Volume 10, Issue 4, 2019, 5679 - 5688 ISSN 2069-5837

Biointerface Research in Applied Chemistry

www.BiointerfaceResearch.com

https://doi.org/10.33263/BRIAC104.679688

Original Research Article Open Access Journal

Received: 25.02.2020 / Revised: 25.03.2020 / Accepted: 26.03.2020 / Published on-line: 29.03.2020

Molecular biology's symphony orchestra from DNA to ribosome: a sonification from gene to protein

Majid Monajjemi [1, *]

[1]Department of chemical engineering, Central Tehran Branch, Islamic Azad University, Tehran, Iran

*corresponding author e-mail address: ***maj.monajjemi@iauctb.ac.ir*** | Scopus ID 6701810683

ABSTRACT

Ribosome sonification contains total steps of DNA, m-RNA, t-RNA and amino acids consequences that convert the bio-macromolecules data derived from biology systems into acousmatic music are a novel approach in a symphony orchestras. NMR data of the ^{13}C are particularly well suited data sources for DNA, mRNA and amino acids sonification. One of the important directions in ribosome sonification is time-series-sonification data (TSSD), due to auditory imagination is very sensitive to changes in time. Although, their resonant frequencies are basically in the MHz range, the resonant frequencies span around kHz. The ribosome of E. *coli* is consisting of several genes which one of them might be divided into 8 series of codons and anti-codons for eight octaves of notes. During NMR calculation with AB-initio methods, these signals are routinely mixed down into the audible frequencies ranges, rendering the need for any additional frequencies transpositions unnecessary. The concert pitches vary from ensemble to ensemble and have varied largely over music methods. The most general advance tuning standard corresponds to 440 Hz for An above middle C as a sequence note. This concept is also applied for distinguishing among the "nominal" (written), and "real" (sounding) notes of a transposing instrument that refers to the sounding pitch on a non-transposing instrument. By this study, E .coli's gene sequences into musical notes for a revealing auditory algorithm has been converted. Estimations of their calculation and optimization of those codons have been done and the total frequencies of each nucleotide have been converted to several music notes and distinguishing those using variations of chemical shifts including pitch, time duration length of notes and even rhythm have been accomplished.

Keywords: *DNA; mRNA; E .coli; concert pitches; sonification, classical music notes.*

1. INTRODUCTION

Ribosome is associated with biological macromolecules machine, existed within all living biological cells, that acts as translation of protein synthesis. Ribosomes make strength of jointed amino acids together based on m-RNA molecules [1]. Claude, first observed ribosomes in 1941 and two major components are included in ribosome, one is the small ribosomal subunits, that read the m-RNA , and the second term is larger subunits, which link amino acids for forming the polypeptides chains. Each subunit consists of one or more ribosomal RNA (r-RNA) molecules and a variety of ribosomal proteins . Ribosome works such a factory, therefore, is known as ribonucleoprotein factories (RNP) [2]. As ribosome can be found in mitochondria and chloroplast, they are called organelle within organelle. Brown and Robinson first discovered ribosomes in plant cells in 1953 and two years next Palade, isolated ribosomes from animal cells and detected RNA in them.

In 1958 R.B. Roberts coined the term ribosome. In contrast mature RBC and sperm, the ribosomes appear in both prokaryotic and eukaryotic cells. In prokaryotic, ribosomes are found freely scattered in the cytoplasm, but in eukaryotic cells it appears free in the cytoplasmic that attached to the outer surfaces of the rough endoplasmic reticulum and nuclear envelopes [3]. Ribosome appears individually in monosomes, while clusters shape in polysomes and during the protein synthesis 6-8 ribosomes temporarily join with a mRNA for forming a cluster which called poly ribosome (polysome or ergo some). The amount of ribosomes in the cells depends on protein synthesis. The popular ribosomes consist of a somewhat flat, elongate small subunit and also a roughly hemispherical large subunit, which associate at the initiation step and dissociates upon termination of the proteins synthesis. The ribosome helps as a physical scaffold, serve to bring together in correct orientations [4]. In addition, the mRNA, representing a transcript of the DNA segment to be translated (t-RNA), bearing the related amino acids due to anticodon for the corresponding m-RNA codon.

Majority, has catalytic activity which placed in the peptidyl-transferase center, which is required for transferring the related t-RNA- amino acids to the nascent polypeptides in each step of elongation. The small subunit in ribosome exhibits a one third/two-thirds distribution of mass into a head and body portion, which extends along the interface with the large subunit. The roughly triangular head tapers off into a scythe-shaped extension, curved away from the large subunit that is especially pronounced in eukaryotes [5]. The large subunits in ribosome are roughly hemispherical, and bears three prominent extensions that serve as landmarks. The genetic specification in living organisms is saved in the genome sequences of their DNA.

Most amounts of these sequences encode proteins which carry out most of the functional tasks in all extant organisms. The DNA information is made available by *transcription* of the genes to mRNAs (messenger ribonucleic acids) that subsequently are *translated* into the various amino acid sequences of all the proteins of an organism.

This is the central dogma of molecular biology in its simplest form as; DNA-gene *transcription)* → mRNA *(translation)* → Protein peptide sequences. The genetic codes in DNA are preserved via *replication* of the genome accomplished via DNA polymerase. In all biological systems, transcription of

DNA into mRNA is done through RNA polymerase, and translation of mRNA is done via the ribosome. The mRNA sequence includes ribonucleotides with either one of four bases which are known as adenine, cytosine, guanine and uracil. The amino acids are encoded through several codons such as *UUU* or UUC for phenylalanine, and also termination of translation and initiation of translation mainly have been recognized via (UAG, UAA) and AUG, respectively (encoding the methionine)[3-5]. The m-RNA sequences are decoded starting with AUG codons which followed via the sequences of codons, specifying the order of insertion of amino acids in the nascent proteins that are followed through the termination codons, signaling which the proteins are ready for dissociation in the ribosome for subsequent folding into its functional state. The links among the m-RNA and the peptide sequences are t-RNA. In the bacterial cells there are 64 different kinds of t-RNA molecules and each one is composed of about 80 nucleotides. They have a CCA-end, to which an amino acid can be linked by an ester bond, and an anticodon, which can read m-RNA codon cognates to the amino acid links to the CCA-end of the t-RNA.

An enzyme recognizing t-RNAs is assigned for each amino acid with an anticodon complementary to the m-RNA codon cognates to these amino acids [6]. Consequently, the enzyme recognizes the amino acids and its cognates of t-RNA(s) and then pairs them together at the expense of ATP hydrolysis to the higher standard free energies complexes that called aminoacyl-t-RNA [4-6] (Fig.1).

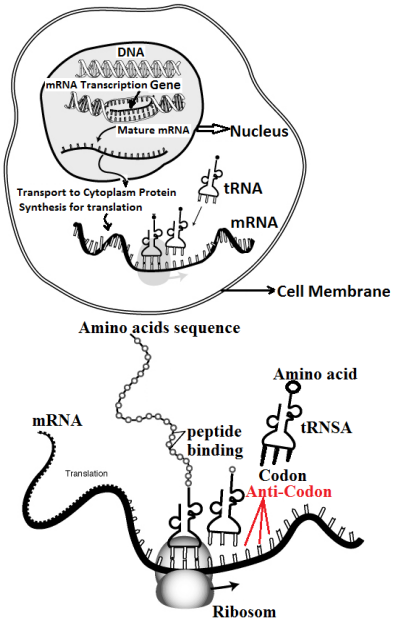

Figure 1. DNA-gene *transcription)* → mRNA *(translation)* → Protein peptide sequences

1.2. Precision of m-RNA translation.

Precision translations of the genetic codes from sequences of related proteins via recognition of aminoacyl-t-RNAs cognate to m-RNA codons demonstrated in the A site based on the Gipps free energies (ΔGo) among cognates and non-cognates codon-anticodon base pairs. These ΔGo -data for the competition among cognates and non-cognates t-RNAs at all the 61 amino acid encoding codons in m-RNAs, the ribosome can enhance the precision and therefore reduce the frequencies of amino acids substitution errors in nascent peptides chains via the principle of proofreading. Amino-acyl-t-RNAs enter the ribosome in A ternary complex consist of EF-Tu and GTP.

