

Crystal structure, physicochemical, DFT, optical, keto-enol tautomerization, docking, and anti-diabetic studies of (Z)-pyrazol β -keto-enol derivative

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ABSTRACT

The new (Z)-pyrazol β -keto-enol as model-molecule has been prepared in accepted high yield; the structure was investigated by X-ray single crystal diffraction (XRD) and Density Functional Theory (DFT) modeling. Several hydrogen bonds interactions were recorded experimentally via XRD and theoretically via Hirshfeld surface analysis (HSA) calculations. The recorded vibrational frequencies FT-IR were further compared to computed ones. Natural Population Analysis (NPA), Mulliken Atomic Charge (MAC), and Molecular Electrostatic Potential (MEP) has been carried out to complete the set of theoretical tools. The HOMO/LUMO, density of state (DOS) and TD-SCF/DFT were applied to compare these quantum parameters with experimental electron transfer and direct optical activity. DFT calculations, natural bond orbital (NBO) analysis and non-covalent interactions (NCI) analysis were used to explore the mechanism of the single proton keto-enol intra-migration tautomerization reaction. Additionally, the desired compound was screened for its *in-vitro* α -amylase and α -glucosidase inhibitory activities. The title compound reflected a potent inhibitory activity α -glucosidase enzyme with IC_{50} value of $72.20 \pm 1.50 \mu M$. Moreover, the solved 3D-crystal structure was used for 1BNA DNA docking evaluation.

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1. Introduction

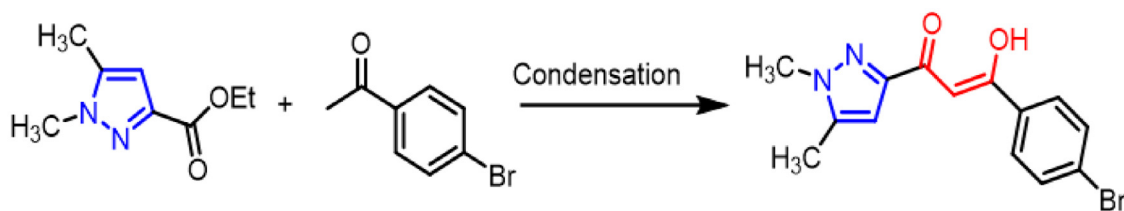
β -ketoenols compounds are interesting in pharmaceutical and medical fields, and are used as drugs against cancer, HIV, influenza, anti-inflammatory and antioxidant substances [1–8]. Derivatives of

the β -keto-enol were used as chelate O₂O ligands that play a good turn in developing the coordination and complexation chemistry, since such compounds can stabilize several transition metals complexes via their polydentate mode of coordination [9–11].

The ketoenol associated with a pyrazole unit revealed molecules with combination properties; the chelate effect is supported furthermore via nitrogen atoms in the pyrazole part, which raised up the poly-chelate properties of the ligand that allowed the development of cluster coordination science [10–12].

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Scheme 1. Synthetic route for the desired (Z)-pyrazol β -keto-enol compound.

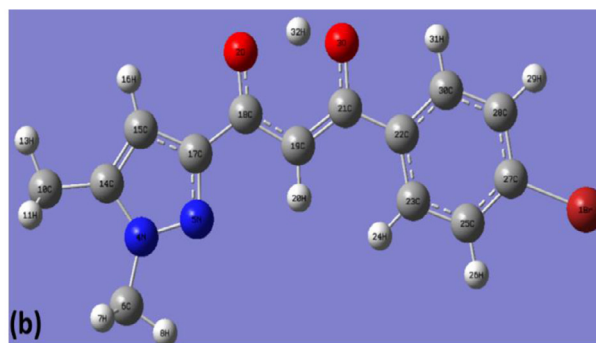
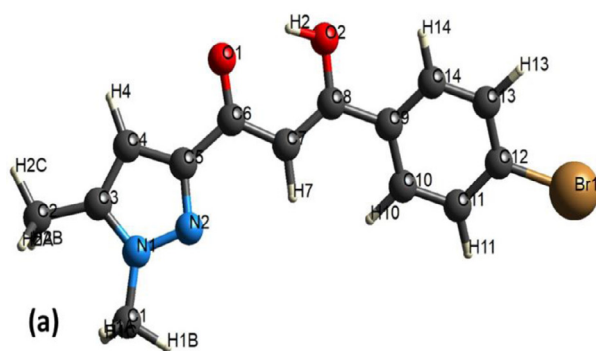


Fig. 1. (a) ORTEP, and (b) B3LYP/6-311++G(d,p) structures.

One of the simplest process and most significant one that have recently raised an immense interest is the intramolecular proton transfer (IPT). Most of the possible IPT phenomena have been found in keto-enol molecules having intra proton acceptors (C=O, C=N) and intra proton donors (N-H, O-H) modes *via* authentic synthesis of type *n* [S(*n*)] intramolecular hydrogen bonds tautomerisms [13].

Keto-enol tautomerism services a decisive turn in molecules holding carbonyl functional group. Requesting the carbonyl tautomeric in molecules are significant to substantiate their critical biological applications and to comprehend biochemical reactions [14–19]. The best-known examples of tautomerism in organic materials with keto-enol functional groups are nitrogenous bases, which preserve the DNA double-strand structure *via* protons transfer to form new hydrogen bonds from the keto isomer. Keto-enol tautomerism of proton in hydroxyl group to its neighbor carbonyl functional group via single or double protons intra-migration have been investigated by means of experimental and theoretical methods [11–18]. However, several experimental and theoretical studies condoned the function of tautomeric process; nature of the proton movements (intra- or inter-molecular migration), accelerating or depressing factors, general mechanism and the role of H-bonding in stabilized both Keto and enol isomers structures [12–19].

In this work, we synthesized a new (Z)-pyrazol β -keto-enol compound which was subjected to XRD-analysis, HSA, spectral and several DFT-quantum, docking evaluation and DFT of the single proton keto-enol intra-migration tautomerization process. Moreover, the compound was screened for their *in-vitro* α -glucosidase and α -amylase inhibitory activities.

2. Experimental section

2.1. Computations and XRD

The DFT-calculations were performed at DFT/B3LYP/6-311++G(d,p) in gaseous phase via Gaussian09 program [20]. CRYSTAL EXPLORER 3.1 software was employed for HSA calculation [21]. The XRD-structure was employed using SHELXS program, respectively [22]. (Table S1 Supplementary Material)

2.2. BNA docking

Docking calculations were carried out at Intel(R) Core(TM) i7 CPU (3 GHz) with Windows 2010 software. The structure was drawn by ChemDraw. The docking was performed by assigning Gastegier charges. Water molecules were erased, and merging of non-polar hydrogen atoms was done using AutoDock.4 [23]. The X-ray crystal of PDB ID: 1BNA DNA was collected free from the Protein Data Bank [24].

2.2.1. Synthesis of (Z)-3-(4-Bromophenyl)-1-(1,5-dimethyl-1H-pyrazol-3-yl)-3-hydroxyprop-2-en-1-one

The β -keto-enol pyrazole derivative studied in this paper was prepared according to the experimental procedure described in our previous work [25]. 7.6 mmol of sodium metal was suspended in 30 mL of toluene before it was traded with 6.0 mmol of pyrazolic carboxylate dissolved also in 20 mL of toluene. Under 0 °C, 6.0 mmol of 3-bromophenyl methyl ketone 10 mL in toluene was added. The reaction mixture was stirred for 3 days at ambient air and room temperature. A precipitate was filtered, then cleaned well using aqueous acetic acid to pH = 5. The extracted organic product using CH₂Cl₂ was left to evaporate at room temperature. Yield ~ 40%.

