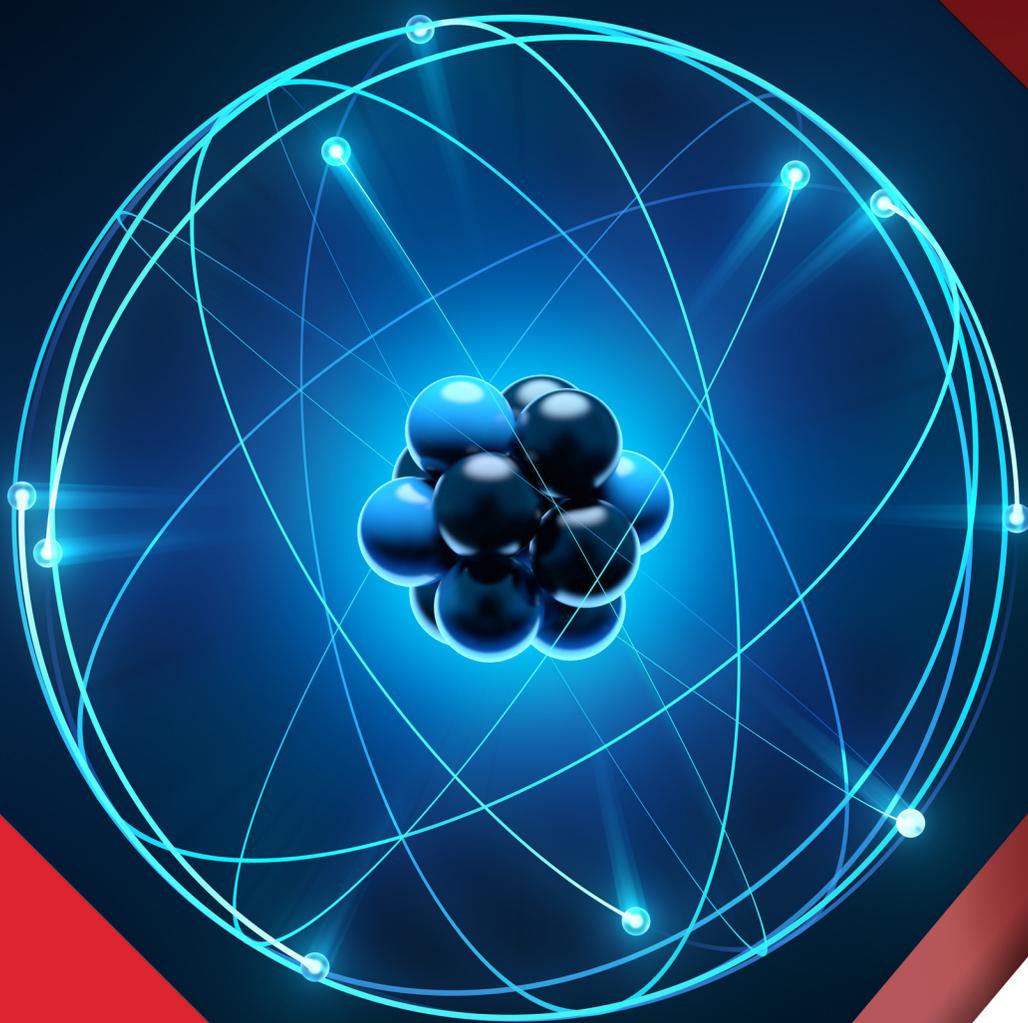


# DFT BASED STUDIES ON BIOACTIVE MOLECULES



**Ambrish Kumar Srivastava**  
**Neeraj Misra**

**Bentham Books**

# **DFT Based Studies on Bioactive Molecules**

Authored by

**Ambrish Kumar Srivastava**

*Department of Physics  
Deen Dayal Upadhyaya Gorakhpur University  
Gorakhpur  
Uttar Pradesh  
India*

&

**Neeraj Misra**

*Department of Physics  
University of Lucknow  
Lucknow Uttar  
Pradesh  
India*

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Authors: Ambrish Kumar Srivastava and Neeraj Misra

ISBN (Online): 978-981-4998-36-9

ISBN (Print): 978-981-4998-37-6

ISBN (Paperback): 978-981-4998-38-3

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# CONTENTS

FOREWORD .....	i
PREFACE .....	ii
<b>CHAPTER 1 THE ESSENCE OF DENSITY FUNCTIONAL THEORY</b> .....	1
<b>INTRODUCTION</b> .....	1
The Schrödinger Equation .....	1
Born-Oppenheimer Approximation .....	2
Electron Density and Wavefunction .....	3
<b>THE KOHN-SHAM APPROACH</b> .....	4
First Theorem .....	4
Second Theorem .....	4
Kohn-Sham Energy .....	4
KS Equations and Solution .....	6
<b>THE EXCHANGE-CORRELATION ENERGY FUNCTIONAL</b> .....	8
The Local Density Approximation (LDA) .....	8
Generalized Gradient Approximation (GGA) .....	9
Hybrid Functionals .....	10
<b>THE BASIS SETS</b> .....	13
<b>PROS AND CONS OF DFT</b> .....	15
Pros .....	15
Cons .....	15
<b>TIME-DEPENDENT DENSITY FUNCTIONAL THEORY (TDDFT)</b> .....	16
<b>CONCLUDING REMARKS</b> .....	18
<b>CONSENT FOR PUBLICATION</b> .....	18
<b>CONFLICT OF INTEREST</b> .....	18
<b>ACKNOWLEDGEMENTS</b> .....	18
<b>REFERENCES</b> .....	19
<b>CHAPTER 2 APPLICATIONS OF DFT ON MOLECULAR SYSTEMS: HOW GAUSSIAN WORKS</b> .....	21
<b>INTRODUCTION</b> .....	21
<b>GEOMETRY OPTIMIZATION AND FREQUENCY CALCULATIONS</b> .....	22
<b>INTRODUCTION TO THE GAUSSIAN</b> .....	26
<b>THERMODYNAMIC PARAMETERS IN GAUSSIAN</b> .....	34
<b>POPULATION ANALYSIS IN GAUSSIAN: MOLECULAR ORBITALS AND ELECTRONIC PARAMETERS</b> .....	36
<b>POPULATION ANALYSIS IN GAUSSIAN: ATOMIC CHARGES AND MULTIPOLE MOMENTS</b> .....	38
<b>NMR CALCULATIONS IN GAUSSIAN</b> .....	41
<b>NLO PARAMETERS IN GAUSSIAN</b> .....	43
<b>NBO ANALYSIS IN GAUSSIAN</b> .....	46
<b>TDDFT CALCULATION OF UV-VIS-NIR SPECTRUM IN GAUSSIAN</b> .....	50
<b>CONCLUDING REMARKS</b> .....	52
<b>CONSENT FOR PUBLICATION</b> .....	52
<b>CONFLICT OF INTEREST</b> .....	52
<b>ACKNOWLEDGEMENTS</b> .....	53
<b>REFERENCES</b> .....	53
<b>CHAPTER 3 DFT STUDY ON SOME SYNTHETIC COMPOUNDS: (2,6), (2,4) AND (3,4) DICHLORO SUBSTITUTED PHENYL-N-(1,3-THIAZOL-2-YL) ACETAMIDES</b> .....	55

<b>INTRODUCTION</b> .....	55
<b>MOLECULAR GEOMETRIES</b> .....	56
<b>MOLECULAR ORBITALS AND ELECTRONIC PROPERTIES</b> .....	58
<b>NBO ANALYSIS</b> .....	59
Charge Distribution .....	59
Coordination Ability .....	59
<b>SCALING OF NORMAL MODES OF VIBRATION</b> .....	62
Higher Wavenumber Region (Above 1400 cm <sup>-1</sup> ) .....	63
Lower Wavenumber Region (Below 1400 cm <sup>-1</sup> ) .....	65
Which is Better, Scale Factor or Scaling Equation? .....	65
<b>COMPARISON OF VIBRATIONAL MODES OF 24DTA AND 34DTA</b> .....	67
Phenyl Ring (R1) Vibrations .....	67
Thiazol Ring (R2) Vibrations .....	70
Fragment (-NHCOCH <sub>2</sub> -) Vibrations .....	73
<b>CONCLUDING REMARKS</b> .....	73
<b>CONSENT FOR PUBLICATION</b> .....	74
<b>CONFLICT OF INTEREST</b> .....	74
<b>ACKNOWLEDGEMENTS</b> .....	74
<b>REFERENCES</b> .....	74
<b>CHAPTER 4 DFT STUDY ON AN UNNATURAL AMINO ACID: 4-HYDROXYPROLINE</b> ....	77
<b>INTRODUCTION</b> .....	77
<b>CIS-4-HYDROXY-L-PROLINE AND TRANS-4-HYDROXY-L-PROLINE</b> .....	78
Structural Properties .....	78
Vibrational Properties .....	80
<i>Spectral Region above 2800 cm<sup>-1</sup></i> .....	83
<i>Spectral Region 1800–1000 cm<sup>-1</sup></i> .....	84
<i>Spectral Region below 1000 cm<sup>-1</sup></i> .....	85
Electronic Properties .....	85
<b>CIS-4-HYDROXY-D-PROLINE AND ITS DIMER</b> .....	86
Molecular Geometry and Potential Energy Surface .....	86
Frontier Orbitals, MESP Surfaces and Charge Distribution .....	89
Inter-Molecular Interaction and NBO Analyses .....	91
Vibrational Spectroscopic Analysis .....	92
Ring Vibrations .....	94
Groups Vibrations .....	96
Electronic and Thermodynamic Parameters (Monomer and Dimer) .....	96
<b>CONCLUDING REMARKS</b> .....	97
<b>CONSENT FOR PUBLICATION</b> .....	98
<b>CONFLICT OF INTEREST</b> .....	98
<b>ACKNOWLEDGEMENTS</b> .....	98
<b>REFERENCES</b> .....	98
<b>CHAPTER 5 DFT STUDY ON SOME NATURAL PRODUCTS: TRICLISINE, RUFESCINE, AND IMERUBRINE</b> .....	100
<b>INTRODUCTION</b> .....	100
<b>TRICLISINE AND RUFESCINE</b> .....	101
Molecular Structures .....	101
Infrared Spectroscopic Analysis .....	102
<i>Wavenumber Range Above 1500 cm<sup>-1</sup></i> .....	104
<i>Wavenumber Range Below 1500 cm<sup>-1</sup></i> .....	104
<b>HOMO, LUMO AND MESP SURFACES</b> .....	106

Electronic and Thermodynamic Parameters .....	108
<b>IMERUBRINE</b> .....	108
Molecular Structure .....	108
Vibrational Spectroscopic Analysis .....	109
<i>C-H Vibrations</i> .....	109
<i>C-C Vibrations</i> .....	112
<i>C-N Vibrations</i> .....	113
<i>C-O and C=O Vibrations</i> .....	113
NMR Spectroscopic Analysis .....	113
Chemical Reactivity .....	115
<i>HOMO, LUMO, and MESP Analyses</i> .....	115
<i>Reactivity Descriptors</i> .....	116
<b>CONCLUDING REMARKS</b> .....	116
<b>CONSENT FOR PUBLICATION</b> .....	117
<b>CONFLICT OF INTEREST</b> .....	117
<b>ACKNOWLEDGEMENTS</b> .....	117
<b>REFERENCES</b> .....	117
<b>CHAPTER 6 A COMPREHENSIVE DFT STUDY ON A THIONE COMPOUND AND ITS TAUTOMER</b> .....	120
<b>INTRODUCTION</b> .....	120
<b>METHODS</b> .....	121
Experimental .....	121
Computational .....	122
<b>RESULTS AND DISCUSSION</b> .....	122
Synthesis and Thermodynamics .....	122
Infrared Spectroscopic Analysis .....	126
<i>Ring Vibrations</i> .....	129
<i>Group Vibrations</i> .....	130
UV-Visible Spectroscopic Analysis .....	131
NMR Spectroscopic Analysis .....	134
MESP and Electronic Parameters .....	136
<b>CONCLUSIONS AND REMARKS</b> .....	138
<b>CONSENT FOR PUBLICATION</b> .....	138
<b>CONFLICT OF INTEREST</b> .....	138
<b>ACKNOWLEDGEMENTS</b> .....	139
<b>REFERENCES</b> .....	139
<b>CHAPTER 7 INTER- AND INTRA-MOLECULAR INTERACTIONS BY QUANTUM THEORY OF ATOMS IN MOLECULE</b> .....	143
<b>INTRODUCTION</b> .....	143
<b>QUANTUM THEORY OF ATOMS IN MOLECULE (QTAIM)</b> .....	144
Existence of H-Bond .....	144
Characterization of H-Bond .....	144
Strength of H-Bond .....	144
The AIMAll Program .....	145
<b>INTRA-MOLECULAR INTERACTIONS</b> .....	146
Synthetic Compounds .....	146
Natural Products .....	146
<b>INTER-MOLECULAR INTERACTIONS</b> .....	149
DFT versus QTAIM .....	149
Inter-Molecular Interactions in CHDP Dimer .....	150

<b>CONCLUDING REMARKS</b> .....	151
<b>CONSENT FOR PUBLICATION</b> .....	152
<b>CONFLICT OF INTEREST</b> .....	152
<b>ACKNOWLEDGEMENTS</b> .....	152
<b>REFERENCES</b> .....	152
<b>APPENDIX</b> .....	154
<b>SUBJECT INDEX</b> .....	1; 7

## FOREWORD

Density functional theory (DFT) based methods use the description of the electronic density of an atom or molecule to calculate a host of important properties, many of which are not easily obtained via experimental methods. Some attributes that may be accessed in this manner include molecular geometry, vibrational frequencies, dipole moments and higher-order moments, thermochemical properties, and so forth.

It gives me great pleasure in writing the foreword of this book. It is an outcome of a rigorous amount of effort, which has been devoted to conceptualizing, planning, and finally writing the book. The book contains all the ingredients required to understand, practice, and perform the DFT based studies. The first chapter of the book introduces the concept of DFT and the second chapter deals with its application to explore molecular systems using the popular *Gaussian* program. The subsequent chapters of the book discuss the results obtained by DFT calculations of various biologically important molecules. The last chapter exclusively focuses on the quantum theory of atoms in molecules, used for the study of various inter- and intra-molecular interactions. The book is also complemented with a sample output of the *Gaussian* as an appendix, which can be used to extract and interpret the results of DFT based calculations.

Despite the availability of high-performance computing and the emergence of new theoretical approaches, understanding of structure↔function correlation in molecular and macromolecular systems remains an elusive goal. I am confident that this book shall be of immense value for students, young researchers, scientists, teachers, and all those interested in exploiting DFT methods for molecular systems, particularly biologically active compounds. This book will help to learn and master the technique of applying the DFT based methods and the *Gaussian* program for analyzing various properties of biologically active molecules.

With best wishes,

**Sugriva Nath Tiwari**

Dean, Faculty of Science, Professor and Former Head, Department of Physics  
Deen Dayal Upadhyaya Gorakhpur University, Gorakhpur, India  
& Former President, Indian Science Congress Association (Physical Sciences Section)

## PREFACE

The very idea of writing a book on density functional theory (DFT) based studies on molecular systems arose from the volume of work carried out by us over a while. We have always felt the need for a concise literature on the theory and practice of DFT followed by a proper compilation of the research work using the well-known suite of programs, such as, the *Gaussian*. The sole perspective of initiating this project was to make available a good pool of literature, which can presumably be of immense help to the young researchers and experimentalists among others, who are planning to work or have been already working in this rapidly growing and exciting field of research.

The book has been organized into seven chapters and written from the beginners' perspective in such a way that anyone interested to work on molecular systems using the DFT based methods and the *Gaussian* program, can get an exhaustive and a very apropos idea of "how to employ the DFT on molecules" to explore the various properties of the systems under study. The chapters of the book have been methodically presented so that before starting to work on any molecular system, it is assumed that the reader gets well acquainted with the basics of DFT. After becoming friendly with the fundamentals of DFT, the reader is exposed to the applications of DFT on molecular systems with the focus on the *Gaussian* and its usage in a much applied way. Thereafter, many interesting themes have been covered in the form of the subsequent chapters of the book, namely, DFT studies on synthetic compounds, unusual amino acids, and natural products followed by a chapter on a comprehensive account on the way theory is used to complement the experiment. Considering the role of interactions in biologically active molecules, an exclusive chapter on the quantum theory of atoms in molecule (QTAIM) has been included. To supplement the second chapter and make the content more digestive, an appendix has also been added.

All in all, we tried every effort to present a concise and at the same time, complete picture of DFT and its role, action, and applications on some biologically active molecules. We believe that this book will serve its purpose and all the readers, irrespective of their field and level of experience would benefit in some way or the other.

We wish you a happy DFT.

**Ambrish Kumar Srivastava**  
Department of Physics Deen Dayal Upadhyaya Gorakhpur University  
Gorakhpur, Uttar Pradesh  
India

&

**Neeraj Misra**  
Department of Physics University of Lucknow  
Lucknow, Uttar Pradesh  
India

**CHAPTER 1****The Essence of Density Functional Theory**

**Abstract:** This chapter outlines the basic principles of the density functional theory (DFT). The introduction of electron density to develop the Kohn-Sham approach has been systematically presented. The various approximations such as LDA, GGA, and hybrid functional for the exchange-correlation energy have been discussed. A separate discussion on the basis sets has also been included. The advantages and shortcomings of DFT based techniques are also revealed. The formulation of time-dependent DFT has been presented in a concise manner. This chapter is intended to provide an overview of the theoretical background of the methods adopted in the succeeding chapters.

**Keywords:** Basis sets, DFT, Electron density, Exchange-correlation energy, Gaussian, Generalized-gradient approximation, Gradient-corrected functional, Hohenberg-Kohn theorem, Hybrid functional, Kohn-Sham approach, Local density approximation, TDDFT.

**INTRODUCTION**

The central idea behind the density functional theory (DFT) is a different variant of quantum mechanics, and like the wavefunction-based methods, some DFT methods do not use any empirical parameters and are derived from the first principles. In contrast to wavefunction-based methods, however, instead of using approximate molecular orbital wavefunctions, DFT uses the knowledge of the overall electron density to solve for the desired properties. Methods based on DFT have gained in popularity due to recent theoretical advancements that often allow it to achieve greater accuracy, at a lower or similar cost in computation time, than commonly used wavefunction-based methods such as the Hartree-Fock (HF) theory.

Since the book is intended for the application of density functional theory (DFT) and time-dependent DFT methods, it is very relevant to describe the formulation of the theory.

