

## **ab initio/DFT calculations $^{13}\text{C}$ , $^1\text{H}$ NMR chemical shifts and bond length in synthesized spirooxindol**

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**Abstract:** Pure spirooxindol was synthesized and studied by both the experimental and calculational methods of NMR and X-ray spectroscopy. Theoretical methods of substantial quality can be used to calculate NMR data using the gauge including atomic orbital (GIAO) method, yielding data comparable with those of the experiment. *ab initio* and DFT calculations of  $^{13}\text{C}$  and  $^1\text{H}$  NMR chemical shifts of the Novel Spirooxindol Compound were reported. The structure of this molecule at first was optimized with the Gaussian 03 program. After the optimization,  $^{13}\text{C}$  and  $^1\text{H}$  chemical shifts were calculated with GIAO method, using corresponding TMS shielding calculated at the same theoretical levels as the reference. Calculations have been performed with using three different basis sets: 6-31G, 6-31G(d,p) and 6-31+G(d,p) at HF and DFT levels of theories. The results, especially for  $^{13}\text{C}$  chemical shifts are in agreement with the experimental values of NMR. In this work the bond lengths of the Spirooxindol was calculated and the results compared with those of the experimental data obtained by X-Ray crystallography. All the computations were done using an IBM x225 Xeon computer that has 2048 MB ram.

**Keywords:**  $^{13}\text{C}$  NMR; GIAO; Gaussian; Spirooxindol Compound; DFT; HF.

### **Introduction**

Spirooxindole ring system is a structural feature found in a variety of oxindole alkaloids [1,2]. The structure of a spirooxindol by the multicomponent 1,3-dipolar cycloaddition of azomethine ylide, derived from 5-nitroisatin and proline by a decarboxylative route, and trans- $\beta$ -nitrostyrene has been synthesized and reported by one of us [3]. The experimental studies in 1,3-dipolar cycloaddition reactions [4] initiated recently are now extended to the theoretical methods [5].

During the past decade numerous *ab initio* methods have been developed, implemented and tested. Several theoretical overviews [4,5,6] and routinely applicable implementations of methods are currently available. Theoretical methods of substantial quality can be used to calculate NMR data using the gauge including atomic orbital (GIAO) method, yielding data comparable with those of the experiment. However these methods not only may interpret the synthetic results obtained thus far but also can be used for the investigation of some useful practical predictions.

The aim of this work is to synthesis a spirooxindol by

some modification of the method and to calculate NMR chemical shift and bond length of the structure of the new compound,  $\text{C}_{20}\text{H}_{18}\text{N}_4\text{O}_5$ , and compare the obtained crystallography and NMR experimental data with the theoretical calculations.

### **Results and Discussion**

Two regioisomers A and B For the titled spirooxindol compound could be imagined (see figure 1). The NMR of spirooxindol of the prepared product before further purification and after purification has been obtained. NMR spectrum of the product before purification showed the presence of the two regioisomers but with the dominant isomer A. Replacement  $\text{NO}_2$  with phenyl causes a small  $^1\text{H}$  deshielding on the connected carbons in the structures A and B. These two sets of signals are there together in the spectrum of the mixed regioisomers. After re-crystallization product related  $^1\text{H}$  signals of isomer B removed from the spectrum. The obtained chemical shifts of isomer A are listed in the end column of Table 1.

In addition on the base of calculated energies in Gaussian for the two structures we concluded the

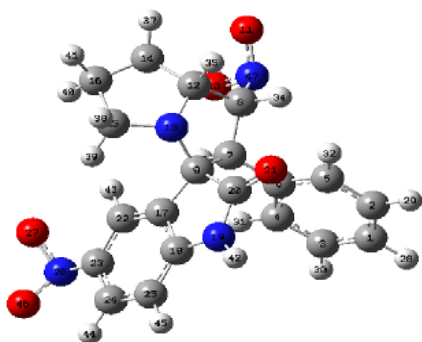
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structure A is more stable than the B. For calculation NMR and X-ray parameters of the A isomer of spirooxindol at first, the structures of the both two isomers of this molecule were optimized with the Gaussian 03 program. The numbering and modeling of optimized structure of spirooxindol (isomer A) are illustrated in Figure 2. The chemical shifts of the molecule in question and the bond lengths were calculated with standard Gaussian 03 program. Calculations have been performed with using three different basis sets: 6-31G, 6-31G(d,p) and 6-31+G(d,p) by both RHF and B3LYP methods.

