

NMR and Solvent Effect Study on the Active Site of Oxidized Azurin

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ABSTRACT

We have evaluated the NMR shielding tensors for active site of oxidized azurin. Azurin is classified to a type I copper protein with ET functionality. We have computed NMR shielding tensors at B3LYP and HF levels by using 6-31G basis set in the gas phase and in different solvents such as water, DMSO, Nitromethane, methanol, ethanol, acetone, dichloroethane. These solvents represent a wide range of solvent properties from the point of view of polarity as well as hydrogen bonding interactions. The NMR shielding tensors were calculated using the GIAO and CSGT methods. Our results reveal that NMR chemical shielding parameters are strongly affected by inducing different solvent media. Regarding to our plotted graphs of σ_{iso} , σ_{aniso} , $\Delta\sigma$, η , δ versus c , the largest σ_{iso} values obtained in ethanol and water for Cu atom whereas the smallest one belonged to DMSO. It is interesting to note that the opposite trend have been observed for asymmetry parameters (η).

Also, calculations at the HF in CSGT and GIAD methods have shown that molecular geometry and shielding properties are better than the other methods, B3LYP in GIAO and CSGT methods.

Keywords: Azurin; NMR parameters; Blue copper protein; Solvent effect

INTRODUCTION

The metalloproteins have attracted considerable interest among many researchers because of their various functionalities, such as electron transfer (ET), redox reaction, oxygen transportation, and activation. Blue copper protein is one of metalloproteins, which can be classified into three types on the basis of spectroscopic properties.

Type I copper protein has an absorption peak near 592-625 nm; type II copper protein has a similar peak to that of the general Cu(II) complex. Type III copper protein exhibits antiferromagnetism and has an absorption peak near 300 nm.

Azurin is classified to a type I copper protein with

ET functionality. The active site of azurin consists of one copper ion and five ligand residues: Gly 45, His46, Cys112, His117, and Met121. The copperon is strongly coordinate-bonding to His46, Cys112, and His117, and bonds weakly to other residues [1].

The Cu site has a distorted trigonal geometry that is intermediate between that preferred by Cu(I) complexes (tetrahedral) and that preferred by Cu(II) complexes (tetragonal). Thus, the change in geometry with redox is limited, and the energy required for this structural rearrangement is small [2]. These observations

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led to the induced rack theory [3] and the entatic state theory[4], based on the hypotheses that the protein matrix forces the Cu(II) site into a catalytically poised geometry similar to the Cu(I) geometry.These theories, which trace the peculiar properties of the cupredoxins and their electron transfer capability back to the strained geometry of their active site, have been challenged recently[5,6], and the issue has been addressed through different theoretical methods.



Fig.1.Overview of the second structure of azurin. The active site consists of the copper ion and five ligand residues: Gly45, His46, Cys112, His117, and Met121[1].

Ryde et al.[5,6] performed quantum-mechanical(QM) optimization in vacuo of the geometry of the oxidized and reduced Cu sites, using the B3LYP hybrid density functional (DFT) method[6,7] .Surprisingly, the results of the calculations on the copper site were in clear contrast with the rack and entatic state hypotheses. The in vacuo optimized geometry of the isolated Cu(II) site was highly similar to the experimental geometry of the site in the protein structure. This suggested that the geometry of the Cu (II) site in cupredoxins is not strained by the protein matrix [8, 9].

Swart investigated the electronic structure of the active site of azurin by density functional

theory (DFT) and carried out MD simulation using the results.

Sugiyama et al.[1] have also carried out MD simulation of oxidized and reduced azurins and have analyzed their backbone dynamics. Nuclear magnetic resonance (NMR) spectroscopy is a valuable technique for obtaining chemical information. This is because the spectra are very sensitive to changes in the molecular structure. This name sensitivity makes NMR a difficult case for molecular modeling [10-12].

NMR Spectroscopy is a powerful tool for study the structure dynamics and interaction of biological molecule such as protein and nucleic acids in solution [13-16].

