

Synthesis, spectroscopic investigations, quantum chemical studies, molecular docking and antiviral activity of 5-chloro-N-(2-chlorophenyl)pyrazine-2-carboxamide

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The FT-IR and FT-Raman spectra of 5-chloro-N-(2-chlorophenyl)pyrazine-2-carboxamide were recorded and the vibrational wavenumbers are computed using DFT method. On the basis of potential energy distribution the complete vibrational assignments were performed. From the molecular electrostatic potential study the negative potential regions are mainly localized over the carbonyl group and phenyl ring and are possible sites for electrophilic attack. The calculated HOMO and LUMO energies confirm that charge transfer occurs within the molecule. The geometrical parameters of the title compound are in agreement with that of similar compounds. The calculated first hyperpolarizability value is comparable with that of similar derivatives and the study of second hyperpolarizability reveals that the title compound is an attractive object for future studies in nonlinear optics. From the molecular docking study, the docked ligand title compound forms a stable complex with glucosamine 6-phosphate deaminase from *E.coli* and gives a binding affinity value of -6.4kcal/mol. The results suggest that the compound might exhibit inhibitory activity against glucosamine 6-phosphate deaminase. The title compound was tested for *in vitro* activity against various DNA and RNA viruses, but no activity was observed.

1. INTRODUCTION

Pyrazines occur almost ubiquitously in nature and obtained from fused oil, galbanum oil, cocoa butter, cocoa bean, coffee bean, green peas, mandibular gland secretion of ponerine ants, molds like *Aspergillus (A) flacus*, *A.sclerotiorii*, *A.oryzae*, *A.ochraceus* etc [1]. The beauty of pyrazine derivatives is that ring carbon atoms can be substituted to get different derivatives [2]. Pyrazines are found naturally in many vegetables, insects, terrestrial vertebrates, and marine organisms, and they are produced by microorganisms during their primary or secondary metabolism [3-6]. The widespread occurrence of simple pyrazine molecules in nature, especially in the flavours of many food systems, their effectiveness at very low concentrations as well as the still increasing applications of synthetic pyrazines in the flavor and fragrance industry are responsible for the high interest in these compounds [7]. Certain pyrazines, especially dihydropyrazines, are essential for all forms of life

due their DNA strand-breakage activity and/ or by their influencing of apoptosis [8]. Pyrazinamide (pyrazine-2-carboxamide) is a first-line antitubercular drug and pyrazinamide derivatives are still in the focus of antitubercular research. The title compound of this article, 5-chloro-N-(2-chlorophenyl)pyrazine-2-carboxamide, possessed *in vitro* antimycobacterial activity against *M. tuberculosis* H37Rv with minimum inhibitory concentration of 0.78-3.13 µg/mL [9]. Certain pyrazine carboxamide derivatives were found to show good inhibitory activity against influenza viruses [10, 11], bovine virus diarrhea [12], yellow fever [13-15] and Puna Toro virus [16]. Therefore, based on the presence of the pyrazine-2-carboxamide moiety, the title compound 5-chloro-N-(2-chlorophenyl)pyrazine-2-carboxamide was tested for *in vitro* activity against a broad panel of viruses, including those mentioned above.



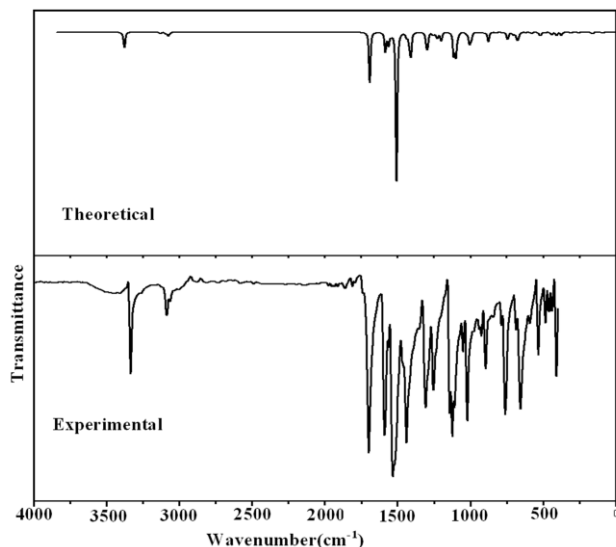


Figure 1. FT-IR spectrum of 5-chloro-N-(2-chlorophenyl) pyrazine-2-carboxamide.

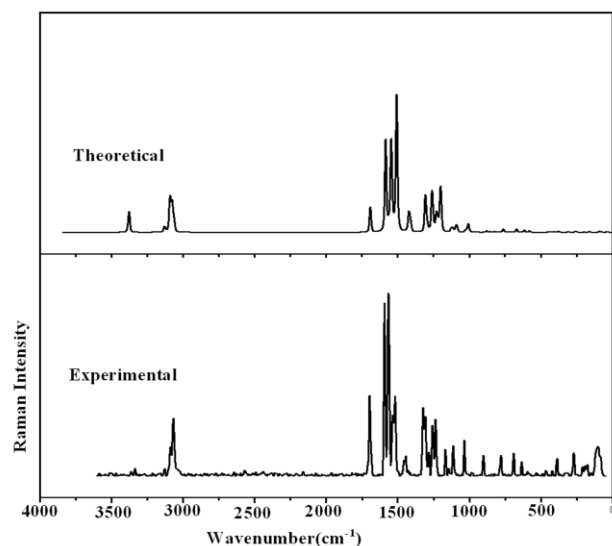


Figure 2. FT-Raman spectrum of 5-chloro-N-(2-chlorophenyl) pyrazine-2-carboxamide.

2. MATERIALS AND METHODS

2.1. General

The sample of the title compound was obtained from the authors of previous study of this compound [9]. The identity and purity of the sample was checked by melting point, NMR spectra and TLC analysis. Obtained results were fully consistent with those reported in literature [17]. The FT-IR spectrum (Figure 1) was recorded using KBr pellets on DR/Jasco FT-IR spectrometer and the FT-Raman spectrum (Figure 2) was obtained on a Bruker RFS 100/s, Germany.