Between these, the cognate ternary complex is selected for GTP hydrolysis with high probability, while non-cognate ternary complexes dissociate with high probability. In this item, the same standard free energies between cognates and non-cognates- t-RNAs can be applied several times [6,7]. In Fig.2 (A), the ratios among cognates and non-cognates peptides have been defined for concentrations of cognates and non-cognates ternary complexes.

The genetic codes are redundant; there are 20 canonical amino acids but sixty one sense codons, all of which are used in mRNA [5,7]. As instance, in *E. coli* there are 5 ISO-accepting t-RNAs for leucine. In addition related t-RNA can read several codons via accepting mismatches in the third codon position based on wobble hypothesis such as, t-RNA (Phenylalanine) (anticodon GAA) reads the two phenylalanine codons UUU, UUC, the ISO-accepting t-RNALeu2 (anticodon GAG) reads the leucine codons CUU, CUC and tRNALeu3 (anticodon UAG) reads CUG, CUA and CUU [5-7]. The physical and chemical phenomenon occurring third codon position wobble has been another unanswered question during past years of ribosome research. The treatment of codon reading on the ribosome can be tuned up or down by mutations in ribosomal RNA and ribosomal proteins. These Precision tuning features have also remained mysterious, since they often relate to events far from the decoding center (Fig.2).

Due to the 30S subunit structures at high resolution in complexes with various ligands, the reason " how the ribosome can enhance the ΔGo values for t-RNA" has cleared in initial selection *and* proofreading, and also how the wobble mechanism done or how ribosomal mutation has been answered in a simple and coherent manner [8].

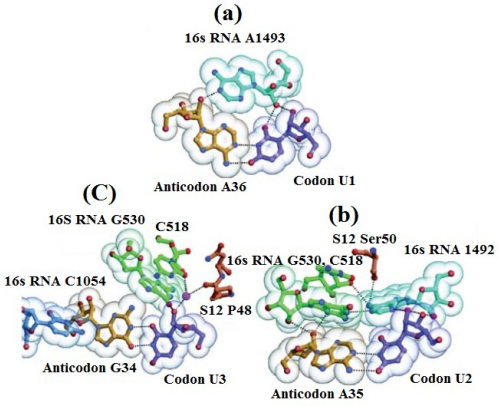

Figure 2. (a) the geometry of base pairing between U1 in first codon (A36 in the anticodon is examining by A1493). (b) Base pairing between U_2 in second codon position and A35 in amino-acyl-t-RNA (examine by A1492 and G530), (C) the geometry of the base pairing in third codon position (U3:G34)

In a summary ribosome has 1-mRNA binding site in smaller sub-unit 2- A-site or amino acyl-t-RNA site, 3- P-site or peptidyl-t-RNA site and 4- E-site or exit site to which uncharged t-RNA come before leaving the ribosome (Fig.3). Structurally, ribosomal subunits include tightly folded ribosomal RNA, (r-RNA) and many surrounded proteins. The mole ratio of r-RNA to proteins in prokaryotic and eukaryotic cells is sixty/forty and fifty/fifty by weight respectively [7-9]. The ribosome's protein may be basic, chemical structural or enzymatic in functions.

The bigger subunit contains an important enzyme – peptidyl transferase, which brings about the formation of peptide bond. Because the r-RNA remains fully covered with proteins inside the ribosome, they are therefore, ribonucleoprotein particles (RNP)[6-10].

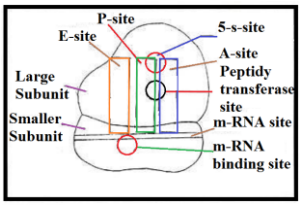

Figure 3. A ribosome showing different active sites.

1.2. Convert DNA sequence to music.

Mc-Millan [11, 12] used the artificial intelligence networks to convert the IR spectrum to music via acoustic foundation. Non-scientist musicians usually do not feel that chemical molecules oscillate and play imaginary music under various conditions (due to fast vibration of the atoms in macro-molecules which are orders of a large magnitude faster than acoustic vibrations).

This perspective seems more amazing by the fact that each molecule has a specific spectrum in a wide region of music. In any simulation of molecular properties towards musical sonification any wave might be matched to the melodies, rhythms, pitches or duration of acoustics that are the meaning of "Sonification" from bio-macro-molecules to music. There are long and distinguished histories, within this field of music, of composers using non-musical systems as root and sources for any further composition. For example some items can be noted, (1): Brazilian composer "Heitor Villa-Lobos" compositions his "Symphony No. 6: On the Profiles of the Mountains of Brazile" (1945) for the orchestra;(2): Famous American composer "John Cage's Atlas Eclipticalis (1960-61) for interesting orchestra; Etudes Borealis (1977) for cello and/or piano, which made via tracing star maps onto score paper; (3) Charles Dodge's another American composer "The Earth's Magnetic Field" (1971) for computer, which mapped magnetic field measurements into the basic notes of diatonic musical scales; (4) Clark and Dunn's works, especially their paper "Life Music: The Sonification of Proteins" and their several collaborative CDs of DNA music are paradigm for those sonification. In each of them, the non-music sources are converted to a music that often has quite unfamiliar aspects [12-15].

The approach supposed of the "DNA sonification" is based on the translation of DNA sequences representations into musical notes that not only permits to create a musical instrument but also allows exploiting deep neural network models for representing and designing in the audio spaces. Sonification, basically focuses on creating the spectrum of overlapping vibrations either to mimic the waves and sounds of related concepts that do not naturally appear. Therefore, have been considered sonification of spider webs and whole ribosome structures, consist of [P-site] = violin, E-site=Piano, A-site= Cello, 5s-site = Saxophone, peptidyl-transfers= Oboe, m-RNA site= Both violin & Clarinet and whole ribose is the orchestra 'leader. By this work, a formulation of sonification method by which the nucleotide sequence of DNA and amino acids in ribosome, have been applied to produce audible sound through the chemical and physical properties of those components such as NMR, NBO, QSAR and Normal mode analysis [15,16].

The supposed sound-based generative algorithms are based on the natural vibrational frequencies of nucleotides and amino acids. Commonly, the vibrational spectra of those nucleotides can be computed via computational chemistry methods such as abinitio methods, molecular dynamics (MD) and especially QM/MM. A computer system can convert these kind inaudible sounds into a range of musical frequencies. By converting these waves of the DNA, t-RNA and amino acids, they can then be used to express musical sounds that are based on the complex spectrum of those vibrations. It is notable that t-RNA, m-RNA and DNA play rolling of information processing, mutations and memories in the brain. Hereby through artificial intelligence, the structures of ribosome components in orchestra space have been modeled via the translational approach and then translation back to ribosome components. The summarize chart of this work is as follows. (1) Analyzing of the translation of the vibrational spectra of each ribosome's components towards audio signals using the concept of trans-positional equivalency. (2) Generating known gene structures into musical scores by sonification. (3) Finding a model of converting ^{13}C-NMR data of nucleotides, di-nucleotide (Bas pairs) and three nucleotides (codons) sequences, t-RNA and amino acids components to musical notes. (4) Presenting a model for overcoming the jump between consecutive notes as a consequence of the ribosome components to any range of genes with NMR & normal modes data. The main problem is the question of how to incorporate rhythm into the sequence of those notes [16].

1.3. Codes for DNA, t-RNA and amino acids interpreation.

The codes for sonification might be linearly converted to the musical sounds, in an approach that has an implied cellular biology context. Interpretation of DNA and t-RNA and amino acids information as musical sounds, which clearly cross the divide among sciences and arts fields [17]. For achieving this goal and targets, they can connect the Amino acids, t-RNA and DNA sequence data to the perceptual specification of sounds [18]. The sonification ways and their auditory help analyze the concept of related sequences by the musical sounds and it should be useful for definition of these codes of DNA, m-RNA and t-RNA sequence interpretation during sonification [19].

The algorithm permits users to inputting their own DNA sequences to produce an auditory display in real time. The major action is the reading frame codons (algorithm) that are extracted from the genetic code, whereby the codons are mapped to musical notes on a scale and also there is no optional handling work for reducing the number of notes to make the auditory display more musical. The DNA bases can be specified as codons in each of three possible reading frames leading to three interlaced streams of notes [20].

2. MATERIALS AND METHODS

2.1. NMR spectroscopy converting.

DNA, m-RNA, t-RNA and amino acids related to codons and anticodons specification in ribosome can be turned by sonification of NMR spectroscopy directly into musical sound, including Infra-red spectroscopies "IR" or nuclear magnetic resonance "NMR". Through IR spectroscopy, it can be measured

the vibrational behavior of those components in ribosome has been applied for the musical sounds in sonification [19-21].