As we know the effect of solvent molecules on proteins plays an important role in the chemical behavior of them and the effects span a considerable range and are governed primarily by solvent polarity. So in our current research, we have theoretically studied the effects of DMSO, nitromethane, methanol, ethanol, acetone, dichloroethane, water and gas phase on the chemical shielding parameters of ^{13}C , ^{15}N , ^{17}O , ^{64}Cu , ^{32}S nuclei involving in active site and its structural stability. The Gauge Including Atomic Orbitals (GIAO) and Continuous Set of Gauge Transformations (CSGT) approaches within the SCF-Hartree-Fock and B3LYP approximation have been used in order to investigate the influence different solvent media on the magnetic shielding tensors through Hartree-Fock and B3LYP approximation using 6-31G basis set. This basis set seems proper, because the CPU-consuming calculations using the HF method generally inhibit its application for NMR calculations of biological macromolecules with large basis sets.

COMPUTATIONAL DETAILS

In the present work, extensive quantum extensive quantum mechanical calculation of electronic structure of the active site of oxidized azurin (Fig.1) and solvent effects on ^{13}C , ^{15}N , ^{17}O , ^{64}Cu , ^{32}S -NMR parameters have been performed in different solvent media and in two available methods using GAUSSIAN 98 program.

We have studied the influence of OMSO, nitromethane, methanol, ethanol, acetone, dichloromethane, water and gas phase on

chemical shielding tensors. There are different methods of salvation. One family of models for systems in solution is referenced to as Self-Consistent Reaction Field (SCRF) method. The simplest SCRF model is the Onsager reaction field model. For the simulation of a polar environment, this model was used as implemented in GAUSSIAN 98. In this model the solvent is considered as a uniform dielectric with a given dielectric constant.

At first, we have modeled the active site of azurin with chem. Office package and then optimized at the Hartree-Fock and B3LYP levels of theory with 6-31G basis set.

In view of the fact that the results of our earlier works [17-18] proved that addition of a greater number of polarization functions and extension of the basis set did not lead to a significant improvement of the results, the choice

of the middle basis set 6-31G was in our opinion justified.

After fully optimization of active site, we have calculated NMR parameters using the density functional B3LYP and HF method by Gauge Including Atomic Orbitals (GIAO) and Continuous Set of Gauge Transformations (CSGT) and have been reported in table 1(a,b,c). For more investigation of solvent effect, the graphs of obtained NMR parameters versus dielectric constant have been evaluated.

RESULTS AND DISCUSSION

In figs. 2-4, chemical shift anisotropy asymmetry (η), isotropy (σ_{iso}), anisotropy (σ_{aniso}), and $\Delta\sigma$ and chemical shift tensor (δ) are observed for ^{13}C , ^{15}N , ^{17}O , ^{64}Cu , ^{32}S nuclei in active site of oxidized azurin with respect to dielectric constants.