2.2. Antiviral Evaluation

Antiviral activity in cell culture was assessed by cytopathic effect (CPE) reduction assays. To perform the tests, the virus was added to semiconfluent cell cultures in 96-well plates and, simultaneously, serial dilutions of the test compound were added. The plates were incubated until clear CPE was reached (typically 3-6 days). The antiviral activity was expressed as EC_{50} , which is the effective concentration causing 50%

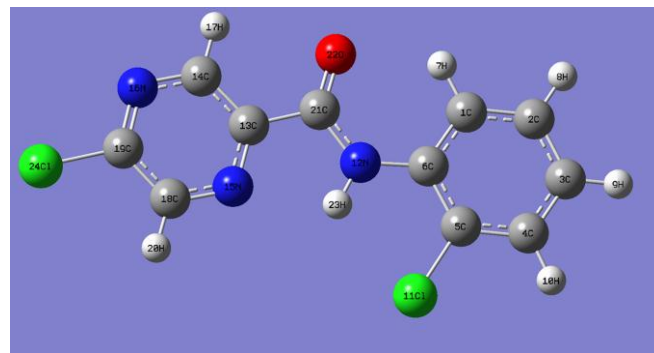


Figure 3. Optimized geometry of 5-chloro-N-(2-chlorophenyl) pyrazine-2-carboxamide.

reduction of CPE compared no non-treated infected cells. The CPE was evaluated by visual microscopy and/or by standard colorimetric formazan-based MTS cell viability assay. Viruses examined in Crandell-Rees Feline Kidney (CRFK) cells: feline coronal virus; feline herpes virus. Viruses examined in human embryonic lung fibroblast (HEL) cells: herpes simplex virus type 1 (HSV-1); a thymidine kinase-deficient (TK) HSV-1 KOS strain resistant to aciclovir; herpes simplex virus type 2 (HSV-2); vaccinia virus; human adenovirus type 2; and vesicular stomatitis virus (VSV). Viruses examined in human cervix carcinoma (HeLa) cells: VSV; Coxsackie B4 viurs; and respiratory syncytial virus (RSV). Viruses examined in African Green Monkey (Vero) cells: para-influenza-3 virus; reovirus-1; Sindbis virus; Coxsackie B4 virus and Punta Toro virus. Viruses examined in Madin-Darby canine kidney (MDCK) cells: human influenza A/H1N1, A/H3N2 and B viruses. Finally, activity against human immunodeficiency virus (HIV) type 1 and type 2 was studied in human MT-4 lymphoblast cells.

2.3. Computational Details

Gaussian09 [18] software was used for all the theoretical calculations and structure of the title compound was optimized using the Becke-Lee-Yang-Parr hybrid exchange correlation three-parameter functional (B3LYP) with CC-pVDZ (5D, 7F) basis set [19]. A scaling factor of 0.9613 had to be used for obtaining a considerably better agreement with experimental data [20]. Structural parameters corresponding to the optimized geometry of the title compound (Figure 3) are given in Table 1. The assignments of the calculated frequencies are done using Gaussview [21] and GAR2PED [22] software.

3. RESULTS AND DISCUSSION

3.1. Geometrical Parameters

In the following discussion, the phenyl and pyrazine ring are designated as Ph and Pz, respectively. The C-C bond lengths in the phenyl ring lie in the range 1.3927-1.4117Å and for benzene the C-C bond length is 1.3993Å [23] and for benzaldehyde 1.3973Å [24]. In the present case, the bond lengths, $C_{13}-C_{21}=1.5084$, $C_{21}-O_{22}=1.2256$, $C_{21}-N_{12}=1.3685$, $C_6-N_{12}=1.4006$ Å are and the corresponding reported values are 1.5248, 1.2486, 1.3521, 1.4109Å [25]. For the title compound, the pyrazine bond lengths, $C_{13}-C_{14}=1.3992$, $C_{14}-N_{16}=1.3402$, $C_{19}-N_{16}=1.3221$, $C_{19}-C_{18}=1.4055$, $C_{18}-N_{15}=1.3300$ and $C_{13}-N_{15}=1.3437$ Å and the corresponding reported values are 1.3955, 1.3482, 1.3521, 1.4109, 1.3532, 1.3477Å [25]. The C-N bond lengths in the pyrazine ring of the title compound are much shorter than the normal C-N single bond that is referred to 1.49Å [25] and the same results are shown for the two C-C bonds lengths in the pyrazine ring and are also smaller than that of the normal C-C single bond of 1.54Å [26]. The bond lengths $C_{21}-N_{12}=1.3685$ and $C_6-N_{12}=1.4006$ Å are also shorter than the normal C-N single bond of 1.49Å, which confirms this bond to have some character of a double or conjugated bond [27]. For the

Table 1. Optimized geometrical parameters of 5-chloro-N-(2-chlorophenyl)pyrazine-2-carboxamide.**Bond lengths (Å)**

C1-C2	1.3948	C1-C6	1.4082	C1-H7	1.0870
C2-C3	1.3968	C2-H8	1.0919	C3-C4	1.3964
C3-H9	1.0914	C4-C5	1.3927	C4-H10	1.0903
C5-C6	1.4117	C5-Cl11	1.7670	C6-N12	1.4006
N12-C21	1.3685	N12-H23	1.0194	C13-C14	1.3992
C13-N15	1.3437	C13-C21	1.5084	C14-N16	1.3402
C14-H17	1.0914	N15-C18	1.3300	N16-C19	1.3221
C18-C19	1.4055	C18-H20	1.0922	C19-Cl24	1.7524
C21-O22	1.2256				

Bond angles (°)

C2-C1-H7	121.3	C6-C1-H7	118.3
C2-C1-C6	120.4	C3-C2-H8	120.1
C1-C2-C3	121.0	C1-C2-H8	118.9
C2-C3-C4	119.5	C2-C3-H9	120.8
C4-C3-H9	119.8	C3-C4-C5	119.7
C3-C4-H10	121.2	C5-C4-H10	119.2
C4-C5-C6	121.7	C4-C5-Cl11	118.6
C6-C5-Cl11	119.7	C1-C6-N12	123.2
C1-C6-C5	117.8	C5-C6-N12	119.0
C6-N12-C21	128.6	C6-N12-H23	116.8
C21-N12-H23	114.6	C14-C13-N15	121.3
C14-C13-C21	119.6	N15-C13-C21	119.1
C13-C14-N16	121.7	C13-C14-H17	120.3
N16-C14-H17	118.0	C13-N15-C18	117.4
C14-N16-C19	116.1	N15-C18-C19	120.2
N15-C18-H20	118.4	C19-C18-H20	121.4
N16-C19-C18	123.3	N16-C19-Cl24	117.9
C18-C19-Cl24	118.9	N12-C21-C13	112.9
N12-C21-O22	126.5	C13-C21-O22	120.7

