Supporting information for

Antimicrobial Pharmacophore Screening of Imidazole[1,2-a] Pyrazine Derivatives: A Quantitative Structure-Activity Relationship Approach

K. J. Rajimon[1, 2] and Renjith Thomas[1, 2,*]

[1] *Department of Chemistry, St Berchmans College (Autonomous), Changanassery, Kerala, 686101, India*

[2] *Centre for Theoretical and Computational Chemistry, St Berchmans College (Autonomous), Changanassery, Kerala, 686101, India*

**Email:* renjith@sbcollege.ac.in (R. Thomas)

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Table S1: Theoretical prediction of ADME properties of the studied compounds.

Molecules	MW	H-bond acceptors	H-bond donors	Rotatable bonds	Molar refractivity	Lipophilicity
1(A)	311.34	4	1	4	91.01	3.48
2(B)	281.36	2	2	3	86.59	2.97
3(C)	255.23	4	1	2	71.65	1.84
4(D)	225.25	2	2	1	67.23	1.33
5(E)	311.34	4	1	4	91.01	3.48
6(F)	281.36	2	2	3	86.59	2.97
7(G)	337.38	4	1	4	98.47	4.31
8(H)	225.25	2	2	1	67.23	1.33
9(I)	309.41	2	1	4	96.39	3.78
10(J)	253.3	2	1	2	77.03	2.13

Table S2: Statistical validation of the GA-MLR model.

Model	R^2_Train	R^2_Test	RMSE_Train	RMSE_Test	R^2_Adjusted
GA-MLR	0.9150714	0.2291822	0.1858331	3.014309	0.4054999

Lack_of_Fit	F_Value	CV_R^2	CV_RMSE	Intercept	Q^2
0.2532489	1.795767	0.8231608	1,076.319	1.534504	-5.861005

Q^2_loo	Y_Scrambling_Mean	Y_Scrambling_SD
0.9150714	1	0.000000000000000115816

Table S3: Validation criteria.

R^2_train	R^2_adj	R^2_R^2adj	LOF
0.9150714	0.4054999	0.5095715	0.2532489

Kxx	Delta_K	RMSE_tr	MAE_tr
0.5032384	2	0.1858331	0.1416266

RSS_tr	CCC_tr	s	F
0.7597468	0.9556525	0.5032384	1.795767

Q^2loo	R^2_Q^2loo	RMSE_cv	MAE_cv
0.9150714	-0.000000000000000001110223	1,076.319	0.1416266

PRESS_cv	CCC_cv	Q^2LMO	R^2Yscr
0.7597468	0.9556525	-5.861005	1

Q^2Yscr	RMSE_AV_Yscr	R^2Xrnd	Q^2Xrnd
1	0.000000000000000001115816	1	1

R^2Yrnd	Q^2Yrnd	RMSE_ext	MAE_ext
1	1	3.014309	1.579153

PRESS_ext	R^2ext	Q^2_F1	Q^2_F^2
63.6024	0.2291822	-5.228338	-5.861005

$Q^2\_F^3$	CCC_ext	r^2m_aver	r^2m_delta
-5.228338	-0.3478359	-2.815911	6.090187

Table. S4: Virtual screening of molecules based on activity model data.

Molecule_ID	final_response	Rank
8	0.02924920	1
3	0.09303062	2
4	0.12321198	3
10	2.30315848	4
6	5.73753726	5
5	5.85973614	6
1	8.60595267	7
2	23.46013693	8
7	26.79833894	9
9	82.17119809	10

NB: Values are as per the activity units (µg/mL)

Table S5: Binding free energy components for the Staphylococcus aureus Pyruvate Carboxylase bound to MOLECULE 8 calculated by MM-GBSA.

Energies (kcal/mol)	Staphylococcus aureus Pyruvate Carboxylase bound to MOLECULE 8
ΔG_{bind}	-68.86
$\Delta G_{bindLipo}$	-21.91
$\Delta G_{bindvdW}$	-34.45
$\Delta G_{bindCoulomb}$	31.65
$\Delta G_{bindHbond}$	-4.01
$\Delta G_{bindSolvGB}$	43.81
$\Delta G_{bindCovalent}$	3.19
$\Delta G_{bindPacking}$	-5.42