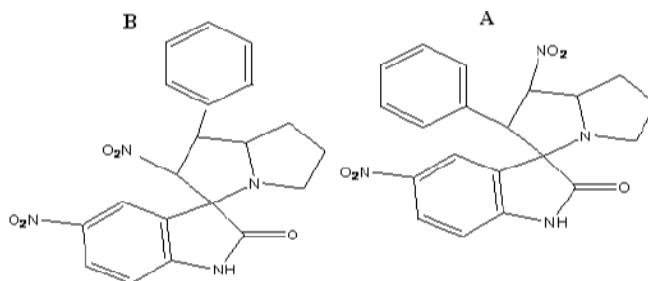
For both the RHF and the B3LYP methods, with the above basis sets, a geometry optimization was first performed for the molecule and for TMS. The NMR shielding tensors were computed with: the GIAO (gauge independent atomic orbital) method. RHF/GIAO denotes the following procedure: the geometry minimized the corresponding RHF energy and the wave function was calculated at the RHF level, presuming calculation of the optimum geometry. Tables 1 gives calculated  $^{13}\text{C}$  and  $^1\text{H}$  chemical shifts which were obtained by NMR the theoretical methods. The results of the chemical shift calculations with the three basis sets specially 6-31G(d,p) are in reasonable agreement with the experimental values

The geometrical parameters (bond length) were computed and listed in Table 2. As could be seen, these results are in good agreement with those of the experimental data obtained by X-Ray crystallography.

**Figure 1.** Atoms numbering of title compound which is analyzed.



**Figure 2.** The structure of two regioisomers of spirooxindol



**Table 1.** Calculated (RHF and B3LYP) and experimental  $^1\text{H}$  and  $^{13}\text{C}$  NMR chemical shift data for some significant atoms in spirooxindol compound

Atom	Method	6-31G	6-31G(d,p)	6-31+G(d,p)	Experimental
$\text{C}_8$	HF	121.797	91.784	112.223	90.305
	B3LYP	124.448	120.197	124.239	
$\text{C}_9$	HF	78.820	73.916	73.732	74.670
	B3LYP	84.902	82.647	84.280	
$\text{C}_{21}$	HF	203.575	180.227	190.748	178.135
	B3LYP	184.277	179.780	182.277	
$\text{C}_{24}$	HF	160.733	140.014	149.594	149.875
	B3LYP	178.364	174.324	177.251	
$\text{H}_{35}$	HF	7.615	6.725	7.123	4.850
	B3LYP	7.252	7.074	7.071	
$\text{H}_{36}$	HF	7.059	5.928	6.463	6.402
	B3LYP	10.463	9.670	9.740	
$\text{H}_{37}$	HF	6.684	5.752	6.173	4.580
	B3LYP	6.677	6.278	6.599	
$\text{H}_{45}$	HF	11.698	9.948	11.468	8.900
	B3LYP	9.657	9.733	10.035	
$\text{H}_{46}$	HF	11.917	9.857	11.323	8.180
	B3LYP	9.663	9.613	7.255	