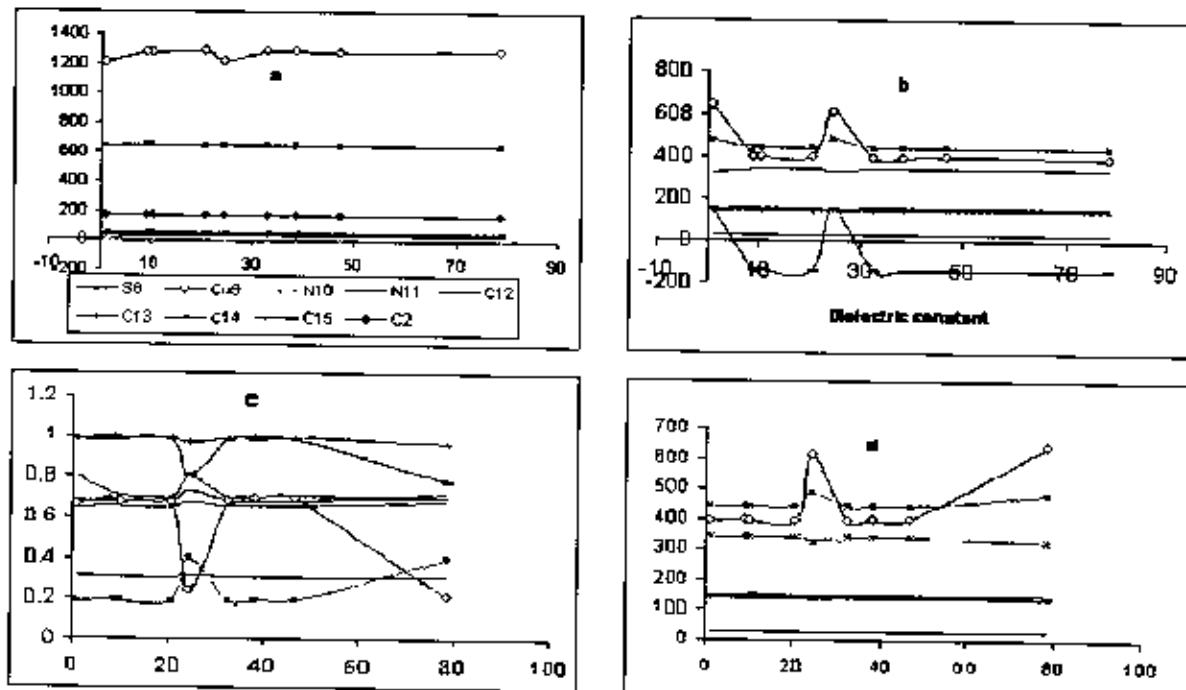


Fig. 2. The graphs of a) isotropic shielding values (σ_{iso}), b) indirect shielding ($\Delta\sigma$), c) asymmetry parameters (η), d) anisotropic shielding value (σ_{aniso}), of propnase atoms of active site azurin in different solvent media at the level of HF/6-31G theory in CSGT method.

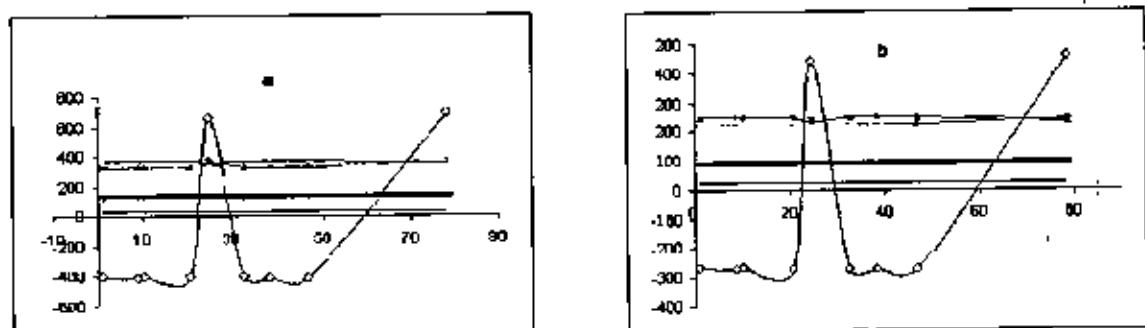


Fig. 3. The graphs of a) indirect shielding ($\Delta\sigma$). b) chemical shift tensor(δ). of propose atoms of active site azurin in different solvent media at the level of HF/6-31G theory in GIAO method

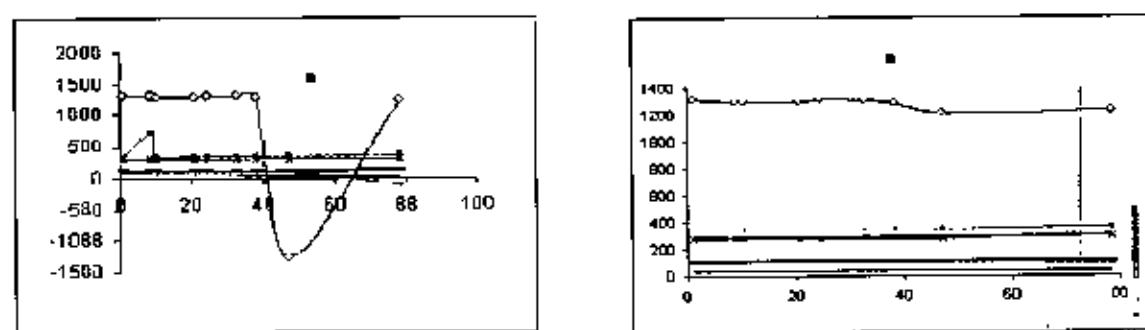


Fig. 4. The graphs of a) isotropic shielding values (σ_{iso}). b) chemical shift tensor(δ). of propose atoms of active site azurin in different solvent media at the level of B3LYP/6-31G theory in CSGT method.