**The Schrödinger Equation**

DFT attempt to solve the non-relativistic Schrödinger wave equation:

$$\hat{H}\Psi = E\Psi \quad (1)$$

Here  $\Psi$  is the wavefunction,  $\hat{H}$  is time-independent non-relativistic Hamiltonian, and  $E$  is the energy of the system.

$$\hat{H} = \hat{T} + \hat{V} \quad (2)$$

The kinetic energy operator  $\hat{T}$  can be expanded into the following components:

$$\hat{T} = -\sum_{i=1}^N \frac{1}{2} \nabla_i^2 - \sum_{A=1}^M \frac{1}{2M_A} \nabla_A^2 \quad (3)$$

where the first term is the kinetic energy for the electrons and the second is that for the nuclei. Similarly, the potential energy operator ( $\hat{V}$ ) is given by.

$$\hat{V} = -\sum_{A=1}^M \sum_{i=1}^N \frac{Z_A}{r_{iA}} + \sum_{i=1}^N \sum_{j>i}^N \frac{1}{r_{ij}} + \sum_{A=1}^M \sum_{B>A}^M \frac{Z_A Z_B}{R_{AB}} \quad (4)$$

Here the first, second, and third terms represent the electron-nucleus attraction, the electron-electron repulsion, and the nucleus-nucleus repulsion, respectively.

Needless to mention that the Schrödinger equation can't be solved "exactly" for any system other than the simplest (single-electron) atomic system [1]. To solve this, therefore, we require certain approximations as discussed below.

### Born-Oppenheimer Approximation

The complete non-relativistic Hamiltonian using eq. (2), (3) and (4) is given below,

$$\hat{H} = -\sum_{i=1}^N \frac{1}{2} \nabla_i^2 - \sum_{A=1}^M \frac{1}{2M_A} \nabla_A^2 - \sum_{A=1}^M \sum_{i=1}^N \frac{Z_A}{r_{iA}} + \sum_{i=1}^N \sum_{j>i}^N \frac{1}{r_{ij}} + \sum_{A=1}^M \sum_{B>A}^M \frac{Z_A Z_B}{R_{AB}} \quad (5)$$

One can write  $\hat{H}$  into two parts considering the nuclear and electronic motions separately,

$$\hat{H}_{\text{elec}} = -\sum_{i=1}^N \frac{1}{2} \nabla_i^2 - \sum_{A=1}^M \sum_{i=1}^N \frac{Z_A}{r_{iA}} + \sum_{i=1}^N \sum_{j>i}^N \frac{1}{r_{ij}} \quad (6)$$

$$\hat{H}_{\text{nucl}} = -\sum_{A=1}^M \frac{1}{2M} \nabla_A^2 + \sum_{A=1}^M \sum_{B>A}^M \frac{Z_A Z_B}{R_{AB}} \quad (7)$$

According to the Born-Oppenheimer approximation, the motion of the electrons in a molecule can be considered in a field of fixed nuclei. This is based on the fact the nuclei are much heavier than the electrons. This implies that the kinetic energy of the nuclei, the first term in eq. (7) can be neglected and the nuclear repulsion energy, the second term in eq. (7), becomes constant for a specific molecular geometry [2]. Therefore, one has to deal with the electronic Hamiltonian, eq. (6). The eq. (6) can be solved for the electronic energy ( $E_{\text{elec.}}$ ) considering a fixed set of nuclear coordinates. The total energy is then simply a sum of  $E_{\text{elec}}$  and the constant nuclear repulsion energy.

### Electron Density and Wavefunction

Note that the electronic wavefunction ( $\psi$ ) obtained by solving eq. (6) is not measurable or observable. The experiments can measure several parameters of molecular systems, including electron density ( $\rho$ ), which is measurable by X-ray diffraction or electron diffraction. It might be a great idea to use one-electron density instead of many-electron wavefunctions for calculating the molecular geometries, energies, *etc.* In Table 1, we compare the properties of wavefunction and electron density.

**Table 1. Comparison of electron density and wavefunction.**

Electron density	Wavefunction
Observable	Not observable
Real	Complex
One electron	Many electrons
3 coordinates for $N$ -electron systems	$3N$ coordinates for $N$ -electron systems

In the Born interpretation, the probability density at any point is nothing but the one-electron wavefunction ( $\psi$ ) squared (having the same unit as that of the wavefunction at that point). For multi-electron wavefunction, the relation between  $\rho$  and  $\psi$  is more complicated. Nevertheless, the relation between  $\rho$  and  $\psi$  reads,

**CHAPTER 2****Applications of DFT on Molecular Systems: How Gaussian Works**

**Abstract:** This chapter focuses on the practical application of DFT in molecular systems. We discuss the process of “geometry optimization” and the idea behind it, which is the very first step of every DFT calculation. We introduce the *Gaussian*, a popular software program to perform such calculations. We continue to discuss the capability of this program with a brief theoretical background, wherever needed. We talk about several kinds of calculations to be performed by the *Gaussian* such as thermodynamics, population analysis, NMR, NLO, NBO, TDDFT calculations to name a few. More importantly, we discuss how to perform these calculations, extract, and interpret the results. Ideally, this chapter provides all the ingredients needed to grasp the results discussed in the forthcoming chapters.

**Keywords:** DFT, Frequency calculation, Gaussian, GaussView, Geometry optimization, MESP, Molecular orbital, NBO, NLO, NMR, Population analysis, TDDFT, Thermodynamics, UV-vis-NIR.

**INTRODUCTION**

Having chosen an appropriate DFT method, *i.e.*, the suitable combination of exchange-correlation functional and basis set, the primary task of any DFT calculation is to obtain the “correct” structure of a molecular system. This is what is known as the geometry optimization of a molecule. The initial configuration of the molecular system required for this task can be derived from crystallographic parameters or modelled hypothetically. The process of geometry optimization has to be followed by the vibrational frequency calculation. This is to ensure that the optimized configuration of a molecule is stable, *i.e.*, its energy is “truly” minimum. Therefore, we shall first discuss these two terms.

Further applications of DFT on the molecular systems depend on the nature and/or property of the systems under study. For instance, if the molecule contains an electron-donating or withdrawing group, one might be interested in the charge distribution. Likewise, if the molecule is asymmetric, one might be interested in its optical activity and so forth.

**GEOMETRY OPTIMIZATION AND FREQUENCY CALCULATIONS**

The objective of geometry optimization is to find an atomic arrangement that makes the molecule most stable. Molecules are most stable when their energy attains the lowest possible value. This is achieved by creating a “potential energy surface” (PES). Before we discuss the PES, let’s first have a look over the minimization of a potential energy function in one-dimension,  $V(x)$ .

A “stationary point” of  $V(x)$  is characterized by:

$$\frac{dV(x)}{dx} = 0 \quad (1)$$

The  $V(x)$  is said to have a minimum if,

$$\frac{d^2V(x)}{dx^2} > 0 \quad (2)$$

and it has a maximum if,

$$\frac{d^2V(x)}{dx^2} < 0 \quad (3)$$

But it is neither maximum nor minimum for,

$$\frac{d^2V(x)}{dx^2} = 0 \quad (4)$$

In Fig. (1), we have plotted the  $V(x)$ , which shows the minimum and maximum stationary points. The “global” minimum is the point that is the lowest among all local minima.

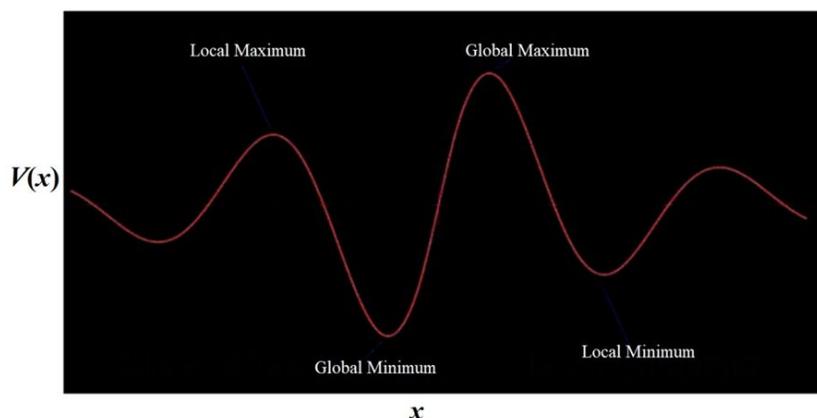


Fig. (1). Variation of  $V(x)$  with respect to the coordinate  $x$ . Various stationary points have also been shown.

The generalization of  $V(x)$  to the three dimensions leads to the concept of a PES. Thus, the PES is a mathematical relationship between different molecular geometries and their corresponding energies. These values are usually displayed in a three-dimensional graph, representing the bond angle, bond distance and, energy values as shown in Fig. (2).

For a molecular system of  $N$  atoms, there are  $3N$  coordinates ( $r$ ). Therefore, eq. (1) can be written as follows:

$$|\nabla V(\vec{r}^{3N})| = 0 \quad (5)$$

The energy of a molecule system near its equilibrium structure (stationary points) becomes:

$$E = T + V = \frac{1}{2} \sum_{i=1}^{3N} q_i^2 + V_{\text{eq}} + \sum_{i=1}^{3N} \sum_{j=1}^{3N} \left( \frac{\partial^2 V}{\partial q_i \partial q_j} \right)_{\text{eq}} q_i q_j \quad (6)$$

**CHAPTER 3****DFT Study on Some Synthetic Compounds: (2,6), (2,4) and (3,4) Dichloro Substituted Phenyl-N-(1-3-thiazol-2-yl) Acetamides**

**Abstract:** In this chapter, we present and discuss DFT study on three dichloro substituted (1, 3-thiazol-2-yl) acetamides; 26DTA, 24DTA and 34DTA using the B3LYP/6-31+G(d,p) method. We focus on the need of scaling the normal modes of vibrations and test two scaling schemes on 26DTA. We analyze their performance by comparing the scaled values against FTIR data. Subsequently, a detailed comparative study on the spectroscopic properties of 24DTA and 34DTA has been performed using a better scaling scheme. In addition, the NBO analysis is employed to explain the coordination ability of molecules and several electronic parameters are obtained to describe their chemical reactivity. This chapter is expected to provide the first flavor of the real application of DFT on biologically active molecules.

**Keywords:** Acetamide, B3LYP, Coordination ability, DFT, Electron parameters, FTIR, HOMO, LUMO, NBO, NPA, Scaling equation, Scaling factor, Vibrational spectra.

**INTRODUCTION**

Acetamide based heterocycles having nitrogen and sulphur atoms, form a distinct group of pharmacologically important compounds with an amide bond similar to that between amino acids in proteins (Chapter 4 will specifically address unusual amino acids). Several natural products and drug compounds contain such heterocyclic moieties [1, 2], including the derivatives of thiazole, which have several biological activities [3, 4]. For instance, the thiazoles have been used in the development of drugs for the cure of several diseases [5 - 12], fibrinogen receptor antagonists with antithrombotic activity [13] an inhibitor of bacterial DNA gyrase B [14]. It is, therefore, desirable to explore some novel compounds based on the thiazole ring. In this chapter, we present DFT based studies on three molecules, namely, 2-(2,6-Dichlorophenyl)-N-(1,3-thiazol-2-yl) acetamide [26DTA], 2-(2,4-Dichlorophenyl)-N-(1,3-thiazol-2-yl) acetamide [24DTA], and 2-(3,4-Dichlorophenyl)-N-(1,3-thiazol-2-yl) acetamide [34DTA]. The results [15 - 17] were obtained by the B3LYP functional and 6-31+G(d,p) basis set.

## MOLECULAR GEOMETRIES

The crystal structures obtained by X-Ray diffraction (XRD) of these compounds can be found in the literature [18 - 20], which were employed to generate the input structure of these molecules to be used for geometry optimization. The molecular structures, after optimization, of 26DTA, 24DTA, and 34DTA are displayed in Fig. (1) and some structural parameters can be found in Table 1. The C–C bond lengths in the vicinity of Cl atoms become a bit longer than others. The bond angle C6-C1-C2 is decreased by 3-4° in molecules 26DTA and 24DTA having at least one substitution of Cl at *ortho* position. The positional change in the substitutions leads to the decrease in the dihedral C1-C2-C7-C8 continuously from molecule 24DTA to 34DTA. In the crystal phase [18 - 20], the existence of N··H–N hydrogen bonds modifies their structural parameters. These inter-molecular interactions can't be considered by performing calculations on an isolated molecule in the gas phase. These molecules also possess intra-molecular hydrogen bonds (see Chapter 7).

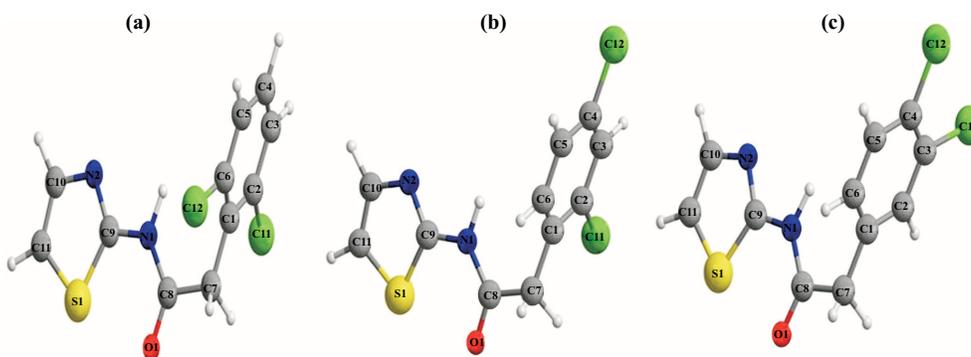


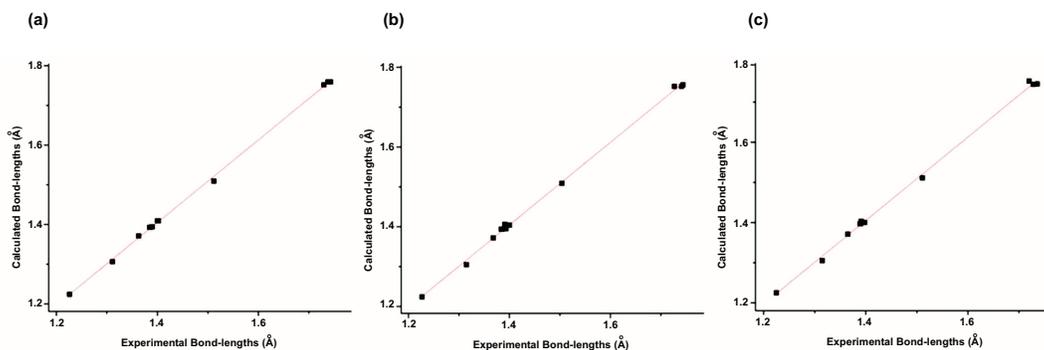
Fig. (1). Molecular structures of (a) 26DTA, (b) 24DTA, and (c) 34DTA at the B3LYP/6-31+G(d,p) level [17].

Table 1. Selected structural parameters at the B3LYP/6-31+G(d,p) level [17]. The corresponding experimental data are taken from Ref. [18-20].

Structural Parameters (Å, °)	26DTA		24DTA		34DTA	
	Calc.	Expt. [18]	Calc.	Expt. [19]	Calc.	Expt. [20]
C1-C2	1.409	1.400	1.406	1.391	1.400	1.398
C2-C3	1.394	1.390	1.395	1.393	1.397	1.389
C3-C4	1.393	1.386	1.394	1.386	1.401	1.392
C4-C5	1.393	1.385	1.394	1.384	1.397	1.390
C1-C6	1.409	1.402	1.404	1.400	1.403	1.391
C1-C7	1.509	1.512	1.509	1.504	1.511	1.511

(Table 3) cont....

C8-O1	1.224	1.226	1.224	1.227	1.225	1.225
C8-N1	1.371	1.363	1.372	1.368	1.371	1.365
C9-N2	1.306	1.311	1.305	1.315	1.305	1.315
C9-S1	1.752	1.730	1.752	1.727	1.752	1.720
C-C11	1.759	1.743	1.756	1.744	1.745	1.736
C-C12	1.759	1.738	1.752	1.741	1.744	1.728
C6-C1-C2	115.7	115.6	116.8	117.2	118.3	118.7
C5-C4-C3	120.2	120.3	121	122.2	119.3	119.3
C6-C1-C7	122.1	122.4	120.5	120.8	121	122.3
C1-C7-C8	118	110.3	117.7	113	117.9	111.9
C8-N1-C9	125.7	123.2	125.7	123.9	125.7	122.9
N1-C9-N2	120.4	121.1	120.4	120.6	120.4	120.8
C9-N2-C10	110.1	109.5	110.1	109.7	110.1	109.2
C9-S1-C11	87.7	88.8	87.7	88.7	87.7	88.7
C6-C1-C7-C8	90.4	91.89	100.3	112.4	86.8	110.9
C1-C7-C8-N1	0	125.3	14.8	172.5	3.7	-166.9



**Fig. (2).** Correlation between calculated and experimental bond lengths; **(a)**  $d_{\text{calc.}} = 1.040 d_{\text{expt.}} - 0.051$ ,  $R^2 = 0.9991$  for 26DTA, **(b)**  $d_{\text{calc.}} = 1.035 d_{\text{expt.}} - 0.044$ ,  $R^2 = 0.9986$  for 24DTA, and **(c)**  $d_{\text{calc.}} = 1.039 d_{\text{expt.}} - 0.050$ ,  $R^2 = 0.9980$  for 34DTA.

In Table 1, we have also listed the bond length obtained from XRD on these compounds for comparison. In Fig. (2), we have plotted correlation graphs between calculated and experimental bond-lengths, excluding the C-H bond-lengths. We obtain a nice linear correlation having a correlation coefficient ( $R^2$ ) of 0.9980-0.9991, which verifies that the present computational method is quite appropriate to reproduce the experimental geometry.

## CHAPTER 4

## DFT Study on an Unnatural Amino Acid: 4-Hydroxyproline

**Abstract:** 4-hydroxy-*l*-proline is formed by hydroxylation of proline, an amino acid found in protein, whose inhibition results in hair problems in humans, causing scurvy disease. In this chapter, we discuss the DFT study on *cis* and *trans* conformers of 4-hydroxy-*l*-proline, *i.e.*, CHLP and THLP using the B3LYP/6-31+G(d,p) level. The equilibrium structures of both conformers are obtained to analyze their vibrational properties. We have also discussed the results of an in-depth study on *cis*-4-hydroxy-*d*-proline (CHDP). The scan of potential energy surface provides the global minimum structure of CHDP along with its possible conformers. HOMO, LUMO, and MESP surfaces as well as charge distribution, are used to explain the chemical reactivity. The equilibrium geometry of CHDP dimer has been obtained and intermolecular interactions are explored by the NBO analyses. Vibrational analysis has been carried out on CHLP, THLP, and CHDP (monomer and dimer). A complete assignment to vibrational modes has been presented based on their potential energy distribution. The calculated frequencies, after proper scaling, are compared with experimental FT-IR frequencies recorded by KBr disc and Nujol mull techniques. Several electronic as well as thermodynamic parameters have also been reported.

**Keywords:** B3LYP, Charge distribution, DFT, Dimer, Electronic parameter, FT-IR, H-bond, HOMO-LUMO, Hydroxyproline, Inter-molecular interaction, MESP, NBO, Proline, Thermodynamic parameter, Vibrational spectra.