title compound C=O bond length is 1.2256 Å and the corresponding reported values are 1.2253 Å [28], 1.2486 Å [25] and 1.2253 Å [29] and according to literature [30, 31] the changes in bond lengths in C=O and C-N are consistent with the following interpretation: that is, hydrogen bond decreases the double bond character of C=O bond and increases the double bond character of C-N bond. At N₁₂ position, the angles C₆-N₁₂-H₂₃ is 116.8°, C₂₁-N₁₂-H₂₃ is 114.6° and C₆-N₁₂-C₂₁ is 128.6° and this asymmetry of angles at N₁₂ position indicates the weakening of N₁₂-H₂₃ bond resulting in proton transfer to the oxygen atom O₂₂ [32]. At C₁₃ position the angles C₁₄-C₁₃-N₁₅ is increased by 1.3° and N₁₅-C₁₃-C₂₁ is reduced by 0.9° from 120° and this asymmetry reveals the interaction between the amide moiety and the pyrazine ring. At C₂₁ position, the bond angles are C₁₃-C₂₁-N₁₂ = 112.9°, C₁₃-C₂₁-O₂₂ = 120.7° and N₁₂-C₂₁-O₂₂ = 126.5° and this asymmetry gives the interaction between carbonyl group and the neighbouring pyrazine ring.

3.2. IR and Raman spectra

The observed IR, Raman bands, calculated (scaled wavenumbers) and assignments are given in Table 2. For the title compound, the C-Cl stretching mode is assigned at 664 cm⁻¹ in the IR spectrum and at 703, 668 cm⁻¹ theoretically as expected [33, 34]. The C-Cl stretching modes are reported at 671 cm⁻¹ [35], 660 (IR), 666 (Raman), 670, 657 cm⁻¹ (DFT) [36]. For the title compound the C=O stretching mode is observed at 1698 cm⁻¹ in the IR spectrum and at 1696 cm⁻¹ in the Raman spectrum. The corresponding theoretical value is 1691 cm⁻¹ and according to literature, C=O stretching modes are expected in

the range 1715-1600 cm⁻¹ [37, 38]. The NH stretching mode of the title compound is assigned at 3350 (IR), 3345 (Raman) and 3378 cm⁻¹ (DFT) which is expected in the region 3390 ± 60 cm⁻¹ [37]. In the present case, the NH deformations are assigned at 1507, 1210 cm⁻¹ (DFT) and the reported values are 1500, 1239 (IR), 1497, 1248 cm⁻¹ (DFT) [25]. The out-of-plane NH deformation mode is assigned at 681 cm⁻¹ in the IR spectrum, 683 cm⁻¹ in the Raman spectrum and at 679 cm⁻¹ theoretically which is expected in the region 790 ± 70 cm⁻¹ [37]. The C-N stretching mode coupled with NH deformation is active in the region 1275 ± 55 cm⁻¹ [37, 38] and in the present case bands at 1230 (Raman), 1227, 1210 cm⁻¹ (DFT) are assigned as the CN stretching modes. The reported values are 1265, 1239 (IR) and 1261, 1248 cm⁻¹ (DFT) for a similar derivative [25]. Mary et al. [39] reported the NH modes at 1547, 1250, 650 (IR) and 1580, 1227, 652 cm⁻¹ (theoretically) for a similar derivative.

The pyrazine ring stretching modes are assigned at 1542, 1520, 1307, 1200, 1084 cm⁻¹ in the IR spectrum, 1542, 1309 cm⁻¹ in the Raman spectrum and in the range 1544-1088 cm⁻¹ theoretically for the title compound. The reported values of the pyrazine ring stretching modes are 1527, 1481, 1219, 1207, 1177 cm⁻¹ [40], 1550, 1518, 1193, 1152, 1045 cm⁻¹ [25]. The ring breathing mode of the pyrazine ring is assigned at 1115 cm⁻¹ theoretically for the title compound and the ring breathing mode is reported at 1126 cm⁻¹ [40] and at 1131 cm⁻¹ [41]. The CH modes of the pyrazine ring are assigned at 3088, 3071, (DFT), 3071 cm⁻¹ (Raman) (stretching modes), 1230 (Raman), 1251, 1227 cm⁻¹ (DFT) (in-plane deformation) and 943, 896 (IR), 901 (Raman), 945, 898 cm⁻¹ (DFT)

Table 2. Calculated (scaled) wavenumbers, observed IR, Raman bands and assignments of 5-chloro-N-(2-chlorophenyl)pyrazine-2-carboxamide.