Brown powder; yield: 32%; m.p 150 °C; R_f = 0.93 (CH₂Cl₂/MeOH 9/1)/silica. IR (KBr, cm⁻¹): ν (OH)=3500–3300; ν (C=O) = 1670; ν (enolic C=C)=1565; ¹H NMR (CDCl₃): δ 2.30 (s, 3H, Pz-CH₃); 3.63 (s, 3H, CH₃-N); 3.76 (s, 0.1H, keto, CH₂); 6.52 (s, 1H, pz-H); 6.69 (s, 0.9H, C-H); 7.72 (m, 2H, Ar-H_{3,5}); 7.85 (m, 2H, Ar-H_{2,6}). ¹³C NMR (CDCl₃): δ 11.38 (1C, Pz-CH₃); 37.04 (1C, CH₃-N); 48.78 (1C, keto CH₂); 94.56 (1C, enol C-H); 106.45 (1C, -CH-pz); 121.94 (1C, Ar-C₄); 126.09 (2C, Ar-C_{3,5}); 129.22(2C, Ar-C_{2,6}); 180.54 (1C, C-OH); 183.59 (1C, C=O). Anal. Calcd. for C₁₄H₁₃BrN₂O₂: C 52.36, H 4.08, N 8.72. Found C 52.27, H 4.03, N 8.8; m/z : 321 (M+H)⁺.

2.3. Antidiabetic activity

2.3.1. α -Glucosidase inhibition assay

The α -glucosidase inhibitory activity was performed in PBS (0.1M; pH 6.7), using *p*-nitrophenyl- α -D-glucopyranoside (*p*NPG) as a substrate, following the method described by Lakbaibi et al.

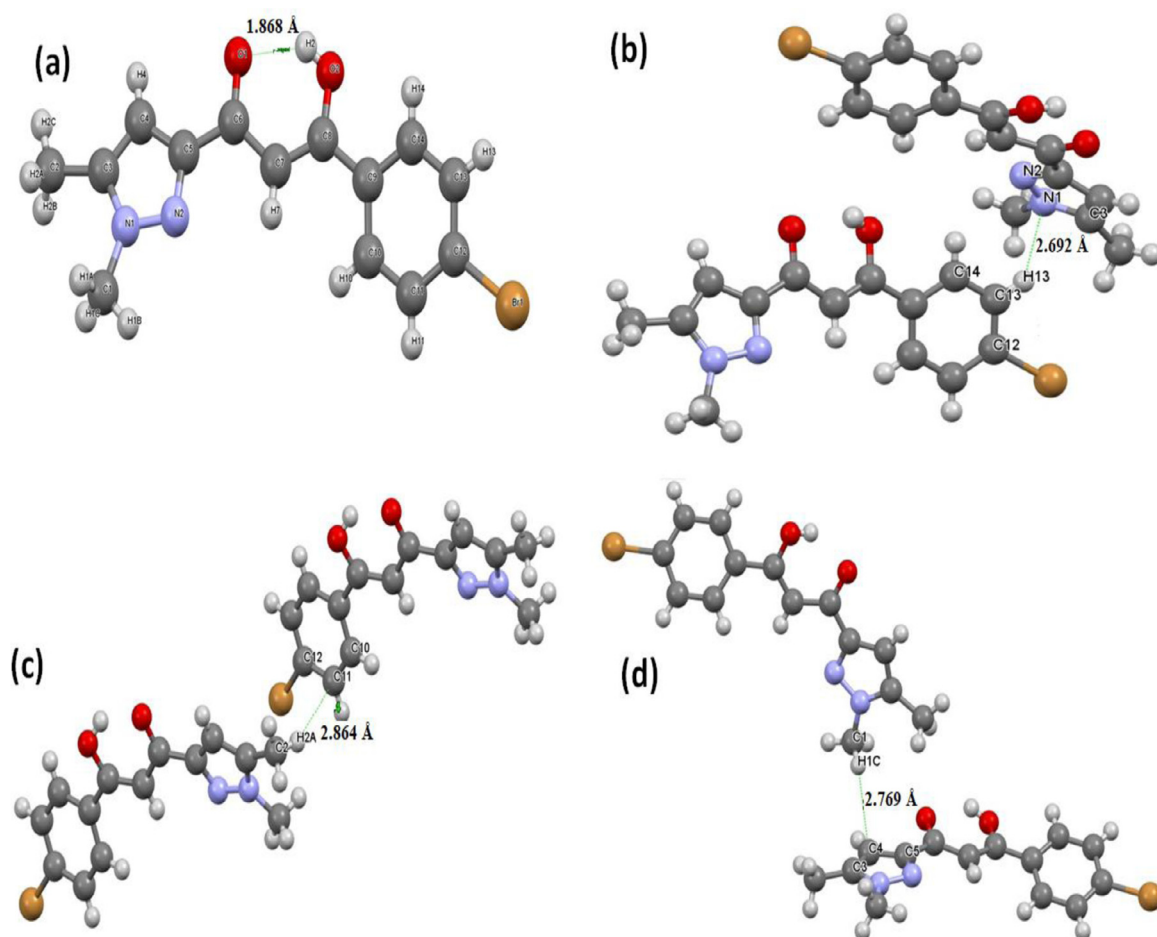


Fig. 2. H-bonds types and bond lengths.

[26], with some slight modifications. The samples were prepared by dissolving the title compound in DMSO and diluted in PBS to a series of different concentrations. Briefly, a mixture of 150 μL of the test sample and 100 μL of PBS containing the Baker's yeast α -Glucosidase enzyme solution (0.1 U/mL) were incubated at 37 $^{\circ}\text{C}$ for 10 min. Then, 200 μL of ρNPG (1 mM) was added to the mixture to initiate the reaction. After incubation at 37 $^{\circ}\text{C}$ for 30 min, 1 mL Na_2CO_3 (0.1 M) was added to stop the reaction and the absorbance was measured at $\lambda = 405$ nm. The results were expressed as percentage inhibition and calculated using the following formula:

$$\text{Inhibition (\%)} = \left[\frac{(1 - (A_{\text{sample}} - A_{\text{b sample}}))}{(A_{\text{control}} - A_{\text{b control}})} \right] \times 100$$

Where A_{control} refers to the absorbance of the control (enzyme and buffer); $A_{\text{b control}}$ refers to the absorbance of control blank (buffer without enzyme); A_{sample} refers to the absorbance of the sample (enzyme and inhibitor); and $A_{\text{b sample}}$ is the absorbance of sample blank (inhibitor without enzyme). Acarbose was used as positive control.

2.3.2. α -amylase inhibition assay

The α -amylase inhibitory assay was performed by the protocol of Lakbaibi et al. [26] with some modifications. At first, the substrate was prepared by dissolving 200 mg starch in 25 mL of sodium hydroxide (0.4 M) with heating at 80 $^{\circ}\text{C}$ for 5 min. After cooling, pH was adjusted to 7.0 ± 0.1 and the final volume was completed to 100 mL with distilled water. Samples solution at varying concentrations (150 μL) were mixed with 500 μL of 0.02 M PBS (pH 6.9, 0.006M NaCl) containing the Human Pancreatic α -amylase enzyme (1.5 U/mL) and incubated for 10 min at 37 $^{\circ}\text{C}$.