**Table2.** X-ray crystallography and Calculated bond length data

Entry	Calculated	X-ray	Entry	Calculated	X-ray
$C_{21} - O_{22}$	1.2327	1.223(2)	$C_{16} - H_{39}$	1.12599	0.9700
$O_{28} - N_{27}$	1.34675	1.230(3)	$C_{16} - H_{40}$	1.12281	0.9700
$O_{47} - N_{27}$	1.3471	1.232(3)	$C_{17} - C_{15}$	1.52307	1.519(3)
$O_{12} - N_{10}$	1.34478	1.223(3)	$C_{17} - H_{41}$	1.11769	0.9700
$O_{11} - N_{10}$	1.34566	1.224(2)	$C_{17} - H_{42}$	1.11700	0.9700
$N_{20} - C_{21}$	1.40595	1.357(3)	$C_{15} - C_{13}$	1.53806	1.535(3)
$N_{20} - C_{19}$	1.3972	1.398(3)	$C_{13} - H_{36}$	1.01279	0.9800
$N_{20} - H_{43}$	0.98659	0.8600	$C_8 - C_7$	1.54662	1.516(3)
$N_{14} - C_9$	1.46879	1.470(3)	$C_8 - C_{35}$	1.13085	0.9800
$N_{14} - C_{16}$	1.45841	1.478(3)	$C_7 - C_6$	1.48803	1.389(3)
$N_{14} - C_{13}$	1.48263	1.483(3)	$C_7 - H_{34}$	1.31100	0.9300
$N_{27} - C_{24}$	1.46945	1.466(3)	$C_6 - C_4$	1.40494	1.393(3)
$N_{10} - C_8$	1.49394	1.500(3)	$C_5 - C_6$	1.40055	1.392(3)
$C_{21} - C_9$	1.58404	1.550(3)	$C_2 - C_5$	1.39483	(1.383(3))
$C_{18} - C_{19}$	1.43467	1.513(3)	$C_5 - H_{33}$	1.10343	0.9300
$C_{23} - C_{24}$	1.41640	1.568(3)	$C_1 - C_2$	1.39431	1.385(3)
$C_{23} - H_{44}$	1.10169	0.9700	$C_2 - H_{30}$	1.10025	0.9300
$C_{24} - C_{25}$	1.40563	1.374(3)	$C_1 - C_3$	1.39529	0.9300
$C_{25} - C_{26}$	1.39768	1.386(3)	$C_1 - H_{29}$	1.009943	0.9300
$C_{25} - H_{45}$	1.10186	0.9300	$C_3 - C_4$	1.39335	1.385(3)
$C_{18} - C_{19}$	1.38046	1.347(3)	$C_3 - H_{31}$	1.385(3)	1.39335
$C_{24} - C_{25}$	1.40563	1.526(3)	$C_4 - H_{32}$	0.9300	1.10023
$C_{25} - C_{26}$	1.39768	1.521(3)	$C_5 - H_{33}$	0.9300	1.10007
$C_{26} - H_{46}$	1.09767	0.9700			
$C_{16} - C_{17}$	1.53748	1.521(3)			

Furthermore, by looking at the data on Table 1 the basis set and theory level dependence of  $^{13}\text{C}$  and  $^1\text{H}$  chemical shifts on calculated  $^{13}\text{C}$  and  $^1\text{H}$  chemical shifts of HF and DFT (B3LYP) method using the three basis sets 6-31G, 6-31G(d,p) and 6-31+G(d,p) in spirooxindol compound are obvious. For demonstrating the accuracy for the HF method and this three basis sets the static data are presented in Table 3 and 4. In accordance with these statistical data HF/6-31G(d,p) in calculation both  $^1\text{H}$  and  $^{13}\text{C}$  chemical shifts, statistically provide an improvement over the two other basis sets in used as judged by the static data.

**Table 3.** Statistical data for  $^{13}\text{C}$  chemical shifts calculated by HF method

Basis sets	6-31G	6-31G(d,p)	6-31+g(d,p)
Min error	10.8582	2.0915	0.2806
Max error	31.4916	11.4787	21.9175
Mean absolute error	19.8	8.5	8.9
Standard deviation of absolute error	10.289	4.3538	10.3426
RMS error	21.7996	9.3411	12.653

**Table 4.** Statistical parameter for  $^1\text{H}$  NMR chemical shifts calculated by HF method

Basis sets	6-31G	6-31G(d,p)	6-31+g(d,p)
Min error	6.1417	1.6443	4.1418
Max error	34.1433	29.8914	13.9342
Mean absolute error	19.8	16	18.8
Standard deviation of absolute error	13.6542	13.3459	21.0019
RMS error	23.0206	19.7362	22.419

## Experimental

Pure spirooxindol (1',5-dinitro-2'-phenyl-1', 2', 5', 6', 7', 7 a'- hexahydrospiro [indoline-3, 3'- pyrrolizin]- 2-one) was synthesized according the literature [3] with some modifications. Briefly, a mixture of 0.192 g (1 mmol) 5-nitroisatin, 0.115 g (1 mmol) proline and 0.149 g (1 mmol *trans*- $\alpha$ -nitrostyrene) in ethanol (10 ml) was refluxed for an hour. Completion of the reaction was tested by TLC. After completion, a portion of 20 ml water was added to solution and then the precipitated solid was separated by filtration. The pure cycloadduct was obtained by recrystallization from ethanol. NMR and X-ray analysis of this compound have been carried out and the results were the same as reference [3]. The bond lengths and  $^1\text{H}$ ,  $^{13}\text{C}$  chemical shifts of

Spirooxindol Compound were calculated with Gaussian 03 software, using B3LYP/GIAO, RHF/GIAO methods.

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