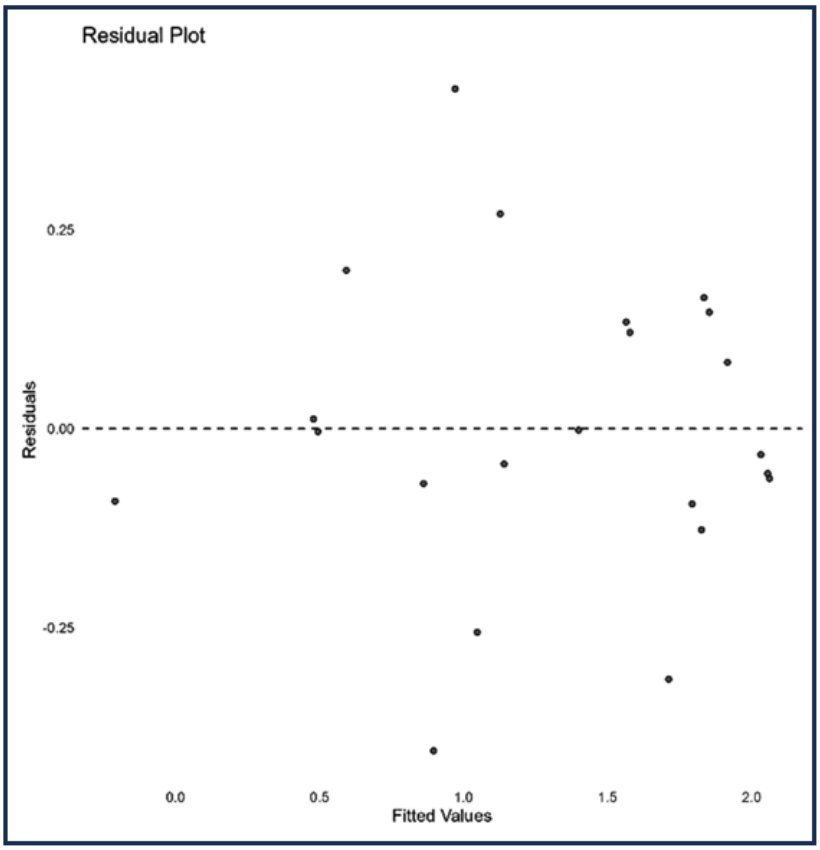

Fig. S1: Residual plot showing the residuals versus fitted values.

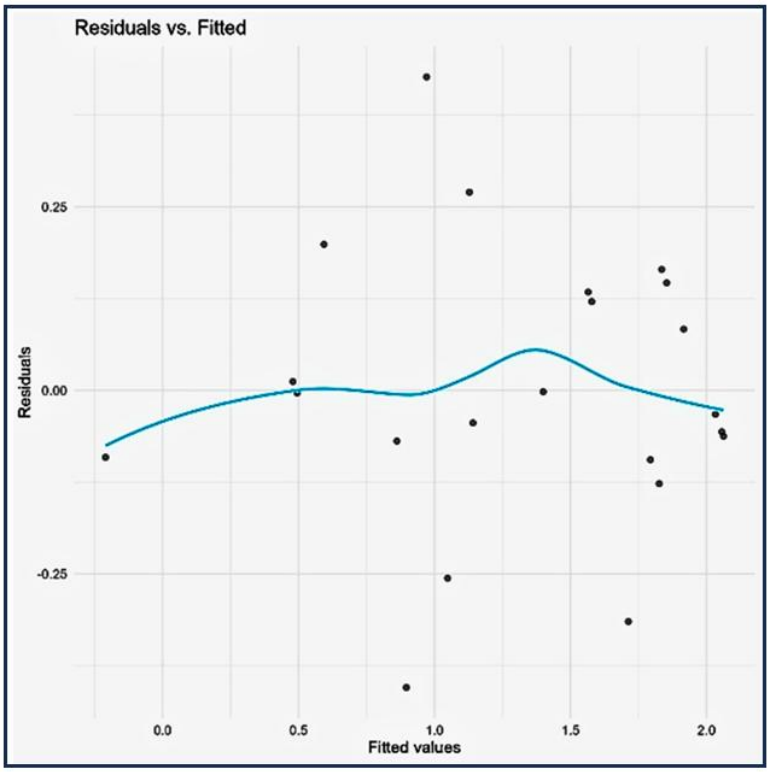

Fig. S2: Plot showing residuals versus fitted values.

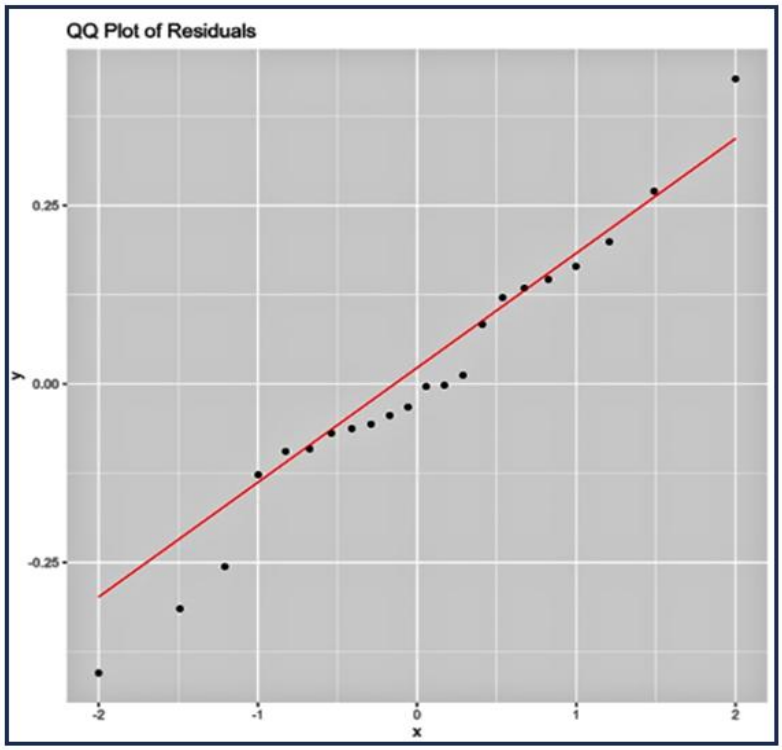

Fig. S3: QQ plot of residuals to check the normality assumption.