Usually, these kind approaches have to be made during the sonification concluding musical's notes, pitches, melodies, Rythms and Chords to be designed in viewpoints of different physical and chemicals images. By this study, ^{13}C-NMR spectroscopy is used as the novel source for ribosome components. NMR is occasionally applied in structure illumination and confirmation that are extremely sensitive for conformation and changing of those components in ribosome. The data of NMR calculation has been yielded from B3LYP/6-31G* level of methods for Guanine, Cytosine, Adenine, and Thymine which are shown in Figs 4&5.

The human genes are as follows; group including; ATG,ATC,TGC,GCA,CAT, AGC, TCA,CTG, group group(1) ATT,TGG,GCC, CAA, AGG, ,GAA,CTT, (2) ATG,TGC, GCA,CAT, AGC, TCA, GAT,CTG , (3) AAT,TTG,GGC,CCA, AAG,TTC, GGA,CCT, (4) ATA, TGT, GCG, CAC, TAT, GTG, CGC, ACA (5); AGT,TCG,GAC,CTA, AGC , TCA, GAT,CTG, (6) AAA,TTT,GGG,CCC,ATG,TGC,GCA,CAT which are shown in Figures 3-5 .

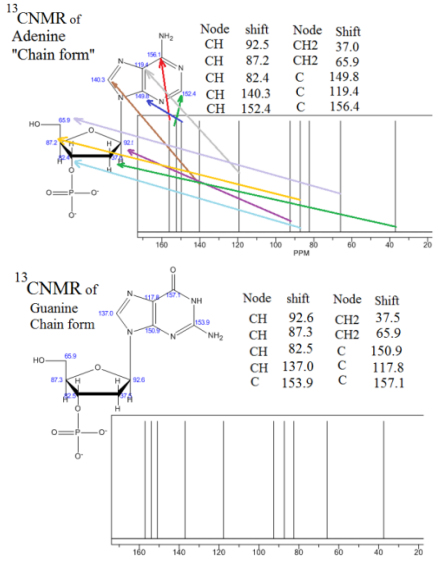

Figure 4. NMR data from B3LYP/6-31G**, for G and C base pairs.

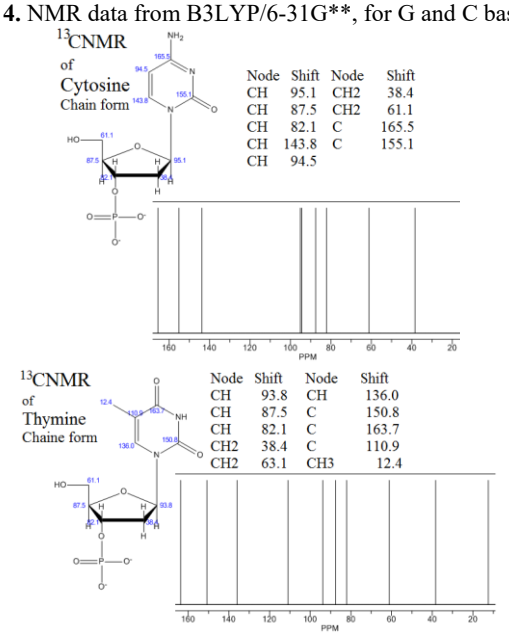

Figure 5. NMR data from B3LYP/6-31G**, for A and T base pairs.

It is complicates to explain the phenomenon of NMR mechanisms for analyzing data without introducing a wide concept of scientific subjects. Therefore, scientifically, in these spectroscopies, each of molecules has various atomic resonances which are split to a few resonances by somewhat differences in the values of frequencies if there are other magnetic nuclei nearby. The resonances are estimated via locating a sample in powerful magnetic fields, then using the pulse of radio frequencies. Basically, the biomolecules can be defined with tiny bells that are made audible through being hit with the radio frequencies hammer [22].

The conversions of those spectrums to the audible sounds are known as NMR sonification that has been used for a few gens with this work (Figs. 6 & 7) .

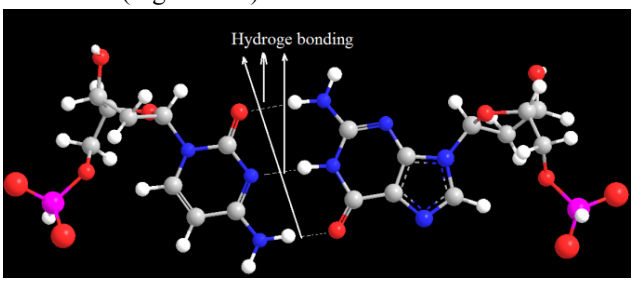

Figure 6. Optimized G-C nucleic acid base pairs through B3LYP/6-31G**, including 3 hydrogen bonds.

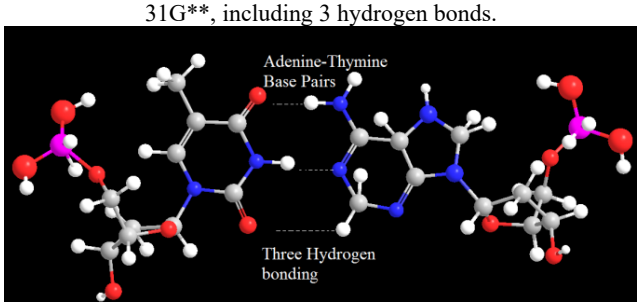

Figure 7. Optimized A-T nucleic acid base pairs through B3LYP/6-31G**, including 3 hydrogen bonds.

The optimized structures and energies data due to particular methods and basis sets are used in a model, in other words data during optimization of molecules and codons are not equal with difference of basis sets or methods. So, the conversion of sonification based on musical frequencies related to the notes may be different for each codon in table 1. Pitch, is one of the major components of the music's notes in the symphonies that pivotal section of acoustics is dependent on it. In abinitio quantum chemistry each basis sets and methods including DFT, MP$_n$, RHF, UHF, ROHF and even semi empirical methods are related to the type of pitches.

2.2. Concert pitch.

Pitch refers to that group of musical instruments that are tuned to the performance. The concert pitches vary from ensemble to ensemble, and have varied largely over music methods. The most general advance tuning standard corresponds to 440 Hz for An above middle C as a sequence note. This concept is also applied for distinguishing among the "nominal" (written), and "real" (sounding) notes of a transposing instrument that refers to the sounding pitch on a non-transposing instrument. Music to transpose tools is transposed via different keys from that of non-transposing tools, such as, playing a written C on a "B ♭ " clarinet or trumpet produces a non-transposing instrument's "B ♭ " that referred to as "concert B before 20th century, there was no coordinated effort for standardizing musical pitches, and the

levels across Europe varied widely. The term normally applied for the unit of pitch, cycle per second (CPS) were renamed the hertz (Hz) in the 20th century in honor of Heinrich.

A = 440 Hz is the most official standard which is used widely in the world and many orchestras comported to this standard as concert pitch but some orchestras such as the New York Philharmonic, use A = 442 Hz. The latter is seldom used as the tuning frequencies in European countries, especially in Italy, Norway and France. Nearly all modern symphony orchestras in Germany, Austria, Russia, Sweden and Spain tune to A = 443 Hz. Some orchestras tune applying the electronic tone generators and when playing with fixed-pitch tools such as the piano, the orchestra will basically tuned to the orchestra's normal pitches. In other words it is thought that the normal trend since the middle of the 20th century has been for standard pitches to rise, though they have been rising far more andante than they have in the past.

Many advanced ensembles that specialize in the efficiency of Baroque music have agreed with the standard of A = 415 Hz. An exact equal-tempered semitone lower than 440 Hz would be 415.30 Hz. Basically, it permits to play with fixed-pitch tools if their transposed down a semitone. Although general efficiency practice, especially in the German Baroque idiom, for tuning certain works to *Chorton*, a semitone higher than 440 Hz (460–470 Hz) such as Pre-Leipzig period cantatas of Bach). Orchestras in Cuba basically use A436 as the pitch so which strings, that are complicated for obtaining, last longer. Treble clef symbol indicates that the second line from the bottom is "G". On any staff, the notes are always arranged so that the next letter is always on the next higher line or space. The last note letter, G, is always followed by another A (Fig.8).