B3LYP) with CC-pVDZ (5D, 7F)			IR $\nu(\text{cm}^{-1})$	Raman $\nu(\text{cm}^{-1})$	Assignments ^a
$\nu(\text{cm}^{-1})$	IR _t	R _A			
3378	77.68	217.34	3350	3345	$\nu\text{NH}(99)$
3128	8.20	56.13	3125	3130	$\nu\text{CHPh}(98)$
3091	6.26	225.73	3091	3090	$\nu\text{CHPh}(96)$
3088	0.73	83.26	-	-	$\nu\text{CHPz}(99)$
3077	11.95	182.20	-	-	$\nu\text{CHPh}(98)$
3071	6.06	90.07	-	3071	$\nu\text{CHPz}(99)$
3063	2.69	77.50	3063	-	$\nu\text{CHPh}(95)$
1691	223.61	146.38	1698	1696	$\nu\text{C}=\text{O}(80)$
1584	83.62	513.38	1588	1588	$\nu\text{Ph}(61), \delta\text{Ph}(10)$
1563	62.71	38.21	1564	1565	$\nu\text{Ph}(59)$
1544	13.99	554.63	1542	1542	$\nu\text{Pz}(63), \delta\text{CHPz}(15)$
1518	9.57	68.24	1520	-	$\nu\text{Pz}(77)$
1507	654.47	731.04	-	1510	$\delta\text{NH}(51), \nu\text{Ph}(10)$
1438	19.77	6.85	1440	1440	$\nu\text{Ph}(44), \delta\text{CHPh}(34)$
1420	42.27	139.51	-	-	$\delta\text{CHPz}(15), \nu\text{Pz}(51)$
1410	133.07	43.25	-	-	$\delta\text{CHPh}(30), \nu\text{Ph}(24), \delta\text{CHPz}(12)$
1306	13.36	192.30	1307	1309	$\nu\text{Pz}(41), \nu\text{Ph}(23)$
1296	111.57	52.06	-	1293	$\nu\text{Ph}(59)$
1260	6.36	208.92	1261	1260	$\delta\text{CHPh}(47), \nu\text{CN}(41)$
1251	12.07	51.91	-	-	$\delta\text{CHPz}(43), \nu\text{Pz}(26), \nu\text{CC}(11)$
1227	37.40	138.53	-	1230	$\delta\text{CHPz}(46), \nu\text{CN}(39)$
1210	3.10	40.79	-	-	$\delta\text{NH}(47), \nu\text{CN}(38)$
1200	36.05	222.91	1200	-	$\nu\text{Pz}(51), \delta\text{CHPz}(10)$
1127	1.00	26.33	-	-	$\delta\text{CHPh}(85)$
1115	99.14	18.28	1118	1114	$\nu\text{CN}(19), \nu\text{Pz}(50)$
1100	101.92	6.00	1104	-	$\delta\text{CHPh}(19), \nu\text{Pz}(16), \nu\text{Ph}(22)$
1088	30.73	53.09	1084	-	$\nu\text{CN}(13), \nu\text{Pz}(57)$
1026	5.74	15.62	1024	1030	$\nu\text{Ph}(46), \delta\text{CHPh}(23), \delta\text{Ph}(12)$
1009	46.08	42.99	-	-	$\delta\text{CHPh}(49), \nu\text{CCl}(17), \nu\text{Ph}(20)$
996	49.34	6.53	-	993	$\delta\text{Pz}(57), \nu\text{Pz}(24)$
970	0.63	0.45	972	-	$\gamma\text{CHPh}(82), \tau\text{Ph}(12)$
945	1.73	1.86	943	-	$\gamma\text{CHPz}(80), \tau\text{Ph}(10)$
929	2.15	0.18	926	-	$\gamma\text{CHPh}(89)$
898	5.29	0.45	896	901	$\gamma\text{CHPz}(81)$
876	42.58	8.60	-	-	$\delta\text{NH}(23), \delta\text{C}=\text{O}(28)$
855	0.92	3.56	853	850	$\gamma\text{CHPh}(78)$
822	2.66	4.83	-	-	$\delta\text{Ph}(37), \nu\text{CN}(15), \nu\text{Ph}(13)$
780	1.84	2.89	782	782	$\tau\text{Pz}(53), \gamma\text{CC}(19), \gamma\text{C}=\text{O}(14)$
761	0.76	15.24	760	-	$\delta\text{Pz}(40), \nu\text{CCl}(13)$
743	42.79	1.51	-	-	$\gamma\text{CHPh}(91)$
709	4.46	1.96	-	-	$\tau\text{Ph}(54), \gamma\text{CN}(15), \gamma\text{CCl}(12)$
703	11.15	0.32	-	-	$\tau\text{Ph}(15), \tau\text{Pz}(19), \nu\text{CCl}(40)$
679	40.85	2.73	681	683	$\gamma\text{C}=\text{O}(30), \gamma\text{NH}(36), \tau\text{Pz}(19)$
668	15.92	14.97	664	-	$\delta\text{Ph}(27), \nu\text{CCl}(46)$
617	1.15	13.57	-	-	$\delta\text{Pz}(77)$
579	5.61	9.73	-	-	$\delta\text{Ph}(68)$
536	0.30	0.21	535	533	$\tau\text{Ph}(56), \gamma\text{CN}(21)$

Table 2. Calculated (scaled) wavenumbers, observed IR, Raman bands and assignments of 5-chloro-N-(2-chlorophenyl)pyrazine-2-carboxamide. (Continued)

519	22.39	0.29	-	-	δ CC(27), ν CCl(16), δ C=O(27)
486	3.02	0.04	486	-	γ CCl(33), τ Pz(31), γ CC(19)
443	10.42	3.91	-	-	ν CCl(39), δ CN(12)
437	4.07	0.60	438	-	τ Ph(56), γ CCl(26)
408	11.33	0.13	410	412	τ Pz(85)
405	3.18	3.68	-	-	δ CCl(36), δ CN(16)
375	16.25	6.15	-	380	δ CCl(35), δ CN(13), δ Ph(17)
309	3.49	1.92	-	315	δ CCl(34), δ Pz(24), δ CC(10)
304	0.01	0.33	-	-	τ Ph(23), γ CC(14), γ NH(19), γ CCl(18)
261	0.95	2.40	-	266	δ CCl(49), δ NH(14), δ C=O(15)
252	1.52	3.85	-	-	γ CC(19), γ CCl(24), τ Ph(23)
197	1.72	0.55	-	195	δ NH(16), δ CCl(14), δ Pz(11), δ Ph(10)
162	7.08	1.58	-	166	δ CN(30), δ CC(23), δ CCl(29)
160	0.03	2.01	-	-	τ Ph(56), γ CCl(14)
92	2.41	1.71	-	-	τ C=O(54), τ CN(18), τ NH(15)
86	1.45	3.89	-	-	τ Pz(41), τ NH(25), τ Ph(10)
57	0.09	0.24	-	-	τ C=O(34), δ CC(23), τ NH(22)
39	0.54	0.73	-	-	τ CN(40), τ C=O(26), τ NH(22)
28	0.63	1.05	-	-	τ NH(46), τ CN(25)

^a ν -stretching; δ -in-plane deformation; γ -out-of-plane deformation; τ -torsion; Ph-phenyl ring; Pz-pyrazine ring; potential energy distribution (%) is given in brackets in the assignment column.

(out of-plane deformation) which are in agreement with literature [34, 25, 40].