Soluble starch (0.2%, PBS 0.02M, pH 6.9, 0.006M NaCl) was added to the mixture and further incubated at 37 $^{\circ}\text{C}$ for 10 min. The reaction was stopped by adding 250 μL of HCl (1M), followed by the addition of 300 μL of iodine reagent (5 mM), and the absorbance was measured at $\lambda = 630$ nm. The α -amylase inhibitory activity was expressed as percentage inhibition, and the IC_{50} values were determined. Acarbose was used as positive control.

3. Result and discussion

3.1. Synthesis CHN-EA and MS

The (Z)-pyrazol β -keto-enol compound was prepared in high yield via condensation of ethyl 1,5-dimethyl-1H-pyrazole-3-carboxylate with 2-(4-bromophenyl)-2-oxoethan-1-ylum at room temperature stirring for 48 h [20–25], as seen in Scheme 1.

Mass spectrometry of the desired compound was found to be 320.02 (theoretical 321.02), and the CHN-elemental analysis was found to be C, 52.42; H, 4.10 and N, 8.84, compared to the calculated from the general formula $\text{C}_{14}\text{H}_{13}\text{BrN}_2\text{O}_2$ to be C, 52.36; H, 4.08 and N, 8.72%.

3.2. XRD and DFT-structure analysis

The desired β -keto-enol crystallized in Z-kinetic favored isomer form with monoclinic, $P2_1/n$ space-group, with four molecules in the unit-cell ($Z = 4$), as illustrated in Fig. 1a. The compound was stabilized in planar structure with very short intra-hydrogen bond

Table 1
DFT-calculated angles (°) and bond lengths (Å) compared to experimental XRD data.

Bond No.	Bonds	Exp. XRD	DFT	Angles No.	Angles (°)	Exp. XRD	DFT
1	Br1 C12	1.905	1.9282	1	N2 N1 C1	119	119.3
2	O1 C6	1.264	1.2888	2	N2 N1 C3	112.9	112.25
3	O2 C8	1.327	1.3442	3	C1 N1 C3	128	128.45
4	N1 N2	1.359	1.3907	4	N1 N2 C5	104.1	103.65
5	N1 C1	1.455	1.464	5	N1 C3 C2	123.2	122.82
6	N1 C3	1.364	1.3829	6	N1 C3 C4	106	106.21
7	N2 C5	1.337	1.352	7	C2 C3 C4	130.7	130.97
8	C2 C3	1.500	1.4972	8	C3 C4 C5	105.6	105.88
9	C3 C4	1.372	1.3822	9	N2 C5 C4	111.4	112.01
10	C4 C5	1.412	1.4165	10	N2 C5 C6	121.8	122.35
11	C5 C6	1.465	1.4591	11	C4 C5 C6	126.7	125.64
12	C6 C7	1.429	1.4251	12	O1 C6 C5	117.8	118.47
13	C7 C8	1.376	1.3792	13	O1 C6 C7	121.5	122.15
14	C8 C9	1.464	1.4746	14	C5 C6 C7	120.7	119.38
15	C9 C10	1.402	1.4032	15	C6 C7 C8	120.9	118.96
16	C9 C14	1.400	1.4035	16	O2 C8 C7	120.9	120.74
17	C10 C11	1.380	1.3916	17	O2 C8 C9	114.2	114.83
18	C11 C12	1.393	1.3914	18	C7 C8 C9	124.9	124.43
19	C12 C13	1.368	1.3903	19	C8 C9 C10	121.9	122.81
20	C13 C14	1.383	1.3911	20	C8 C9 C14	119.4	118.3

of type O-H...O=C [25–28]. In the gaseous phase, the B3LYP/6-311++G(d,p) optimized structure reflected also the presence of intra-hydrogen bond which is consistent with XRD-exp. result as seen in Table 1 and Fig. 1b.

DFT/XRD angles and bonds lengths values are in an excellent agreement (Table 1 and Fig. S1 of Supporting Materials), Bond length DFT and experimental values it was seen in Fig. S1, where the graphical correlation was found to be 0.9931 as in Fig. S1 b. closely, the graphical correlation between the DFT/XRD angles found to be 0.9844 (Fig. S1 c and d). The DFT parameters are slightly longer than the XRD ones since they are performed in the gaseous state, whereas the XRD was carried out in the solid-state.

3.3. Crystal interactions and HSA investigation

Two main H-bonds of types H...O and H...N were recorded in the lattice of the crystal [27–30], each molecule is binding with its surrounding via four total interactions (Fig. 2). Two H-bonds and two H... π interactions. The shortest interaction is in the β -keto-enol part since the proton of enol binds to the carbonyl oxygen of the keto part as O-H...O=C with 1.868 Å to form a S6 intra-synthon (Fig. 2a). An inter hydrogen bond of type C_{ph}-H...N_{pyrazole} with 2.692 Å, forming a 1D supramolecular system was observed (Fig. 2b). The other H... π bonds were detected as C_{Me}-H... π _{ph} 2.864 Å (Fig. 2c) and C_{Me}-H... π _{pyrazole} 2.769 Å (Fig. 2d).

In HSA, four red dots on the d_{norm} surface of the ligand molecule were detected [28–32]; all the d_{norm} big dots are due to the intra H...O and inter H...N hydrogen bonds formation (Fig. 3a). The shape index Fig. 4b reflected clearly the formation of H... π _{ring} bonds interactions. The number and the type of the H-bonds detected by HSA were matching with XRD-result interactions result (Fig. 3b). The HSA 2D-FP result plots over the ligand surface molecule revealed the presence of 58.5% H...overall connections. Atom-to-atom inter-contacts ratios are depicted in Fig. 3c with five types of H...interactions as: H...H (35.6%) > H...C (9.2%) > H...O (5.7%) > H...Br (4.9%) > H...N (4.9%).

3.4. MEP and atomic charge populations

The MEP suggested the presence of electrophilic/nucleophilic sites in the molecule surface as seen in Fig. 4a and b. For instance, the red color reflected hydroxyl oxygen, carbonyl O and pyrazole N atoms as the strongest nucleophile site. The Br atom with green color indicating that it is between electrophilic and nucleophilic

centers. The blue colors of methyl and phenyl protons atoms reflected the electrophilic positions, except the proton atom of the hydroxide which is in green color since this atom is busy with intra-hydrogen bond, therefore it is not highlighted with blue color. Since both blue and red colors were detected via MEP, therefore several H-bonds were predictable [27,28]. These results matched well the XRD and HAS results.

MAC and NPA charges population revealed digital e-poor or e-rich molecule atoms as in Fig. 4c. Generally, MAC reflected less atomic-charges values compared to NPA. The MAC and NPA proved all the N and O atoms and (C6, C10, C15, C19, C20, C22, C23, C27, C28 and C30) atoms are with negative e-values (nucleophilic sites). The electrophilic sites are C14 and C21 atoms and all hydrogen atoms since they are with positive e values, therefore its electrophilic sites (see Table 2). Moreover, the NPA and MAC charges results are fitted well with the MEP, XRD and HSA results.