### INTRODUCTION

The protein structure and its functions have been the subject of investigation for a long time [1]. Proteins contain many amino acids of different types with complex structures. One of them is proline, which is unique due to the fact that the amine nitrogen is attached to two alkyl groups. Consequently leading it to a secondary amine. Proline possesses an enormous conformational rigidity due to the distinguishable cyclic form of its side-chain. This side-chain also changes the rate of the formation of peptide bonds among proline and other amino acids. The incorporation of unnatural amino acids leads to the exploration of protein structure and functions [2, 3]. Proline and related compounds are frequently employed in organic reactions as asymmetric catalysts. Furthermore, proteins with

excess proline interact with polyphenols to form haze (turbidity) during brewing [4, 5].

4-Hydroxyproline is derived from proline by substituting a hydroxyl ( $-OH$ ) to the gamma carbon atom. Despite the fact that it is not directly found into proteins, it consists of almost 4% of all amino acids obtained in animal tissue, which exceeds several translationally incorporated amino acids [6]. Hydroxyproline becomes a main constituent of the protein collagen [7], playing an important role in collagen stability [8] by facilitating the sharp twisting of the collagen helix [9]. Therefore, it can be exploited as an indicator to estimate the amount of collagen and/or gelatin. The glycoproteins incorporating hydroxyproline have also been obtained in plant cell walls [10]. The hydroxylation of proline needs ascorbic acid, whose absence in humans results in the reduced stability of the collagen due to defect in the hydroxylation of proline residues of collagen, leading to scurvy disease. Nevertheless, the increased serum and urine levels of hydroxyproline are obtained in the case of Paget's disease [11]. 4-hydroxyproline is also found in the toxic cyclic peptides from *Amanita* mushrooms (e.g. alpha-amanitin and phalloidin) [12].

Many chemical and/or biological properties are closely associated with the molecular structures or geometries. The different conformations of the same molecule may lead to different chemical properties. The aim of the present study includes detailed structural and vibrational analyses of two potential conformers of 4-hydroxyproline, namely, *cis*-4-hydroxy-*l*-proline (CHLP) and *trans*-4-hydroxy-*l*-proline (THLP). In this chapter, we will first provide a comparative analysis of CHLP and THLP [13]. Subsequently, we will focus on the *cis*-4-hydroxy-*d*-proline (CHDP) and its dimer [14]. The CHLP and CHDP can be differentiated on the basis of the circular dichroism or optical rotatory dispersion, which will not be discussed here. All results described in this chapter are obtained at the B3LYP/6-31+G\*\* or B3LYP/6-31+G(d,p) level using the *Gaussian 09* program.

## CIS-4-HYDROXY-L-PROLINE AND TRANS-4-HYDROXY-L-PROLINE

### Structural Properties

The optimized geometries of CHLP and THLP are shown in Fig. (1) and respective bond-lengths can be found in Table 1. 4-hydroxyproline is composed of one hetero-pentagonal ring with one carbon replaced by nitrogen. This pentagonal ring deviates from planarity because of the repulsion due to non-bonding electrons of nitrogen. The covalent bond between the side-chain and nitrogen backbone has relevant structural consequences on the properties of both conformers. However, there is a strict dependence between the main- and side-

chain proline conformations. This is reflected in the non-bonding distances between backbone atoms, R(1–4) which is 2.12 Å for CHLP and 2.118 Å for THLP and R(1–5), 2.128 Å (CHLP) and 2.12 Å (THLP) (not given in Table 1).

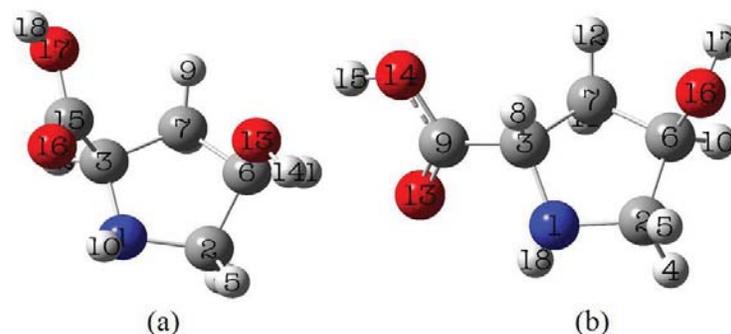


Fig. (1). Optimized geometries of (a) CHLP and (b) THLP [13].

In *cis* and *trans* conformers, the same groups (–OH and –COOH) are present at different angular positions of the hetero-pentagonal ring. This results in the change in ring geometries which have also been proven to be a sensitive indicator of the interaction between the substituent and the ring. Consequently, a re-adjustment takes place in the ring due to the presence of these groups in both *cis* and *trans* conformations. The average bond-length of C–C in the ring for CHLP (1.52 Å) takes a slightly lower value than in THLP (1.53 Å). However, C–N bond-length in *cis* (1.47 Å) becomes slightly higher than that in *trans* conformer, 1.46 Å (see Table 1). In general, calculated bond-lengths are consistent with the observed values for 4-hydroxyproline [15] by X-ray and neutron diffraction. For instance, the C–C bond-lengths in 4-hydroxyproline are observed to be between 1.52 Å and 1.53 Å.

Table 1. Bond-lengths (R, in Å) of CHLP and THLP calculated at the B3LYP/6-31+G(d,p) level. Refer to (Fig. 1) for atomic labeling [13].

CHLP				THLP			
Parameter	Value	Parameter	Value	Parameter	Value	Parameter	Value
R(1-2)	1.475	R(6-7)	1.528	R(1-2)	1.475	R(6-7)	1.539
R(1-3)	1.469	R(6-11)	1.099	R(1-3)	1.462	R(6-10)	1.098
R(1-10)	1.016	R(6-13)	1.432	R(1-18)	1.017	R(6-16)	1.434
R(2-4)	1.099	R(7-8)	1.094	R(2-4)	1.094	R(7-11)	1.097
R(2-5)	1.096	R(7-9)	1.091	R(2-5)	1.095	R(7-12)	1.094
R(2-6)	1.537	R(13-14)	0.966	R(2-6)	1.553	R(9-13)	1.214

## DFT Study on Some Natural Products: Triclisine, Rufescine, and Imerubrine

**Abstract:** This chapter deals with three biologically active natural products, triclisine, rufescine, and imerubrine. The B3PW91/6-311+G(d,p) level of DFT is used to obtain the optimized structures of molecules under study. We carried out vibrational analyses of triclisine and rufescine at their optimized structures and provided detailed assignments of the prominent vibrational modes. The computed infrared frequencies are found to be in good agreement with the experimentally determined FT-IR spectra of both molecules. Similarly, their properties are also studied with the help of HOMO, LUMO, MESP surfaces, and several electronic as well as thermodynamic parameters. The vibrational spectrum of imerubrine is analyzed and the normal modes are accurately assigned based on the potential energy distribution. The nuclear magnetic resonance shifts of imerubrine are also obtained, analyzed, and compared with the corresponding experimental values. The chemical reactivity of imerubrine is also explained using HOMO, LUMO, and MESP surfaces as well as a number of reactivity descriptors.

**Keywords:** Azafluoranthenes, B3PW91, DFT, Electronic parameter, FT-IR, H-bond, HOMO, Imerubrine, LUMO, MESP, Natural product, NMR, Rufescine, Thermodynamic parameter, Triclisine, Vibrational spectra.

### INTRODUCTION

Amazonian wines *Abuta rufescens* and *Triclisia gillettii* are employed to extract triclisine and rufescine, respectively, which are natural products belonging to the azafluoranthene group. The azafluoranthenes are present everywhere in nature, having their parent bases in the cigarette smoke, coal tar, street dust, rivers, and lake sediments [1, 2]. These compounds containing nitrogen-heterocycles have become one of the major contaminants in environment [3, 4]. Nevertheless, the natural products of the azafluoranthene group have been found to show potential-biological activities as antifungal, anti-HIV and cytotoxic agents [5 - 7]. For instance, the azafluoranthene eupolauridine exhibit the cytotoxic activity by targeting the DNA topoisomerase II [8]. Apart from the aforementioned biological activities, the molecules with the azafluoranthene core possess interesting spectral properties due to extensive conjugation. This makes them ideal for luminescent

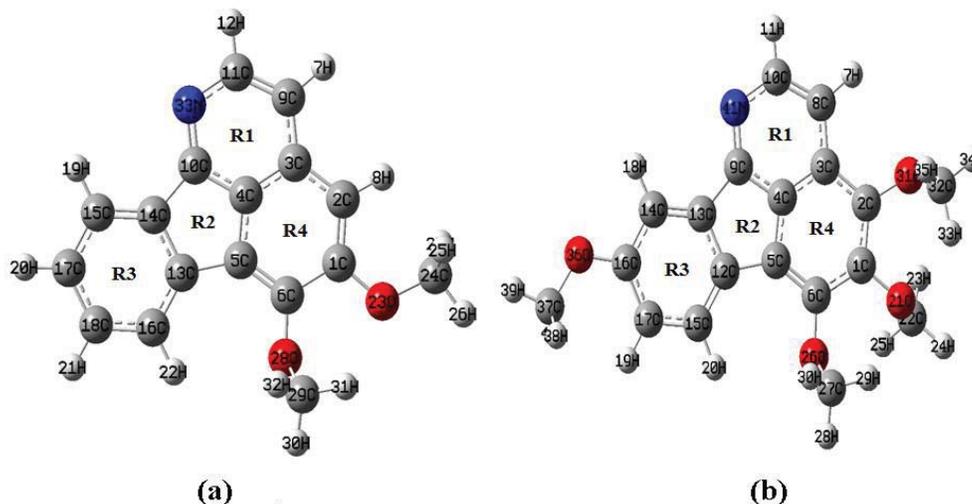
applications and electroluminescent devices [9 - 12]. The direct arylation [13] and electrocyclization [14] can be used to synthesize the azafluoranthene compounds and their derivatives. The comparative DFT study of triclisine and rufescine has been reported by us [15].

Likewise, *Abuta imene* is used to extract imerubrine, which belongs to the rare natural products from tropoloisoquinolines [16]. Biosynthetically, it is an analogue of alkaloids of azafluoranthene [17]. Boger and Takahashi [18] along with Lee and Cha [19] have reported the total syntheses of imerubrine and associated compounds using the cycloaddition reaction. The structure of imerubrine is derived from rufescine such that extra oxygen is attached to a phenyl ring, as studied by us [20]. Hence, it becomes obvious to perform a comparative analysis of imerubrine and rufescine. In this chapter, we present the results of triclisine, rufescine, and imerubrine at the B3PW91/6-311+G(d,p) level.

## TRICLISINE AND RUFESCINE

### Molecular Structures

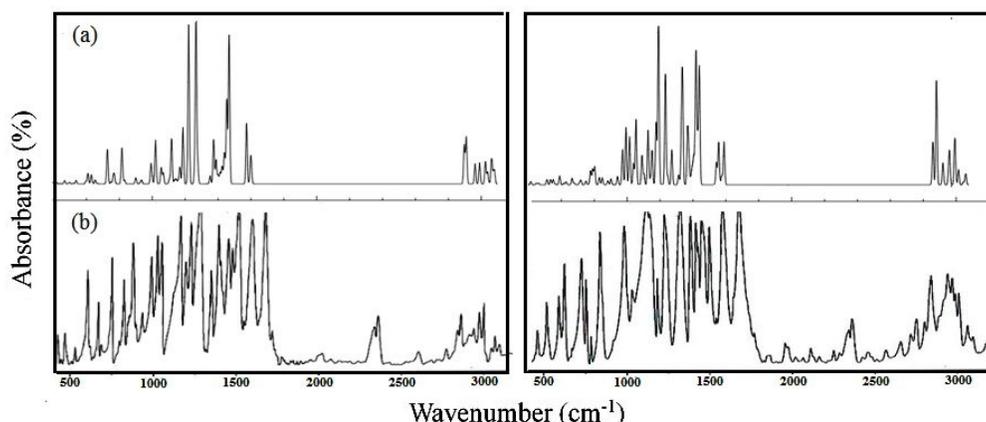
The optimized structures of triclisine and rufescine molecules are shown in Fig. (1) with the labeling of atoms. The structural similarities in these compounds is due to the presence of four six-membered rings including a heterocyclic ring (R1) with the substitution of nitrogen and the functionalized ring (R4) having two  $-OCH_3$  groups. In addition, there exist two more  $-OCH_3$  groups, in rufescine, linked at the C2 and C16 sites of ring R4 and R3, respectively.



**Fig. (1).** Optimized molecular geometries of (a) triclisine and (b) rufescine (reproduced from [15] with the permission of Elsevier).

### Infrared Spectroscopic Analysis

Infrared frequencies (wavenumbers) of both molecules are also calculated using the B3PW91/6-311+G(d,p) level. The calculated wavenumbers are scaled with the factor of 0.9648 as discussed in the previous chapters. The Perkin Elmer 1800 Spectrophotometer has been employed for recording the FT-IR spectra of these compounds in the region 4000-400  $\text{cm}^{-1}$  using samples in CsI pellet as mentioned earlier [15]. The calculated spectra have been plotted in Fig. (2) along with corresponding FT-IR spectra for a quick comparison.



**Fig. (2).** (a) Simulated IR and (b) experimental FT-IR spectra of (left) triclisine and (left) rufescine (reproduced from [15] with the permission of Elsevier).

Tables 1 and 2 list the prominent vibrational modes for triclisine and rufescine, respectively. The detailed vibrational assignments of normal modes have been offered and respective FT-IR wavenumbers are also listed. To simplify the discussion, the vibrational spectrum has been divided into two parts, greater than 1500  $\text{cm}^{-1}$  and less than 1500  $\text{cm}^{-1}$ .

**Table 1. Infrared spectral analysis of significant vibrations of triclisine (adopted from [15] with the permission of Elsevier).**

Wavenumber ( $\text{cm}^{-1}$ )		FT-IR Value ( $\text{cm}^{-1}$ )	IR Int. (a.u.)	Vibrational Assignments*
Calculated	Scaled			
3209	3094	3090	9.3	$\nu(\text{CH})\text{R3}$
3209	3093	-	6.6	$\nu(\text{CH})\text{R4}$
3201	3086	-	13.0	$\nu(\text{CH})\text{R3}$
3191	3076	3080	23.0	$\nu(\text{CH})\text{R1}$

## A Comprehensive DFT Study on a Thione Compound and its Tautomer

**Abstract:** In this chapter, we present an exhaustive study on a synthetic compound, 4-Amino-3-(4-hydroxybenzyl)-1H-1,2,4-triazole-5(4H)-thione (4AHT) and its tautomer employing both experimental and theoretical methods. 4AHT was synthesized by the reaction of 4-hydroxyphenylacetic acid and thiocarbohydrazide. The derivatives of 1,2,4-triazole are known to display antiviral, antidepressant, antimicrobial and anti-inflammatory activities. A DFT study on thione and thiol tautomers of 4AHT has been performed using the B3LYP/6-31+G(d,p) level. The calculated geometrical parameters are obtained to be in compliance with corresponding crystallographic values. The FT-IR spectrum of 4AHT obtained by the KBr disc technique has been explained by assigning the normal modes based on their potential energy distributions. The UV-visible spectrum of the title compound has been discussed by calculating the electronic transitions in several excited states using the TD-DFT method. The <sup>1</sup>H-NMR spectrum has also been studied by the GIAO method, which provides a good linear correlation between calculated and experimental chemical shifts. These spectroscopic results propose the dominance of the thione form of 4AHT in the solid-state and NH-SH tautomerism in the liquid form. This chapter is designed to provide a complete picture of the DFT based studies on molecular systems.

**Keywords:** B3LYP, DFT, Electronic parameter, Electronic transition, Experiment, FT-IR, HOMO, LUMO, MESP, NH-SH tautomerism, NMR, PES, Reaction, Synthesis, Tautomer, TD-DFT, Thermodynamics, Thiol, Thione, UV-visible.

### INTRODUCTION

The well known heterocyclic triazoles have been recently in focus due to their adaptability for the synthesis of various heterocyclic systems. There exist two tautomers of triazoles, namely, the 1,2,3-triazole, symbolized as 1H and the 1,2,4-triazole, symbolized as 4H. The planar 4H rings are aromatic with 6 $\pi$ -electron-systems, which are very important in chemical science [1, 2]. The derivatives 1,2,4-triazole exhibit several biological activities, and hence, many 4H derivatives along with their N-bridged compounds were paid attention to in the past [3, 4]. The 1,2,4-triazole derivatives have been found to show anti-inflammatory [5],

antiviral [6], antimicrobial [7], and antidepressant [8] activities. Therefore, the synthesis and extensive study of these heterocyclic systems are of immense importance.

Schiff bases [9, 10] and related heterocycles including triazoles [11 - 13] become potent corrosion inhibitors. Their chemisorption primarily takes place due to the  $\text{-C=N-}$  group interaction [10] and electronegative atoms such as N, O, S, *etc.* in the Schiff bases make them efficient corrosion inhibitors. Several compounds based on triazoles are reported to be good corrosion inhibitors for steel in acid media [14 - 17]. The synthesis of a few 1,2,4-triazole-5(4H)-thione compounds have been reported by Salgın-Gökşen *et al.* [18] along with their antimicrobial, analgesic, and anti-inflammatory activities. In this chapter, a comprehensive experimental and theoretical study of 4-Amino-3-(4-hydroxybenzyl)-1H-1,2,4-triazole-5(4H)-thione (4AHT) is presented, which was performed by us [19]. The 4AHT compound was synthesized by fusing a well-triturated mixture of 4-hydroxyphenylacetic acid ( $\text{C}_8\text{H}_8\text{O}_3$ ) and thiocarbohydrazide ( $\text{CH}_6\text{N}_4\text{S}$ ) in a round bottom flask for one hour on an oil bath at 413 K and subsequently cooling to room temperature [20]. The compound, thus obtained, was dried and recrystallized using methanol, yielding colourless block-like crystals, being triclinic with a  $P_1$  symmetry group.

The reaction thermodynamics for the synthesis and spectroscopic analyses are performed using the density functional theory (DFT) based method. The chemical reactivity of 4AHT is studied with the help of molecular electrostatic potential (MESP) surface and several descriptors. The biological activities of 4AHT are also anticipated. We are of the firm view that these results will be useful in the future works on the 1,2,4-triazole-5(4H)-thione and related systems.

## METHODS

### Experimental

The sample has been estimated as 100% pure using the HPLC method. The Shimadzu 8400S spectrometer with the resolution of  $\pm 4 \text{ cm}^{-1}$  was employed to record the FT-IR spectrum of sample in the wavenumber range 4000-400  $\text{cm}^{-1}$  using the KBr pellet (see Chapter 4). The Bruker 400 MHz NMR spectrometer was used to record the  $^1\text{H}$ -NMR spectrum of 4AHT with dimethyl sulfoxide (DMSO) solvent. The Shimadzu UV-2550 double-beam spectrophotometer having 1 cm matched quartz cell to measure the absorbance was utilized to record the UV-visible spectrum of 4AHT with ethyl alcohol (ethanol) solvent.