In the basis of the above diagrams, table 1(a,b,c) list values of the σ_{iso} , σ_{aniso} , $\Delta\sigma$, δ , η values for ^{13}C , ^{15}N , ^{17}O , ^{64}Cu , ^{32}S nuclei in different dielectric constants

As expected, the NMR shielding tensors of ^{13}C , ^{15}N , ^{17}O , ^{64}Cu , ^{32}S nuclei are drastically affected by what it is bonded to and the type of bond to its neighbor. Our obtained results yielded strong evidence that intermolecular effects such as electron transfer interactions play very important role in determining the ^{13}C , ^{15}N , ^{17}O , ^{64}Cu , ^{32}S -NMR chemical shielding tensors of active site of oxidized azurin and some systematic trends appeared from the analysis of the calculated values.

On the basis of both geometrical positions of ^{13}C , ^{15}N , ^{17}O , ^{64}Cu , ^{32}S existing in active site of oxidized azurin and computed results, for nuclei involved in electron transfer the obtained NMR parameters are not the same as those computed for other atoms.

For Cu₉ atom which behaves as electron donor, the σ_{iso} component showed the largest intermolecular effects and it shows positive shielding values, i.e., the electron transfer interaction produced a deshielding in this position.

Comparison of σ_{iso} , σ_{aniso} , $\Delta\sigma$ and δ values of Cu₉ atom with another shielding values in table 1 and also analysis of graphs of σ_{iso} , σ_{aniso} , $\Delta\sigma$ and δ 's versus dielectric constant exhibited in figs 2-4 revealed that, the largest values observed for ethanol and water, whereas the smallest belongs to DMSO. It is interesting to note that on the contrary, the opposite trend have been observed for asymmetry parameter (η). This logical behavior may be readily understood in accord with biological conception.

The metal ion in the electron-transfer copper proteins such as the type I copper proteins has been proposed to exist in an entatic state. These studies as well as earlier reports suggest that the metal-ligand interactions in the blue copper proteins indeed play an important role in imparting extra stability to the metal binding site of the protein[19].

Table 1. NMR parameters of C, N, O, Cu, S nuclei involving in active site azurin in different solvent media at the levels of RHF/6-31G and B3LYP/6-31G theory in GIAO and CSGT methods(a),(b),(c) (n)