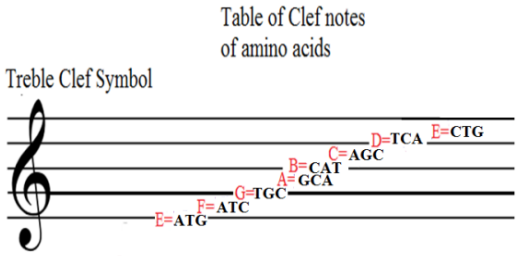

Figure 8. Calculations of Treble Clef Symbol of 8 codons

2.3. Basic music theory.

In the standard notations, musical sound can be written as the series of notes. The major item in the pieces of music needs to clear about a note in the pitches, or, what is its duration among the notes (time scale) or how long it lasts or stops.

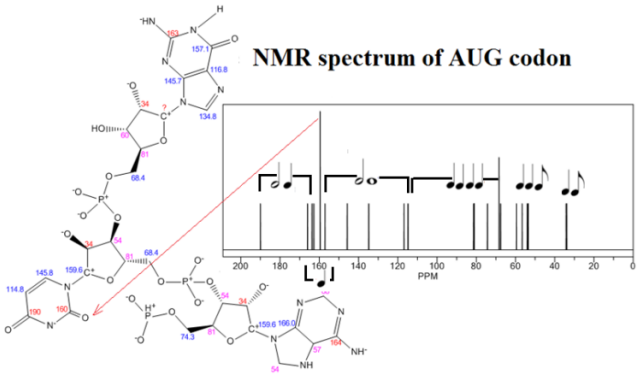

Figure 9. Time scales and note Lengths of AUG codon based on distances between chemical shifts, each 10 ppm is one unite.

Table 1. Normal modes (B3LYP/6-31G*) analysis based on Music's note

Base	Maximum frequency (HZ) of Normal modes	Intensity	degeneracy	Music's note
Adenine	3701	556	1	$A^{\#}_7/B^{b}_7$
Cytosine	1899	1531	1	$A^{\#}_6/B^{b}_6$
Guanine	2826	491	1	F_7
Thymine	3494	438	1	A_7
Bas Pairs				
G-C	6005	6501	1	$G^{\#}_8/A^{b}_8$
A-T	7400	2333	1	$A^{\#}_8/B^{b}_8$

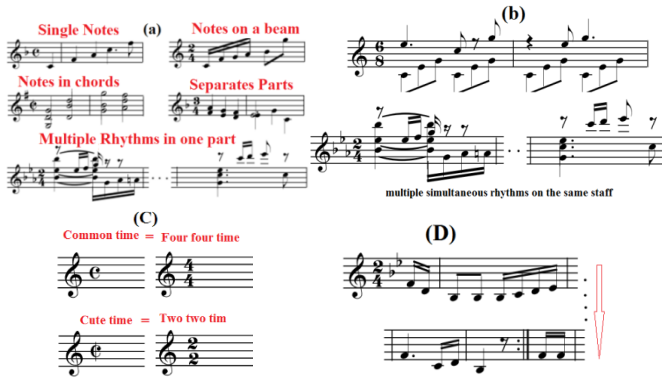

Figure 10. Multiple rhythm, Rests, Signature, Meter and Measure marks in the notes.

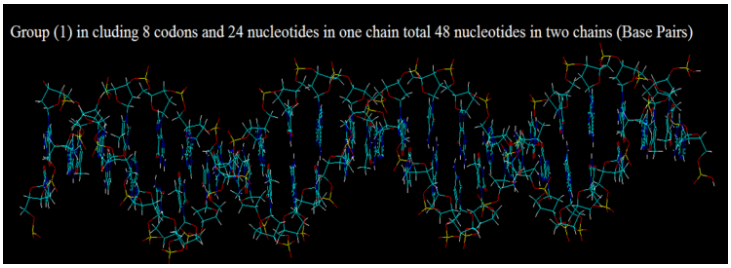

Figure 11. Optimized of group (1) , Helix form is B form and sugar form is 2`and Caps are from 3` to 5`.

For definition the pitches, must be looked at the clef and the key signature, and then look to the line which the notes are located on or between the lines. In the NMR figures the distances among chemical shifts explain the time scale among those notes (Fig .9).

The dots which are some places other than next to the head of the note do not affect the rhythm. Other dots are articulation marks. They may affect the actual length of the note (the amount of time it sounds), but do not affect the amount of time it must be given (Figs 9-11).

In table 1 chemical and musical reaction are listed

Chemical reaction: Adenine +Thymine → Adenine- Thymine (Bas pairs) Musical reaction: $(A^{\#}_7/B^{b}_7) + (A_7) \rightarrow (A^{\#}_8/B^{b}_8)$

Chemical reaction: Guanine +Cytosine → Guanine-Cytosine (Bas pairs) & Musical reaction is: $(F_7) + (A^{\#}_6/B^{b}_6) \rightarrow (G^{\#}_8/A^{b}_8)$

The note lengths are defined based on how long the notes last compared to the whole notes. A note which lasts half as long as a whole note is a half note. The note that lasts a quarter compare to whole notes are a quarter notes. The pattern continues with eighth notes, sixteenth notes, thirty-second notes, sixty-fourth notes, and so on, each type of note is half the length of the previous type (Fig.10-a).

When the rhythms are complex, this is necessary to make the rhythm in each part clear (Fig.10-b). The time signatures are the mark that is written at the beginning of the pieces of music, but

the meter of a pieces is the sequence of its rhythms in a repetitive pattern of strong and weak beats.

Meters can be classified via counting the number of beats from the strongest beat to the next one. The meter of a piece of music is their foundation rhythm; the time signature is a symbol that tells you the meter of each piece (Fig.10-c). At the ends of the music, a measure should be interrupted via a double bar were located the pickup notes in the correct place and assures that repeats have the correct number of the beats. When this occurs, the bar lines would be still appearing at the end of the completed measure (Fig.10-d). The whole calculations and theoretical approaches and experimental methods have been done based on our previous works [23-78] in viewpoints of theory an mathematical conversion ofrelated physical chemistry properties to those biological systems to conversion museical notes.

3. RESULTS

3.1. The oboe charachteristic on leading the orchestra in tuning.

The sound of the oboe stands out from the orchestra, so it's easy for all the musicians for hearing. The oboes have stable pitches and the others pitches are unstable. The only way of altering the pitch of an oboe is to adjust the breadth or length of the reeds; it is nearly impossible to make any sudden changes on the day of the efficiency. Nearly all musical tools have usually been unstable in subjects of pitch due to the differences in heat, humidity, and the like. Generally, the musical tools have such as mechanism which allows efficiency for tuning them. However, due to its structure, the oboe's pitches might only be changed via removing and inserting reeds[79,80]. They are not possible for changing how high-pitched the tones are the way that can be done by removing a clarinet's barrel or altering the tension of a violin's strings[80-83].

The only techniques of altering the pitches of the oboes are to adjust the breadth or length of the reeds; it is nearly impossible for making any suddenly changing. It is complicated to adjust the pitches of the oboes[84,85]. So, it would appear which the other musical tools must be made to match, and that is the explanation of why the oboes are the standard for tuning. Its pitch is also steadier than strings, so it's a more reliable tuning source. This was especially true when all violin strings were made from gut[86]. Longevities also have more and more for doing with it: over time flutes, bassoons, French horns and clarinets drifted in and out of the orchestra; but oboe was nearly always written into orchestral scores. So they became the standard instrument for tuning[87-89]. As same as any other musical tools, oboes might be tuned sharp or flat. But most oboists use an electronic tuner for making sure their 'A' is on point. Theoretically, the whole orchestra must use the electronic tuner for tuning which probably yields a more consistently accurate note than an oboe, as well. Some part notes in the ribosome symphony are exhibited in Figs.12& 13 [90-94].

3.2. The structure of *E. coli* ribosome.

In the 1960s, regulation of ribosome synthesis yields a simple linear relationship among growth rates and cellular concentrations of ribosomes. In past decades, microbiologists had been interested in various items that influence growth. Bacterial physiological scientist was interested in the subject of what really determines growth rates. Consequently, the main question of regulation of its synthesis, growth rate-dependent control, is based on definition of how bacterial cells adjust ribosome synthesis in relation to synthesis of other cellular component so that the optimize growth rates are attained under middle to fast growth situations[95-98].