## Computational

The optimization of the structure of 4AHT was performed with no constraints on symmetry in the potential energy surface (PES) with DFT at the B3LYP [21, 22] functional and a 6-31+G(d,p) basis set. The UV-visible spectrum was replicated by applying the time-dependent DFT (TD-DFT) approach using the equilibrium structure of 4AHT at the B3LYP level. The gauge independent atomic orbital (GIAO) method was used to calculate the  $^1\text{H-NMR}$  chemical shifts at the same level. The polarizable continuum model devised by Tomasi *et al.* [23] has been exploited to incorporate the solvent effect during spectroscopic calculations. These computations were carried out by the *Gaussian 09* software [24].

## RESULTS AND DISCUSSION

### Synthesis and Thermodynamics

Fig. (1) displays the schematic of the reaction for the synthesis of 4AHT. The thermodynamics of this reaction can be analyzed by calculating various thermal parameters of reactants and products using room temperature. Table 1 lists the room temperature values of total electronic energy ( $E$ ), thermal Enthalpy ( $H$ ), Gibbs' free energy ( $G$ ), and entropy ( $S$ ) for these reactants ( $\text{C}_8\text{H}_8\text{O}_3$ ,  $\text{CH}_6\text{N}_4\text{S}$ ) and products ( $\text{C}_9\text{H}_{10}\text{N}_4\text{OS}$ ,  $2\text{H}_2\text{O}$ ).

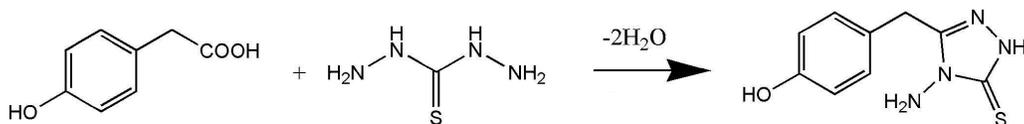


Fig. (1). Synthesis scheme of 4AHT [20].

One can see that the change in enthalpy change ( $\Delta H_{\text{Reaction}}$ ), Gibbs free energy ( $\Delta G_{\text{Reaction}}$ ), and entropy ( $\Delta S_{\text{Reaction}}$ ) for this reaction are calculated to be -0.3010 a.u., -0.0415 a.u. and 24.8 cal/mol.K, respectively (1 a.u. = 627.5 kcal/mol). Thus,  $\Delta H_{\text{Reaction}}$  and  $\Delta G_{\text{Reaction}}$  possess negative values but the value of  $\Delta S_{\text{Reaction}}$  is positive. This clearly reveals that the synthesis of 4AHT is favourable at room temperature due to the spontaneous and exothermic nature of the reaction.

Since both  $H$  and  $S$  favour the reaction path and so does  $G$  because  $\Delta G = \Delta H - T \Delta S$ . The equilibrium constant ( $K_{\text{eq}}$ ) and  $\Delta G_{\text{Reaction}}$  at temperature ( $T$ ) are related as  $K_{\text{eq}} = e^{-\Delta G/RT}$ , which decides the nature (direction) of a chemical reaction. The  $K_{\text{eq}}$  value for the above mentioned reaction is found to be  $1.285 \times 10^{19}$  at  $R = 1.987 \times 10^{-3}$  kcal/mol.K and  $T = 298.15$  K. This further suggests that the reaction proceeds

## CHAPTER 7

## Inter- and Intra-Molecular Interactions by Quantum Theory of Atoms in Molecule

**Abstract:** In this exclusive chapter, we present a brief overview of the quantum theory of atoms in molecule (QTAIM) proposed by R. F. W. Bader. This theory is based on the topological analysis of the electron density and related parameters. One of the strengths of this theory is the accurate prediction, characterization, and quantification of various interactions, including H-bond and van der Waals interactions. Herein, we discuss the important aspects of QTAIM regarding the intra- and intermolecular interactions in biologically active molecules discussed in the preceding chapters. Within the framework of the QTAIM, I mention the criteria of H-bonds and characterize the various H-bonds on the basis of topological parameters, and continue to quantify the strength of the H-bond. I will also describe a very user-friendly software *AIMAll* to perform the QTAIM analysis and explain the obtained results. In order to provide the contents digested, I will include examples of molecules from Chapters 3, 4, and 5. I believe that this chapter will guide the readers interested in various kinds of interactions in biologically active molecules.

**Keywords:** AIM, AIMAll, BCP, Bond strength, BSSE, Characterization, Complex, Counterpoise, Dimer, Electron density, H-bond, Intermolecular interaction, Intramolecular interaction, Laplacian, Molecular graph, QTAIM, RCP, Reactivity, Stabilization, Supermolecular approach, Topology.

### INTRODUCTION

H-bonds play a key role in determining the shapes, properties, and functions of biomolecules and biologically active systems [1]. Despite the dominant role of H-bonding in nature, accurate data on the respective stabilization or interaction energies are quite rare. The situation with extended H-bonded complexes is, despite enormous progress in various experimental techniques, even less satisfactory and accurate data on stabilization energies of these complexes are almost unavailable. Reliable and consistent information on the stability of various types of inter-molecular H-bonded complexes, from the very weak to the strongest, comes from the high-level correlated quantum chemical wavefunction-based method or density functional theory (DFT) calculations, and these methods, thus, represent one of the most promising sources of relevant data. On the cont-

rary, the intra-molecular H-bonds can not be directly quantified from a DFT calculation and this requires an alternative approach.

### QUANTUM THEORY OF ATOMS IN MOLECULE (QTAIM)

The QTAIM [2] describes the interactions between atomic basins. It exploits some topological parameters *viz.* electron density ( $\rho$ ) and its Laplacian ( $\nabla^2\rho$ ), kinetic energy density ( $G$ ), potential energy density ( $V$ ), and total electron energy density ( $H$ ) at the bond critical point (BCP) of interaction atoms or fragments. The theory efficiently characterizes and quantifies various types of H-bonded and other interactions.

#### Existence of H-Bond

In QTAIM, the existence of H-bond follows Koch and Popelier criterion [3], which requires:

1. The existence of bond critical point (BCP) for the ‘proton (H)···acceptor (A)’ contact.
2. The value of electron density should lie in the range of 0.002–0.040 a.u.
3. The corresponding Laplacian ( $\nabla^2\rho$ ) should be within the range of 0.024–0.139 a.u.

#### Characterization of H-Bond

The three types of H-bond are characterized on the basis of topological parameters. According to Rozas *et al.* [4], the characterization demands at BCP:

1.  $\nabla^2\rho < 0$  and  $H < 0$  for strong H-bond of covalent nature.
2.  $\nabla^2\rho > 0$  and  $H < 0$  for medium H-bond of partially covalent nature.
3.  $\nabla^2\rho > 0$  and  $H > 0$  for weak H-bond of electrostatic character.

#### Strength of H-Bond

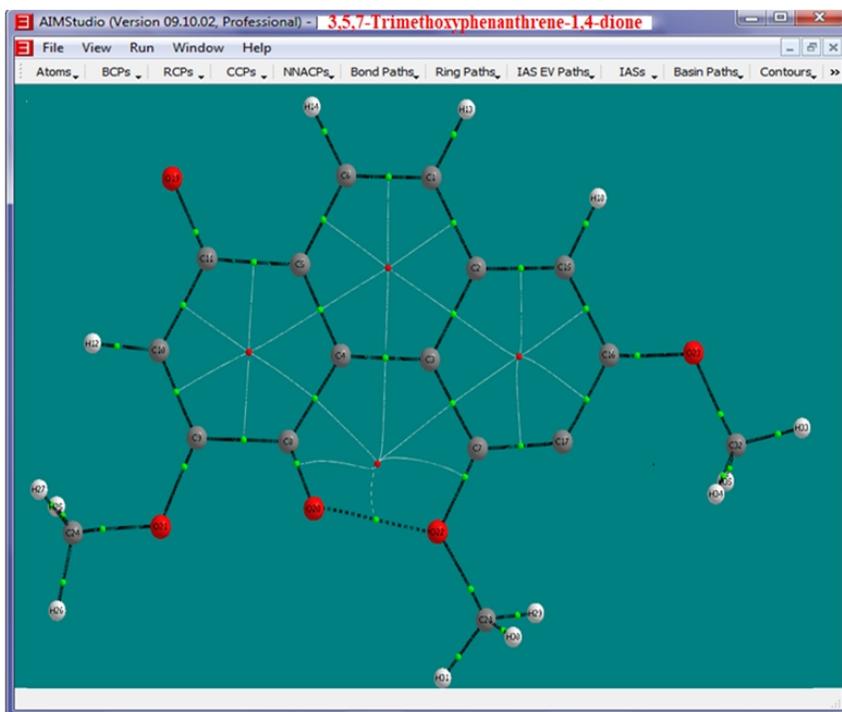
According to Espinosa *et al.* [5], the interaction energy of A···B contact is defined as,

$$\Delta E = -\frac{1}{2}V \quad (1)$$

at BCP.

### The AIMAll Program

There are various programs available to perform the QTAIM analysis, such as *AIMPAC* [6], *AIM2000* [7], *AIMAll* [8, 9], *etc.* In this chapter, we use the *AIMAll* program in order to explore intra-molecular and inter-molecular H-bond interactions such as hydrogen bonds (H-bonds). *AIMAll* is a user-friendly and efficient program. The graphical user interface of *AIMAll* is displayed in Fig. (1). It uses the formatted checkpoint (.fch or .fchk) file generated by the *Gaussian* program (see Chapter 2) as an input and automatically performs QTAIM analysis for the system under study. The basis set on reliability and stability in the values of QTAIM parameters have been studied and found that they are almost independent of the basis set in the case of used functional B3LYP in DFT [10].



**Fig. (1).** The graphical user interface of *AIMAll* program displaying the molecular graph of 3,5,7-Trimethoxyphenanthrene-1,4-dione (TPD). The intra-molecular interaction is shown by a dotted line. Green and red points represent BCPs and RCPs, respectively.

The QTAIM calculations on TPD [11] reveal an intra-molecular  $O20 \cdots O22$  interaction as depicted in the molecular graph shown in Fig. (1). The bond-distance  $O20 \cdots O22$  calculated at B3LYP/6-31+G\*\*method is 2.643 Å. The values of topological parameters at BCP of  $O22 \cdots O21$  are as follows:

## APPENDIX

### **Gaussian Output File of Methane (CH<sub>4</sub>)**

Entering Link 1 = C:\G09W\1.exe PID= 3188.

Copyright (c) 1988,1990,1992,1993,1995,1998,2003,2009,2010,  
Gaussian, Inc. All Rights Reserved.

This is part of the Gaussian(R) 09 program. It is based on  
the Gaussian(R) 03 system (copyright 2003, Gaussian, Inc.),  
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the Gaussian 92(TM) system (copyright 1992, Gaussian, Inc.),  
the Gaussian 90(TM) system (copyright 1990, Gaussian, Inc.),  
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-----  
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-----

Cite this work as:

Gaussian 09, Revision B.01,

M. J. Frisch, G. W. Trucks, H. B. Schlegel, G. E. Scuseria,  
M. A. Robb, J. R. Cheeseman, G. Scalmani, V. Barone, B. Mennucci,  
G. A. Petersson, H. Nakatsuji, M. Caricato, X. Li, H. P. Hratchian,  
A. F. Izmaylov, J. Bloino, G. Zheng, J. L. Sonnenberg, M. Hada,  
M. Ehara, K. Toyota, R. Fukuda, J. Hasegawa, M. Ishida, T. Nakajima,

Y. Honda, O. Kitao, H. Nakai, T. Vreven, J. A. Montgomery, Jr.,  
J. E. Peralta, F. Ogliaro, M. Bearpark, J. J. Heyd, E. Brothers,  
K. N. Kudin, V. N. Staroverov, T. Keith, R. Kobayashi, J. Normand,  
K. Raghavachari, A. Rendell, J. C. Burant, S. S. Iyengar, J. Tomasi,  
M. Cossi, N. Rega, J. M. Millam, M. Klene, J. E. Knox, J. B. Cross,  
V. Bakken, C. Adamo, J. Jaramillo, R. Gomperts, R. E. Stratmann,  
O. Yazyev, A. J. Austin, R. Cammi, C. Pomelli, J. W. Ochterski,  
R. L. Martin, K. Morokuma, V. G. Zakrzewski, G. A. Voth,  
P. Salvador, J. J. Dannenberg, S. Dapprich, A. D. Daniels,  
O. Farkas, J. B. Foresman, J. V. Ortiz, J. Cioslowski,  
and D. J. Fox, Gaussian, Inc., Wallingford CT, 2010.

\*\*\*\*\*

Gaussian 09: IA32W-G09RevB.01 12-Aug-2010

29-Nov-2020

\*\*\*\*\*

%chk=C:\Users\hp\Desktop\ch4.chk

-----

# opt freq b3lyp/6-311+g(d) geom=connectivity

-----

1/14=-1,18=20,19=15,26=3,38=1,57=2/1,3;

2/9=110,12=2,17=6,18=5,40=1/2;

3/5=4,6=6,7=11,11=2,16=1,25=1,30=1,71=1,74=-5/1,2,3;

4//1;

5/5=2,38=5/2;

6/7=2,8=2,9=2,10=2,28=1/1;

7//1,2,3,16;

1/14=-1,18=20,19=15/3(2);

2/9=110/2;

99//99;

2/9=110/2;

3/5=4,6=6,7=11,11=2,16=1,25=1,30=1,71=1,74=-5/1,2,3;

4/5=5,16=3/1;

5/5=2,38=5/2;

7//1,2,3,16;

1/14=-1,18=20,19=15/3(-5);

2/9=110/2;

6/7=2,8=2,9=2,10=2,19=2,28=1/1;

99/9=1/99;

-----

Title Card Required

-----

Symbolic Z-matrix:

Charge = 0 Multiplicity = 1

C 1.76692 0.56391 0.

H 2.12357 -0.4449 0.

H 2.12359 1.06831 0.87365

H 2.12359 1.06831 -0.87365

H 0.69692 0.56392 0.

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Berny optimization.

Initialization pass.

-----

! Initial Parameters !

! (Angstroms and Degrees) !

-----  
! Name Definition Value Derivative Info. !  
-----

! R1 R(1,2) 1.07 estimate D2E/DX2 !  
! R2 R(1,3) 1.07 estimate D2E/DX2 !  
! R3 R(1,4) 1.07 estimate D2E/DX2 !  
! R4 R(1,5) 1.07 estimate D2E/DX2 !  
! A1 A(2,1,3) 109.4712 estimate D2E/DX2 !  
! A2 A(2,1,4) 109.4712 estimate D2E/DX2 !  
! A3 A(2,1,5) 109.4712 estimate D2E/DX2 !  
! A4 A(3,1,4) 109.4713 estimate D2E/DX2 !  
! A5 A(3,1,5) 109.4712 estimate D2E/DX2 !  
! A6 A(4,1,5) 109.4712 estimate D2E/DX2 !  
! D1 D(2,1,4,3) -120.0 estimate D2E/DX2 !  
! D2 D(2,1,5,3) 120.0 estimate D2E/DX2 !  
! D3 D(2,1,5,4) -120.0 estimate D2E/DX2 !  
! D4 D(3,1,5,4) 120.0 estimate D2E/DX2 !  
-----

Trust Radius=3.00D-01 FncErr=1.00D-07 GrdErr=1.00D-06

Number of steps in this run= 24 maximum allowed number of steps= 100.

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Input orientation:  
-----

Center Atomic Atomic Coordinates (Angstroms)

Number Number Type X Y Z

---

1 6 0 1.766917 0.563910 0.000000  
2 1 0 2.123572 -0.444900 0.000000  
3 1 0 2.123590 1.068308 0.873652  
4 1 0 2.123590 1.068308 -0.873652  
5 1 0 0.696917 0.563923 0.000000

---

Distance matrix (angstroms):

1 2 3 4 5  
1 C 0.000000  
2 H 1.070000 0.000000  
3 H 1.070000 1.747302 0.000000  
4 H 1.070000 1.747302 1.747303 0.000000  
5 H 1.070000 1.747303 1.747303 1.747303 0.000000

Stoichiometry CH<sub>4</sub>

Framework group T[O(C),4C3(H)]

Deg. of freedom 1

Full point group T NOp 12

Largest Abelian subgroup D2 NOp 4

Largest concise Abelian subgroup D2 NOp 4

Standard orientation:

---

Center Atomic Atomic Coordinates (Angstroms)

Number Number Type X Y Z

---

1 6 0 0.000000 0.000000 0.000000  
2 1 0 0.617765 0.617765 0.617765  
3 1 0 -0.617765 -0.617765 0.617765  
4 1 0 -0.617765 0.617765 -0.617765  
5 1 0 0.617765 -0.617765 -0.617765

-----  
Rotational constants (GHZ): 164.2463768 164.2463768 164.2463768

Standard basis: 6-311+G(d) (5D, 7F)

There are 10 symmetry adapted basis functions of A symmetry.

There are 8 symmetry adapted basis functions of B1 symmetry.

There are 8 symmetry adapted basis functions of B2 symmetry.

There are 8 symmetry adapted basis functions of B3 symmetry.

Integral buffers will be 262144 words long.

Raffenetti 2 integral format.

Two-electron integral symmetry is turned on.

34 basis functions, 56 primitive gaussians, 35 cartesian basis functions

5 alpha electrons 5 beta electrons

nuclear repulsion energy 13.6865184815 Hartrees.

NAtoms= 5 NActive= 5 NUniq= 2 SFac= 4.00D+00 NAtFMM= 50 NAOKFM=F Big=F

One-electron integrals computed using PRISM.

NBasis= 34 RedAO= T NBF= 10 8 8 8

NBsUse= 34 1.00D-06 NBFU= 10 8 8 8

Harris functional with IExCor= 402 diagonalized for initial guess.

ExpMin= 4.38D-02 ExpMax= 4.56D+03 ExpMxC= 6.82D+02 IAcc=2 IRadAn= 0 AccDes=  
0.00D+00

HarFok: IExCor= 402 AccDes= 0.00D+00 IRadAn= 0 IDoV= 1

ScaDFX= 1.000000 1.000000 1.000000 1.000000

FoFCou: FMM=F IPFlag= 0 FMFlag= 100000 FMFlg1= 0

NFxFlg= 0 DoJE=T BraDBF=F KetDBF=T FulRan=T

Omega= 0.000000 0.000000 1.000000 0.000000 0.000000 ICntrl= 500 IOpCl= 0

NMat0= 1 NMatS0= 1 NMatT0= 0 NMatD0= 1 NMtDS0= 0 NMtDT0= 0

IICent= 4 NGrid= 0.

Petite list used in FoFCou.

Initial guess orbital symmetries:

Occupied (A) (A) (T) (T) (T)

Virtual (A) (T) (T) (T) (T) (T) (T) (A) (T) (T) (T) (T)

(T) (T) (A) (A) (E) (E) (T) (T) (T) (A) (T) (T)

(T) (T) (T) (T) (A)

The electronic state of the initial guess is 1-A.

Requested convergence on RMS density matrix=1.00D-08 within 128 cycles.