3.5. IR investigations

The solid state Exp.-IR and the DFT gaseous state of the desired ligand showed the presence of couple of functional groups in the backbone of the ligand. The O-H bond was not detected in both states with its expected frequencies at 3500–3300 cm⁻¹ that supported the presence of intra hydrogen bond [25]. C-H_{ph} stretching vibrations were found at ~ 3110 cm⁻¹, C-H_{CH3} stretching vibrations at 2950–2840 cm⁻¹ and C=O stretching vibrations at 1670 cm⁻¹ as seen in Fig. 5a. Moreover, a high degree of correlation between the DFT-IR and Experiment was observed (Fig. 5b). This high degree of compatibility can be translated via 0.9927 graphical correlation values as seen in Fig. 5c.

3.6. HOMO-LUMO, DOS, optical and TD-DFT/e-transfer

HOMO/LUMO shapes and energy diagram (Fig. 6a) and DOS (Fig. 6b) showed the e-donation ability in the UV area with $\Delta E_{HOMO/LUMO}$ = 4.2327 and 4.2520 eV, respectively.

Experimentally, Tauc relation [33] can be used to check the energy matching between DOS and HOMO/LUMO theoretical result with optical band gap energy (ΔE_g) using DMSO solvent yielding to ΔE_g = 4.22 eV (Fig. 6c). The result is approximated to both $\Delta E_{HOMO/LUMO}$ and ΔE_{DOS} energy.

The experimental electron transfer and computed TD-DFT/B3LYP/6-311++G(d,p) in DMSO solvents was illustrated in Fig. 6d. Experimentally, two broad bands at λ_{max} = 230 and

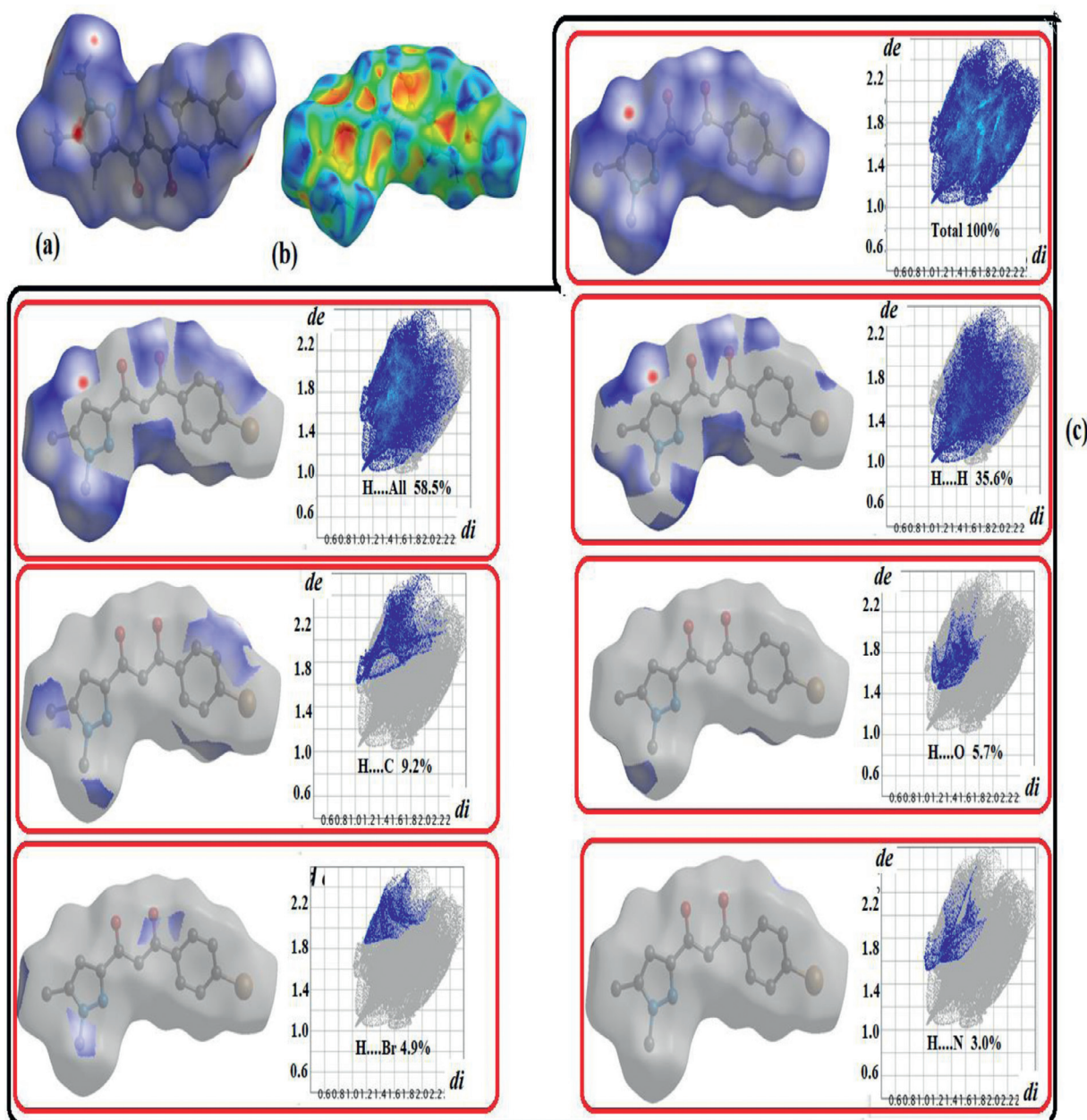


Fig. 3. (a) d_{norm} mapped (b) shape index, and (c) Fingerprint inside...outside atoms.

Table 2
Mac and NPA charge population.

Atoms No.	Atom type	MAC	NPA	Atoms No.	Atom type	MAC	NPA
1	Br	0.206289	0.11132	17	C	0.290033	0.08653
2	O	-0.49037	-0.48656	18	C	0.396422	0.43962
3	O	-0.58526	-0.64112	19	C	-0.28694	-0.36893
4	N	-0.3949	-0.24405	20	H	0.214996	0.24463
5	N	-0.37777	-0.24946	21	C	0.308859	0.34069
6	C	-0.40481	-0.46671	22	C	-0.02027	-0.10469
7	H	0.218281	0.23159	23	C	-0.1937	-0.20566
8	H	0.23553	0.24695	24	H	0.213562	0.2449
9	H	0.218747	0.22675	25	C	-0.14534	-0.22184
10	C	-0.62864	-0.70448	26	H	0.212826	0.25359
11	H	0.219565	0.2462	27	C	-0.34902	-0.1623
12	H	0.22655	0.24964	28	C	-0.14271	-0.24011
13	H	0.229027	0.25655	29	H	0.213245	0.25463
14	C	0.264418	0.14908	30	C	-0.18116	-0.19156
15	C	-0.27179	-0.30214	31	H	0.219605	0.2597
16	H	0.198791	0.25947	32	H	0.385917	0.48778

