International Journal of Advances in Scientific Research and Engineering (ijasre)

E-ISSN : 2454-8006

DOI: 10.31695/IJASRE.2023.9.5.5

Volume 9, Issue 5
May - 2023

Geometric Modelling and Analysis of the Amino Acid: Phenylalanine

Arzu ÖZGEN[1], Sinem GÜRKAN AYDIN[2]

[1]Department of Medical Services and Techniques

[2]Department of Faculty of Applied Sciences, Aircraft Maintenance and Repair

Istanbul Gelisim University, Turkey

ABSTRACT

L-phenylalanine (Phe), an essential amino acid, is necessary for the synthesis of proteins such as catecholamine and melanin, and is also the precursor of the amino acid L-tyrosine (Tyr). In this paper, optimized structures of Phe, were calculated by using semi-empirical models such as AM1, PM3 and MNDO; Density Functional models (DFT) at B3LYP and Hartreefock methods (HF) with 6-311++G (d,p) level. The energies and geometric parameters of Kaempferol were also determined.

Key Words: DFT, Geometric analysis, HF, Phenylalanine.

1. INTRODUCTION

Animals, including humans, cannot synthesize some amino acids necessary for protein synthesis and homeostasis of metabolic nitrogen (N). These molecules, called essential amino acids, must be provided directly or indirectly from a plant source [1]. L-Phe, which is an essential amino acid and serves as a precursor molecule for thousands of vital and special compounds, contains 8.5% nitrogen. About 20-30% of the photosynthetically fixed carbon is for the synthesis of Phe [2-3]. L-Phe, the precursor of the L-tyrosine amino acid, is also required in the synthesis of thyroxine, melanin, norepinephrine, and epinephrine [2-4]. Phe, which is a crucial substance of proteins in all living organisms, is also the precursor amino acid for many natural products such as cell wall components, pigments, hormones and alkaloids in plants. Phe provides the carbon skeleton for the phenylpropanoid pathway, a pathway that makes thousands of different chemicals used for structure, defence in organism physiology [5-8].

Phe is synthesized from chorismate, which is converted to prephenate by chorismate mutase [8-9-10]. Phe, which has a vital importance for seed formation in plants [11-12]. Phe is an amino acid found in breast milk and a number of foods, including poultry, meat, cottage cheese, lentils, fish, and sesame seeds. When the daily recommended total protein intake is met, adequate intake is achieved, and the daily adult requirement for Phe and tyrosine (Tyr) is 39 mg/kg [13-14]. Approximately 80% of dietary Phe is converted to Tyr for protein synthesis [15]. Phenylalanine hydroxylase enzyme deficiency causes the disease known as Phenylketonuria (PKU) disorder of Phe metabolism [2]. Untreated patients develop severe intellectual disability, epilepsy, and psychiatric, and movement problems [16].

Very large molecules are often studied only by molecular mechanics, because other methods (quantum mechanical methods based on Schrödinger's equation: quasi-experimental, ab initio and DFT) take too long. New molecules with unusual structures are best investigated by ab initio or possibly Density functional calculations (DFT) calculations [17].

DFT calculations are like ab initio and quasi-experimental calculations based on the Schrödinger equation. However, unlike the other two methods, DFT does not calculate a wave function, but instead directly derives the electron distribution. DFT is somewhat new: chemically useful DFT computational chemistry dates back to the 1980s, while "serious" computational chemistry was done by the ab initio method in the 1970s and by quasi-experimental approaches in the 1950s [17].

The B3LYP functional is a hybrid of several components whose relative weights were selected based on experimental thermochemical data. The accuracy of such hybrid functionals in predicting molecular geometries and vibrational frequencies has not yet been fully characterized [18].

The B3LYP functional has exactly eight empirical parameters in total. Sousa et al. reported in their 2007 paper that from 2002 to 2006 the names of functionals accounted for approximately 80% of journal articles and abstracts each year, the popularity of which is clearly better for almost any particular application. Despite the fact that a functional can be found, Sousa et al. said circa 2007 that "B3LYP still remains a viable and particularly fruitful alternative to the 'mean' quantum chemistry problem" [19-17].

In this study, the optimized structures of Phe, was calculated by using semi-empirical models such as AM1, PM3 and MNDO; Density Functional models (DFT) at B3LYP and Hartreefock methods (HF) with 6-311++G (d,p) level. The energies and geometric parameters of Kaempferol were also determined.

2. COMPUTATIONAL DETAILS

Optimization, structure parameters, geometric parameters have been obtained by using semi-empirical models such as AM1, PM3 and MNDO; Density Functional models (DFT) at B3LYP and Hartreefock methods (HF) with 6-311++G (d,p) and 6-31G* levels. Gaussian 09 package and Gauss-View molecular visualization programs have been used for all computations [20-21].