Requested convergence on MAX density matrix=1.00D-06.

Requested convergence on energy=1.00D-06.

No special actions if energy rises.

Keep R1 ints in memory in canonical form, NReq=1118393.

SCF Done: E(RB3LYP) = -40.5269656822 A.U. after 7 cycles

Conv = 0.1651D-08 -V/T = 2.0025

\*\*\*\*\*

Population analysis using the SCF density.

\*\*\*\*\*

Orbital symmetries:

Occupied (A) (A) (T) (T) (T)

Virtual (A) (T) (T) (T) (T) (T) (T) (A) (T) (T) (T) (T)

(T) (T) (A) (A) (E) (E) (T) (T) (T) (A) (T) (T)

(T) (T) (T) (T) (A)

The electronic state is 1-A.

Alpha occ. eigenvalues -- -10.14229 -0.70375 -0.39971 -0.39971 -0.39971

Alpha virt. eigenvalues -- 0.01085 0.05743 0.05743 0.05743 0.15177

Alpha virt. eigenvalues -- 0.15177 0.15177 0.21540 0.40328 0.40328

Alpha virt. eigenvalues -- 0.40328 0.60964 0.60964 0.60964 0.61552

Alpha virt. eigenvalues -- 0.87392 1.25394 1.25394 1.59531 1.59531

Alpha virt. eigenvalues -- 1.59531 2.34714 2.44084 2.44084 2.44084

Alpha virt. eigenvalues -- 3.13406 3.13406 3.13406 23.45834

Condensed to atoms (all electrons):

1 2 3 4 5

1 C 5.438146 0.375862 0.375862 0.375862 0.375862

2 H 0.375862 0.471076 -0.027446 -0.027446 -0.027446

3 H 0.375862 -0.027446 0.471076 -0.027446 -0.027446

4 H 0.375862 -0.027446 -0.027446 0.471076 -0.027446

5 H 0.375862 -0.027446 -0.027446 -0.027446 0.471076

Mulliken atomic charges:

1

1 C -0.941595

2 H 0.235399

3 H 0.235399

4 H 0.235399

5 H 0.235399

Sum of Mulliken atomic charges = 0.00000

Mulliken charges with hydrogens summed into heavy atoms:

1

1 C 0.000000

Sum of Mulliken charges with hydrogens summed into heavy atoms = 0.00000

Electronic spatial extent (au):  $\langle R^{**2} \rangle = 35.2014$ 

Charge= 0.0000 electrons

Dipole moment (field-independent basis, Debye):

X= 0.0000 Y= 0.0000 Z= 0.0000 Tot= 0.0000

Quadrupole moment (field-independent basis, Debye-Ang):

XX= -8.4501 YY= -8.4501 ZZ= -8.4501

XY= 0.0000 XZ= 0.0000 YZ= 0.0000

Traceless Quadrupole moment (field-independent basis, Debye-Ang):

XX= 0.0000 YY= 0.0000 ZZ= 0.0000

XY= 0.0000 XZ= 0.0000 YZ= 0.0000

Octapole moment (field-independent basis, Debye-Ang\*\*2):

XXX= 0.0000 YYY= 0.0000 ZZZ= 0.0000 XYY= 0.0000

XXY= 0.0000 XXZ= 0.0000 XZZ= 0.0000 YZZ= 0.0000

YYZ= 0.0000 XYZ= 0.7305

Hexadecapole moment (field-independent basis, Debye-Ang\*\*3):

XXXX= -16.6677 YYYY= -16.6677 ZZZZ= -16.6677 XXXY= 0.0000

XXXZ= 0.0000 YYYYX= 0.0000 YYYZ= 0.0000 ZZZX= 0.0000

ZZZY= 0.0000 XXYY= -5.0946 XXZZ= -5.0946 YYZZ= -5.0946

XXYZ= 0.0000 YYXZ= 0.0000 ZZXY= 0.0000

N-N= 1.368651848151D+01 E-N=-1.207227515305D+02 KE= 4.042785986351D+01

Symmetry A KE= 3.449759076308D+01

Symmetry B1 KE= 1.976756366809D+00

Symmetry B2 KE= 1.976756366809D+00

Symmetry B3 KE= 1.976756366809D+00

Calling FoFJK, ICntrl= 2127 FMM=F ISym2X=1 IICent= 0 IOpCIX= 0 NMat=1 NMatS=1  
NMatT=0.

\*\*\*\*\* Axes restored to original set \*\*\*\*\*

-----  
Center Atomic Forces (Hartrees/Bohr)

Number Number X Y Z

-----  
1 6 0.000000000 0.000000000 0.000000000  
2 1 0.004838637 -0.013686260 -0.000000012  
3 1 0.004838896 0.006843035 0.011852598  
4 1 0.004838876 0.006843049 -0.011852598  
5 1 -0.014516409 0.000000176 0.000000012  
-----

Cartesian Forces: Max 0.014516409 RMS 0.007496241

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Berny optimization.

Internal Forces: Max 0.014516409 RMS 0.007759347

Search for a local minimum.

Step number 1 out of a maximum of 24

All quantities printed in internal units (Hartrees-Bohrs-Radians)

Mixed Optimization -- RFO/linear search

Second derivative matrix not updated -- first step.

The second derivative matrix:

R1 R2 R3 R4 A1

R1 0.37230

R2 0.00000 0.37230  
R3 0.00000 0.00000 0.37230  
R4 0.00000 0.00000 0.00000 0.37230  
A1 0.00000 0.00000 0.00000 0.00000 0.16000  
A2 0.00000 0.00000 0.00000 0.00000 0.00000  
A3 0.00000 0.00000 0.00000 0.00000 0.00000  
A4 0.00000 0.00000 0.00000 0.00000 0.00000  
A5 0.00000 0.00000 0.00000 0.00000 0.00000  
A6 0.00000 0.00000 0.00000 0.00000 0.00000  
D1 0.00000 0.00000 0.00000 0.00000 0.00000  
D2 0.00000 0.00000 0.00000 0.00000 0.00000  
D3 0.00000 0.00000 0.00000 0.00000 0.00000  
D4 0.00000 0.00000 0.00000 0.00000 0.00000  
A2 A3 A4 A5 A6  
A2 0.16000  
A3 0.00000 0.16000  
A4 0.00000 0.00000 0.16000  
A5 0.00000 0.00000 0.00000 0.16000  
A6 0.00000 0.00000 0.00000 0.00000 0.16000  
D1 0.00000 0.00000 0.00000 0.00000 0.00000  
D2 0.00000 0.00000 0.00000 0.00000 0.00000  
D3 0.00000 0.00000 0.00000 0.00000 0.00000  
D4 0.00000 0.00000 0.00000 0.00000 0.00000  
D1 D2 D3 D4  
D1 0.00499  
D2 0.00000 0.00499

D3 0.00000 0.00000 0.00499

D4 0.00000 0.00000 0.00000 0.00499

ITU= 0

Eigenvalues --- 0.05269 0.05891 0.08766 0.16000 0.16000

Eigenvalues --- 0.37230 0.37230 0.37230 0.37230

RFO step: Lambda=-2.25043714D-03 EMin= 5.26881002D-02

Linear search not attempted -- first point.

Iteration 1 RMS(Cart)= 0.02071637 RMS(Int)= 0.00000000

Iteration 2 RMS(Cart)= 0.00000000 RMS(Int)= 0.00000000

Clncor: largest displacement from symmetrization is 4.65D-14 for atom 3.

Variable Old X -DE/DX Delta X Delta X Delta X New X

(Linear) (Quad) (Total)

R1 2.02201 0.01452 0.00000 0.03876 0.03876 2.06076

R2 2.02201 0.01452 0.00000 0.03876 0.03876 2.06076

R3 2.02201 0.01452 0.00000 0.03876 0.03876 2.06076

R4 2.02201 0.01452 0.00000 0.03876 0.03876 2.06076

A1 1.91063 0.00000 0.00000 0.00000 0.00000 1.91063

A2 1.91063 0.00000 0.00000 0.00000 0.00000 1.91063

A3 1.91063 0.00000 0.00000 0.00000 0.00000 1.91063

A4 1.91063 0.00000 0.00000 0.00000 0.00000 1.91063

A5 1.91063 0.00000 0.00000 0.00000 0.00000 1.91063

A6 1.91063 0.00000 0.00000 0.00000 0.00000 1.91063

D1 -2.09440 0.00000 0.00000 0.00000 0.00000 -2.09440

D2 2.09440 0.00000 0.00000 0.00000 0.00000 2.09440

D3 -2.09440 0.00000 0.00000 0.00000 0.00000 -2.09440

D4 2.09440 0.00000 0.00000 0.00000 0.00000 2.09440

Item Value Threshold Converged?

Maximum Force 0.014516 0.000450 NO

RMS Force 0.007759 0.000300 NO

Maximum Displacement 0.038757 0.001800 NO

RMS Displacement 0.020716 0.001200 NO

Predicted change in Energy=-1.131979D-03

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Input orientation:

-----  
Center Atomic Atomic Coordinates (Angstroms)

Number Number Type X Y Z

-----  
1 6 0 1.766917 0.563910 0.000000

2 1 0 2.130408 -0.464237 -0.000001

3 1 0 2.130427 1.077976 0.890397

4 1 0 2.130426 1.077977 -0.890397

5 1 0 0.676408 0.563923 0.000001  
-----

Distance matrix (angstroms):

1 2 3 4 5

1 C 0.000000

2 H 1.090509 0.000000

3 H 1.090509 1.780794 0.000000

4 H 1.090509 1.780794 1.780794 0.000000

5 H 1.090509 1.780794 1.780794 1.780794 0.000000

Stoichiometry CH4

Framework group TD[O(C),4C3(H)]

Deg. of freedom 1

Full point group TD NOp 24

Omega: Change in point group or standard orientation.

Old FWG=T [O(C1),4C3(H1)]

New FWG=TD [O(C1),4C3(H1)]

Largest Abelian subgroup D2 NOp 4

Largest concise Abelian subgroup D2 NOp 4

Standard orientation:

-----  
Center Atomic Atomic Coordinates (Angstroms)

Number Number Type X Y Z

-----  
1 6 0 0.000000 0.000000 0.000000

2 1 0 0.629606 0.629606 0.629606

3 1 0 -0.629606 -0.629606 0.629606

4 1 0 -0.629606 0.629606 -0.629606

5 1 0 0.629606 -0.629606 -0.629606  
-----

Rotational constants (GHZ): 158.1265094 158.1265094 158.1265094

Standard basis: 6-311+G(d) (5D, 7F)

There are 10 symmetry adapted basis functions of A symmetry.

There are 8 symmetry adapted basis functions of B1 symmetry.

There are 8 symmetry adapted basis functions of B2 symmetry.

There are 8 symmetry adapted basis functions of B3 symmetry.

Integral buffers will be 262144 words long.

Raffenetti 2 integral format.

Two-electron integral symmetry is turned on.

34 basis functions, 56 primitive gaussians, 35 cartesian basis functions

5 alpha electrons 5 beta electrons

nuclear repulsion energy 13.4291161863 Hartrees.

NAtoms= 5 NActive= 5 NUniq= 2 SFac= 4.00D+00 NAtFMM= 50 NAOKFM=F Big=F

One-electron integrals computed using PRISM.

NBasis= 34 RedAO= T NBF= 10 8 8 8

NBsUse= 34 1.00D-06 NBFU= 10 8 8 8

Initial guess read from the read-write file.

B after Tr= 0.000000 0.000000 0.000000

Rot= 1.000000 0.000000 0.000000 0.000000 Ang= 0.00 deg.

Initial guess orbital symmetries:

Occupied (A1) (A1) (T2) (T2) (T2)

Virtual (A1) (T2) (T2) (T2) (T2) (T2) (T2) (A1) (T2) (T2)

(T2) (T2) (T2) (T2) (A1) (A1) (E) (E) (T2) (T2)

(T2) (A1) (T2) (T2) (T2) (T2) (T2) (A1)

Harris functional with IExCor= 402 diagonalized for initial guess.

ExpMin= 4.38D-02 ExpMax= 4.56D+03 ExpMxC= 6.82D+02 IAcc=2 IRadAn= 0 AccDes= 0.00D+00

HarFok: IExCor= 402 AccDes= 0.00D+00 IRadAn= 0 IDoV= 1

ScaDFX= 1.000000 1.000000 1.000000 1.000000

FoFCou: FMM=F IPFlag= 0 FMFlag= 100000 FMFlg1= 0

NFxFlg= 0 DoJE=T BraDBF=F KetDBF=T FulRan=T

Omega= 0.000000 0.000000 1.000000 0.000000 0.000000 ICntrl= 500 IOpCl= 0

NMat0= 1 NMatS0= 1 NMatT0= 0 NMatD0= 1 NMtDS0= 0 NMtDT0= 0

IICent= 4 NGrid= 0.

Petite list used in FoFCou.

Requested convergence on RMS density matrix=1.00D-08 within 128 cycles.

Requested convergence on MAX density matrix=1.00D-06.

Requested convergence on energy=1.00D-06.

No special actions if energy rises.

Keep R1 ints in memory in canonical form, NReq=1119085.

SCF Done: E(RB3LYP) = -40.5280818642 A.U. after 6 cycles

Conv = 0.6849D-08 -V/T = 2.0052

Calling FoFJK, ICntrl= 2127 FMM=F ISym2X=1 IICent= 0 IOpCIX= 0 NMat=1 NMatS=1  
NMatT=0.

\*\*\*\*\* Axes restored to original set \*\*\*\*\*

-----  
Center Atomic Forces (Hartrees/Bohr)

Number Number X Y Z

-----  
1 6 0.000000000 0.000000000 0.000000000  
2 1 0.000050603 -0.000143133 0.000000000  
3 1 0.000050606 0.000071565 0.000123956  
4 1 0.000050606 0.000071565 -0.000123956  
5 1 -0.000151814 0.000000002 0.000000000  
-----

Cartesian Forces: Max 0.000151814 RMS 0.000078397

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Berny optimization.

Using GEDIIS/GDIIS optimizer.

Internal Forces: Max 0.000151814 RMS 0.000081148

Search for a local minimum.

Step number 2 out of a maximum of 24

All quantities printed in internal units (Hartrees-Bohrs-Radians)

Mixed Optimization -- En-DIIS/RFO-DIIS

Update second derivatives using D2CorX and points 1 2

DE= -1.12D-03 DEPred=-1.13D-03 R= 9.86D-01

SS= 1.41D+00 RLast= 7.75D-02 DXNew= 5.0454D-01 2.3254D-01

Trust test= 9.86D-01 RLast= 7.75D-02 DXMaxT set to 3.00D-01

The second derivative matrix:

R1 R2 R3 R4 A1

R1 0.37188

R2 -0.00042 0.37188

R3 -0.00042 -0.00042 0.37188

R4 -0.00042 -0.00042 -0.00042 0.37188

A1 0.00000 0.00000 0.00000 0.00000 0.16000

A2 0.00000 0.00000 0.00000 0.00000 0.00000

A3 0.00000 0.00000 0.00000 0.00000 0.00000

A4 0.00000 0.00000 0.00000 0.00000 0.00000

A5 0.00000 0.00000 0.00000 0.00000 0.00000

A6 0.00000 0.00000 0.00000 0.00000 0.00000

D1 0.00000 0.00000 0.00000 0.00000 0.00000

D2 0.00000 0.00000 0.00000 0.00000 0.00000

D3 0.00000 0.00000 0.00000 0.00000 0.00000

D4 0.00000 0.00000 0.00000 0.00000 0.00000

A2 A3 A4 A5 A6

A2 0.16000

A3 0.00000 0.16000

A4 0.00000 0.00000 0.16000

A5 0.00000 0.00000 0.00000 0.16000

A6 0.00000 0.00000 0.00000 0.00000 0.16000

D1 0.00000 0.00000 0.00000 0.00000 0.00000

D2 0.00000 0.00000 0.00000 0.00000 0.00000

D3 0.00000 0.00000 0.00000 0.00000 0.00000

D4 0.00000 0.00000 0.00000 0.00000 0.00000

D1 D2 D3 D4

D1 0.00499

D2 0.00000 0.00499

D3 0.00000 0.00000 0.00499

D4 0.00000 0.00000 0.00000 0.00499

ITU= 1 0

Use linear search instead of GDIIS.

Eigenvalues --- 0.05269 0.05891 0.08766 0.16000 0.16000

Eigenvalues --- 0.37063 0.37230 0.37230 0.37230

RFO step: Lambda= 0.00000000D+00 EMin= 5.26881002D-02

Quartic linear search produced a step of 0.01120.

Iteration 1 RMS(Cart)= 0.00023197 RMS(Int)= 0.00000000

Iteration 2 RMS(Cart)= 0.00000000 RMS(Int)= 0.00000000

Clncor: largest displacement from symmetrization is 1.12D-14 for atom 4.

Variable Old X -DE/DX Delta X Delta X Delta X New X

(Linear) (Quad) (Total)

R1 2.06076 0.00015 0.00043 0.00000 0.00043 2.06120  
R2 2.06076 0.00015 0.00043 0.00000 0.00043 2.06120  
R3 2.06076 0.00015 0.00043 0.00000 0.00043 2.06120  
R4 2.06076 0.00015 0.00043 0.00000 0.00043 2.06120  
A1 1.91063 0.00000 0.00000 0.00000 0.00000 1.91063  
A2 1.91063 0.00000 0.00000 0.00000 0.00000 1.91063  
A3 1.91063 0.00000 0.00000 0.00000 0.00000 1.91063  
A4 1.91063 0.00000 0.00000 0.00000 0.00000 1.91063  
A5 1.91063 0.00000 0.00000 0.00000 0.00000 1.91063  
A6 1.91063 0.00000 0.00000 0.00000 0.00000 1.91063  
D1 -2.09440 0.00000 0.00000 0.00000 0.00000 -2.09440  
D2 2.09440 0.00000 0.00000 0.00000 0.00000 2.09440  
D3 -2.09440 0.00000 0.00000 0.00000 0.00000 -2.09440  
D4 2.09440 0.00000 0.00000 0.00000 0.00000 2.09440

Item Value Threshold Converged?

Maximum Force 0.000152 0.000450 YES

RMS Force 0.000081 0.000300 YES

Maximum Displacement 0.000434 0.001800 YES

RMS Displacement 0.000232 0.001200 YES

Predicted change in Energy=-1.239284D-07

Optimization completed.

-- Stationary point found.

-----

! Optimized Parameters !

! (Angstroms and Degrees) !

-----

! Name Definition Value Derivative Info. !

