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Subtle Bond of Amino Acids

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Abstract: *The subtle bond of amino acids isdiscussed.*

Keywords: *subtle bond, quantized energy, subtle bond number, terahertz frequency, amino acids*

1. INTRODUCTION

In the previous paper the subtle bond was presented on the example of fluorine atoms of Carbon tetrafluoride (CF_4).[1]In this paper we will pay attention to the subtle bond of amino acids.

2. SUBTLE BOND ENERGY

The energyshould bereleased at subtle bond forming between equal atoms at curved distance $n = \pi D$ and is given by the next equation:

$$E_{subtle\ \ bond} = Ry.\alpha^{-1}\left(-\frac{1}{\frac{s(n)}{2}} + \frac{1}{s\left(\frac{n}{2}\right)}\right) < 0. \quad (1)$$

Taking into account$Ry = 13.605\ 693\ 009\ eV$multiplied by $\alpha^{-1} = 137.035\ 999\ 146$as well asapplyingthe double surface geometry

$$s(n) = n\left(2 - \frac{1}{\sqrt{1+\frac{\pi^2}{n^2}}}\right). \quad (2)$$

Here $n$counts Compton wavelengths of the electron on the elliptic surface and showing the result $s(n)$ on the average elliptic-hyperbolic surface. In a classical approach we are dealing with rigidorbits sothe curved distance between atoms is determined bynatural numbers $n = 1, 2, 3$ ... On the other hand, ina non-classical approach we are dealing with doubled orbits at the expense of the available kinetic energy of the electronso also half values come into consideration$n = 0.5, 1, 1.5, 2, 5, 3$ ...The subtle bond energy is thus quantizedand a limited selection of energy is possible being in inverse proportion to the mentioned specific number n. Combining equations (1),(2) we can write:

$$E_{subtle\ \ bond} = \frac{2Ry.\alpha^{-1}}{n}\left(-\frac{1}{\left(2 - \frac{1}{\sqrt{1+\frac{\pi^2}{n^2}}}\right)} + \frac{1}{\left(2 - \frac{1}{\sqrt{1+4\frac{\pi^2}{n^2}}}\right)}\right). \quad (3)$$

3. ENERGY RANGE

Subtle bond energy range is determined on the lower side by the number$n = 0.5$,andon the upper side by the non-number $n = \infty$ as follows:

$$E_{subtle\ \ bond}\,(0.5) = Ry.\alpha^{-1}\left(-\frac{1}{\frac{s(0.5)}{2}} + \frac{1}{s\left(\frac{0.5}{2}\right)}\right) = -3883\ eV. \quad (4)$$

And

$$E_{subtle\ \ bond}\ (\infty) = Ry.\alpha^{-1}\left(-\frac{1}{\frac{s(\infty)}{2}}+\frac{1}{s\left(\frac{\infty}{2}\right)}\right) = 0\ eV. \qquad (5)$$

Thus, the upper limit of released subtle bond energy is 3883 eV, the lower limit of released energy is zero, andthere should be some space available in the middlefor the attainable values of the subtle bond energy. Of course, this energy can be expressed in frequency equivalents, too.Let's test the theory in THz region of proteinogenicamino acidswhose absorption peaks are given with sufficient precision.[2]

4. Amino Acid

Amino acid [3], any of a group of organic molecules that consist of a basic amino group (—NH_2), an acidic carboxyl group (—COOH), and an organic *R* group (or side chain) that is unique to each amino acid. The term *amino acid* is short for *α-amino [alpha-amino] carboxylic acid*. Each molecule contains a central carbon (C) atom, called the α-carbon, to which both an amino and a carboxyl group are attached. The remaining two bonds of the α-carbon atom are generally satisfied by a hydrogen (H) atom and the *R* group.The amino acids differ from each other in the particular chemical structure of the side chain (*R* group) as illustrated in Figure 1:

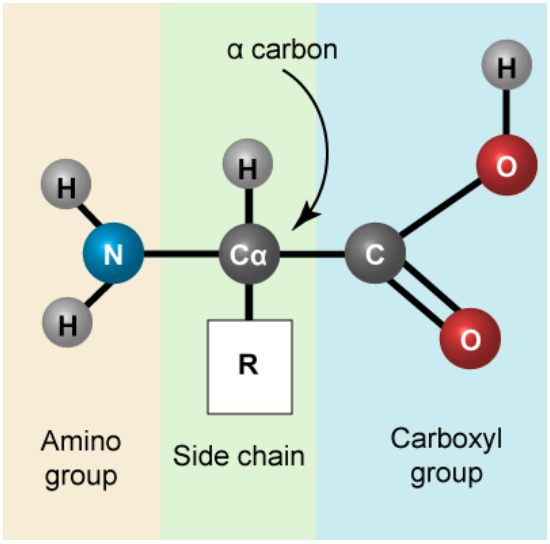

Figure1. *Amino acid*

5. Absorption Peaks of TwentyAmino Acids in the Range of 0.8 to 2.5 THz

The terahertz absorption peaks of20protein creating amino acids are presented in Table1. Their recently measured frequency [2] is given in the second column. The subtle bond original orbit length is attributed to the measured frequency in the third column. The nearest theoretical subtle bond original orbit number is chosen in the fourth column. And the nearest theoretical subtle bond frequency is given in the fifth column.

