLR method for 2D QSAR and SA kNN method for 3D QSAR. Best model was selected based on the various statistical parameters. This study revealed some key descriptors which would positively contribute to the biological activity. Using the finding of QSAR studies derivatives were designed and subjected to Lipinski filter to determine their drug likeness.

About Authors

Dr. Trupti Chitre, M.Pharm, Ph.D, Associate Professor in Dept. of Pharmaceutical Chemistry, AISSMS College of Pharmacy. Her area of research includes drug design, synthesis of Anti-HIV and Anti TB entities.

Anagha G. Sujalegaonkar, PG student in Dept. of Pharmaceutical chemistry in AISSMS College of Pharmacy.

Shital Patil, M.Pharm, Assistant Professor in Dept. of Pharmaceutical Chemistry, AISSMS College of Pharmacy. Her area of research includes drug design, synthesis of Anti-HIV and Anti-TB entities.

Kalyani Asgaonkar, M.Pharm, Assistant Professor in Dept. of Pharmaceutical chemistry, AISSMS College of Pharmacy. Her area of research includes drug design, synthesis of Anti-HIV and Anti-TB entities.

Cite this article: Chitre TS, Patil SM, Sujalegaonkar AG, Asgaonkar KD. Designing of Thiazolidin-4-one Pharmacophore using QSAR Studies for Anti-HIV Activity. Indian J of Pharmaceutical Education and Research. 2021;55(2):581-9.