-----

! R1 R(1,2) 1.0905 -DE/DX = 0.0002 !  
 ! R2 R(1,3) 1.0905 -DE/DX = 0.0002 !  
 ! R3 R(1,4) 1.0905 -DE/DX = 0.0002 !  
 ! R4 R(1,5) 1.0905 -DE/DX = 0.0002 !  
 ! A1 A(2,1,3) 109.4712 -DE/DX = 0.0 !  
 ! A2 A(2,1,4) 109.4712 -DE/DX = 0.0 !  
 ! A3 A(2,1,5) 109.4712 -DE/DX = 0.0 !  
 ! A4 A(3,1,4) 109.4712 -DE/DX = 0.0 !  
 ! A5 A(3,1,5) 109.4712 -DE/DX = 0.0 !  
 ! A6 A(4,1,5) 109.4712 -DE/DX = 0.0 !  
 ! D1 D(2,1,4,3) -120.0 -DE/DX = 0.0 !  
 ! D2 D(2,1,5,3) 120.0 -DE/DX = 0.0 !  
 ! D3 D(2,1,5,4) -120.0 -DE/DX = 0.0 !  
 ! D4 D(3,1,5,4) 120.0 -DE/DX = 0.0 !

-----

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Input orientation:

-----

Center Atomic Atomic Coordinates (Angstroms)

Number Number Type X Y Z

-----

1 6 0 1.766917 0.563910 0.000000  
 2 1 0 2.130408 -0.464237 -0.000001  
 3 1 0 2.130427 1.077976 0.890397

4 1 0 2.130426 1.077977 -0.890397

5 1 0 0.676408 0.563923 0.000001

-----  
Distance matrix (angstroms):

1 2 3 4 5

1 C 0.000000

2 H 1.090509 0.000000

3 H 1.090509 1.780794 0.000000

4 H 1.090509 1.780794 1.780794 0.000000

5 H 1.090509 1.780794 1.780794 1.780794 0.000000

Stoichiometry CH4

Framework group TD[O(C),4C3(H)]

Deg. of freedom 1

Full point group TD NOp 24

Largest Abelian subgroup D2 NOp 4

Largest concise Abelian subgroup D2 NOp 4

Standard orientation:

-----  
Center Atomic Atomic Coordinates (Angstroms)

Number Number Type X Y Z

-----  
1 6 0 0.000000 0.000000 0.000000

2 1 0 0.629606 0.629606 0.629606

3 1 0 -0.629606 -0.629606 0.629606

4 1 0 -0.629606 0.629606 -0.629606

5 1 0 0.629606 -0.629606 -0.629606

-----  
 Rotational constants (GHZ): 158.1265094 158.1265094 158.1265094

\*\*\*\*\*

Population analysis using the SCF density.

\*\*\*\*\*

Orbital symmetries:

Occupied (A1) (A1) (T2) (T2) (T2)

Virtual (A1) (T2) (T2) (T2) (T2) (T2) (T2) (A1) (T2) (T2)

(T2) (T2) (T2) (T2) (A1) (A1) (E) (E) (T2) (T2)

(T2) (A1) (T2) (T2) (T2) (T2) (T2) (T2) (A1)

The electronic state is 1-A1.

Alpha occ. eigenvalues -- -10.15133 -0.69745 -0.39634 -0.39634 -0.39634

Alpha virt. eigenvalues -- 0.00991 0.05736 0.05736 0.05736 0.14637

Alpha virt. eigenvalues -- 0.14637 0.14637 0.21072 0.40418 0.40418

Alpha virt. eigenvalues -- 0.40418 0.59906 0.59906 0.59906 0.60278

Alpha virt. eigenvalues -- 0.86494 1.25797 1.25797 1.59542 1.59542

Alpha virt. eigenvalues -- 1.59542 2.35038 2.42329 2.42329 2.42329

Alpha virt. eigenvalues -- 3.10057 3.10057 3.10057 23.43988

Condensed to atoms (all electrons):

1 2 3 4 5

1 C 5.441470 0.372433 0.372433 0.372433 0.372433

2 H 0.372433 0.475956 -0.027063 -0.027063 -0.027063

3 H 0.372433 -0.027063 0.475956 -0.027063 -0.027063

4 H 0.372433 -0.027063 -0.027063 0.475956 -0.027063

5 H 0.372433 -0.027063 -0.027063 -0.027063 0.475956

Mulliken atomic charges:

1

1 C -0.931204

2 H 0.232801

3 H 0.232801

4 H 0.232801

5 H 0.232801

Sum of Mulliken atomic charges = 0.00000

Mulliken charges with hydrogens summed into heavy atoms:

1

1 C 0.000000

Sum of Mulliken charges with hydrogens summed into heavy atoms = 0.00000

Electronic spatial extent (au):  $\langle R^{**2} \rangle = 35.9778$ 

Charge= 0.0000 electrons

Dipole moment (field-independent basis, Debye):

X= 0.0000 Y= 0.0000 Z= 0.0000 Tot= 0.0000

Quadrupole moment (field-independent basis, Debye-Ang):

XX= -8.5144 YY= -8.5144 ZZ= -8.5144

XY= 0.0000 XZ= 0.0000 YZ= 0.0000

Traceless Quadrupole moment (field-independent basis, Debye-Ang):

XX= 0.0000 YY= 0.0000 ZZ= 0.0000

XY= 0.0000 XZ= 0.0000 YZ= 0.0000

Octapole moment (field-independent basis, Debye-Ang<sup>\*\*2</sup>):

XXX= 0.0000 YYY= 0.0000 ZZZ= 0.0000 XYY= 0.0000

XXY= 0.0000 XXZ= 0.0000 XZZ= 0.0000 YZZ= 0.0000

YYZ= 0.0000 XYZ= 0.7811

Hexadecapole moment (field-independent basis, Debye-Ang<sup>\*\*3</sup>):

XXXX= -17.2201 YYYX= -17.2201 ZZZZ= -17.2201 XXXY= 0.0000

XXXZ= 0.0000 YYYX= 0.0000 YYYZ= 0.0000 ZZZX= 0.0000

ZZZY= 0.0000 XXYY= -5.2429 XXZZ= -5.2429 YYZZ= -5.2429

XXYZ= 0.0000 YYXZ= 0.0000 ZZXY= 0.0000

N-N= 1.342911618634D+01 E-N=-1.201307897495D+02 KE= 4.031684346614D+01

Symmetry A KE= 3.447981936062D+01

Symmetry B1 KE= 1.945674701840D+00

Symmetry B2 KE= 1.945674701840D+00

Symmetry B3 KE= 1.945674701840D+00

1|1|UNPC-LAPTOP-VBAQNH7H|FOpt|RB3LYP|6-311+G(d)|C1H4|HP|29-Nov-2020|0|

|# opt freq b3lyp/6-311+g(d) geom=connectivity||Title Card Required||0

,1|C,1.76691739,0.563909725,0.|H,2.1304079871,-0.4642365757,-0.0000009

202|H,2.1304274232,1.077975738,0.8903970013|H,2.1304259205,1.077976800

6,-0.8903970013|H,0.6764082293,0.5639229371,0.0000009202||Version=IA32

W-G09RevB.01|State=1-A1|HF=-40.5280819|RMSD=6.849e-009|RMSF=7.840e-005

|Dipole=0.,0.,0.|Quadrupole=0.,0.,0.,0.,0.,0.|PG=TD [O(C1),4C3(H1)]||@

WERE I TO AWAIT PERFECTION, MY BOOK WOULD NEVER BE FINISHED.

-- HISTORY OF CHINESE WRITING

TAI T'UNG, 13TH CENTURY

Job cpu time: 0 days 0 hours 0 minutes 3.0 seconds.

File lengths (MBytes): RWF= 5 Int= 0 D2E= 0 Chk= 1 Scr= 1

Normal termination of Gaussian 09 at Sun Nov 29 23:31:54 2020.

Link1: Proceeding to internal job step number 2.

-----

#N Geom=AllCheck Guess=TCheck SCRF=Check GenChk RB3LYP/6-311+G(d) Freq

-----  
1/10=4,29=7,30=1,38=1,40=1/1,3;  
2/12=2,40=1/2;  
3/5=4,6=6,7=11,11=2,14=-4,16=1,25=1,30=1,70=2,71=2,74=-5,116=1/1,2,3;  
4/5=101/1;  
5/5=2,98=1/2;  
8/6=4,10=90,11=11/1;  
11/6=1,8=1,9=11,15=111,16=1/1,2,10;  
10/6=1/2;  
6/7=2,8=2,9=2,10=2,18=1,28=1/1;  
7/8=1,10=1,25=1/1,2,3,16;  
1/10=4,30=1/3;  
99//99;

-----  
Title Card Required  
-----

Redundant internal coordinates taken from checkpoint file:

C:\Users\hp\Desktop\ch4.chk

Charge = 0 Multiplicity = 1

C,0,1.76691739,0.563909725,0.

H,0,2.1304079871,-0.4642365757,-0.0000009202

H,0,2.1304274232,1.077975738,0.8903970013

H,0,2.1304259205,1.0779768006,-0.8903970013

H,0,0.6764082293,0.5639229371,0.0000009202

Recover connectivity data from disk.

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Berny optimization.

Initialization pass.

-----

! Initial Parameters !

! (Angstroms and Degrees) !

-----

! Name Definition Value Derivative Info. !

-----

! R1 R(1,2) 1.0905 calculate D2E/DX2 analytically !

! R2 R(1,3) 1.0905 calculate D2E/DX2 analytically !

! R3 R(1,4) 1.0905 calculate D2E/DX2 analytically !

! R4 R(1,5) 1.0905 calculate D2E/DX2 analytically !

! A1 A(2,1,3) 109.4712 calculate D2E/DX2 analytically !

! A2 A(2,1,4) 109.4712 calculate D2E/DX2 analytically !

! A3 A(2,1,5) 109.4712 calculate D2E/DX2 analytically !

! A4 A(3,1,4) 109.4712 calculate D2E/DX2 analytically !

! A5 A(3,1,5) 109.4712 calculate D2E/DX2 analytically !

! A6 A(4,1,5) 109.4712 calculate D2E/DX2 analytically !

! D1 D(2,1,4,3) -120.0 calculate D2E/DX2 analytically !

! D2 D(2,1,5,3) 120.0 calculate D2E/DX2 analytically !

! D3 D(2,1,5,4) -120.0 calculate D2E/DX2 analytically !

! D4 D(3,1,5,4) 120.0 calculate D2E/DX2 analytically !

-----

Trust Radius=3.00D-01 FncErr=1.00D-07 GrdErr=1.00D-07

Number of steps in this run= 2 maximum allowed number of steps= 2.

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Input orientation:

-----

Center Atomic Atomic Coordinates (Angstroms)

Number Number Type X Y Z

-----

1 6 0 1.766917 0.563910 0.000000

2 1 0 2.130408 -0.464237 -0.000001

3 1 0 2.130427 1.077976 0.890397

4 1 0 2.130426 1.077977 -0.890397

5 1 0 0.676408 0.563923 0.000001

-----

Distance matrix (angstroms):

1 2 3 4 5

1 C 0.000000

2 H 1.090509 0.000000

3 H 1.090509 1.780794 0.000000

4 H 1.090509 1.780794 1.780794 0.000000

5 H 1.090509 1.780794 1.780794 1.780794 0.000000

Stoichiometry CH4

Framework group TD[O(C),4C3(H)]

Deg. of freedom 1

Full point group TD NOp 24

Largest Abelian subgroup D2 NOp 4

Largest concise Abelian subgroup D2 NOp 4

Standard orientation:

-----  
 Center Atomic Atomic Coordinates (Angstroms)

Number Number Type X Y Z  
 -----

1 6 0 0.000000 0.000000 0.000000

2 1 0 0.629606 0.629606 0.629606

3 1 0 -0.629606 -0.629606 0.629606

4 1 0 -0.629606 0.629606 -0.629606

5 1 0 0.629606 -0.629606 -0.629606  
 -----

Rotational constants (GHZ): 158.1265094 158.1265094 158.1265094

Standard basis: 6-311+G(d) (5D, 7F)

There are 10 symmetry adapted basis functions of A symmetry.

There are 8 symmetry adapted basis functions of B1 symmetry.

There are 8 symmetry adapted basis functions of B2 symmetry.

There are 8 symmetry adapted basis functions of B3 symmetry.

Integral buffers will be 262144 words long.

Raffenetti 2 integral format.

Two-electron integral symmetry is turned on.

34 basis functions, 56 primitive gaussians, 35 cartesian basis functions

5 alpha electrons 5 beta electrons

nuclear repulsion energy 13.4291161863 Hartrees.

NAtoms= 5 NActive= 5 NUniq= 2 SFac= 4.00D+00 NAtFMM= 50 NAOKFM=F Big=F

One-electron integrals computed using PRISM.

NBasis= 34 RedAO= T NBF= 10 8 8 8

NBsUse= 34 1.00D-06 NBFU= 10 8 8 8

Initial guess read from the checkpoint file: C:\Users\hp\Desktop\ch4.chk

B after Tr= 0.000000 0.000000 0.000000

Rot= 1.000000 0.000000 0.000000 0.000000 Ang= 0.00 deg.

Initial guess orbital symmetries:

Occupied (A1) (A1) (T2) (T2) (T2)

Virtual (A1) (T2) (T2) (T2) (T2) (T2) (T2) (A1) (T2) (T2)

(T2) (T2) (T2) (T2) (A1) (A1) (E) (E) (T2) (T2)

(T2) (A1) (T2) (T2) (T2) (T2) (T2) (T2) (A1)

Requested convergence on RMS density matrix=1.00D-08 within 128 cycles.

Requested convergence on MAX density matrix=1.00D-06.

Requested convergence on energy=1.00D-06.

No special actions if energy rises.

Keep R1 ints in memory in canonical form, NReq=1119085.

SCF Done: E(RB3LYP) = -40.5280818642 A.U. after 1 cycles

Conv = 0.7046D-09 -V/T = 2.0052

Range of M.O.s used for correlation: 1 34

NBasis= 34 NAE= 5 NBE= 5 NFC= 0 NFV= 0

NROrb= 34 NOA= 5 NOB= 5 NVA= 29 NVB= 29

Symmetrizing basis deriv contribution to polar:

IMax=3 JMax=2 DiffMx= 0.00D+00

G2DrvN: will do 6 centers at a time, making 1 passes doing MaxLOS=2.

Calling FoFCou, ICntrl= 3107 FMM=F I1Cent= 0 AccDes= 0.00D+00.

FoFDir/FoFCou used for L=0 through L=2.

End of G2Drv Frequency-dependent properties file 721 does not exist.

End of G2Drv Frequency-dependent properties file 722 does not exist.

IDoAtm=11111

Differentiating once with respect to electric field.

with respect to dipole field.

Differentiating once with respect to nuclear coordinates.

Keep R1 ints in memory in canonical form, NReq=1020123.

There are 9 degrees of freedom in the 1st order CPHF. IDoFFX=4.

9 vectors produced by pass 0 Test12= 1.61D-15 1.11D-08 XBig12= 7.20D+00 1.49D+00.

AX will form 9 AO Fock derivatives at one time.

9 vectors produced by pass 1 Test12= 1.61D-15 1.11D-08 XBig12= 2.01D-01 2.19D-01.

9 vectors produced by pass 2 Test12= 1.61D-15 1.11D-08 XBig12= 6.03D-04 7.70D-03.

9 vectors produced by pass 3 Test12= 1.61D-15 1.11D-08 XBig12= 1.57D-06 4.26D-04.

9 vectors produced by pass 4 Test12= 1.61D-15 1.11D-08 XBig12= 5.58D-10 7.80D-06.

4 vectors produced by pass 5 Test12= 1.61D-15 1.11D-08 XBig12= 3.26D-13 2.44D-07.

Inverted reduced A of dimension 49 with in-core refinement.

Isotropic polarizability for W= 0.000000 13.81 Bohr\*\*3.

End of Minotr Frequency-dependent properties file 721 does not exist.

End of Minotr Frequency-dependent properties file 722 does not exist.

\*\*\*\*\*

Population analysis using the SCF density.

\*\*\*\*\*

Orbital symmetries:

Occupied (A1) (A1) (T2) (T2) (T2)

Virtual (A1) (T2) (T2) (T2) (T2) (T2) (T2) (A1) (T2) (T2)

(T2) (T2) (T2) (T2) (A1) (A1) (E) (E) (T2) (T2)

(T2) (A1) (T2) (T2) (T2) (T2) (T2) (T2) (A1)

The electronic state is 1-A1.

Alpha occ. eigenvalues -- -10.15133 -0.69745 -0.39634 -0.39634 -0.39634

Alpha virt. eigenvalues -- 0.00991 0.05736 0.05736 0.05736 0.14637

Alpha virt. eigenvalues -- 0.14637 0.14637 0.21072 0.40418 0.40418

Alpha virt. eigenvalues -- 0.40418 0.59906 0.59906 0.59906 0.60278

Alpha virt. eigenvalues -- 0.86494 1.25797 1.25797 1.59542 1.59542

Alpha virt. eigenvalues -- 1.59542 2.35038 2.42329 2.42329 2.42329

Alpha virt. eigenvalues -- 3.10057 3.10057 3.10057 23.43988

Condensed to atoms (all electrons):

1 2 3 4 5

1 C 5.441470 0.372433 0.372433 0.372433 0.372433

2 H 0.372433 0.475956 -0.027063 -0.027063 -0.027063

3 H 0.372433 -0.027063 0.475956 -0.027063 -0.027063

4 H 0.372433 -0.027063 -0.027063 0.475956 -0.027063

5 H 0.372433 -0.027063 -0.027063 -0.027063 0.475956

Mulliken atomic charges:

1

1 C -0.931204

2 H 0.232801

3 H 0.232801

4 H 0.232801

5 H 0.232801

Sum of Mulliken atomic charges = 0.00000

Mulliken charges with hydrogens summed into heavy atoms:

1

1 C 0.000000

Sum of Mulliken charges with hydrogens summed into heavy atoms = 0.00000

APT atomic charges:

1

1 C -0.015942

2 H 0.003985

3 H 0.003985

4 H 0.003985

5 H 0.003985

Sum of APT charges= 0.00000

APT Atomic charges with hydrogens summed into heavy atoms:

1

1 C 0.000000

2 H 0.000000

3 H 0.000000

4 H 0.000000

5 H 0.000000

Sum of APT charges= 0.00000

Electronic spatial extent (au):  $\langle R^{**2} \rangle = 35.9778$ 

Charge= 0.0000 electrons

Dipole moment (field-independent basis, Debye):

X= 0.0000 Y= 0.0000 Z= 0.0000 Tot= 0.0000

Quadrupole moment (field-independent basis, Debye-Ang):

XX= -8.5144 YY= -8.5144 ZZ= -8.5144

XY= 0.0000 XZ= 0.0000 YZ= 0.0000

Traceless Quadrupole moment (field-independent basis, Debye-Ang):

XX= 0.0000 YY= 0.0000 ZZ= 0.0000

XY= 0.0000 XZ= 0.0000 YZ= 0.0000

Octapole moment (field-independent basis, Debye-Ang<sup>\*\*2</sup>):

XXX= 0.0000 YYY= 0.0000 ZZZ= 0.0000 XYY= 0.0000

XXY= 0.0000 XXZ= 0.0000 XZZ= 0.0000 YZZ= 0.0000

YYZ= 0.0000 XYZ= 0.7811

Hexadecapole moment (field-independent basis, Debye-Ang<sup>3</sup>):

XXXX= -17.2201 YYYY= -17.2201 ZZZZ= -17.2201 XXXY= 0.0000

XXXZ= 0.0000 YYYYX= 0.0000 YYYZ= 0.0000 ZZZX= 0.0000

ZZZY= 0.0000 XXYY= -5.2429 XXZZ= -5.2429 YYZZ= -5.2429

XXYZ= 0.0000 YYXZ= 0.0000 ZZXY= 0.0000

N-N= 1.342911618634D+01 E-N=-1.201307898411D+02 KE= 4.031684350874D+01

Symmetry A KE= 3.447981938511D+01

Symmetry B1 KE= 1.945674707876D+00

Symmetry B2 KE= 1.945674707876D+00

Symmetry B3 KE= 1.945674707876D+00

Exact polarizability: 13.812 0.000 13.812 0.000 0.000 13.812

Approx polarizability: 16.443 0.000 16.443 0.000 0.000 16.443

Calling FoFJK, ICntrl= 100127 FMM=F ISym2X=1 IICent= 0 IOpCIX= 0 NMat=1  
NMatS=1 NMatT=0.