3. RESULTS AND DISCUSSION

With theoretical calculation methods, many properties such as geometric and electronic properties of molecules can be started to be calculated without the need for experiments. With the theoretical calculation methods used today, it can be easily applied and desired results can be obtained even for compounds that are obtained and/or not obtained/not obtained, even for compounds that cannot be formed under real conditions. In some studies, more sensitive and reliable results can be obtained than the experimental method. It is quite easy to get the desired results in theoretical calculations made with a computer. The calculated ground state optimized structures of phenylalanine are shown in Figure 1.

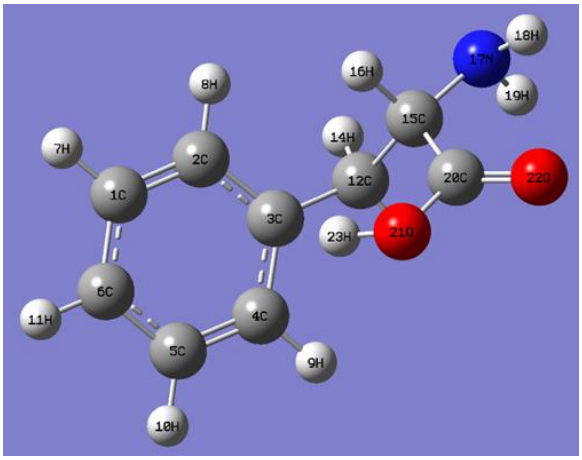

Figure 1. Optimized structure of Phenylalanine

In a molecule, there are only rotations around the sigma bond (single bond). Temporary molecular shapes resulting from the rotation of groups around the sigma bond are called conformations of the molecule. The analysis of the energy change undergone by the molecule as a result of the rotation of the groups around the sigma bond is called conformation analysis. Different conformations of molecules can cause them to display different properties. For example, for a biomolecule to function, that molecule must be in a certain conformation. These are usually low-energy conformations. Since the molecule has more than one single bond-centred dihedral angle and there may be free rotations around these bonds, conformation analysis is performed to find the most stable state of such flexible molecules, and the energies and geometries of the formed conformations are determined (Table 1a,b,c,d,e).

Table 1.a. Calculated geometric parameters of Phenylalanine.

Geometric parameters Bond lengths(A)	DFT/B3LYP 6-31G (d,p)	Calculated values HF 6-311G++(d,p)	AM1	PM3	MNDO
1C-7H	1.08439	1.07226	1.09933	1.09163	1.09257
6C-11H	1.08401	1.07195	1.09272	1.08866	1.08739
5C-10H	1.08417	1.07216	1.09923	1.09143	1.09237
4C-9H	1.08581	1.07362	1.09873	1.09302	1.09333
2C-8H	1.08231	1.06891	1.09881	1.09304	1.09332
3C-12C	1.51919	1.51654	1.46936	1.48563	1.49015
12C-4H	1.09651	1.08382	1.12533	1.10334	1.11828

DOI: 10.31695/IJASRE.2023.9.5.5

12C-3H	1.09678	1.08380	1.12209	1.10345	1.11709
12C-5C	1.56270	1.55421	1.54911	1.55012	1.57471
15C-6H	1.09552	1.08276	1.13347	1.11805	1.12334
15C-7N	1.47420	1.45897	1.45222	1.49238	1.47106
17N-9H	1.02876	1.00650	1.00250	0.99894	1.00867

Table 1.b. Calculated geometric parameters of Phenylalanine.

Geometric parameters Bond Angles (^{0})	Calculated values DFT/B3LYP 6-31G (d,p)	Calculated values HF 6-311G++(d,p)
C3C12 -H13	109.32722	109.14481
H9-C4-C3	119.57153	119.76839
H10-C5-C4	119.85307	119.81858
H11-C6-C5	120.14222	120.21305
H7-C1-C6	119.87473	119.91147
H8-C2-C3	118.10271	118.91977
C2-C3-C12	120.88648	121.06837
C3-C12-H14	110.74323	110.63072
C3-C12-H13	109.32722	109.14481
C12-C15-H16	108.49075	108.73524
C12-C15-C20	108.38801	108.71233
C12-C15-N17	110.34692	110.11769
C15-C20-O22	123.80980	124.24008
C15-C20-O21	115.69965	115.21360
C20-O21-H23	111.28015	115.10762
C15-N17-H19	108.30658	111.23550
C15-N17-H18	111.40950	113.42966

Table 1.c. Calculated geometric parameters of Phenylalanine.