Solvent	Method	Atoms	GIAO					CSGT				
			δ_{iso}	δ_{aniso}	$\Delta\sigma$	η	δ	δ_{iso}	δ_{aniso}	$\Delta\sigma$	η	δ
78.39	HF B3LYP	C2	187.18	34.14	34.14	0.5276	22.263	173.85	28.197	28.197	8.6812	18.748
			169.76	37.91	37.91	0.5377	25.277	157.68	32.883	32.883	0.627	21.869
		S6	740.4	332.09	332.09	0.3817	221.397	651.4	442.155	442.16	0.185	294.77
			566.54	344.81	344.81	0.68	229.476	498.78	412.355	432.36	8.5289	288.237
		Cu9	1758.5	260.43	-405.19	0.285	-270.13	1292.3	394.373	394.38	0.666	262.915
			168.64	1312.34	1312.34	0.9158	874.898	411.46	1151.17	-1058.5	0.694	-905.666
		N10	8.25	361.85	361.84	0.351	241.229	14.294	332.85	332.85	0.29	221.9
			21.45	275.11	275.11	0.1024	183.105	11.892	256.303	256.3	0.1327	170.868
		N11	8.23	369.04	369.83	0.3577	246.022	13.162	341.554	341.55	0.3059	227.702
			24.56	298.67	298.67	8.184	199.112	11.998	275.877	275.88	0.1984	183.918
		C12	55.32	146.41	146.41	0.6943	97.003	58.938	154.149	154.35	0.6529	102.899
			47.46	122.03	122.03	0.557	81.45	33.428	129.221	129.22	0.472	86.149
		C13	62.89	127.57	127.56	8.9525	85.043	131.052	140.947	140.95	0.9967	93.965
			65.7	90.95	90.95	0.9493	64.638	39.791	103.257	-103.3	0.9902	-68.865
		C14	61.83	138.47	138.47	0.3494	92.315	35.055	148.58	148.58	0.7003	99.054
			59.19	189.55	109.55	0.6586	73.025	41.766	119.154	119.15	0.5946	79.436
		C15	62.68	128.79	129	0.9713	85.56	14.131	141.648	-142.58	0.9864	-95.055
			58.01	182.07	182.07	0.8136	68.047	31.508	111.963	111.96	0.8837	74.642
47.8	HF B3LYP	C2	187.23	34.17	34.17	0.5278	22.778	173.88	28.222	28.224	0.6815	18.815
			169.85	37.81	37.81	0.5315	25.247	157.75	32.721	32.721	0.6207	21.814
		S6	739.9	332.83	332.83	0.382	221.58	650.75	443.025	443.83	0.1899	293.35
			565.8	341.47	716.01	0.678	227.647	497.87	428.762	428.76	0.5285	285.84
		Cu9	1744.4	262.51	-413.12	0.27	-275.41	1282.9	400.404	400.4	0.6963	266.936
			169.81	1288.84	1298.84	0.925	865.89	411.19	1139.48	-1351	0.6868	-900.67
		N18	8.59	361.62	361.62	0.3496	241.079	-11.806	332.385	332.38	0.29	221.59
			21.75	276.03	276.03	0.1022	184.019	12.081	257.174	257.17	0.1275	171.45
		N11	8.83	368.08	368.89	8.3539	245.388	-13.03	340.546	340.55	0.3019	227.03
			24.5	299.14	299.14	0.1865	199.42	14.864	275.946	275.95	0.1991	183.963
		C12	55.41	146.29	146.29	0.6991	97.527	39.024	154.166	154.17	8.658	102.778
			47.4	122.19	122.19	0.556	81.46	33.386	129.318	129.32	0.47	86.212
		C13	62.92	127.33	127.33	8.9548	84.885	34.124	149.641	140.64	0.9983	93.761
			65.51	91.01	91.01	8.9506	60.676	39.603	103.264	-103.41	0.9972	-68.938
		C14	62.05	138.21	138.21	0.7535	92.142	45.196	148.341	148.34	0.7044	98.894
			58.24	188.48	109.48	8.66	72.985	43.793	119.883	119.08	0.5955	79.389
		C15	62.73	128.77	128.77	0.9695	85.848	34.203	141.523	-142.27	8.9895	-94.846
			58.02	102.18	102.18	0.8124	68.118	33.51	111.959	111.96	0.8835	74.639
38.22		C2	187.19	34.15	34.15	0.5277	22.764	173.86	28.2	28.2	0.6813	18.8
			169.77	37.89	37.9	0.5314	25.263	157.67	32.796	32.796	0.6229	21.864
		S6	740.31	332.18	332.18	0.38188	221.451	651.3	442.237	442.24	0.186	294.825
			585.82	343.04	343.04	0.677	228.695	498.12	438.164	430.16	0.528	286.776
		Cu9	1749.8	260.97	-406.52	0.2838	-271.02	1291	395.214	395.22	0.672	263.476
			172.16	1294.77	1294.77	0.9235	863.18	-410.35	1137.09	-1346	0.689	-897.343
		N10	8.29	361.83	361.83	0.3509	241.22	-94.247	332.787	332.79	0.291	221.858

Table I. Continue.

(b)