The phenyl CH stretching modes are assigned at 3125, 3091, 3063 (IR), 3130, 3090 (Raman) and 3128, 3091, 3077, 3063 cm^{-1} theoretically for the title compound according to literature [37]. For the title compound, the phenyl ring stretching modes are observed at 1588, 1564, 1440 cm^{-1} in the IR spectrum and at 1588, 1565, 1440, 1293 cm^{-1} in the Raman spectrum, which is expected in the region 1250-1601 cm^{-1} [37]. In ortho di-substitution the ring breathing mode has three wavenumber intervals depending on whether both substituents are heavy, or one of them is heavy, while the other is light, or both of them are light. In the first case, the interval is 1100-1130 cm^{-1} , in the second case 1020-1070 cm^{-1} while in the third case it is between 630 and 780 cm^{-1} [37, 42]. The reported values of the ring breathing mode of ortho substituted phenyl ring are 1030 (IR), 1030 (Raman), 1022 cm^{-1} (DFT) [43], 1041 cm^{-1} [44], 1011 cm^{-1} [45], 1020 cm^{-1} [46], 1022, 1027 cm^{-1} [47]. For the title compound the ring stretching mode is assigned at 1024 cm^{-1} in IR, 1030 cm^{-1} in Raman and at 1026 cm^{-1} theoretically [37, 42]. The CH deformations of the phenyl ring are expected above 1000 cm^{-1} (in-plane bending modes) and below 1000 cm^{-1} (out-of-plane bending modes [37] and in the present case these modes are assigned at 1261, 1104 (IR), 1260 (Raman), 1260, 1127, 1100, 1009 cm^{-1} (DFT) (in-plane bending modes) and at 972, 926, 853 (IR), 850 (Raman), 970, 929, 855, 743 cm^{-1} (DFT) (out-of-plane bending modes). The ring deformation modes are also identified and assigned Table 2) and most of the modes are not pure but contains significant contributions from other modes also. The root mean square value between the calculated and observed wavenumbers were calculated in order to investigate the performance of the vibrational wavenumbers of the title compound and the RMS errors are 5.32 for IR bands and 6.42 for Raman bands.

3.3. Nonlinear optical properties

The computational approach allows the determination of nonlinear optical properties as an inexpensive way to design molecules

by analyzing their potential before synthesis and to determine the hyperpolarizability values [48]. The polarizability values represent the nonlinear contribution to the induced dipole moment and are noteworthy because of their fundamental role in the interpretation of the nonlinear properties in the molecular systems [49]. Many organic molecules, containing conjugated π electrons characterized by large values of hyperpolarizabilities were analyzed by means of vibrational spectroscopy [50]. The calculated values of the dipole moment and polarizability are 1.864 Debye and 7.728×10^{-23} esu. The first order hyperpolarizability of the title compound is calculated and is found to be 10.15×10^{-30} esu which is comparable with the reported values of similar derivatives [25, 40]. The calculated hyperpolarizability of the title compound is 78.08 times that of the standard NLO material urea (0.13×10^{-30} esu) [51]. The theoretical second order hyperpolarizability was calculated using the Gaussian09 software and is equal to -15.04×10^{-37} e.s.u. We conclude that the title compound and its derivatives are an attractive object for future studies of nonlinear optical properties. For the title compound, the calculated C-N distances in the molecular structure are intermediate between those of C-N single and C=N double bond and therefore, the calculated data suggest an extended π -electron delocalization of the pyrazine ring and carboxamide moiety [52] which is responsible for the nonlinearity of the molecule.

3.4. Frontier molecular orbitals

Molecular orbital and their properties, like energy are very useful for predicting the most reactive position in π -electron systems and also explained several types of reaction in conjugated systems [53]. The HOMO-LUMO energy gap has been used to prove the bioactivity from the intermolecular charge transfer [54]. The HOMO-LUMO energy gap shows that the energy gap reflects the chemical reactivity and the level of conductivity of the molecule [55]. Smaller the value of energy gap, the easier electron transfer occurs from HOMO to LUMO. Relatively large gap means the molecule would not be kinetically stable [56]. In the present case the energy values of HOMO and LUMO are -7.827 and -



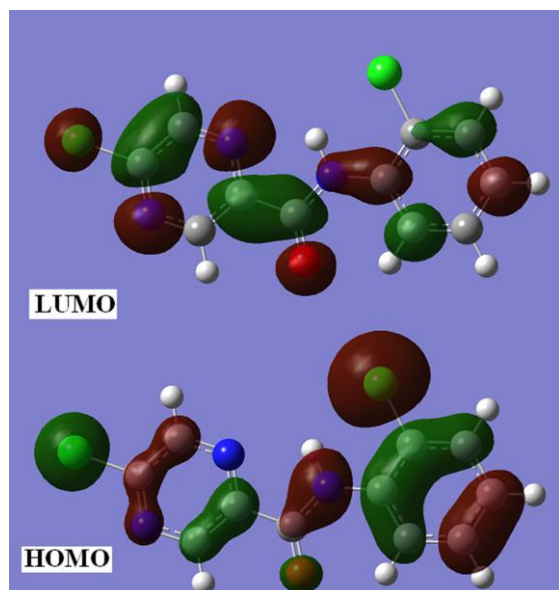


Figure 4. HOMO-LUMO plots of 5-chloro-N-(2-chlorophenyl)pyrazine-2-carboxamide.

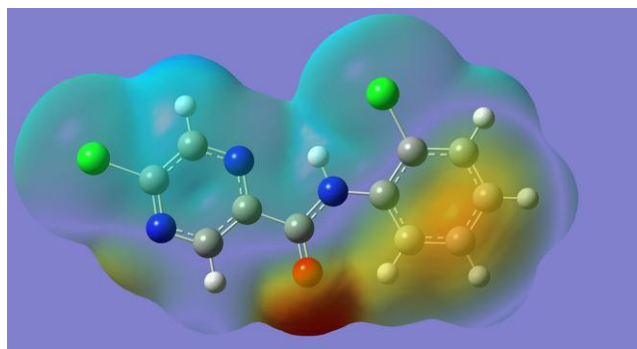


Figure 5. MEP plot of 5-chloro-N-(2-chlorophenyl)pyrazine-2-carboxamide.

4.845 eV, respectively. The ionization energy and electron affinity can be expressed as: $I = -E_{\text{HOMO}}$ and $A = -E_{\text{LUMO}}$; $I = 7.827$ and $A = 4.845$ eV. The different global descriptors are given by, hardness $\eta = (I-A)/2$, chemical potential $\mu = -(I+A)/2$ and electrophilicity index $\omega = \mu^2/2\eta$ [57, 58]. In the present case the values of these descriptors are $\eta = 1.491$, $\mu = -6.336$ and $\omega = 13.46$ and the energy gap between HOMO and LUMO orbitals is 2.982 eV. Figure 4 shows the distributions of the HOMO and LUMO orbitals and the HOMO is localized over the entire molecule while the LUMO is over the entire molecule, except the chlorine atom attached with the phenyl ring. Both the HOMO and LUMO are mainly localized on the pyrazine ring, indicating that the HOMO-LUMO are mostly the π -anti-bonding type orbital.