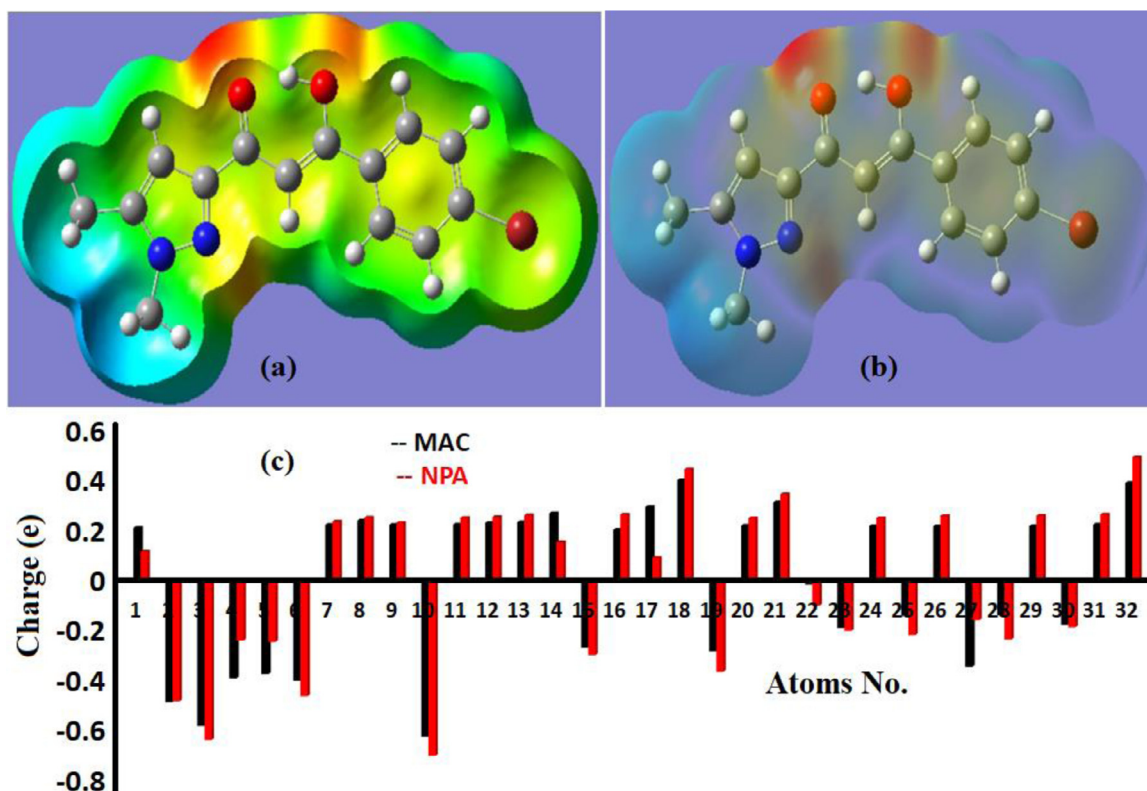


Fig. 4. (5) B3LYP/MEP, (a) labeled map and (b) BPA (■) and MAC (■) charge populations.

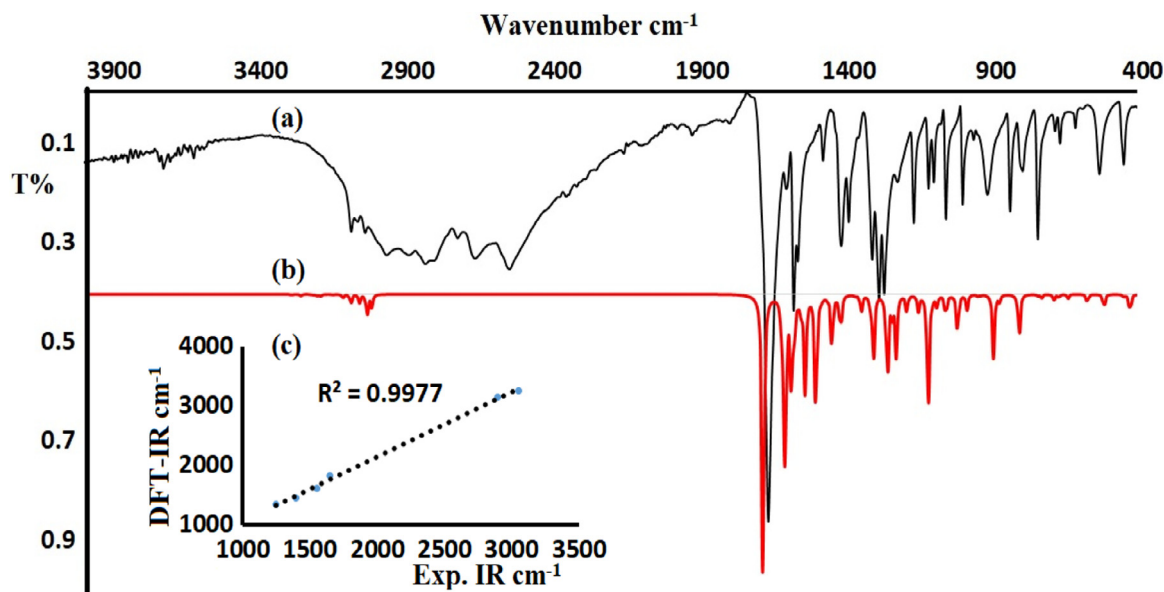


Fig. 5. IR of desired ligand (a) Exp. solid state (b) gaseous state DFT and (c) Exp./DFT graphical correlation.

$\lambda_{\text{max}} = 312 \text{ nm}$ corresponding mainly to $\pi \rightarrow \pi^*$ and $n \rightarrow \pi^*$ e-transition, were observed. No more bands were detected in the visible area. TD-DFT reflected a similar absorption behavior (Fig. 6d), two peaks with $\lambda_{\text{max}} = 236$ and $\lambda_{\text{max}} = 315 \text{ nm}$ were reported in DMSO, which is meanly assigned to HOMO-1 > LUMO+1 (12%), HOMO > LUMO+1 (18%), HOMO > LUMO+2 (50%) HOMO-5 > LUMO (7%), HOMO-5 > LUMO+1 (4%) and HOMO-4 > LUMO (4%) for peak at $\lambda_{\text{max}} = 236 \text{ nm}$. Peak at $\lambda_{\text{max}} = 315 \text{ nm}$ is assigned to HOMO-1 > LUMO (11%), HOMO > LUMO (83%) and HOMO-3 > LUMO (2%). The small $\Delta\lambda$ shift between the Exp.

and DFT peaks can be attributed to solvent-solute interaction [27–32].