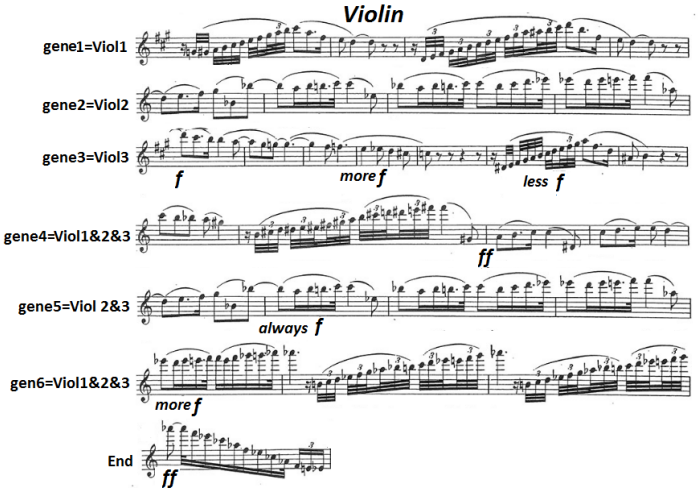

Fig.12. the violin notes which are imaginaries related to p-site of E.coli ribosome cell

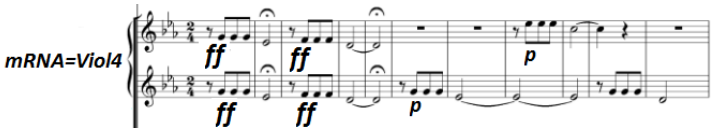

Figure 13. The violin notes which are imaginaries related to mRNA of *E.coli* ribosome cell.

The other basic events dependent on this study of regulation of ribosome synthesis is the discovery of stringent control which has a musical behavior by itself. Although the cessation of stable RNA including both r-RNAs and t-RNAs in auxotrophic bacteria starved for a required amino acid had been known for some time, they were a discovery of the *rela* gene by Gunther Stent and Sydney Brenner. This important finding stimulated the scientist to study the mechanism involved in this regulatory phenomenon[99-101].

Measurements of synthesis rates of r-RNAs, r-protein mRNAs, and r-proteins under several nutritional situations were accomplished through using these isolated genes and more improved techniques via various groups. So, it became clear that under medium to fast growth conditions, the synthesis rates of all r-proteins reflect their accumulation rates. Furthermore, the synthesis rates of r-RNAs also approximately reflect their accumulation rates under these situations. As will be mentioned below, this supposition turned out to be incorrect and eukaryotic cells were found to apply the third possibility mentioned above, i.e., separate and direct regulation of both r-RNA and r-protein syntheses in *E. coli* ribosome. Based on some previous works we have simulated a part of *E. coli* ribosome for a sonification and a partial playing of this mashie yields a simple music as instance can be seen in Figs 12 & 13.

4. CONCLUSIONS

The ribosome of the *E. coli* being analyzed related to the features present by the NMR analysis for musical sonification. In addition, it might be to select ribosome components based on structural features in order to create acoustic music notes. By this study, using the sonification methodology presented to create an acoustic music combination based exclusively on publicly accessible normal modes and NMR data. In addition, it can be useful for applying the sonification of other important DNA motifs such as mutation, transcription, restriction and duplication to unique sounds for highlighting their occurrence. The imaging of codons in t-RNA and anti-codons in m-RNA for writing the related musical notes are instructive and can also be useful for mapping the output of more complex approaches of sequence analyses to an auditory display. DNA sequences can be identified via sonification for providing an impetus for the inclusion of auditory displays within the toolkit of DNA sequences, as an adjunct to existing visual and analytical tools for ribosome. These approaches are strong tools for any further controlling human diseases such as Cancer, Alzheimer, Parkinson and diabetes.

5. REFERENCES

1. Weixlbaumer, A.; Jin, H.; Neubauer, C.; Voorhees, R.M.; Petry, S.; Kelley, A.C.; Ramakrishnan, V. Insights into translational termination from the structure of RF2 bound to the ribosome. *Science* **2008**, *322*, 953-956, https://doi.org/10.1126/science.1164840.
2. Frauenfeld, J.; Gumbart, J.; O. E.; Sluis, V.D.; Funes, S.; Gartmann, M.; Beatrix, B.; Mielke, T.; Berninghausen, O.; Becker, T.; Schulten, K.; Beckmann, R. Cryo-EM structure of the ribosome-SecYE complex in the membrane environment. *Nat. Struct. Mol. Biol.* **2011,** *18*, 614–621, https://doi.org/10.1038/nsmb.2026.
3. Bhushan, S.; Gartmann, M.; Halic, M.; Armache, J.P.; Jarasch, A.; Mielke, T.; Berninghausen, O.; Wilson, D.N.; Beckmann. R. *α*-helical nascent polypeptide chains visualized within distinct regions of the ribosomal exit tunnel. *Nat. Struct. Mol. Biol.* **2010**, *17*, 313–317, https://doi.org/10.1038/nsmb.1756.
4. Berndt, U.; Oellerer, S.; Zhang, Y.; Johnson, A.E.; Rospert, S. A signal-anchor sequence stimulates signal recognition particle binding to ribosomes from inside the exit tunnel. *Proc. Natl. Acad. Sci. USA* **2009**, *106*, 1398–1403, https://doi.org/10.1073/pnas.0808584106.
5. Nissen, P.; Ippolito, J.A.; Ban, N.; Moore, P.B.; Steitz, T.A. Rna tertiary interactions in the large ribosomal subunit: The a-minor motif. *Proc. Natl. Acad. Sci. USA* **2001**, 98:4899–4903, https://doi.org/10.1073/pnas.081082398.
6. Schmeing, T.M.; Huang, K.S.; Kitchen, D.E.; Strobel, S.A.; Steitz, T.A. Structural insights into the roles of water and the 2 hydroxyl of the p site tRNA in the peptidyl transferase reaction. *Molecular Cell* **2005**, *20*, 437–448, https://doi.org/10.1016/j.molcel.2005.09.006.
7. Schmeing, T.M.; Huang, K.S.; Strobel, S.A.; Steitz, T.A. An induced-fit mechanism to promote peptide bond formation and exclude hydrolysis of peptidyl-tRNA. *Nature* **2005**, *438*, 520–524, https://doi.org/10.1038/nature04152.
8. Silva, C.A.; Bertran, J.; Branchadell, V.C.; Oliva, A. Quantum Mechanical Study on the Mechanism of Peptide Bond Formation in the Ribosome. *J. Am.Chem. Soc.* **2011**, *134,* 5817–5831, https://doi.org/10.1021/ja209558d.
9. Voorhees, R.M.; Weixlbaumer, A.; Loakes, D.; Kelley, A.C.; Ramakrishnan, V. Insights into substrate stabilization from snapshots of the peptidyl transferase center of the intact 70S ribosome. *Nat. Struct. Mol. Biol.* **2009**, *16,* 528–533.
10. Sievers, A.; Beringer, M.; Rodnina,M.V.; Wolfenden, R.; The ribosome as an entropy trap. *Proc. Natl. Acad. Sci. USA*, **2004**, *101*, 7897–7901, https://doi.org/10.1038/nsmb.1577.
11. Dombois, F. Auditory Seismology on Free Oscillations, Focal Mechanisms, Explosions and Synthetic Seismograms. *Proceedings of the International Conference on Auditory Display, Kyoto* **2002**, 1-4.
12. McMillan, R. Auditory Analysis of Infrared Spectra Using Artificial Neural Networks for Data Pretreatment. *International Conference on Auditory Display* **1992**.
13. Ohno, S.; Ohno, M. The All Pervasive Principle of Repetitious Recurrence Governs not only Coding Sequence Construction but also Human Endeavor in Musical Composition. *Immunogenetics* **1986,** *24*, 71-78, https://doi.org/10.1007/bf00373112.
14. Albers, M.C. The Varèse System, Hybrid auditory Interfaces, and Satellite Ground Control: Using Auditory Icons and Sonification in a Complex, Supervisory Control System. *Proceedings of the International Conference on Auditory Display,* **1994**, *3*, 13
15. Walker, B.N.; Kramer, G. Mappings and Metaphors in Auditory Displays: An Experimental Assessment. *Proceedings of the 1996 International Conference on Auditory Display* **1996**, *2,* https://doi.org/10.1145/1101530.1101534.
16. Giesa, T.; Spivak, D.I.; Buehler, M.J. Reoccurring Patterns in Hierarchical Protein Materials and Music: The Power of Analogies. *Bionanoscience* **2011**, *1*, 153-161, https://doi.org/10.1007/s12668-011-0022-5.
17. Mossinger, J. Science in culture: The music of life. *Nature* **2005**, *435*, 280, https://doi.org/10.1038/435280a.
18. Barrass, S. A perceptual framework for the auditory display of scientific data. *ACM Trans Appl Percept*. **2005**, *2*, 389–402, https://doi.org/10.1145/1101530.1101532.
19. Delatour, T. Molecular Music, The Acoustic Conversion of Molecular Vibrational Spectra. *Computer Music Journal* **2000**, *24*, 48-68.
20. Delatour, T. Molecular Songs. *Molecular Aesthetics* **2013**, *1*, 293–311.
21. Alexjander, S.; Deamer, D. The Infrared Frequency of DNA bases: Science and Art. *IEEE Engineering in Medicine and Biology Magazine*. **1999**, 18, 74-79.
22. Truax, B. Sound, Listening and Place: The aesthetic dilemma. *Organised Sound* **2012**, *17,* 193–201, https://doi.org/10.1017/S1355771811000380.
23. Mollaamin, F.; Monajjemi, M.; Mehrzad, J. Molecular Modeling Investigation of an Anti-cancer Agent Joint to SWCNT Using Theoretical Methods. *Fullerenes nanotubes and carbon nanostructures* **2014**, *22*, 738-751, https://doi.org/10.1080/1536383X.2012.731582.
24. Mollaamin, F.; Monajjemi, M. DFT outlook of solvent effect on function of nano bioorganic drugs. *Physics and Chemistry of Liquids* **2012**, *50*, 596-604, https://doi.org/10.1080/00319104.2011.646444.
25. Mollaamin, F.; Gharibe, S.; Monajjemi, M. Synthesis of various nano and micro ZnSe morphologies by using hydrothermal method. *International Journal of Physical Sciences* **2011**, *6*, 1496-1500.