3.5. Molecular electrostatic potential

The molecular electrostatic potential has been used for predicting sites and relative reactivities towards electrophilic attack, in studies of biological recognition and hydrogen bonding interactions [59]. The molecular electrostatic potential provides a visual method to understand the relative polarity of a molecule and such surfaces depict the size, shape, charge density and site of chemical reactivity of the molecule. In the MEP surface generated, negative potential corresponds to an attraction of the proton by the concentrated electron density in the molecules (colored as red) and positive electrostatic potential corresponds

to repulsion of the proton by the atomic nuclei in regions where low electron density exists and the nuclear charge is incompletely shielded (colored in shades of blue). The electrostatic potential increases in the order red < orange < yellow < green < blue. As seen from the Figure 5, the regions of negative potential are C=O and phenyl ring where the positive potential regions are other parts of the title molecule.

3.6. Natural bond orbital analysis

The natural bond orbitals (NBO) calculations were performed using NBO 3.1 program [60] at the DFT/B3LYP level in order to understand various second-order interactions and the important results given in Tables 3 and 4. The various strong intra-molecular hyper conjugative interactions are: C_4-C_5 from Cl_{11} of $n_3(Cl_{11}) \rightarrow \pi^*(C_4-C_5)$, $C_{21}-O_{22}$ from N_{12} of $n_1(N_{12}) \rightarrow \pi^*(C_{21}-O_{22})$, $C_{13}-C_{14}$ from N_{15} of $n_1(N_{15}) \rightarrow \sigma^*(C_{13}-C_{14})$, $C_{18}-C_{19}$ from N_{16} of $n_1(N_{16}) \rightarrow \pi^*(C_{18}-C_{19})$, $C_{21}-N_{12}$ from O_{22} of $n_2(O_{22}) \rightarrow \sigma^*(C_{21}-N_{12})$ and $C_{19}-N_{16}$ from Cl_{24} of $n_3(Cl_{24}) \rightarrow \pi^*(C_{19}-N_{16})$ with electron densities, 0.38721, 0.33232, 0.03641, 0.04401, 0.06812, 0.39706e and stabilization energies, 8.43, 69.34, 9.13, 10.04, 22.98, 13.28 KJ/mol. The natural hybrid orbitals with higher energy orbitals and 100% p-character are: $n_3(Cl_{11})$, $n_2(O_{22})$, $n_3(Cl_{24})$ with energies, -0.32753, -0.26062, -0.33242a.u and with low occupation numbers, 1.95067, 1.87423, 1.92203. The orbitals with lower energy values are: $n_1(Cl_{11})$, $n_1(O_{22})$, $n_1(Cl_{24})$ having a lower energy value, -0.92376, -0.70490, -0.92203a.u with p-characters, 15.77, 38.16, 15.02% and high occupation numbers, 1.99419, 1.97655, 1.99478. Thus, a very close to pure p-type lone pair orbital participates in the electron donation to the $\pi^*(C_4-C_5)$ orbital for $n_3(Cl_{11}) \rightarrow \pi^*(C_4-C_5)$, $\pi^*(C_{21}-O_{22})$ orbital for $n_1(N_{12}) \rightarrow \pi^*(C_{21}-O_{22})$, $\sigma^*(C_{13}-C_{14})$ orbital for $n_1(N_{15}) \rightarrow \sigma^*(C_{13}-C_{14})$, $\sigma^*(C_{18}-C_{19})$ orbital for $n_1(N_{16}) \rightarrow \sigma^*(C_{18}-C_{19})$, $\sigma^*(C_{21}-N_{12})$ orbital for $n_2(O_{22}) \rightarrow \sigma^*(C_{21}-N_{12})$ and $\pi^*(N_{16}-C_{19})$ orbital for $n_3(Cl_{24}) \rightarrow \pi^*(N_{16}-C_{19})$ interaction in the compound.

3.7. Antiviral activity

In vitro activity of 5-chloro-N-(2-chlorophenyl)pyrazine-2-carboxamide was determined against a broad panel of various clinically important DNA and RNA viruses. The virus panel (see experimental section for the full list) included pathogens of medical importance such as herpesviruses, respiratory syncytial virus (RSV), HIV and influenza virus. No antiviral activity was detected up to the highest tested concentration, which was (due to limited solubility in the testing medium) 20 μM for most of the viruses, 25 μM for HIV, and 100 μM for influenza viruses.

3.8. Molecular docking

The enzyme glucosamine 6-phosphate deaminase (GlcN6P deaminase,) catalyzes the reversible isomerization and deamination of D-glucosamine 6-phosphate (GlcN6P) into D-fructose 6-phosphate and ammonium ion [61]. Glucosamine-6-phosphate synthase is the only member of the amidotransferase subfamily of enzymes. The molecular mechanism of reaction catalysed by GlcN-6-P synthase is complex and involves both amino transfer and sugar isomerisation. GlcN-6-P synthase is inflicted in phenomenon of hexosamine induced insulin resistance in diabetes [62]. Pyrazine and their derivatives in the past decade and were found to possess promising antitumor, anticonvulsant, antimicrobial, anti-tubercular and anti-diabetic activities [63]. High resolution crystal structure of glucosamine 6-phosphate deaminase was downloaded from the RSCB protein data bank website with PDB ID: 1FQO. All molecular docking calculations were performed on Auto Dock-Vina software [64]. The 3D crystal structure of glucosamine 6-phosphate deaminase was obtained from Protein Data Bank and the protein was prepared for docking by removing the co-crystallized ligands, waters and co-factors. The Auto Dock Tools (ADT) graphical user interface was used to calculate Kollman charges and polar hydrogens. The ligand was prepared for docking by minimizing its energy at B3LYP/6-31G (6D, 7F) level of

Table 3. Second order perturbation theory analysis of Fock matrix in NBO basis corresponding to the intra-molecular bonds of the title compound.