Geometric parameters Bond Angles (0)	Calculated values AM1	Calculated values PM3	Calculated values MNDO
C3C12 -H13	110.99541	111.06067	111.11000
H9-C4-C3	118.66454	118.86078	119.37932
H10-C5-C4	120.23419	120.17911	120.23348
H11-C6-C5	120.68474	120.67242	120.75586
H7-C1-C6	118.83426	118.92814	118.97903
H8-C2-C3	118.56815	118.56187	119.42606
C2-C3-C12	120.84565	118.97854	121.81592
C3-C12-H14	110.05662	110.32040	109.74657
C3-C12-H13	110.99541	111.06067	111.11000
C12-C15-H16	107.31374	108.39467	108.36463
C12-C15-C20	110.34854	110.92445	113.06386
C12-C15-N17	112.94315	110.67393	110.22298
C15-C20-O22	125.18335	126.39785	124.63881
C15-C20-O21	120.89117	121.88374	121.17926
C20-O21-H23	109.86144	107.60760	114.92037
C15-N17-H19	109.85739	109.90290	111.10010
C15-N17-H18	109.66845	110.22575	110.26540

DOI: 10.31695/IJASRE.2023.9.5.5

Table 1.d. Calculated geometric parameters of Phenylalanine.

Geometric parameters Dihedral angles (^{0})	Calculated values DFT/B3LYP 6-31G (d,p)	Calculated values HF 6-311G++(d,p)
C(12)-C(3)-C(2)-H(8)	-2.15278	-1.52448
C(12)-C(3)-C(4)-H(9)	-0.26707	-0.53525
C(3)-C(4)-C(5)-H(10)	179.76201	179.85053
C(3)-C(2)-C(1)-H(7)	179.92975	-179.97018
C(3)-C(12)-C(15)-H(16)	44.80819	41.99360
C(3)-C(12)-C(15)-C(20)	163.82667	160.60164
C(3)-C(12)-C(15)-17(N)	-75.06546	-77.63083
C(20)-C(15)-N(17)-H(18)	-86.85879	-84.10075
O(21)-C(20)-C(15)-H(16)	50.98892	50.80637
O(21)-C(20)-C(15)-N(17)	171.69243	171.15160
O(22)-C(20)-C(15)-N(17)	-11.56202	-11.18216
C(20)-C(15)-N(17)-H(19)	32.41240	40.95443
N(23)-O(21)-C(20)-O(22)	176.22111	174.39444
H(23)-O(21)-C(20)-C(15)	-6.91423	-7.84474

Table 1.e. Calculated geometric parameters of Phenylalanine.

Geometric parameters Dihedral angles (^{0})	Calculated values AM1	Calculated values PM3	Calculated values MNDO
C(12)-C(3)-C(2)-H(8)	-3.75405	-13.61425	-2.02079
C(12)-C(3)-C(4)-H(9)	4.34675	14.86090	2.41555
C(3)-C(4)-C(5)-H(10)	-179.32338	-176.89647	-179.51663
C(3)-C(2)-C(1)-H(7)	179.30515	178.23712	179.64916
C(3)-C(12)-C(15)-H(16)	-45.19527	-62.08556	-49.39553
C(3)-C(12)-C(15)-C(20)	69.69366	55.37274	68.88218
C(3)-C(12)-C(15)-17(N)	-162.64135	-177.36028	-163.82112
C(20)-C(15)-N(17)-H(18)	-36.95753	-45.06867	-49.92295
O(21)-C(20)-C(15)-H(16)	58.72855	67.76860	44.06715
O(21)-C(20)-C(15)-N(17)	175.33463	-175.95747	159.00239
O(22)-C(20)-C(15)-N(17)	-1.11197	15.16324	-17.44354
C(20)-C(15)-N(17)-H(19)	81.46975	74.98038	66.28610
N(23)-O(21)-C(20)-O(22)	-171.33719	-173.22959	-169.42348
H(23)-O(21)-C(20)-C(15)	11.83758	16.33828	13.77939

Gaussian 09W is a very comprehensive program that includes molecular mechanics, semi-experimental and ab initio methods. It has a large selection of theories and foundation sets for all three methods. The energies of atoms and molecules can be calculated, geometric optimizations can be made, energy-dependent vibration frequencies, force constants and dipole moments can be calculated. The program can traverse the potential energy surface, scanning for minimums, transition states, and reaction paths. It can test the stability of the molecular wave function. As seen from the table there are slight differences between them, and this causes some relative geometrical differences.

4. CONCLUSIONS

In this study, the geometric, optical and spectroscopic properties of the Phenylalanine biomolecule were investigated using the density functional theory. Optimization, structure parameters, geometric parameters of the considered biomolecule have been obtained by using semi-empirical models such as AM1, PM3 and MNDO. Phenylalanine is an amino acid used to produce proteins and other important molecules. It is also used to make important molecules in the body. Phenylalanine has been used to treat ailments such as depression, skin conditions, and pain. Therefore, detailed examination is very important for biology situations and pharmaceutical technology.