26. 16. Monajjemi M. Graphene/(h-BN)*n*/X-doped raphene as anode material in lithium ion batteries (X = Li, Be, B AND N). *Macedonian Journal of Chemistry and Chemical Engineering* **2017**, *36*, 101–118, http://dx.doi.org/10.20450/mjcce.2017.1134.
27. Monajjemi, M. Cell membrane causes the lipid bilayers to behave as variable capacitors: A resonance with self-induction of helical proteins. *Biophysical Chemistry* **2015**, *207*, 114-127, https://doi.org/10.1016/j.bpc.2015.10.003.
28. Monajjemi, M. Study of CD5+ Ions and Deuterated Variants (CHxD(5-x)+): An Artefactual Rotation. *Russian Journal of Physical Chemistry A* **2018,** *92*, 2215-2226.
29. Monajjemi, M. Liquid-phase exfoliation (LPE) of graphite towards graphene: An ab initio study. *Journal of Molecular Liquids*, **2017**, *230*, 461–472, https://doi.org/10.1016/j.molliq.2017.01.044.
30. Jalilian, H.; Monajjemi, M. Capacitor simulation including of X-doped graphene (X = Li, Be, B) as two electrodes and (h-BN)m (m = 1–4) as the insulator. *Japanese Journal of Applied Physics* **2015**, *54,* 085101-7.
31. Ardalan, T.; Ardalan, P.; Monajjemi, M. Nano theoretical study of a C 16 cluster as a novel material for vitamin C carrier. *Fullerenes Nanotubes and Carbon Nanostructures* **2014**, *22*, 687-708, https://doi.org/10.1080/1536383X.2012.717561.
32. Mahdavian, L.; Monajjemi, M.; Mangkorntong, N. Sensor response to alcohol and chemical mechanism of carbon nanotube gas sensors *Fullerenes Nanotubes and Carbon Nanostructures* **2009***, 17*, 484-495, https://doi.org/10.1080/15363830903130044.
33. Monajjemi, M.; Najafpour, J. Charge density discrepancy between NBO and QTAIM in single-wall armchair carbon nanotubes. *Fullerenes Nanotubes and Carbon Nano structures* **2014**, *22*, 575-594, https://doi.org/10.1080/1536383X.2012.702161.
34. Monajjemi, M.; Hosseini, M.S. Non bonded interaction of B16 N16 nano ring with copper cations in point of crystal fields. *Journal of Computational and Theoretical Nanoscience* **2013**, *10*, 2473-2477.
35. Monajjemi, M.; Mahdavian, L.; Mollaamin, F. Characterization of nanocrystalline silicon germanium film and nanotube in adsorption gas by Monte Carlo and Langevin dynamic simulation. *Bulletin of the Chemical Society of Ethiopia* **2008**, *22*, 277-286, https://doi.org/10.4314/bcse.v22i2.61299.
36. Lee, V.S.; Nimmanpipug, P.; Mollaamin, F.; Thanasanvorakun, S.; Monajjemi, M. Investigation of single wall carbon nanotubes electrical properties and normal mode analysis: Dielectric effects. *Russian Journal of Physical Chemistry A* **2009**, *83*, 2288-2296, https://doi.org/10.1134/S0036024409130184.
37. Mollaamin, F.; Najafpour, J.; Ghadami, S.; Akrami, M.S.; Monajjemi, M. The electromagnetic feature of B N H (x = 0, 4, 8, 12, 16, and 20) nano rings:Quantum theory of atoms in molecules/NMR approach. *Journal of Computational and Theoretical Nanoscience* **2014**, *11*, 1290-1298.
38. Monajjemi, M.; Mahdavian, L.; Mollaamin, F.; Honarparvar, B. Thermodynamic investigation of enolketo tautomerism for alcohol sensors based on carbon nanotubes as chemical sensors. *Fullerenes Nanotubes and Carbon Nanostructures* **2010**, *18,* 45-55, https://doi.org/10.1080/15363830903291564.
39. Monajjemi, M.; Ghiasi, R.; Seyed, S.M.A. Metal-stabilized rare tautomers: N4 metalated cytosine (M = Li , Na , K , Rb and Cs), theoretical views. *Applied Organometallic Chemistry* **2003**, *17*, 635-640, https://doi.org/10.1002/aoc.469.
40. Ilkhani, A.R.; Monajjemi, M. The pseudo Jahn-Teller effect of puckering in pentatomic unsaturated rings C AE , A=N, P, As, E=H, F, Cl.*Computational and Theoretical Chemistry* **2015**, *1074*, 19-25, http://dx.doi.org/10.1016%2Fj.comptc.2015.10.006.
41. Monajjemi, M. Non-covalent attraction of B N and repulsion of B N in the B N ring: a quantum rotatory due to an external field. *Theoretical Chemistry Accounts* **2015**, *134*, 1-22, https://doi.org/10.1007/s00214-015-1668-9.
42. Monajjemi, M.; Naderi, F.; Mollaamin, F.; Khaleghian, M. Drug design outlook by calculation of second virial coefficient as a nano study. *Journal of the Mexican Chemical Society* **2012**, *56*, 207-211, https://doi.org/10.29356/jmcs.v56i2.323.
43. Monajjemi, M.; Bagheri, S.; Moosavi, M.S. Symmetry breaking of B2N(-,0,+): An aspect of the electric potential and atomic charges. *Molecules* **2015**, *20*, 21636-21657, https://doi.org/10.3390/molecules201219769.
44. Monajjemi, M.; Mohammadian, N.T. S-NICS: An aromaticity criterion for nano molecules. *Journal of Computational and Theoretical Nanoscience* **2015**, *12*, 4895-4914, https://doi.org/10.1166/jctn.2015.4458.
45. Monajjemi, M.; Ketabi, S.; Hashemian, Z.M.; Amiri, A. Simulation of DNA bases in water: Comparison of the Monte Carlo algorithm with molecular mechanics force fields. *Biochemistry (Moscow)* **2006**, *71*, 1-8, https://doi.org/10.1134/s0006297906130013.
46. Monajjemi, M.; Lee, V.S.; Khaleghian, M.; Honarparvar, B.; Mollaamin, F. Theoretical Description of Electromagnetic Nonbonded Interactions of Radical, Cationic, and Anionic NH2BHNBHNH2 Inside of the B18N18 Nanoring. *J. Phys. Chem C* **2010**, *114*, 15315, https://doi.org/10.1021/jp104274z.
47. Monajjemi, M.; Boggs, J.E. A New Generation of BnNn Rings as a Supplement to Boron Nitride Tubes and Cages. *J. Phys. Chem. A* **2013**, *117*, 1670-1684, http://dx.doi.org/10.1021/jp312073q.
48. Monajjemi, M. Non bonded interaction between BnNn (stator) and BN B (rotor) systems: A quantum rotation in IR region. *Chemical Physics* **2013**, *425*, 29-45, https://doi.org/10.1016/j.chemphys.2013.07.014.
49. Monajjemi, M.; Robert, W.J.; Boggs, J.E. NMR contour maps as a new parameter of carboxyl's OH groups in amino acids recognition: A reason of tRNA–amino acid conjugation. *Chemical Physics* **2014**, *433*, 1-11, https://doi.org/10.1016/j.chemphys.2014.01.017.
50. Monajjemi, M. Quantum investigation of non-bonded interaction between the B15N15 ring and BH2NBH2 (radical, cation, and anion) systems: a nano molecularmotor. *Struct Chem* **2012,** *23*, 551–580, http://dx.doi.org/10.1007/s11224-011-9895-8.
51. Monajjemi, M. Metal-doped graphene layers composed with boron nitride–graphene as an insulator: a nano-capacitor. *Journal of Molecular Modeling* **2014**, *20*, 2507, https://doi.org/10.1007/s00894-014-2507-y.
52. Monajjemi, M.; Ketabi, S.; Amiri, A. Monte Carlo simulation study of melittin: protein folding and temperature ependence, *Russian journal of physical chemistry* **2006**, *80,* S 55-S62, https://doi.org/10.1134/S0036024406130103.
53. Monajjemi, M; Heshmata, M; Haeria, H.H. QM/MM model study on properties and structure of some antibiotics in gas phase: Comparison of energy and NMR chemical shift. *Biochemistry-moscow* **2006**, *71,* S113-S122 https://doi.org/10.1134/S0006297906130190.
54. Monajjemi, M.; Afsharnezhad, S.; Jaafari, M.R.; Abdolahi, A.N.; Monajemi, H. NMR shielding and a thermodynamic study of the effect of environmental exposure to petrochemical solvent on DPPC, an important component of lung surfactant. *Russian journal of physical chemistry A* **2007**, *81,* 1956-1963, https://doi.org/10.1134/S0036024407120096.