Donor(i)	Type	ED/e	Acceptor(j)	Type	ED/e	E(2) ^a	E(j)-E(i) ^b	F(i,j) ^c	
C1-C6	σ	1.972	C1-C2	σ^*	0.015	2.15	1.28	0.047	
			C4-C5	σ^*	0.021	3.14	1.26	0.056	
			C5-Cl11	σ^*	0.036	5.27	0.78	0.057	
C4-C5	σ	1.980	C3-C4	σ^*	0.016	2.49	1.30	0.051	
			C5-C6	σ^*	0.031	4.15	1.27	0.065	
			C6-N12	σ^*	0.028	3.45	1.15	0.056	
	π	1.715	C1-C6	π^*	0.387	18.97	0.30	0.069	
			C2-C3	π^*	0.338	15.99	0.31	0.063	
C5-C6	σ	1.978	C1-C6	σ^*	0.022	3.30	1.28	0.058	
			C4-C5	σ^*	0.021	3.51	1.30	0.060	
			C6-N12	σ^*	0.028	1.55	1.15	0.038	
N12-C21	σ	1.989	N12-C21	σ^*	0.068	2.78	1.20	0.052	
			C5-C6	σ^*	0.031	1.83	1.38	0.045	
			C6-N12	σ^*	0.028	2.08	1.26	0.046	
C13-C14	σ	1.987	C13-C14	σ^*	0.036	1.51	1.37	0.041	
			N12-C21	σ^*	0.068	1.78	1.21	0.042	
			C13-N15	σ^*	0.023	1.45	1.23	0.038	
C13-C21	σ	1.975	C13-C21	σ^*	0.070	2.09	1.15	0.044	
			C6-N12	σ^*	0.028	4.21	1.10	0.061	
			C13-C14	σ^*	0.036	1.44	1.21	0.037	
			C13-N15	σ^*	0.023	1.08	1.16	0.032	
			C14-N16	σ^*	0.014	2.51	1.17	0.049	
			N15-C18	σ^*	0.016	3.07	1.18	0.054	
N16-C19	σ	1.989	C18-C19	σ^*	0.044	1.87	1.40	0.046	
	π	1.718	C13-C14	π^*	0.292	21.09	0.34	0.076	
			N15-C18	π^*	0.336	17.46	0.31	0.067	
C18-C19	σ	1.992	N16-C19	σ^*	0.028	1.60	1.28	0.041	
C19-Cl24	σ	1.987	C14-N16	σ^*	0.014	3.29	1.17	0.055	
			N15-C18	σ^*	0.016	2.83	1.18	0.052	
C21-O22	π	1.973	C13-C14	π^*	0.292	4.09	0.36	0.037	
LPCl11	σ	1.994	C5-C6	σ^*	0.031	1.20	1.45	0.037	
	π	1.967	C4-C5	σ^*	0.021	2.87	0.90	0.045	
			C5-C6	σ^*	0.031	2.86	0.86	0.044	
	n	1.951	C4-C5	π^*	0.387	8.43	0.34	0.052	
LPN12	σ	1.627	C1-C6	π^*	0.387	36.08	0.29	0.092	
			C21-O22	π^*	0.332	69.34	0.26	0.121	
LPN15	σ	1.912	C13-C14	σ^*	0.036	9.13	0.92	0.083	
			C13-C21	σ^*	0.070	2.44	0.79	0.039	
			C18-C19	σ^*	0.044	9.02	0.89	0.081	
LPN16	σ	1.901	C13-C14	σ^*	0.036	8.75	0.90	0.081	
			C18-C19	σ^*	0.044	10.04	0.88	0.085	
			C19-Cl24	σ^*	0.074	5.23	0.45	0.044	
LPO22	σ	1.977	N12-C21	σ^*	0.068	2.35	1.16	0.047	
			C13-C21	σ^*	0.070	2.03	1.10	0.043	
	π	1.874	N12-C21	σ^*	0.068	22.98	0.72	0.116	
			C13-C21	σ^*	0.070	18.45	0.66	0.100	
LPCl24	σ	1.995	C18-C19	σ^*	0.044	1.13	1.43	0.036	
	π	1.971	N16-C19	σ^*	0.028	5.05	0.83	0.058	
			C18-C19	σ^*	0.044	3.07	0.83	0.045	
	n	1.922	N16-C19	π^*	0.397	13.28	0.29	0.060	

^aE(2) means energy of hyper-conjugative interactions (stabilization energy in kJ/mol)^bEnergy difference (a.u.) between donor and acceptor i and j NBO orbitals^cF(i,j) is the Fock matrix elements (a.u.) between i and j NBO orbitals

Table 4. NBO results showing the formation of Lewis and non-Lewis orbitals.

Bond(A-B)	ED/e ^a	EDA%	EDB%	NBO	s%	p%
σ C1-C6	1.966	47.95	52.05	0.6925(sp ^{2.03})C+	32.93	67.07
	-0.705			0.7214(sp ^{1.70})C	37.06	62.94
σ C4-C5	1.980	49.09	50.91	0.7007(sp ^{1.91})C+	34.32	65.68
	-0.740			0.7135(sp ^{1.45})C	40.76	59.24
π C4-C5	1.715	45.78	54.22	0.6766(sp ^{1.00})C+	0.00	100.0
	-0.280			0.7363(sp ^{1.00})C	0.00	100.0
σ C5-C6	1.978	49.49	50.91	0.7035(sp ^{1.57})C+	38.92	61.08
	-0.739			0.7170(sp ^{1.86})C	34.98	65.02
σ N12-C21	1.989	62.80	37.20	0.7925(sp ^{1.80})N+	35.64	64.36
	-0.848			0.6099(sp ^{2.08})C	32.40	67.60
σ C13-C14	1.987	51.33	48.67	0.7164(sp ^{1.68})C+	37.26	62.74
	-0.756			0.6976(sp ^{1.73})C	36.59	63.41
σ C13-C21	1.975	52.18	47.82	0.7224(sp ^{2.05})C+	32.79	67.21
	-0.691			0.6915(sp ^{1.85})C	35.04	64.96
σ N16-C19	1.989	59.15	40.85	0.7691(sp ^{1.71})N+	36.78	63.22
	-0.902			0.6391(sp ^{1.90})C	34.52	65.48
π N16-C19	1.718	55.19	44.81	0.7429(sp ^{1.00})N+	0.00	100.0
	-0.352			0.6694(sp ^{1.00})C	0.00	100.0
σ C18-C19	1.992	49.25	50.75	0.7018(sp ^{1.76})C+	36.18	63.82
	-0.780			0.7124(sp ^{1.38})C	42.03	57.97
σ C19-Cl24	1.987	45.58	54.42	0.6751(sp ^{3.27})C+	23.39	76.61
	-0.693			0.7377(sp ^{5.57})Cl	15.15	84.85
π C21-O22	1.973	30.39	69.61	0.5512(sp ^{1.00})C+	0.00	100.0
	-0.370			0.8343(sp ^{1.00})O	0.00	100.0
n1Cl11	1.994 -0.924	-	-	sp ^{0.19}	84.23	15.77
n2Cl11	1.967 -0.334	-	-	sp ^{99.99}	0.56	99.44
n3Cl11	1.951 -0.328	-	-	sp ^{1.00}	0.00	100.0
n1N12	1.627 -0.273	-	-	sp ^{1.00}	0.00	100.0
n1N15	1.912 -0.393	-	-	sp ^{2.48}	28.68	71.32
n1N16	1.901 -0.380	-	-	sp ^{2.51}	28.43	71.57
n1O22	1.977 -0.705	-	-	sp ^{0.62}	61.84	38.16
n2O22	1.874 -0.261	-	-	sp ^{1.00}	0.00	100.0
n1Cl24	1.995 -0.931	-	-	sp ^{0.18}	84.98	15.02
n2Cl24	1.971 -0.333	-	-	sp ^{99.99}	0.09	99.91
n3Cl24	1.922 -0.332	-	-	sp ^{1.00}	0.00	100.0

^aED/e in a.u.