DOI: 10.31695/IJASRE.2023.9.5.5

REFERENCES

[1] Pascual, M. B., El-Azaz, J., de la Torre F. N., Cañas R. A., Avila C., and, Cánovas F. M; 2016. Biosynthesis and Metabolic Fate of Phenylalanine in Conifers. Frontiers in plant science, 7,1030.

[2] Kohlmeier, M; 2003. Phenylalanine. Food Science Technology. Nutrition Metabolism. Cambridge, MA, USA: Academic Press: 314-321.

[3] Bonawitz, N. D., and Chapple, C; 2010. The genetics of lignin biosynthesis: connecting genotype to phenotype. Annual review of genetics, 44, 337-363.

[4] Farishian, R. A., and Writtaker, J. H; 1980. Phenylalanine lowers melanin synthesis in mammalian melanocytes by reducing tyrosinase uptake: implications for pigment reduction in phenylketonuria. Journal of Investigative Dermatology, 74(2), 85-89..

[5] Kliebenstein, D. J; 2004. Secondary metabolites and plant/environment interactions: a view through Arabidopsis thaliana tinged glasses. Plant, Cell & Environment, 27(6), 675-684..

[6] Tzin, V., and Galili, G; 2010. New insights into the shikimate and aromatic amino acids biosynthesis pathways in plants. Molecular plant, 3(6), 956-972.

[7] Korkina, L. G; 2007. Phenylpropanoids as naturally occurring antioxidants: from plant defense to human health. Cellular and molecular biology, 53(1), 15-25.

[8] Maeda, H., and Dudareva, N; 2012. The shikimate pathway and aromatic amino acid biosynthesis in plants. Annual review of plant biology, 63, 73-105..

[9] Yoo, H., Widhalm, J. R., Qian, Y., Maeda, H., Cooper, B. R., Jannasch, A. S., and Dudareva, N; 2013. An alternative pathway contributes to phenylalanine biosynthesis in plants via a cytosolic tyrosine: phenylpyruvate aminotransferase. Nature communications, 4(1), 1-11..

[10] Herrmann, K. M., and Weaver, L. M; 1999. The shikimate pathway. Annual review of plant biology, 50(1), 473-503.

[11] Razal, R. A., Ellis, S., Singh, S., Lewis, N. G., and Towers, G. N; 1996. Nitrogen recycling in phenylpropanoid metabolism. Phytochemistry, 41(1), 31-35

[12] Towers, G. H. N., Singh, S., Van Heerden, P. S., Zuiches, J., and Lewis, N. G; 1998. Integrating nitrogen and phenylpropanoid metabolic pathways in plants and fungi. Lignin and Lignan Biosynthesis, 3, 42-54.

[13] Gibson, N. R., Jahoor, F., Ware, L., and Jackson, A. A; 2002. Endogenous glycine and tyrosine production is maintained in adults consuming a marginal-protein diet. The American journal of clinical nutrition, 75(3), 511-518.

[14] Young, V. R., and Borgonha, S; 2000. "Nitrogen and amino acid requirements: the Massachusetts Institute of Technology amino acid requirement pattern", The journal of Nutrition, 130(7):1841S-1849S.

[15] Matthews, D. E., Marano, M. A., Campbell, R. G; 1993. Splanchnic bed utilization of leucine and phenylalanine in humans. American Journal of Physiology-Endocrinology And Metabolism, 264(1), E109-E118..

[16] Blau, N., Van Spronsen, F. J., and Levy, H. L; 2010. Phenylketonuria, The Lancet, 376(9750), 1417-1427...

[17] Jarrahpour, A. A., and Zarei, M; 2004. Synthesis of 2-({[4-(4-{[(E)-1-(2-hydroxy-3- methoxyphenyl)methylidene amino}phenoxy)phenyl imino}methyl)-6- methoxyl phenol. MolbankM352. ISSN 1422-8599, Retrieved February 22

[18] Tim S; 2010. Organic Chemistry With a Biological Emphasis. University of Minnesota Morris, 2.

[19] Sousa, S. F., Fernandes, P. A., and Ramos, M. J; 2007. General performance of density functionals. The Journal of Physical Chemistry A, 111(42), 10439-10452..

[20] Frisch, M., Trucks, G., Schlegel, H. E. A., Scuseria, G. W., Robb, M. A., Cheeseman, J. R., ... and Pople, A. J; 2004. Gaussian 03, revision C. 02.

[21] Frish, A., Nielsen, A.B., and Holder,A.J; 2001. Gauss View User Manual. Gaussian Inc., Pittsburg, PA,, 4(1), 1-1

DOI: 10.31695/IJASRE.2023.9.5.5