55. Mollaamin, F.; Noei, M.; Monajjemi, M.; Rasoolzadeh, R. Nano theoretical studies of fMet-tRNA structure in protein synthesis of prokaryotes and its comparison with the structure of fAla-tRNA. *African journal of microbiology research* **2011**, *5,* 2667-2674, https://doi.org/10.5897/AJMR11.310.
56. Monajjemi, M.; Heshmat, M.; Haeri, H. H.; et al. Theoretical study of vitamin properties from combined QM-MM methods: Comparison of chemical shifts and energy. *Russian journal of physical chemistry* **2006**, *80,* 1061-1068, https://doi.org/10.1134/S0036024406070119.
57. Monajjemi, M; Chahkandi, B. Theoretical investigation of hydrogen bonding in Watson-Crick, Hoogestein and their reversed and other models: comparison and analysis for configurations of adenine-thymine base pairs in 9 models. *Journal of molecular structure-theochem* **2005**, *714,* 43-60, https://doi.org/10.1016/j.theochem.2004.09.048.
58. Monajjemi, M.; Honarparvar, B.; Haeri, H.H.; Heshmat, M. An ab initio quantum chemical investigation of solvent-induced effect on N-14-NQR parameters of alanine, glycine, valine, and serine using a polarizable continuum model. *Russian journal of physical chemistry* **2006**, *80*, S40-S44, https://doi.org/10.1134/S0036024406130073.
59. Monajjemi, M.; Seyed Hosseini, M. Non Bonded Interaction of $B_{16}N_{16}$ Nano Ring with Copper Cations in Point of Crystal Fields. *Journal of Computational and Theoretical Nanoscience* **2013**, *10*, 2473-2477.
60. Monajjemi, M.; Farahani, N.; Mollaamin, F. Thermodynamic study of solvent effects on nanostructures: phosphatidylserine and phosphatidylinositol membranes. *Physics and chemistry of liquids* **2012**, *50,* 161-172, https://doi.org/10.1080/00319104.2010.527842.
61. Monajjemi, M.; Ahmadianarog, M. Carbon Nanotube as a Deliver for Sulforaphane in Broccoli Vegetable in Point of Nuclear Magnetic Resonance and Natural Bond Orbital Specifications. *Journal of computational and theoretical nanoscience* **2014**, *11,* 1465-1471, https://doi.org/10.1166/jctn.2014.3519.
62. Monajjemi, M.; Ghiasi, R.; Ketabi, S.; Passdar, H.; Mollaamin, F. A Theoretical Study of Metal-Stabilised Rare Tautomers Stability: N4 Metalated Cytosine (M=Be^{2+}, Mg^{2+}, Ca^{2+}, Sr^{2+} and Ba^{2+}) in Gas Phase and Different Solvents. *Journal of Chemical Research* **2004**, *1*, 11-18, https://doi.org/10.3184/030823404323000648.
63. Monajjemi, M.; Baei, M.T.; Mollaamin, F. Quantum mechanics study of hydrogen chemisorptions on nanocluster vanadium surface. *Russian journal of inorganic chemistry* **2008**, *53,* 1430-1437, https://doi.org/10.1134/S0036023608090143.
64. Mollaamin, F.; Baei, M.T.; Monajjemi, M.; Zhiani, R.; Honarparvar, B. A DFT study of hydrogen chemisorption on V (100) surfaces. *RUSSIAN JOURNAL OF PHYSICAL CHEMISTRY A* **2008**, *82,* 2354-2361, https://doi.org/10.1134/S0036024408130323.
65. Monajjemi, M.; Honarparvar, B.; Nasseri, S.M.; Khaleghian, M. NQR and NMR study of hydrogen bonding interactions in anhydrous and monohydrated guanine cluster model: A computational study. *Journal of structural chemistry* **2009**, *50,* 67-77, https://doi.org/10.1007/s10947-009-0009-z.
66. Monajjemi, M.; Aghaie, H.; Naderi, F. Thermodynamic study of interaction of TSPP, CoTsPc, and FeTsPc with calf thymus DNA. *Biochemistry-Moscow* **2007**, *72,* 652-657, https://doi.org/10.1134/S0006297907060089.
67. Monajjemi, M.; Heshmat, M.; Aghaei, H.; Ahmadi, R.; Zare, K. Solvent effect on N-14 NMR shielding of glycine, serine, leucine, and threonine: Comparison between chemical shifts and energy versus dielectric constant. *Bulletin of the chemical society of ethiopia* **2007**, *21*, 111-116, https://doi.org/10.4314/bcse.v21i1.61387.
68. Monajjemi, M.; Rajaeian, E.; Mollaamin, F.; Naderi, F.; Saki, S. Investigation of NMR shielding tensors in 1,3 dipolar cycloadditions: solvents dielectric effect. *Physics and chemistry of liquids* **2008**, *46*, 299-306, https://doi.org/10.1080/00319100601124369.
69. Mollaamin, F.; Varmaghani, Z.; Monajjemi, M. Dielectric effect on thermodynamic properties in vinblastine by DFT/Onsager modelling. *Physics and chemistry of liquids* **2011,** *49,* 318-336, https://doi.org/10.1080/00319100903456121.
70. Monajjemi, M.; Honaparvar, B.; Hadad, B.K.; Ilkhani, A.R.; Mollaamin, F. Thermo-chemical investigation and NBO analysis of some anxileotic as Nano-drugs. *African journal of pharmacy and pharmacology* **2010**, *4,* 521-529.
71. Monajjemi, M.; Khaleghian, M.; Mollaamin, F. Theoretical study of the intermolecular potential energy and second virial coefficient in the mixtures of CH4 and Kr gases: a comparison with experimental data. *Molecular simulation* **2010**, *11,* 865-870, https://doi.org/10.1080/08927022.2010.489557.
72. Monajjemi, M.; Khosravi, M.; Honarparvar, B.; Mollamin, F. Substituent and Solvent Effects on the Structural Bioactivity and Anticancer Characteristic of Catechin as a Bioactive Constituent of Green Tea. *International journal of quantum chemistry* **2011**, *111,* 2771-2777, https://doi.org/10.1002/qua.22612.
73. Tahan, A.; Monajjemi, M. Solvent Dielectric Effect and Side Chain Mutation on the Structural Stability of Burkholderia cepacia Lipase Active Site: A Quantum Mechanical/ Molecular Mechanics Study. *Biotheoretica* **2011**, *59*, 291-312, https://doi.org/10.1007/s10441-011-9137-x.
74. Monajjemi, M.; Khaleghian, M. EPR Study of Electronic Structure of [CoF6](3-)and B18N18 Nano Ring Field Effects on Octahedral Complex. *Journal of cluster science* **2011**, *22*, 673-692, https://doi.org/10.1007/s10876-011-0414-2.
75. Monajjemi, M; Mollaamin, F. Molecular Modeling Study of Drug-DNA Combined to Single Walled Carbon Nanotube, *Journal of cluster science* **2012**, *23*, 259-272, https://doi.org/10.1007/s10876-011-0426-y.
76. Mollaamin, F; Monajjemi, M. Fractal Dimension on Carbon Nanotube-Polymer Composite Materials Using Percolation Theory. *Journal of computational and theoretical nanoscience* **2012**, *9*, 597-601, https://doi.org/10.1166/jctn.2012.2067.
77. Mahdavian, L.; Monajjemi, M. Alcohol sensors based on SWNT as chemical sensors: Monte Carlo and Langevin dynamics simulation. *Microelectronics journal* **2010**, *41,* 142-149, https://doi.org/10.1016/j.mejo.2010.01.011.
78. Monajjemi, M.; Falahati, M.; Mollaamin, F. Computational investigation on alcohol nanosensors in combination with carbon nanotube: a Monte Carlo and ab initio simulation. *Ionics* 2013, *19*, 155-164, https://doi.org/10.1007/s11581-012-0708-x.
79. Kadkhodaie, A.; Rezaee, R. Have you ever head the sound of well logs or reservoir data. *Journal of Petroleum Science and Engineering* **2017**, *156*, 340–347, https://doi.org/10.1016/j.petrol.2017.06.014.
80. Supper, A. Lobbying for the ear, listening with the whole body: the (anti-)visual culture of sonification, *Sound Studies* **2016**, *2,* 69-80, https://doi.org/10.1080/20551940.2016.1214446.
81. Vickers, P.; Holdrich, R. Direct Segmented Sonification of the data domain. *Arxiv. org* **2017**, *1711*.11368.
82. Rosen, A. An introduction to cognitive aging and dementia: a clinical neuropsychologist's perspective. Proceedings of the 2016 CHI. *Conference Extended Abstracts on Human Factors in Computing Systems San Jose*: **2016**, 948–951, https://doi.org/10.1145/2851581.2856690.