		2175	276.17	276.17	8.1025	184.115	12.05	257.34	257.34	0.126	171.56	
	HF B3LYP	N11	8.35	368.88	368.88	0.3569	245.92	-13.509	341.39	341.39	0.3051	227.594
			24.24	298.99	298.99	0.1891	199.33	14.704	276.192	276.19	0.1998	184.129
		C12	55.54	146.39	146.39	0.695	97.592	38.952	154.319	154.32	0.653	102.879
			47.36	122.23	122.23	0.5566	81.487	33.341	129.357	129.36	0.4709	86.238
		C13	62.9	127.52	127.52	0.953	85.017	34.067	140.896	140.9	0.997	93.93
			65.44	91.03	91.03	0.9486	60.684	39.55	103.287	-183.35	0.9987	-68.902
		C14	61.87	138.43	138.43	0.7581	92.285	45.858	148.541	148.54	0.7009	99.027
			58.26	109.4	109.48	0.6611	72.987	43.822	119.077	119.08	0.5961	79.385
		C15	62.7	128.78	128.78	0.971	85.856	34.147	141.623	-142.53	0.9873	-95.818
			57.96	102.19	102.23	0.8125	68.128	33.457	112.054	112.05	0.8825	74.703
315	HF B3LYP	C2	187.2	34.15	34.15	8.5279	22.765	173.86	28.201	28.281	8.6616	18.881
			169.74	37.9	37.9	0.5349	25.268	157.66	32.8	32.8	0.6251	21.867
		S6	740.29	332.25	332.25	0.381	221.5	651.28	442.317	442.32	0.1186	294.878
			585.78	343.28	343.28	0.673	228.852	498.23	430.587	430.59	0.5249	287.058
		Gu9	1749.6	261.05	406.89	0.283	-271.26	1290.6	395.729	395.73	8.672	263.819
			174.64	1294.14	1294.14	0.9193	862.76	-407.93	1139	-1341.8	8.697	-494.557
		N10	8.33	381.82	381.82	0.3507	241.215	-14.212	332.769	332.77	8.2913	221.846
			21.61	276.18	276.19	8.1827	184.13	12.112	257.297	257.3	0.1261	171.53
		N11	8.36	368.85	368.85	0.3568	245.902	-13.498	341.353	341.35	0.305	227.569
			24.33	299.58	299.58	0.1889	199.72	14.652	276.22	276.22	0.1982	184.147
		C12	55.35	148.36	146.38	0.6952	97.586	38.959	154.306	154.3	0.6539	102.87
			47.33	122.24	122.25	0.556	81.495	33.328	129.35	129.35	0.4702	86.233
		G13	82.9	127.51	127.51	0.953	85.009	34.069	140.881	140.88	0.9971	93.921
			65.42	81.1	91.1	0.947	60.736	39.546	103.339	103.34	0.9999	68.893
		C14	61.88	138.42	138.41	0.7503	92.28	45.064	148.534	148.53	0.7011	99.023
			59.24	189.43	109.43	0.6632	72.954	43.8	119.028	119.03	0.598	79.352
		C15	62.7	128.78	128.78	0.971	85.856	34.154	141.616	-142.52	0.9873	-95.01
			57.95	102.32	182.32	0.807	68.211	33.421	112.071	112.07	0.8767	74.714
145	HF B3LYP	C2	184.25	34.5	34.5	0.5652	22.998	171.17	28.435	28.434	0.7339	18.956
			169.7	87.98	37.99	0.539	25.323	157.61	32.865	32.865	0.6277	21.91
		S6	729.6	371.08	371.88	0.502	247.38	645.52	487.887	487.08	8.398	324.725
			566.11	344.66	344.66	6.68	229.77	498.61	431.968	431.97	8.5382	287.979
		Gu9	1857.8	655.76	655.76	0.7365	437.172	1220.8	612.212	612.21	0.2398	408.142
			178.81	1311.36	1311.36	0.918	874.239	-412.36	1151.19	-1358.5	0.6948	-905.634
		N10	21.85	347.64	347.64	0.279	231.76	-2.035	320.209	320.21	8.248	213.47
			21.69	276.86	276.06	0.1019	184.639	12.027	257.1R3	257.18	0.1274	171.455
		N11	17.25	358.88	358.88	0.353	233.923	-5.534	325.345	325.35	8.3094	216.897
			24.41	286.63	298.63	0.1864	199.888	14.881	275.98	275.98	8.1978	184.867
		C12	55.49	144.84	144.84	8.2209	96.561	38.859	153.236	153.23	0.6717	102.157
			47.4	122.14	122.14	0.5566	81.427	33.368	129.284	129.28	0.4712	86.189
		C13	61.87	125.85	125.85	0.9182	83.898	32.922	139.49	139.49	6.9732	92.993
			65.53	91.81	91.01	0.9495	60.671	39.648	103.259	-103.33	0.9987	-68.883
		C14	66.96	131.58	131.58	0.8608	87.718	49.221	143.128	143.13	0.8003	95.419
			59.29	109.51	109.51	0.6608	73.008	43.844	119.107	119.11	0.5959	79.405
		C15	55.34	138.75	138.75	0.7238	92.502	28.178	149.955	149.96	0.3082	99.97
			57.98	182.21	162.21	0.8117	68.141	33.473	112.076	112.08	6.8812	74.717
125		C2	187.21	34.15	34.15	0.5279	22.768	173.87	28.206	28.206	0.6817	18.804
			169.78	37.91	37.91	0.538	25.275	157.68	32.809	32.809	0.6272	21.873
		S6	748.2	332.37	332.37	0.38169	221.583	651.16	442.472	442.47	0.1869	294.98
			567.34	345.75	345.76	0.677	230.5	499.53	413.166	433.17	0.527	288.777
	Gu9		1748.3	261.53	-408.53	0.2803	-272.36	1288.7	396.964	396.97	0.679	264.643
			170.32	1386.63	1306.83	0.92	871.22	-412.51	1145.55	-1355.8	8.689	-913.88

Table 1. Continu..