3.7. Tautomerisation of diketone (DFT study)

3.7.1. Energetic profile of reaction

The transformation of diketone structure through tautomerisation process to (Z)-keto enol, (Z)-enol keto and (E)-enol keto was discussed (Fig. 7) under implicit SMD solvation of toluene, room temperature and 1 atm. All concerned structures out carried basing on DFT computations by applying the B3LYP exchange-correlation

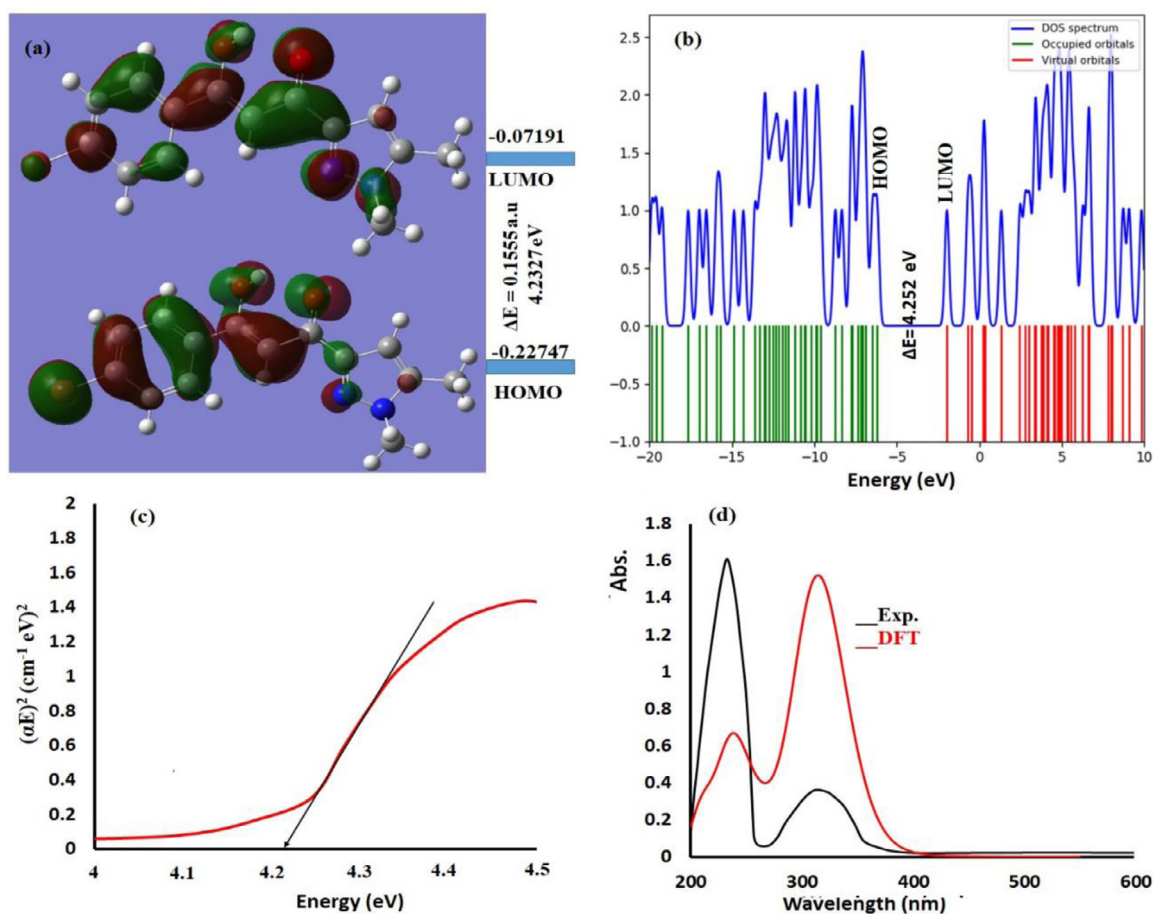


Fig. 6. (a) LUMO/HOMO, (b) TD-DFT, (c) Exp. electronic spectra, and (d) optical band gap energy in DMSO.

functional with 6-311G++(d,p) basis set [25,26]. Therefore, in order to contribute to a better understanding of the mechanism for this reaction and explain the most favorable tautomerization, we realized the various points as follows: a complete analysis of the Gibbs free energy difference profile of the reaction. Yet, a characterization of the transition-state TSs (i.e., TS-(Z)-keto enol and TS-(Z)-enol keto) associated with the tautomerism reaction was made using QST3 approach [34,35] (Fig. 8). All calculations were made at level NBO analysis [36].

According to the Fig. 8, the (Z)-keto enol is slightly more stable than (Z)-enol keto with 2.250 kcal/mol. The diketone tautomerization to both (Z)-keto enol and (Z)-enol keto has almost a similar aspect at level kinetic behavior. Therefore, we have noticed that the formation of (Z)-keto enol is slightly more favored than of (Z)-enol keto. Otherwise, it is noticed that the activation Gibbs free energy barrier corresponding to the formation of (Z)-keto enol is 44.238 kcal/mol, and for the formation of (Z)-enol keto is 46.114 kcal/mol; indicates clearly that the kinetic of formation of (Z)-keto enol is almost the same with (Z)-enol keto. This result indicates that both (Z)-keto enol and (Z)-enol keto products have the potential to form with a small dominance of (Z)-keto enol. As for the formation of (E)-enol keto its formation is difficult from diketone tautomerization (it is not possible).

3.7.2. NCI analysis

NCI analysis was also carried out on the three following possible structures (Z)-keto enol, (Z)-enol keto and (E)-enol keto which formed according to the studied reaction. NCIs analysis evaluates the intermolecular interactions and can be revealed solely by means of the reduced density gradient, S , which is a scalar field of

the electron density (ρ) and can be defined as:

$$S = \frac{|\nabla \rho|}{2(3\pi^2)^{1/3} \rho^{4/3}}$$

The S function has higher values in regions outside the molecule and lower values near the covalent bonds and non-covalent interactions, which appear as peaks in the $S(r)$ diagram [38]. The limiting interaction cases like hydrogen bonds, Van der Waals (VdW) and steric repulsion is reflected here with a coloring scheme (blue, green, and red, respectively). Lu and Chen [39] conducted the non-covalent interactions and their visualization was done with Visual Molecular Dynamics VMD [40].

In other words, we observed from NCI analysis (Fig. 9) that both (Z)-keto enol and (Z)-enol keto present a hydrogen bond interaction between H α and O1 which considered as strong interaction (32.15 and 26.04 kcal/mol, respectively, calculated from NBO analysis), much higher than the usual hydrogen bonds energies of 4–6 kcal/mol [41]. Additionally, as for (E)-enol keto we have remarked that there are existence of repulsive interactions between two hydrogen atoms (H6 & H7) and between oxygen and nitrogen atoms (O5 & N6). It is worth mentioning here that the strong hydrogen bond at the (Z)-keto enol and (Z)-enol keto favor their formation with respect to that of (E)-enol keto (presence of repulsive interactions).

3.8. Anti-diabetic activity

The antidiabetic activity of the title compound has been systematically evaluated against α -glucosidase and α -amylase at different concentration. The IC₅₀ values of the *in-vitro* α -glucosidase