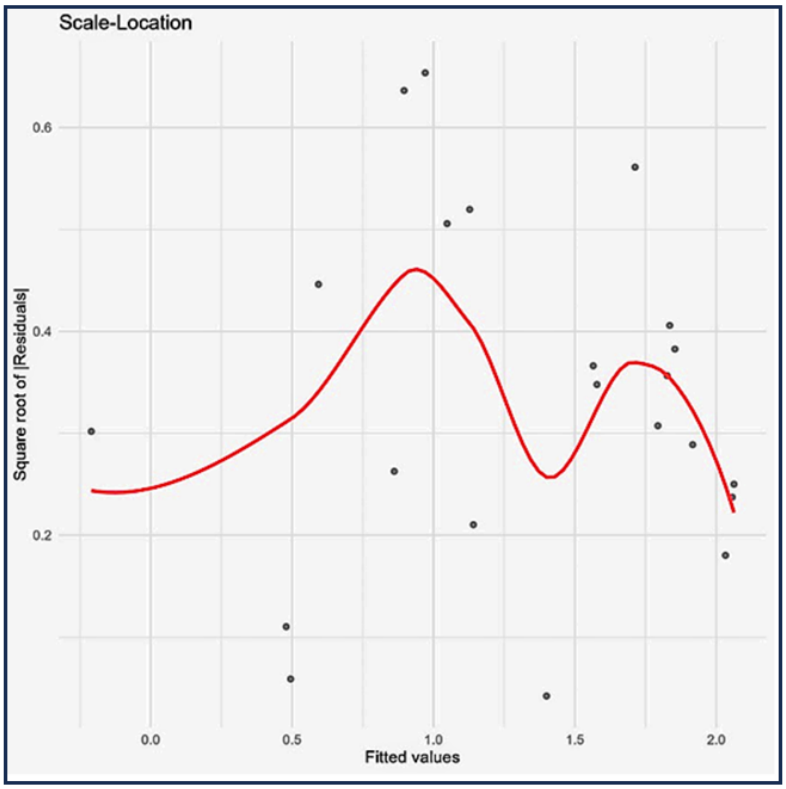

Fig. S4: Scale-Location plot showing the spread of residuals.

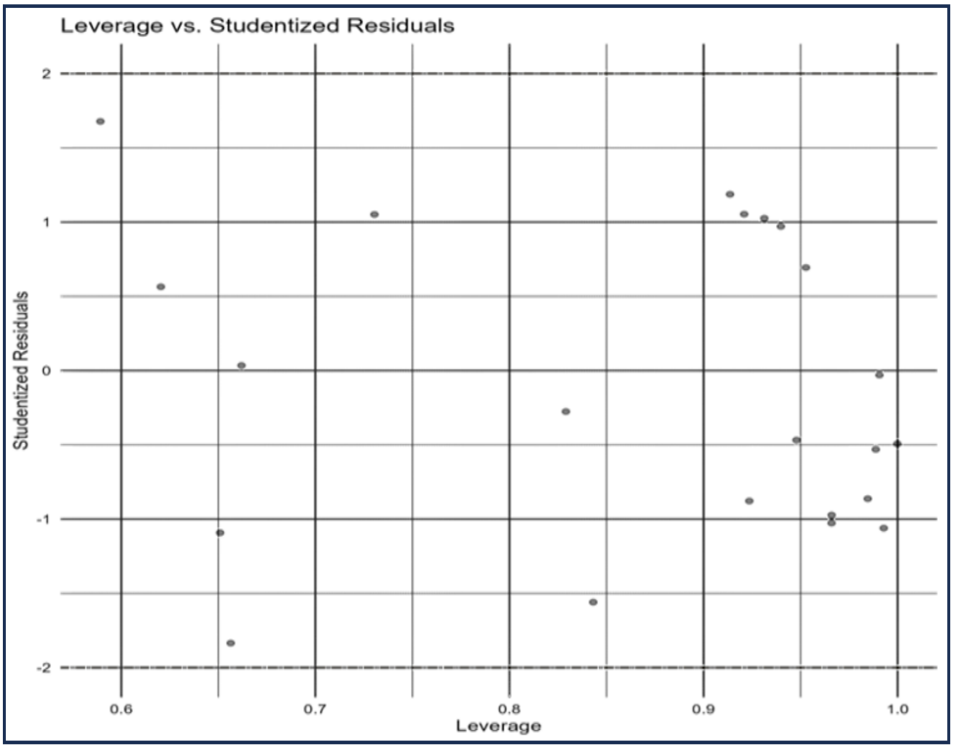

Fig. S5: Plot showing leverage versus studentized residuals.

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