Full mass-weighted force constant matrix:

Low frequencies --- -0.0012 -0.0011 -0.0003 46.1637 46.1637 46.1637

Low frequencies --- 1355.1285 1355.1285 1355.1285

Harmonic frequencies (cm<sup>-1</sup>), IR intensities (KM/Mole), Raman scattering activities (A<sup>4</sup>/AMU), depolarization ratios for plane and unpolarized incident light, reduced masses (AMU), force constants (mDyne/A), and normal coordinates:

1 2 3

T2 T2 T2

Frequencies -- 1355.1285 1355.1285 1355.1285

Red. masses -- 1.1788 1.1788 1.1788

Frc consts -- 1.2754 1.2754 1.2754

IR Inten -- 20.7468 20.7468 20.7468

Atom AN X Y Z X Y Z X Y Z

1 6 -0.02 0.12 0.01 0.12 0.02 0.00 0.00 -0.01 0.12

2 1 0.31 -0.39 0.16 -0.32 0.17 0.26 0.22 0.26 -0.39

3 1 0.28 -0.42 -0.22 -0.33 0.16 -0.28 -0.24 -0.21 -0.35

4 1 -0.15 -0.34 -0.30 -0.40 -0.30 0.18 0.26 -0.20 -0.36

5 1 -0.18 -0.31 0.24 -0.41 -0.29 -0.20 -0.21 0.27 -0.38

4 5 6

E E A1

Frequencies -- 1582.6386 1582.6386 3030.2510

Red. masses -- 1.0078 1.0078 1.0078

Frc consts -- 1.4873 1.4873 5.4525

IR Inten -- 0.0000 0.0000 0.0000

Atom AN X Y Z X Y Z X Y Z

1 6 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00

2 1 -0.32 0.38 -0.07 -0.26 -0.14 0.40 -0.29 -0.29 -0.29

3 1 0.32 -0.38 -0.07 0.26 0.14 0.40 0.29 0.29 -0.29

4 1 0.32 0.38 0.07 0.26 -0.14 -0.40 0.29 -0.29 0.29

5 1 -0.32 -0.38 0.07 -0.26 0.14 -0.40 -0.29 0.29 0.29

7 8 9

T2 T2 T2

Frequencies -- 3135.0616 3135.0616 3135.0616

Red. masses -- 1.1018 1.1018 1.1018

Frc consts -- 6.3804 6.3804 6.3804

IR Inten -- 29.9080 29.9080 29.9080

Atom AN X Y Z X Y Z X Y Z

1 6 0.01 -0.09 0.00 -0.07 -0.01 0.06 -0.06 -0.01 -0.07

2 1 0.24 0.22 0.24 0.05 0.06 0.07 0.43 0.44 0.43

3 1 0.25 0.23 -0.25 0.43 0.44 -0.43 -0.01 -0.01 -0.01

4 1 -0.34 0.32 -0.34 -0.01 0.00 0.01 0.36 -0.38 0.36

5 1 -0.33 0.31 0.33 0.37 -0.38 -0.37 -0.08 0.07 0.06

-----

- Thermochemistry -

-----

Temperature 298.150 Kelvin. Pressure 1.00000 Atm.

Atom 1 has atomic number 6 and mass 12.00000

Atom 2 has atomic number 1 and mass 1.00783

Atom 3 has atomic number 1 and mass 1.00783

Atom 4 has atomic number 1 and mass 1.00783

Atom 5 has atomic number 1 and mass 1.00783

Molecular mass: 16.03130 amu.

Principal axes and moments of inertia in atomic units:

1 2 3

Eigenvalues -- 11.41327 11.41327 11.41327

X 0.04958 0.97439 -0.21932

Y -0.21486 0.22486 0.95041

Z 0.97539 0.00000 0.22050

This molecule is a spherical top.

Rotational symmetry number 12.

Rotational temperatures (Kelvin) 7.58887 7.58887 7.58887  
Rotational constants (GHZ): 158.12651 158.12651 158.12651  
Zero-point vibrational energy 117629.4 (Joules/Mol)  
28.11410 (Kcal/Mol)  
Vibrational temperatures: 1949.73 1949.73 1949.73 2277.06 2277.06  
(Kelvin) 4359.85 4510.65 4510.65 4510.65  
Zero-point correction= 0.044803 (Hartree/Particle)  
Thermal correction to Energy= 0.047669  
Thermal correction to Enthalpy= 0.048613  
Thermal correction to Gibbs Free Energy= 0.027486  
Sum of electronic and zero-point Energies= -40.483279  
Sum of electronic and thermal Energies= -40.480413  
Sum of electronic and thermal Enthalpies= -40.479469  
Sum of electronic and thermal Free Energies= -40.500596  
E (Thermal) CV S  
KCal/Mol Cal/Mol-Kelvin Cal/Mol-Kelvin  
Total 29.913 6.444 44.465  
Electronic 0.000 0.000 0.000  
Translational 0.889 2.981 34.261  
Rotational 0.889 2.981 10.122  
Vibrational 28.135 0.482 0.082  
Q Log10(Q) Ln(Q)  
Total Bot 0.227635D-12 -12.642760 -29.111032  
Total V=0 0.922556D+08 7.964993 18.340074  
Vib (Bot) 0.248057D-20 -20.605449 -47.445800  
Vib (V=0) 0.100532D+01 0.002304 0.005305

Electronic 0.100000D+01 0.000000 0.000000

Translational 0.252295D+07 6.401908 14.740939

Rotational 0.363731D+02 1.560781 3.593830

\*\*\*\*\* Axes restored to original set \*\*\*\*\*

-----  
Center Atomic Forces (Hartrees/Bohr)

Number Number X Y Z

-----  
1 6 0.000000000 0.000000000 0.000000000

2 1 0.000050603 -0.000143132 0.000000000

3 1 0.000050606 0.000071565 0.000123956

4 1 0.000050605 0.000071565 -0.000123956

5 1 -0.000151814 0.000000002 0.000000000

-----  
Cartesian Forces: Max 0.000151814 RMS 0.000078397

GradGradGradGradGradGradGradGradGradGradGradGradGradGradGradGradGrad

Berny optimization.

Internal Forces: Max 0.000151814 RMS 0.000081148

Search for a local minimum.

Step number 1 out of a maximum of 2

All quantities printed in internal units (Hartrees-Bohrs-Radians)

Second derivative matrix not updated -- analytic derivatives used.

The second derivative matrix:

R1 R2 R3 R4 A1

R1 0.34282

R2 0.00246 0.34282

R3 0.00246 0.00246 0.34282  
R4 0.00246 0.00246 0.00246 0.34282  
A1 0.00188 0.00188 -0.00118 -0.00257 0.02004  
A2 0.00294 -0.00076 0.00327 -0.00545 -0.00893  
A3 0.00574 -0.00461 -0.00510 0.00397 -0.01329  
A4 -0.00076 0.00294 0.00327 -0.00545 -0.00893  
A5 -0.00461 0.00574 -0.00510 0.00397 -0.01329  
A6 -0.00519 -0.00519 0.00484 0.00554 0.02442  
D1 -0.00363 -0.00363 -0.00256 0.00983 -0.01360  
D2 0.00299 0.00299 -0.00769 0.00171 0.00826  
D3 -0.00394 0.00693 -0.00385 0.00085 0.00413  
D4 -0.00693 0.00394 0.00385 -0.00085 -0.00413  
A2 A3 A4 A5 A6  
A2 0.03773  
A3 -0.02295 0.07372  
A4 -0.00218 0.02535 0.03773  
A5 0.02535 -0.03581 -0.02295 0.07372  
A6 -0.02902 -0.02701 -0.02902 -0.02701 0.08763  
D1 -0.01083 0.01481 -0.01083 0.01481 0.00564  
D2 -0.00947 0.00693 -0.00947 0.00693 -0.00317  
D3 -0.01438 -0.00049 0.00491 0.00742 -0.00159  
D4 -0.00491 -0.00742 0.01438 0.00049 0.00159  
D1 D2 D3 D4  
D1 0.02992  
D2 0.00149 0.01860  
D3 0.00074 0.00930 0.01889

D4 -0.00074 -0.00930 0.00959 0.01889

ITU= 0

Eigenvalues --- 0.03818 0.04300 0.06530 0.13346 0.13403

Eigenvalues --- 0.34123 0.34124 0.34150 0.35021

Angle between quadratic step and forces= 0.00 degrees.

Linear search not attempted -- first point.

Iteration 1 RMS(Cart)= 0.00023171 RMS(Int)= 0.00000000

Iteration 2 RMS(Cart)= 0.00000000 RMS(Int)= 0.00000000

Clncor: largest displacement from symmetrization is 1.11D-12 for atom 4.

Variable Old X -DE/DX Delta X Delta X Delta X New X

(Linear) (Quad) (Total)

R1 2.06076 0.00015 0.00000 0.00043 0.00043 2.06120

R2 2.06076 0.00015 0.00000 0.00043 0.00043 2.06120

R3 2.06076 0.00015 0.00000 0.00043 0.00043 2.06120

R4 2.06076 0.00015 0.00000 0.00043 0.00043 2.06120

A1 1.91063 0.00000 0.00000 0.00000 0.00000 1.91063

A2 1.91063 0.00000 0.00000 0.00000 0.00000 1.91063

A3 1.91063 0.00000 0.00000 0.00000 0.00000 1.91063

A4 1.91063 0.00000 0.00000 0.00000 0.00000 1.91063

A5 1.91063 0.00000 0.00000 0.00000 0.00000 1.91063

A6 1.91063 0.00000 0.00000 0.00000 0.00000 1.91063

D1 -2.09440 0.00000 0.00000 0.00000 0.00000 -2.09440

D2 2.09440 0.00000 0.00000 0.00000 0.00000 2.09440

D3 -2.09440 0.00000 0.00000 0.00000 0.00000 -2.09440

D4 2.09440 0.00000 0.00000 0.00000 0.00000 2.09440

Item Value Threshold Converged?

Maximum Force 0.000152 0.000450 YES

RMS Force 0.000081 0.000300 YES

Maximum Displacement 0.000433 0.001800 YES

RMS Displacement 0.000232 0.001200 YES

Predicted change in Energy=-1.316197D-07

Optimization completed.

-- Stationary point found.

-----

! Optimized Parameters !

! (Angstroms and Degrees) !

-----

! Name Definition Value Derivative Info. !

-----

! R1 R(1,2) 1.0905 -DE/DX = 0.0002 !

! R2 R(1,3) 1.0905 -DE/DX = 0.0002 !

! R3 R(1,4) 1.0905 -DE/DX = 0.0002 !

! R4 R(1,5) 1.0905 -DE/DX = 0.0002 !

! A1 A(2,1,3) 109.4712 -DE/DX = 0.0 !

! A2 A(2,1,4) 109.4712 -DE/DX = 0.0 !

! A3 A(2,1,5) 109.4712 -DE/DX = 0.0 !

! A4 A(3,1,4) 109.4712 -DE/DX = 0.0 !

! A5 A(3,1,5) 109.4712 -DE/DX = 0.0 !

! A6 A(4,1,5) 109.4712 -DE/DX = 0.0 !

! D1 D(2,1,4,3) -120.0 -DE/DX = 0.0 !

! D2 D(2,1,5,3) 120.0 -DE/DX = 0.0 !

! D3 D(2,1,5,4) -120.0 -DE/DX = 0.0 !

! D4 D(3,1,5,4) 120.0 -DE/DX = 0.0 !

-----  
GradGradGradGradGradGradGradGradGradGradGradGradGradGradGradGradGradGrad

1|1|UNPC-LAPTOP-VBAQNH7H|Freq|RB3LYP|6-311+G(d)|C1H4|HP|29-Nov-2020|0|

|#N Geom=AllCheck Guess=TCheck SCRF=Check GenChk RB3LYP/6-311+G(d) Freq||Title  
Card Required||0,1|C,1.76691739,0.563909725,0.|H,2.1304079871,-0.4642365757-  
-0.0000009202|H,2.1304274232,1.077975738,0.8903970013|H

,2.1304259205,1.0779768006,-  
0.8903970013|H,0.6764082293,0.5639229371,0.0000009202||Version=IA32W-G09RevB.01|  
State=1-A1|HF=-40.5280819|RMSD=7.046e-010|RMSF=7.8-  
0e-005|ZeroPoint=0.0448027|Thermal=0.047669|Dipole=

0.,0.,0.|DipoleDeriv=-0.015942,0.,0.,0.,-0.015942,0.,0.,0.,-0.015942,0

.0578811,0.076215,0.,0.076215,-0.1307508,-0.0000002,0.,-0.0000002,0.08

48261,0.0578782,-0.038109,-0.0660074,-0.038109,0.0309334,-0.0933458,-0.066-  
074,-0.0933458,-0.0768551,0.0578784,-0.0381089,0.0660071,-0.03810  
89,0.0309332,0.093346,0.0660071,0.093346,-0.0768551,  
0.1576958,0.0000029,0.0000002,0.0000029,0.0848261,0.,0.0000002,0.,0.0848261|Polar=13.  
8120382,0.,13.8120382,0.,0.,13.8120382|PG=TD  
[O(C1),4C3(H1)]|NImag=0||0.54767104,0.,0.54767104,0.,0.,0.54767104,-0.07688286,0.0848  
9672,0.0000008,0.07885896,0.08489672,-0.28700193,-0.0000002-  
,-0.09332226,0.30983122,0.0000008,-0.00000021,-0.046868-  
9,-0.0000008,0.00000024,0.04586582,-0.0768860-  
,-0.04245004,0.07352633,0.00331311,0.00442709,0.01113397

,0.07886248,-0.04245004,-0.10690019,-0.10397894,-0.01185643,-0.0127-  
859,-0.02558442,0.04666298,0.11185534,-0.07352633,-0.10397894,-0.2269670  
3,0.00173299,0.00100654,0.00147123,0.08082343,0.11429829,0.24383818,-  
0.07688582,-0.04244995,0.07352603,0.00331309,0.00442711-  
-0.01113397,0.00331337,0.00742900-  
-0.00940146,0.07886221-  
-0.04244995-  
-

0.10690043,0.10397915,-0.01185639,-0.01271862,0.02558442,0.00742897,0.00856605,-0.01  
329531,0.04666288,0.11185561,0.07352603,0.10397915,-0.22696703,-0.0017330-  
,-0.00100656,0.00147128,0.00940143,0.01329533,-0.01981367,-0.080823

09,-0.11429853,0.24383818,-0.31701629,0.00000327,0.00000023,-0.0086023

0,-0.00042865,0.,-0.00860290,0.00021449,0.00037137,-0.00860286,0.00021

449,-0.00037136,0.34282435,0.00000327,-0.04686849,0.,0.03213837,0.0026  
0791,-0.00000002,-0.01606900,-0.00080262,0.00196941,-0.01606904,-0.000  
80262,-0.00196939,-0.00000360,0.04586582,0.00000023,0.,-0.04686849,0.0  
0000002,0.,-0.00193985,-0.02783250,0.00196974,0.00147128,0.02783250,-0  
.00196974,0.00147123,-0.00000025,0.,0.04586582||0.,0.,-0.00005060,0  
.00014313,0.,-0.00005061,-0.00007157,-0.00012396,-0.00005061,-0.000071  
57,0.00012396,0.00015181,0.,0.||@

... FOR AFTERWARDS A MAN FINDS PLEASURE IN HIS PAINS,  
WHEN HE HAS SUFFERED LONG AND WANDERED FAR.

-- HOMER

Job cpu time: 0 days 0 hours 0 minutes 4.0 seconds.

File lengths (MBytes): RWF= 5 Int= 0 D2E= 0 Chk= 1 Scr= 1

Normal termination of Gaussian 09 at Sun Nov 29 23:31:58 2020.