83. Rice, S.L.; Kent, F.P. Clinical pet-mr imaging in breast cancer and lung cancer. *PET Clin* **2016**, *11*, 387–402, https://doi.org/10.1016/j.cpet.2016.05.008.
84. Rungta, A.; Schissler, C.; Rewkowski, N.; Mehra, R.; Manocha, D. Diffraction Kernels for Interactive Sound Propagation in Dynamic Environments. *IEEE Trans. Vis. Comput. Graph*. **2018**, *24*, 1613–1622, https://doi.org/10.1109/TVCG.2018.2794098.
85. Yu, T.; Behm, H.; Bill, R.; Kang, J. Validity of VR Technology on the Smartphone for the Study of Wind Park Soundscapes. *ISPRS Int. J. Geo-Inf.* **2018**, *7*, 152, https://doi.org/10.3390/ijgi7040152.
86. Mysore, A.; Velten, A.; Eliceiri K.W. Sonifcation of Arabidopsis Mitochondria and Cell Membrane. *Figshare* **2016**.
87. Paterson, E.; Sanderson, P.M.; Paterson, N.A.B.; Liu, D.; Loeb, R.G. The effectiveness of pulse oximetry sonification enhanced with tremolo and brightness for distinguishing clinically important oxygen saturation ranges: a laboratory study. *Anaesthesia* **2016**, https://doi.org/10.1111/anae.13424.
88. Connor, M.O.; Deeks, H.M.; Dawn, E.; Metatla, O.; Roudaut, A.; Sutton, M.; Thomas, L.M.; Glowacki, B.R.; Tew, P.; Wonnacott, M.; Bates, P.; Mulholland, A.J.; GLowacki, D.R. Sampling molecular conformations and dynamics in a multi-user virtual reality framework. *ArXiv e-prints* **2018**, *4*, https://doi.org/10.1126/sciadv.aat2731.
89. Rau, B.; Frieb, F.; Krone, M.; Muller, C.; Ertl, T. Enhancing visualization of molecular simulations using sonification. In: *1er workshop international Virtual and Augmented Reality for Molecular Science (VARMS@IEEEVR)*. 2015; pp. 25–30.
90. Commère, L.; Florian, G.; Côté, F.; Rouat, J. Sonification of 3D point clouds for substitution of vision by audition for blind users. 24ème conference international Auditory Display (ICAD 2018), Michigan Technological University, USA, 2018.
91. Larsen P.E. More of an Art than a Science: Using Microbial DNA Sequences to Compose Music. *J Microbiol Biol Educ*. **2016**, *17,* 129–32, https://dx.doi.org/10.1128%2Fjmbe.v17i1.1028.
92. Bywater, R.P.; Middleton, J.N. Melody discrimination and protein fold classification. *Heliyon*. **2016**, *2,* e00175. https://doi.org/10.1016/j.heliyon.2016.e00175.
93. Valery, B.; Scannella, S.; Peysakhovich, V.; Barone, P.; Causse, M. Can an aircraft be piloted via sonification with an acceptable attentional cost? A comparison of blind and sighted pilots. *Applied Ergonomics*, **2017**, *62,* 227-236, https://doi.org/10.1016/j.apergo.2017.03.001.
94. Dyer, J.; Stapleton, P.; Rodger, M. Sonification movement for motor skill learning in a novel bimanual task: Aesthetics & Retention Strategies", School of Psychology & Sonic Arts Research Centre, Queens University Belfast, The 22nd International Conference on Auditory Display. *ICAD*, *Canberra, Australia* **2016,** https://doi.org/10.21785/icad2016.027.
95. Kather, J.K.; Hermann, T.; Bukschat, Y. ;Kramer T.; Schad, L.; Zãűllner, F.G. Polyphonic sonification of electrocardiography signals for diagnosis of cardiac pathologies. *Scientific Reports* **2017**, *7,* 44549, https://doi.org/10.1038/srep44549.
96. Kadkhodaie, A.; Rezaee, R. Have you ever head the sound of well logs or reservoir data. *Journal of Petroleum Science and Engineering* **2017**, *156*, 340–347, https://doi.org/10.1016/j.petrol.2017.06.014.
97. Supper, A. Lobbying for the ear, listening with the whole body: the (anti-)visual culture of sonification, *Sound Studies*, **2016**, *2,* 69-80, https://doi.org/10.1080/20551940.2016.1214446.
98. Vickers, P.; Holdrich, R. Direct Segmented Sonification of the data domain. *Arxiv.org* **2017**, *1711,* 11368.
99. Rosen, A. An introduction to cognitive aging and dementia: a clinical neuropsychologist's perspective. *Proceedings of the 2016 CHI Conference Extended Abstracts on Human Factors in Computing Systems. San Jose, ACM* **2016**, 948–951, https://doi.org/10.1145/2851581.2856690.
100. Rice, S.L.; Kent, F.P. Clinical PET-MR imaging in breast cancer and lung cancer. *PET Clin* **2016**, *11,* 387–402, https://dx.doi.org/10.1016%2Fj.cpet.2016.05.008.
101. Miller-Thomas, M.M.; Sipe, A.L.; Benzinger, T.L.S.;McConathy, J.; Connolly, S.; Schwetye, K.E. Multimodality review of amyloid-related diseases of the central nervous system. *Radiographics* **2016**, *36*, 147–63, https://doi.org/10.1148/rg.2016150172.

6. ACKNOWLEDGEMENTS

Thanks of the Central Tehran Branch, Islamic Azad University for supporting computational software and all necessary equipment.