Table 5. The binding affinity values of different poses of the title compound predicted by Autodock Vina.

Mode	Affinity (kcal/mol)	Distance from best mode (Å)	
		RMSD l.b.	RMSD u.b.
1	-6.4	0.000	0.000
2	-6.3	16.000	17.494
3	-5.9	15.604	16.062
4	-5.9	15.517	16.703
5	-5.5	15.509	16.908
6	-5.4	15.629	16.383
7	-5.4	25.660	24.969
8	-5.3	21.630	22.584
9	-5.2	25.087	26.492

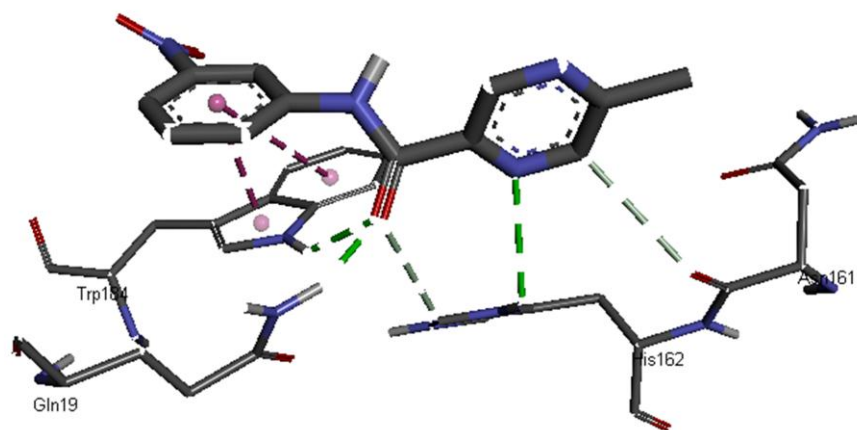


Figure 6. Schematic for the ligand interaction with the active site of glucosamine-6-phosphate deaminase.

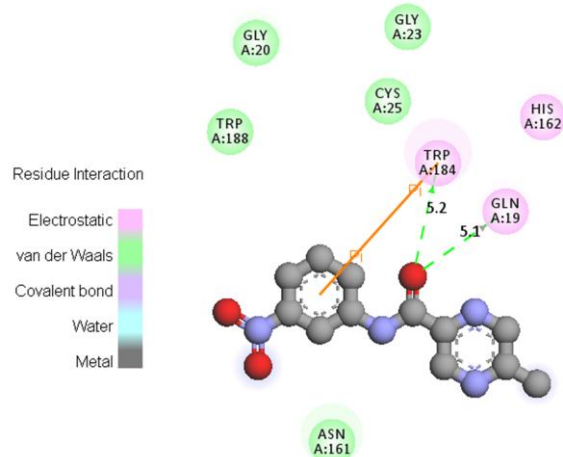


Figure 7. 2D interactive plot of ligand and glucosamine-6-phosphate deaminase receptor.

theory and partial charges were calculated by Geistenger method. The active site of the enzyme was defined to include residues of the active site within the grid size of $40\text{\AA} \times 40\text{\AA} \times 40\text{\AA}$. The most popular algorithm, Lamarckian Genetic Algorithm (LGA) available in Autodock was employed for docking. The docking protocol was tested by extracting co-crystallized inhibitor from the protein and then docking the same. The

docking protocol predicted the same conformation as was present in the crystal structure with RMSD value well within the reliable range of 2\AA [65]. Amongst the docked conformations, one which binds well at the active site was analysed for detailed interactions in Discover Studio Visualizer 4.0 software. The ligand binds at the active site of the substrate (Figures 6 and 7) by weak non-covalent interactions. Amino acid Leu106 forms H-bond with the docked ligand. The docked ligand title compound forms a stable complex with glucosamine 6-phosphate deaminase and gives a binding affinity (ΔG in kcal/mol) value of -6.4 (Table 5). These preliminary results suggest that the compound might exhibit inhibitory activity against glucosamine 6-phosphate deaminase (Figure 8).

4. CONCLUSIONS

The FT-IR and FT-Raman spectra of the title compound were reported experimentally and theoretically. The HOMO and LUMO analysis are used to determine the charge transfer within the molecule. The chemical reactivity is understood from the chemical potential, electrophilicity and global hardness. The stability of the molecule arising from hyperconjugative interaction and charge delocalization has been analyzed using natural bond orbital analysis. MEP predicts the most reactive part in the molecule. Optimized geometrical parameters of the title compound are in agreement with that of similar derivatives. The hyperpolarizability values of the title compound are also determined and from the study reveals that the title compound and its derivatives are attractive objects for future studies in nonlinear optics. The title compound binds at the active site of the substrate by weak non-covalent interactions and the amino acid Leu106 forms H-bond with the docked

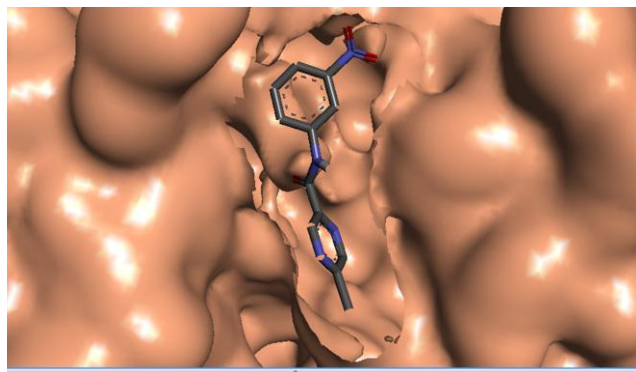


Figure 8. Pictorial representation with docked ligand embedded in the active site of glucosamine-6-phosphate deaminase.

ligand. As an additional test, in vitro antiviral activity of the title compound was evaluated against broad panel of clinically important viruses. No antiviral activity was detected in the tested concentrations.

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