**SUBJECT INDEX****A**

Absolute electro-negativity 58  
Absorption wavelengths 131, 134  
Acetamide fragment 67, 73  
Activities 55, 100, 120, 121  
    anti-inflammatory 120, 121  
    biological 55, 100, 120, 121  
    potential-biological 100  
Adaptability 120  
AIMAll program 145  
Alcolea palafox 62  
Amanita mushrooms 78  
Amazonian wines Abuta 100  
Analysis 92, 106, 121, 138, 143  
    second-order perturbation theory 92  
    spectroscopic 106, 121, 138  
    topological 143  
Animal tissue 78  
Antibonding orbitals 60  
Antidepressant 120, 121  
Antithrombotic activity 55  
Approach 15, 143, 151  
    cost-effective 15  
    supermolecular 143, 151  
Aromatic 113, 130  
    carbon atoms 113  
    CH stretching 130  
    systems 113  
Ascorbic acid 78  
Asymmetric catalysts 77  
Atomic 22, 90  
    arrangement 22  
    charges on CHDP 90  
Atoms 8, 9, 14, 15, 35, 47, 55, 59, 60, 61, 73,  
    84, 89, 113, 114, 134, 135, 143, 144,  
    147, 151  
    hydrogen 14, 89, 134  
    non-hydrogen 14  
    oxygen 60, 73, 84  
    quantum theory of 143, 144  
    sulphur 55

Auxiliary, time-dependent 17  
Avogadro constant 51

**B**

Bacterial DNA gyrase 55  
Bands 63, 73, 84, 85, 94, 104  
    active 94  
    experimental 85, 104  
    intense 73, 84, 85  
    observed FT-IR 63  
Basis sets 14, 143, 149  
    cc-pVTZ 14  
    correlation-consistent 14  
    double-zeta polarized 14  
    superposition errors (BSSE) 143, 149  
Bond 48, 143, 144, 145, 148, 151  
    critical point (BCP) 143, 144, 145, 148,  
    151  
    orbital 48  
    strength 143

**C**

Calculated and scaled wavenumbers 127, 132  
Calculating 33, 42  
    frequencies 33  
    GIAO 42  
Calculations 7, 8, 12, 14, 15, 21, 27, 29, 32,  
    34, 46, 49, 50, 122, 136, 138, 150  
    electron correlation 14  
    spectroscopic 122  
    theoretical 150  
Carbon atoms 58, 59, 78, 89, 94, 113  
    gamma 78  
    neighboring 58  
Carboxylic acid 91  
Charges 30, 38, 51, 58, 60, 61, 67, 89, 94, 137  
    elementary 51  
Charge transfer (CT) 59, 89, 92, 132  
CHDP conformers 87, 88

- Chemical 37, 55, 58, 59, 73, 77, 96, 97, 100, 106, 108, 115, 116, 121, 137, 138, 143  
hardness 37, 58, 108, 137, 138  
reactivity 55, 58, 59, 73, 77, 96, 97, 100, 106, 108, 115, 116, 121  
wavefunction-based method 143
- Chemical shifts 14, 134  
of hydrogen 134  
tensor 41
- Chemisorption 121
- Circular dichroism 78
- Cis conformer 83
- Coefficients 48, 52  
electronic-transition 52
- Collagen 78  
helix 78  
protein 78  
stability 78
- Commercial software package 26
- Comparison of electron density and wavefunction 3
- Comparison of vibrational modes 67
- Compounds 15, 55, 56, 57, 59, 70, 77, 100, 101, 102, 109, 121, 132  
aromatic 109  
azafluoranthene 101  
novel 55  
transition metal 15
- Conformers 77, 78, 80, 87, 88, 91  
low-lying 87
- Continuous set of gauge transformations (CSGT) 41
- Corrections 15, 49  
delocalization 49
- Correlated quantum, high-level 143
- Correlation 9, 12, 14, 57, 62, 80, 81  
local 12
- Correlation coefficient 57, 66, 80, 123, 136, 138  
linear 123, 138
- Coulomb-attenuating method 13
- CP technique 149
- Crystallographic parameters 21, 27, 124  
experimental 124
- Cytotoxic 100
- activity 100  
agents 100
- ## D
- Data 29, 73  
crystallographic 73  
grid 29
- Defining exchange-correlation energy 5
- Density 1, 3, 8, 16, 17, 39, 121, 138, 143  
probability 3  
spin 39  
time-dependent 16
- DFT 1, 11, 16, 21, 122  
application of 16, 21  
hybrid 11  
time-dependent 1, 122
- DFT methods 1, 149  
time-dependent 1
- ## E
- Egap 38, 85  
higher 85
- Electric field 43  
static 43
- Electrocyclization 101
- Electroluminescent devices 101
- Electron 3, 104, 107, 116  
deficiencies 104  
diffraction 3  
donor 107, 116
- Electron correlation 15, 66  
effects 15
- Electron density 1, 3, 4, 6, 8, 9, 11, 15, 16, 17, 113, 115, 116, 143, 144, 146, 151  
and wavefunction 3  
time-dependent 17  
transfer 113, 115, 116
- Electronegative 107, 116, 137
- Electronic 2, 50, 51, 96, 97, 108, 120, 131, 132, 133, 138  
and thermodynamic parameters 96, 108

## Subject Index

and thermodynamic parameters of CHDP monomer 97  
motions 2  
transitions 50, 51, 120, 131, 132, 133, 138  
Electronic parameters 36, 38, 55, 58, 59, 97, 100, 116, 120, 136, 137, 138  
calculated 97  
change 58  
Electrophilic index 37, 137, 138  
Electropositive potentials 89  
Electrostatic 39, 40, 89, 107, 115, 121, 136, 137, 146, 150  
molecular 40, 89, 107, 115, 121, 136, 137  
negative 89  
Energy 1, 2, 3, 4, 5, 6, 8, 9, 10, 12, 16, 17, 21, 22, 23, 25, 31, 32, 35, 36, 37, 43, 47, 51, 60, 86, 91, 92, 97, 108, 122, 131, 132, 149, 150  
binding 9, 91  
calculated 16, 150  
classical repulsion 17  
electron correlation 8  
electron-electron repulsion 5  
electronic 3, 4, 10  
electronic repulsion 6  
exchange-correlation 1, 6, 8, 9  
excitation 12, 131, 132  
kinetic 2, 3, 5, 6, 10  
molecular atomization 12  
nuclear repulsion 3  
stabilisation 60  
thermal 97, 108  
total 3, 43, 51, 86  
total electronic 85, 122, 149  
Energy gap 85, 96, 116, 132  
smaller 116  
Energy values 23, 37, 150, 151  
accurate stabilization 151  
corresponding interaction 150  
Enthalpy change 122  
Equations 1, 7, 11, 18, 24, 62, 66, 97, 136  
linear 66  
non-relativistic Schrödinger wave 1  
standard thermodynamic 97  
Equilibrium geometry 77, 87, 91

## DFT Based Studies on Bioactive Molecules 199

Exchange energy 8, 10, 11  
Excited state transition 50  
densities 50  
Experimental 73, 77, 93, 102, 131  
FT-IR frequencies 77  
FT-IR spectra 93, 102  
FTIR values 73  
UV-visible spectrum 131

## F

Fibrinogen receptor antagonists 55  
Field, electromagnetic 4  
Fock matrix 7, 8, 49, 50  
elements 8, 50  
Forbidden transitions 51  
Frequency-dependent NLO parameters 46  
FT-IR 94, 95, 96, 102, 104, 105, 106, 121, 127, 138  
band 104, 106  
spectrum 121, 127, 138  
value 94, 95, 96, 102, 105, 127  
FT-IR spectra 70, 92, 93, 100, 102, 104, 116  
corresponding experimental 116  
determined 100  
Functionals 5, 9, 10, 12, 15, 16, 17, 18  
gradient-corrected 9  
hybrid 10, 12  
long-range corrected 12, 16

## G

Gauge-independent atomic orbital (GIAO) 41, 113, 122  
Gaussian 12, 13, 15, 27, 28, 52, 145  
and GaussView programs 27, 52  
functions 13  
processes 27  
program 12, 15, 145  
type functions 13  
website 28  
GaussView programs 27, 39, 52  
Generalized gradient approximation (GGA) 1, 9, 10, 12, 18

GIAO method 120  
Gibbs free energy 36  
Glycoproteins 78  
Gyromagnetic ratio 41

## H

Halomethyl radicals 62  
Hamiltonian 2, 3, 41  
  complete non-relativistic 2  
  electronic 3  
  time-independent non-relativistic 2  
Harmonic frequencies 33  
Heterocyclic 55, 101, 108, 116  
  moieties 55  
HF 10, 11, 12, 15, 37  
  exchange energy 11, 12  
  method 10, 37  
  theory 15  
Higher energy 4, 92  
  relatively 92  
Higher intensities, relatively 130  
Highest occupied molecular orbital (HOMO)  
  37, 38, 40, 55, 58, 89, 90, 100, 106, 115,  
  116, 132, 134, 137  
HOMO, low-lying 96  
Homogeneous electron gas 8  
HPLC method 121  
Hybridization 91  
Hydrogen bonding 96, 134, 148  
  intermolecular 134  
Hydrogen bonding interactions 150  
  strong inter-molecular 91  
Hydrogen bonds, intra-molecular 56  
Hydroxyproline 77, 78  
Hyperconjugations 61

## I

Individual Gauges for Atoms 41  
  in molecules (IGAIM) 41  
Infrared 102, 126  
  frequencies 102  
  Spectroscopic Analysis 102, 126

Infrared spectra 92  
  calculated 116  
Infrared spectral analysis 97, 110  
  of iverubrine 110  
Input orientation 31, 44, 45  
Interaction energies 149, 150  
  intermolecular 149  
  inter-molecular H-bond 150  
Interactions 49, 60, 73, 91, 92, 106, 115, 132,  
  134, 136, 143, 144, 145, 146, 147, 148,  
  149, 150, 151  
  charge-transfer 115, 134  
  chemical 106, 115, 132  
  donor-acceptor 92  
  drug-receptor 115, 136  
  hydrogen-bonded 150  
  hyperconjugative 73  
  inter-molecular H-bond 145  
  intramolecular 73, 143, 151  
  ionic 146  
Intermolecular interaction(s) 77, 91, 93, 97,  
  136, 143, 149, 150, 151  
  and NBO analyses 91  
  energy 149  
Isotropic magnetic shielding (IMS) 134  
Iterative process 8

## K

KBr disc technique 120  
Kinetic energy density 144, 146, 151  
Kinetic 2, 96  
  energy operator 2  
  stability 96  
Kohn-Sham 1, 4  
  approach 1, 4  
  energy 4  
Kohn theorem 6  
Koopmans' theorem 37  
KS 6, 7, 8  
  equations 6, 7  
  Fock matrix 8  
  orbital energies 7

**L**

- LCAO method 37
- Lewis structure 46, 91
- Local density approximation (LDA) 1, 8, 9, 10, 12, 18
- Lone-pair (LP) 49, 59, 60, 61, 86, 91, 113
  - delocalization 113
  - interaction 61
- Lowest unoccupied molecular orbital (LUMO) 37, 38, 55, 58, 89, 100, 106, 115, 116, 120, 132, 134, 137
- LP 59, 60
  - interactions of 60
  - one-centre valence 59
- LUMO 38, 40, 58
  - and higher unoccupied molecular orbitals 40
  - energies 38, 58
- LYP correlation 12, 13

**M**

- Magnetic field 41
  - applied 41
  - external 41
- Mass-weighted Cartesian displacements 24
- Matrix 7, 25, 43
  - equation 7
  - mass-weighted force constant 33
- MESP 21, 40, 41, 52, 89, 100, 107, 115, 116, 120, 121, 136, 137
  - analyses 115
  - and electronic parameters 136
  - of imerubrine 116
  - surface of imerubrine 115
  - surfaces and charge distribution 89
- Methods 38, 57, 120
  - computational 57
  - finite-difference 38
  - theoretical 120
- Molecular geometry and potential energy surface 86

- Molecular orbitals (MOs) 6, 11, 13, 14, 21, 36, 37, 39, 40, 52, 58, 132
  - occupied 6, 40
- Mulliken population analysis (MPA) 47, 89, 90

**N**

- Natural 47, 48, 55, 61, 73, 89
  - atomic orbitals (NAOs) 47, 48
  - population analysis (NPA) 47, 48, 55, 61, 73, 89
- Natural bond orbital (NBO) 21, 46, 47, 48, 49, 50, 52, 55, 77, 91
  - ANALYSIS 46, 48
- Nature 122, 137
  - exothermic 122
  - polarized 137
- NBO 46, 49, 97
  - external program 46
  - method 97
  - non-Lewis 49
  - program 46
- NBO analysis 46, 48, 49, 55, 59, 60, 61, 73, 77, 91, 92, 150
  - for lone-pair interaction 61
- NH 83, 130
  - stretching modes 83
  - stretching vibrations 130
- NMR 41, 42
  - calculations 41, 42, 113, 134
  - spectroscopic analysis 113, 134
- Nuclear magnetic 21, 41, 42, 43, 52, 100, 120
  - resonance (NMR) 21, 41, 43, 52, 100, 120
  - shielding tensors 42
- Nucleosides 147
- Nucleus attraction 10
- Nujol mull techniques 77, 93, 98
- Numerical differentiation 25, 43

**O**

- One-electron spatial wavefunctions 4
- Optical 21, 78

- activity 21
  - rotatory dispersion 78
- Optimized molecular geometries 101
- Orbitals 8, 14, 37, 41, 46, 47, 49, 59, 113, 122, 132
  - core atomic 14
  - gauge-independent atomic 41, 113
  - independent atomic 122
  - lone pair 49
  - natural atomic 46, 47
  - non-Lewis 49
- Oscillator strengths 50, 51, 52, 131, 132
- Oxygen 60, 116
  - LP orbitals 60

## P

- Paget's disease 78
- PED analysis 82
- Polarizability tensor 43
- Polarization 14, 15, 97
  - functions 14
  - d-type Gaussian 14
  - p-type 15
  - d-type Gaussian 14
- Popelier criterion 144
- Population analysis 21, 36, 37, 38
- Potent corrosion inhibitors 121
- Potential energy 2, 16, 22, 23, 25, 26, 86, 87, 67, 68, 81, 82, 83, 84, 85, 93, 94, 95, 96, 97, 109, 120, 122, 123, 126, 130, 144, 146, 151
  - density 144, 146, 151
  - distribution (PED) 67, 68, 81, 82, 83, 84, 85, 93, 94, 95, 96, 97, 109, 126, 130
  - function 22
  - operator 2
  - surface (PES) 16, 22, 23, 25, 26, 28, 86, 87, 120, 122, 123
- Proline 77, 78
  - hydroxylation of 77, 78
- Properties 1, 3, 18, 21, 27, 41, 55, 58, 78, 85, 89, 97, 100, 108, 143, 150
  - biological 78

- chemical 78
- electronic 58, 85, 97, 108
- spectral 100
- spectroscopic 55
- Prototype dimers 149

## Q

- QTAIM 143, 145, 146, 148, 150, 151
  - analysis 143, 145, 146, 148, 150, 151
  - calculations 145, 146
  - method 151
- Quantum 1, 9, 143
  - mechanics 1
  - Monte Carlo simulations 9
  - theory 143

## R

- Raman scattering 33
- Reaction 77, 96, 97, 101, 106, 108, 115, 120, 122, 123, 132, 138
  - chemical 96, 97, 122
  - cycloaddition 101
  - kinetics 26
  - organic 77
  - paths 108, 122
  - thermodynamics of 121, 123, 138
- Reactivity descriptors 38, 100, 116
  - chemical 38
- Region 25, 62, 63, 65, 67, 70, 73, 82, 83, 96, 107, 109, 110, 115, 116, 129, 130, 131
  - electron-deficit 107
  - electronegative 115, 116
  - electropositive 115
- Repulsion 2, 5, 8, 78, 86
  - electron-electron 2
  - electronic 86
  - nucleus-nucleus 2
- Runge-Gross theorem 17

## S

- Scaling 55, 62, 65, 66, 73, 98, 126

## Subject Index

equation 55, 62, 65, 66, 73, 98, 126  
of normal modes of vibration 62  
procedure, universal 62  
Schrödinger equation 1, 2, 16  
Scurvy disease 77, 78  
Second order perturbation theory analysis 49  
Self-consistent field (SCF) 31  
Software 27, 122  
visualization 27  
Species 16, 115, 136  
hydrogen-bonded 16  
Spectra, emission 50  
Spectrophotometer 102  
Stabilization 60, 92, 137, 143, 146, 148  
energies 137, 143  
significant 60, 148  
Stationary point 25, 28  
frequency 28  
interpretation in terms of energy 25  
Stretching 63, 65, 67, 70, 73, 82, 83, 96, 103,  
104, 112, 129, 130  
antisymmetric 129  
anti-symmetric 104  
asymmetric 65, 70, 112  
symmetric 65, 70, 112, 129  
Stretching vibrations 70, 83, 96, 109, 126, 131  
Substitutions 56, 59, 67, 70, 89, 101, 104, 108,  
112, 116, 136, 137  
electrophilic 116, 137  
nucleophilic 89, 136  
Sum of Mulliken atomic charges 39  
Systems 2, 4, 5, 6, 7, 8, 9, 10, 11, 14, 16, 17,  
18, 67, 106, 112, 120, 121, 132, 143,  
145, 146  
active 143  
actual 6, 11  
atomic 2  
heterocyclic 120, 121  
multi-electron 16  
one-electron 7  
ring 67, 106, 112, 132  
stationary 17

## DFT Based Studies on Bioactive Molecules 203

### T

TDDFT method 50, 52  
Tetramethylsilane 43, 134  
Theory 1, 8, 18, 49, 143, 144, 151, 152  
linear response 18  
second-order perturbation 49  
Thermal 34, 36, 122  
correction 36  
energies 36  
enthalpies 36, 122  
free energies 36  
Thermochemistry 34, 35  
Thermodynamics, statistical 35  
Thiazole 65, 67  
heterocyclic 67  
rings 65  
Thiocarbohydrazide 120, 121  
Time-dependent density functional theory  
(TDDFT) 1, 16, 17, 18, 21, 50  
Topology 143  
Total 107, 146  
density surface 107  
energy density 146  
Toxic cyclic peptides 78  
Transition 26, 50, 52, 89, 115, 116, 132  
probability 52  
state 26, 52  
velocity 50

### U

UV-visible 120, 121, 122, 131, 132, 138  
spectra 138  
spectroscopic analysis 131  
spectrum 120, 121, 122, 131, 132, 138  
UV-vis-NIR 21, 50, 52  
spectrum 52  
spectrum 50

### V

Valence 14, 15, 47  
consistent-polarized 14

- orbitals 14, 15
- triple-zeta 14
- Vibrational 21, 26, 28, 62, 63, 68, 70, 71, 73, 77, 78, 82, 92, 94, 100, 102, 109
  - analyses 77, 78, 100
  - analysis of CHDP 94
  - bands 26
  - frequencies 26, 28, 62, 73, 82
  - frequency calculation 21
  - spectroscopic analysis 63, 68, 71, 92, 109
  - spectroscopy 62
  - spectrum 100, 102
  - twisting 70
  - wavenumbers 63
- Vibrational modes 62, 66, 67, 81, 83, 85, 93, 94, 100, 104, 106, 109, 110, 112, 113, 130
  - coupling of 62, 113
  - strong 104

**W**

- Waals interactions 16, 143
- Wavefunction 1, 2, 3, 6, 11, 15, 16, 28
  - based methods 1, 15, 16
  - electronic 3
  - multi-electron 3
- Wavenumber difference by scaling schemes 67
- Wigner-Seitz radius 9

**X**

- X-ray 3, 56, 57, 79, 123, 138
  - crystallography 123, 138
  - diffraction (XRD) 3, 56, 57

**Z**

- Zero-point 36, 85, 97, 108
  - correction 36
  - energy (ZPE) 85, 97, 108



**Amrish Kumar Srivastava**

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Dr. Amrish Kumar Srivastava is an Assistant Professor at the Department of Physics in Deen Dayal Upadhyaya Gorakhpur University, Gorakhpur, India. He obtained his Ph.D. from the University of Lucknow, India, and subsequently worked as a National Postdoctoral Fellow at D.D.U. Gorakhpur University. He teaches Biophysics and Advanced Quantum Physics to postgraduate students. His broad research areas include Computational Biophysics and Computational Materials Science. He has published over 110 research papers in various journals of international repute with an h-index of 20. Dr. Srivastava is the Guest Associate Editor of *Frontiers in Chemistry* and also serves the editorial board of many journals including *Current Chinese Science* from Bentham. He has reviewed more than 30 research articles for many journals. His works have been referenced in Wikipedia, the free encyclopedia. He has expertise in dealing with DFT calculations over a wide range of molecular systems. More details can be found at the website: <https://cutt.ly/CMSLab>

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## BOOK SUMMARY

This book is intended for young researchers and experimentalists among others, who wish to explore the DFT on molecular systems. The salient features of the book include concise and complete coverage of DFT on biologically active molecules. It begins with the basics of DFT for beginners followed by its application and usage using a powerful Gaussian program. Subsequently, discussions on synthetic compounds, amino acids, and natural products have been offered. The book also features an exclusive chapter on the quantum theory of atoms in molecule and supplemented by an appendix.

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