(c)

	HF B3LYP	N10	8.39 21.48	361.79 274.81	361.79 274.91	0.3504 0.102	241.195 183.273	-14.129 11.912	332.686 256.083	332.68 256.08	0.291 0.1326	221.791 170.722
		N11	8.48 24.49	368.68 298.75	368.67 298.75	0.356 0.1855	245.784 199.165	-13.38 14.957	341.163 276.058	341.16 276.06	0.3041 0.1994	227.442 184.039
		C12	55.38 47.44	146.36 121.97	146.36 121.97	0.6961 0.558	97.57 81.312	38.975 33.422	154.27 129.182	154.27 120.18	0.6549 0.473	102.847 86.121
		C13	62.91 65.78	127.47 90.98	127.47 90.98	0.9535 0.9482	84.977 60.657	34.084 30.836	140.819 103.276	140.82 103.28	0.9974 0.9999	93.88 68.851
		C14	61.92 59.25	138.37 109.58	138.37 109.58	0.7511 8.6582	92.244 73.057	45.095 43.818	148.485 119.172	148.49 119.17	8.7819 0.594	98.99 79.448
		C15	62.71 57.88	128.78 182.1	128.78 102.08	0.9708 0.8132	85.851 68.066	34.17 33.493	141.588 112.003	-142.45 112	0.9878 0.8829	-94.967 74.669
	DFT B3LYP	C2	187.22 168.73	34.18 37.95	34.16 37.95	0.5279 0.5436	22.776 25.3	173.87 157.63	28.218 32.83	28.218 32.83	0.6815 0.6326	18.812 21.887
		S6	738.94 568.08	332.74 350.16	332.73 358.16	0.3819 0.675	221.82 233.44	650.81 500.12	442.928 436.46	442.93 436.46	0.189 0.528	295.285 290.97
		Cu9	1745.2 166.86	262.11 1285.58	-412.26 1285.57	0.2715 0.9658	-214.84 857.85	1284.2 -417.61	399.489 1123.84	399.49 -1362.1	0.6933 8.65	266.326 -908.081
		N10	8.57 21.67	361.65 275.69	361.65 275.69	0.3496 8.1013	241.1 183.796	-13.923 11.973	332.448 256.915	332.45 256.91	0.2902 0.1277	221.631 171.277
		N11	8.75 24.54	368.22 298.83	368.22 208.83	0.3543 8.1818	245.479 199.219	-13.114 14.973	340.681 275.93	340.68 275.93	0.3023 0.1969	227.12 183.953
		C12	55.4 47.39	146.31 122.15	146.31 122.15	0.556 0.556	8.6984 81.433	97.538 33.372	154.191 129.31	154.19 129.31	8.6573 0.4703	102.794 86.207
		C13	62.92 65.48	127.35 91.09	127.35 91.09	0.9546 0.9476	84.901 60.73	34.015 30.581	140.677 103.343	140.68 -103.38	0.9981 0.9993	93.785 -68.917
		C14	82.81 59.15	138.25 109.37	138.25 109.37	0.7529 0.659	92.166 72.91	45.17 43.75	148.375 118.987	148.38 118.99	0.7038 0.5943	98.917 79.321
		C15	82.74 58.21	128.77 101.75	128.77 101.75	8.9699 8.8177	85.843 67.832	34.201 33.694	141.529 111.646	-142.31 111.65	8.989 0.8867	-94.871 74.431
	DFT B3LYP	C2	184.26 178.64	34.18 38.12	34.18 38.12	0.57 0.599	22.785 25.413	171.18 158.12	28.335 33.3	28.339 33.3	0.7226 8.6798	18.89 22.2
		S6	728.54 885.61	364.7 385.21	364.7 365.21	0.4999 8.473	243.136 243.471	644.67 540.91	480.694 456.891	480.69 456.89	0.3463 0.38	328.462 304.594
		Cu8	1649.7 485.5	878.57 1231.35	678.57 1231.35	0.70187 0.287	452.38 820.9	1214.1 -87.266	644.821 1152.54	644.85 1152.5	0.2139 0.62	429.887 768.356
		N18	20.94 31.67	348.04 293.44	348.04 293.44	0.2799 0.179	232.03 195.629	-2.06 16.801	320.544 270.447	320.54 270.44	0.248 8.0537	213.696 180.298
		N11	18.33 25.25	349.48 305.08	349.48 305.09	8.3499 0.262	232.936 203.393	-4.61 11.499	323.97 281.465	323.97 281.47	8.3114 0.194	215.98 187.644
		C12	55.25 58.82	144.9 123.87	144.9 123.87	0.7266 0.544	96.599 82.578	38.656 35.509	153.34 130.295	153.14 130.29	0.6756 0.467	102.226 86.863
		C13	61.87 69.13	126.17 87.58	126.17 -90.24	0.9072 0.941	84.111 -60.159	32.976 40.887	139.737 98.925	139.74 -105.14	0.9653 0.8817	93.158 -70.095
		C14	67.21 63.99	131.65 110.19	131.65 110.19	0.8605 0.687	87.765 73.458	49.464 47.499	143.161 119.074	143.16 119.07	0.8009 0.6224	95.441 79.383
		C15	54.25 60.68	148.15 186.38	148.15 108.38	0.6902 0.6803	93.433 72.254	27.209 34.516	151.195 117.446	151.2 117.45	0.7794 8.784	100.797 78.298