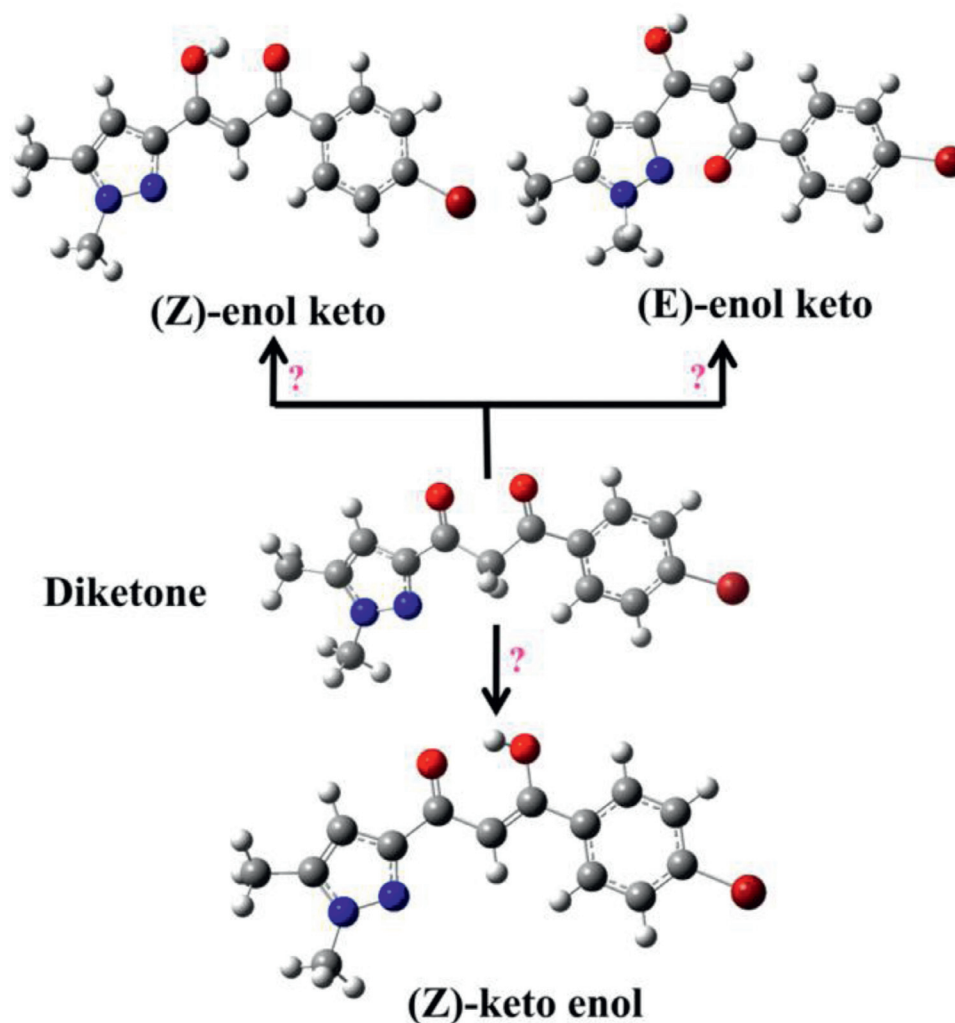


Fig. 7. Possible structures from diketone tautomerisation.

Table 3
Antidiabetic activity of (Z)-pyrazol β -keto-enol

Compound	IC ₅₀ (μ M) ^a	
	α -glucosidase	α -amylase
(Z)-pyrazol β -keto-enol	72.20 $\pm$ 1.50	211.10 $\pm$ 1.06
Acarbose	72.58 $\pm$ 1.39	101 $\pm$ 1.95

^a The IC₅₀ values are mean $\pm$ SEM of three independent experiments.

and α -amylase inhibitory activities of the title molecule, compared to acarbose as reference drug are shown in Table 3. *In-vitro* study on the inhibition of α -glucosidase shows that the (Z)-pyrazol β -keto-enol has potent activity with IC₅₀ value of 72.20 $\pm$ 1.50 μ M, compared to acarbose (IC₅₀ = 72.58 $\pm$ 1.39 μ M). The results of the *in-vitro* α -amylase inhibitory activity reveal that (Z)-pyrazol β -keto-enol has a good inhibitory activity with IC₅₀ value of 211.10 $\pm$ 1.06 μ M. This value is 2.09-fold lower than that of acarbose (IC₅₀ = 101 $\pm$ 1.95 μ M) (Table 3).

3.9. Molecular docking

The solved XRD-structure of the desired ligand was docked to the DNA (PDB ID: 1BNA) available data [41], compound was cross-linked to both two DNA helix via four basic hydrogen bonds to

form the [DNA:ligand] complex similar to *cis-plat* mode of binding (Fig. 10a). One of two Me functional group contributed to non-sufficient DNA binding via very long H-bonds 3.76 Å, since it is not impeded well in between the DNA helix, which supported the minor groove DNA intercalation. The docking effect can be considered as good data when the Root Mean Square Deviation (RMSD) value is less than 2 Å [32]. The other three H-bonds were detected with Guanine and adenosines Nuclides in one DNA helix but with shorter H-bonds binding to the as seen in Fig. 10b. The interactions are located at DNA DA17: H3–O=C (ligand) with 2.03 Å, DNA DG16:H22–O=C(ligand) with 2.49 Å H-bond and DNA DA18:O4....H-O(ligand) with 1.88 Å (Fig. 10c). The total binding energy was found to be -8.12 Kcal/mol. Therefore, the docking interactions and energy result reflected the ligand as a very good binder. H-bonds positions were consistent with the H-bonds detected in the crystal lattice.

4. Conclusion

The (Z)-pyrazol β -keto-enol was proved by the XRD-crystal and the DFT/XRD-structure parameters showed a high matching. Moreover, the H-bonds that were computed via MEP and HSA reflected an excellent matching with the experimental XRD-packing result too. MAC and NPA population charge analysis detected both electrophilic and nucleophilic sites on the molecule surface. The HOMO/LUMO, TD-SCF/DFT, DOS and B3LYP-IR, calculations are in

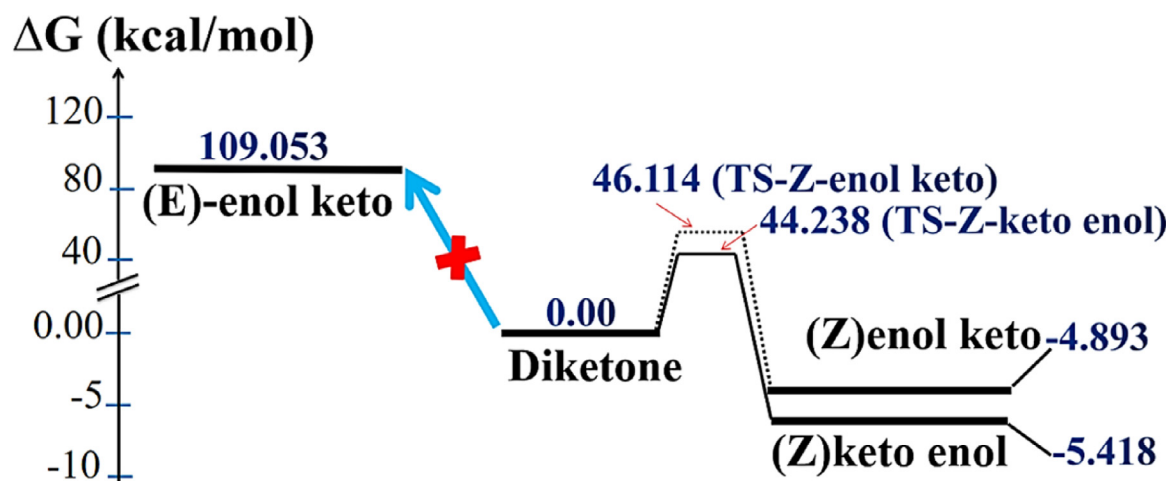


Fig. 8. Gibbs free energy difference profile vs. reaction coordinate for tautomerism structure diketone including implicit SMD solvation [37] of toluene at 273.15 K and 1 atm. All Gibbs free energies are obtained relatively to the Gibbs free energy value of diketone (-3385.694 a.u.); where 1 u.a. = 627.509 kcal/mol.