Table1.*The absorption peaks in the range of 0.8 to 2.5 THzof 20 proteinogenicamino acids. Sign "–"means no absorption peak at this range is available*

Amino acid	Measured absorption peaks (THz)	Attributed subtle bond original orbit length(λ_e)	Theoretical subtle bond original orbit number n	Theoretical subtle bond frequency(THz)
Beta-Alanine	-			
D-Alanine	**2.226**	**181.5645**	**181.5**	**2.228374385**
L-Alanine	**2.226**	**181.5645**	**181.5**	**2.228374385**
D-Arginine	**0.99** 1.435	**237.9254** 210.2120	**238** 210	**0.989070114** 1.439347523
L-Arginine	**1.002** 1.508	**236.9711** 206.7606	**237** 207	**1.001633673** 1.502777887
D-Aspartic acid	-			
L-Aspartic acid	-			

D-Glutamic acid	1.216 **2.038** **2.443**	222.1526 **186.9908** **176.0142**	222 **187** **176**	1.218508211 **2.037700235** **2.443590882**
L-Glutamic acid	**1.235** 1.967	**221.0066** 189.2167	**221** 189	**1.235109996** 1.973766663
D-Serine	-			
L-Serine	-			
DL-Tyrosine	-			
L-Tyrosine	0.975 **1.929** 2.076	239.1402 **190.4525** 185.8415	239 **190.5** 186	0.976715756 **1.927560557** 2.070704054
Glycine	-			
L-Leucine	**0.854** **1.48** 1.683 2.198	**249.9471** **208.0575** 199.3230 182.3332	**250** **208** 199.5 182.5	**0.853458097** **1.481227676** 1.678530720 2.191988719
L-Lysine	0.956 **2.069**	240.7152 **186.0511**	241 **186**	0.952617410 **2.070704054**
L-Methionine	-			
L-Threonine	**1.418** 2.034	**211.0496** 187.1134	**211** 187	**1.418998451** 2.037700235
L-Tryptophan	1.447 **1.88** **2.285**	209.6288 **192.0949** **179.9862**	209.5 **192** **180**	1,449668049 **1.882785130** **2.284477786**
L-Valine	**1.678** 2.236	**199.5211** 181.2932	**199.5** 181.5	**1.678530720** 2.228374385

We can see in bold print that all twelve acids out of twenty whichhave absorption peaks in the range of 0.8 to 2.5 THz possess at least one frequency that is very close tothe theoretical subtle bondfrequency. Theoretical subtle bond original orbit numbers are distributed around the number210which belongs to D-arginine as well as to ammonia NH_3. (See appendix 1).So, the subtle bonds could be attributed to the hydrogen atoms$H$in amino group $-NH_2$ wheresubtle bond issomehow contracted or stretchedby the influence ofthe side chain$R$ (See figure 1).The present subtle bondoriginal orbit numbersattributedto the measured absorption peaks[2]support this argument, since theyoccupy acceptable valuesof 180 to 250 what is within the range of subtle bond orbit numbers of hydrogen atoms in the amino group (See appendix2). The subtle bonds could be also attributed to the hydrogen atoms H ofother groups,for instance $-CH_3$, beingpresent in the side chain R (See appendix 3).

6. Conclusion

Absorption peaks in the range of 0.8 to 2.5 THzof protein creatingamino acids indicate the presence of a subtle bondwhich is suspected to bedependent onthe basic amino group $-NH_2$and theorganic$R$group(side chain).

Dedication

To the touch of life

Figure2. *Touch of life [4]*

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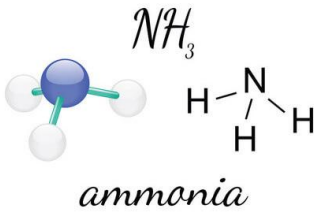
Appendix 1

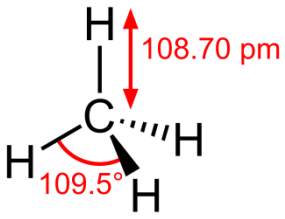


The distance between hydrogen atoms$H \ldots H$in ammonia $NH_3$is$162.42\ pm$[5]which expressed in Compton wavelengths of the electronequals $66.941\ \lambda_e$. The curved distance is π- times longer. Yielding $210.30\ \lambda_e$ it is longer than thestablesubtle orbit length $s(n) = 210.023\ \lambda_e$as well as unstable subtle orbit length $2\ x\ s\left(\frac{n}{2}\right) = 210.093$. So, the subtle bond (stable or unstable) can be formed with the help of energy release.

Appendix 2

The distance between nitrogen atom$N$ and hydrogen atom$H$ in ammonia$NH_3$is $101.24\ pm$[5]which expressed in Compton wavelengths of the electronequals $41.726\ \lambda_e$. The curved distance is π- times longer yielding $131.09\ \lambda_e$. The stretched distance between hydrogen atoms in amino group $-NH_2$should not exceed twice of this value, what means thatthe subtle orbit number should not exceed 262.In our case we are the witness of the maximum number $250 < 262$.

Appendix 3



The distance between carbon atom C and hydrogen atom$H$ in methane CH_4 is $108.70\ pm$[5]which expressed in Compton wavelengths of the electronequals $44{,}801\ \lambda_e$. The curved distance is π- times longer yielding $140.75\ \lambda_e$. The stretched distance between hydrogen atoms in carbon group $-CH_3$ should not exceed twice of this value, what means that the subtle orbit number should not exceed 281. In our case we are the witness of the maximum number $250 < 281$.

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