The metal ion in the electron-transfer copper proteins such as the type I copper proteins has been proposed to exist in an entatic state. These studies as well as earlier reports suggest that the metal-ligand interactions in the blue copper proteins indeed play an important role in imparting extra stability to the metal binding site of the protein[19].

As expected, after Cu₆, S₆ shows positive shielding values. Cys 112 is among the ligand residues the one that more strongly hybridizes with the Cu orbitals. The covalency of the copper-ligand bonds is very anisotropic and it was suggested that this should favor hole super exchange pathways that couple to the Cu through the Cys112 ligand[20]. The cysteine ligand decreases the reorganization energy. This decrease is caused by the transfer of charge from the negative charged thiolate group to Cu^{II}, which makes the oxidized and reduced structures quite similar[21].

For both N₁₀ and N₁₁ atoms which are fused in imidazole ring, shielding tensors are close to each other but according to our obtained results of fig. 2, as the dielectric constant in passing from the nitromethane to water, the σ_{aniso} and $\Delta\sigma$ of N₁₁ and N₁₀ increase and the η decrease in the ethanol which is expected to result in a significant shielding of this nitrogen nuclei at the Hartree-Fock level of theory with CSGT method.

Nitrogen ligands give up an appreciably lower reorganization energy than water, owing to the lower Cu-N force constant[21].

Figure 4 shows that, as the dielectric constant of the solvent increases, the $\Delta\sigma$ and σ_{aniso} of C₁₅ and C₁₃ increase and the η of C₁₅ and C₁₃ decreased in the ethanol at the Hartree-Fock level of theory with GIAO method.

Also, calculations at the HF in CSGT method (Fig. 2) and the HF in GIAO method (Fig. 3) have shown that molecular geometry and shielding properties are better than the other methods, B3LYP in GIAO and CSGT methods (fig. 4).

CONCLUSION

The results reported in this paper indicates that it is possible to measure NMR tensors of various nuclei involving in biological compounds either in

gas phase or in the presence of different solvent molecules theoretically. Several conclusions can be made on the basis of the observed results of the present study. Such amount of theoretical data can provide us important insights into the nature of molecular structures in biological systems.

Our main findings from the point of view of solvent effects can be summarized as follows:

optimization at the HF level of theory provides a suitable computational model in terms of calculated NMR parameters and relative energies.

NMR parameters are very sensitive to small changes in molecular geometry and chemical environment exhibited significant sensitivity to the intramolecular interactions. So, our obtained theoretical results emphasized on the influence of the environment factors

The largest σ_{iso} value of mentioned nuclei of active site azurin observed for ethanol and water, whereas the smallest one belongs to DMSO. It is interesting to note that the opposite trend have been observed for asymmetry parameters(η). This usual behavior may be readily understood in accord with biotechnological conceptions.⁷

The calculation of nuclear magnetic resonance (NMR) parameters using ab initio techniques seems to be a major and a remarkable tool for investigation of how variations of biological systems and provides information on the local environment of selected species and their next nearest neighbors. However, combination of NMR study embedded in solvent medium reveals a logical interpretation of the observed results.

In conclusion, we have shown that theoretical calculations can be used to successfully solve biochemical problems. In similarly with experimental methods, they involve assumptions and interpretation, and they have their limitations, but there are many problems that are best studied by theory. Thus, theoretical methods have become a competitive alternative to experiments for biochemical investigations.

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