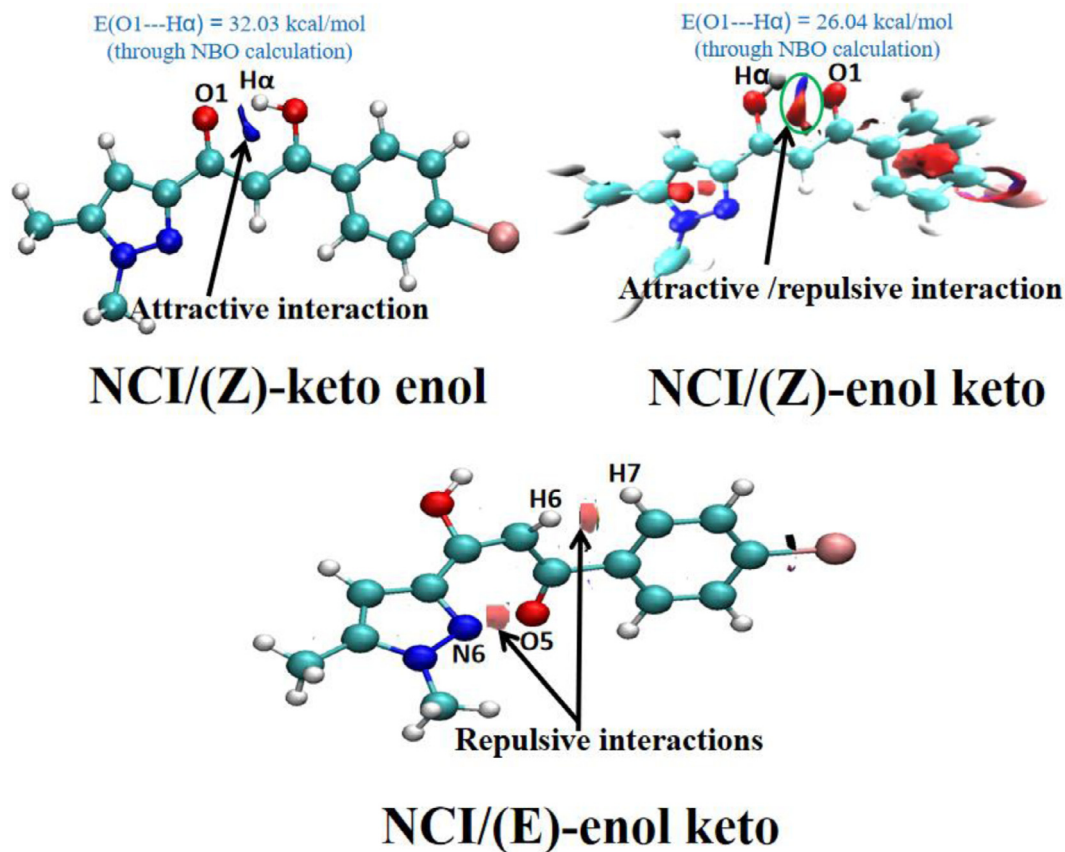


Fig. 9. NCI analysis of (Z)-keto enol, (Z)-enol keto and (E)-enol keto.

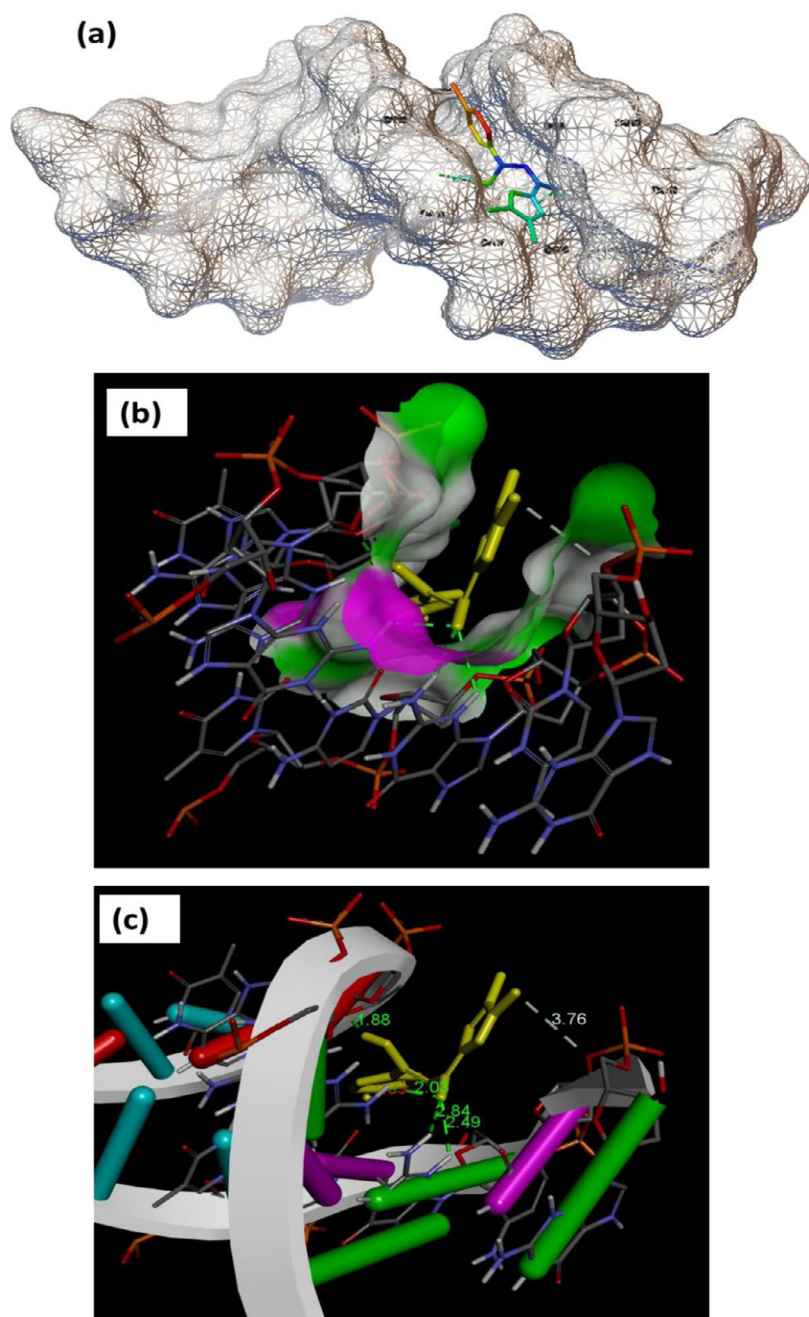


Fig. 10. (a) DNA-ligand binding position representation, (b) tow helix interactions and (c) ligand:Nuclides H-bonds.

an excellent agreement with exp. direct Tauc ΔE_g , UV-visible, FT-IR, spectra. DFT computations and both NBO and NCI analysis. They together indicate clearly that the formation of keto-enol is kinetically more favored than enol-keto; in high approval with experimental data. The results of *in-vitro* antidiabetic activity reflected that the desired molecule exhibited a potent α -glucosidase inhibition with IC₅₀ value of 72.20 ± 1.50 μ M. The desired compound showed a very good DNA-docking effect and double helix minor groove with four H-bonds binding mode were detected.

Declaration of Competing Interest

The authors declare that they have no conflicts of interest.

CRediT authorship contribution statement

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Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:[10.1016/j.molstruc.2021.131308](https://doi.org/10.1016/j.molstruc.2021.131308).

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