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With Respect to Quantum Perspectıve Model, Can Euler Numbers be Related to Bıochemıstry?

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Abstract- This article researches whether there is a link between Euler's numbers and genetic codes. At first, the sum of the numbers of the first fifteen "15" digits of Euler's numbers after the comma are converted to bases in genetic codes. Secondly, after the comma, Euler's numbers with eighteen fifteen groups are converted to nucleotide bases. So, the results obtained by this way are expressed as nucleotide bases (A, T, C, G, U). (A)Adenine, (T)Thymine, (C)Cytosine, (G),Guanine, (U)Uracil. Thirdly, the search result is similar to ZEBRAFISH-DANIO RERIO, and even bat coronavirus after the NCBI (National Biotechnology Information Center) searched this sequence "AUGUUGAUAUTAAUCATC". Fourtly, the genetic codes of Zebrafish have been proven to be very similar to human genetic codes. Fifthly, multiple spawning of these fish species also means that Euler's numbers are increasing. In sum, the relationship between the Euler's numbers in mathematical science and the atomic weights of atomic elements in genetic codes also shed lights on Biochemistry.

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Keywords: zebrafish-danio rerio, biochemistry, euler's numbers, bat coronavirus, quantum perspective model, and NCBI (national biotechnology ınformation center).

I. Euler Numbers

Euler's numbers are e:

2.718281828459045235360287471352662497757247093699959574966967627724076630353547594571382178525166427427466391932003059921817413596629043572900334295260595630738132328627943490763233829880753195251019011573834187930702154089149934884167509244761460668082264800168477411853 [1]

II. Methods and Discussion

The chemical structures of bases include Carbon(C), Nitrogen (N), Oxygen (O), and Hydrogen (H). Calculation of bases with chemical atoms (See also Table-1). (Ölmez T, 2020).

Ref

1. Farrell R E. RNA Methodologies A Laboratory Guide For Isolation and Characterization. 4th Edition, Amsterdam Elsevier Acad. Press, Pennsylvania State University York, 2010; 704-710.

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Table 1: Representation of nucleotide bases (A, T, C, G and U) in chemical atoms

ATOMS / NUCLEOTIDE BASES	C=6	H=1	O=8	N=7	SUM
ADENINE: C5H5N5	5	5	-	5	70
THYMINE: C5H6N2O2	5	6	2	2	66
CYTOSINE: C4H5N3O1	4	5	1	3	64
GUANINE: C5H5N5O1	5	5	1	5	78
URACIL : C4H4N2O2	4	4	2	2	58

The atomic numbers of them: Carbon(C): 6, Nitrogen (N): 7, Oxygen (O): 8, Hydrogen (H): 1 (Wieser E M et al, 2013).

The chemical structures of bases (A, T, C, G, and U) are shown at below. (Ölmez T, 2020)

(A) Adenine: C5H5N5:70;

(T) Thymine: C5H6N2O2:66,

(C) Cytosine: C4H5N3O1:64,

(G) Guanine: C5H5N5O1:78, and

(U) Uracil: C4H4N2O2: 58

(Lodish H et al, 2018).

III. Calculation of Euler Numbers and Genetic Codes

Euler's numbers are e:

2.718281828459045235360287471352662497757247093699959574966967627724076630353547594571382178525166427427466391932003059921817413596629043572900334295260595630738132328627943490763233829880753195251019011573834187930702154089149934884167509244761460668082264800168477411853 [1]

Euler's numbers fifteen groups can be shown as [AUGUUGAUAUTAAUCATC]

The first fifteen groups of Euler's numbers after the comma:

7+1+8+2+8+1+8+2+8+4+5+9+0+4+5+9+0+4+5=72. Just like as in Adenine (A): 70.

The second fifteen groups of Euler's numbers after the comma:
2+3+5+3+6+0+2+8+7+4+7+1+3+5+2=58. Just like as in Uracil (U): 58.

The third fifteen groups of Euler's numbers after the comma:
6+6+2+4+9+7+7+5+7+2+4+7+0+9+3=78. Just like as in Guanine (G): 78

The fourth fifteen groups of Euler's numbers after the comma:
6+9+9+9+5+9+5+7+4+9+6+6+9+6+7=106*. Just like as in Uracil (U): 58*

The fifth fifteen groups of Euler's numbers after the comma:
6+2+7+7+2+4+0+7+6+6+3+0+3+5+3=61. Just like as in Uracil (U): 58.

Ref

1. Farrell R. E. RNA Methodologies A Laboratory Guide For Isolation and Characterization. 4th Edition, Amsterdam Elsevier Acad. Press, Pennsylvania State University York, 2010; 704-710.

The sixth fifteen groups of Euler's numbers after the comma:
5+4+7+5+9+4+5+7+1+3+8+2+1+7+8=76. Just like as in Guanine (G): 78.

The seventh fifteen groups of Euler's numbers after the comma:
5+2+5+1+6+6+4+2+7+4+2+7+4+6+6=67. Just like as in Adenine (A): 70

The eighth fifteen groups of Euler's numbers after the comma:
3+9+1+9+3+2+0+0+3+0+5+9+9+2+1=56. Just like as in Uracil (U): 58

The ninth fifteen groups of Euler's numbers after the comma:
8+1+7+4+1+3+5+9+6+6+2+9+0+4+3=68. Just like as in Adenine (A): 70

The tenth fifteen groups of Euler's numbers after the comma:
5+7+2+9+0+0+3+3+4+2+9+5+2+6+0=57. Just like as in Uracil (U): 58.

The eleventh fifteen groups of Euler's numbers after the comma:
5+9+5+6+3+0+7+3+8+1+3+2+3+2+8=65. Just like as in Thymine (T): 66

The twelfth fifteen groups of Euler's numbers after the comma:
6+2+7+9+4+3+4+9+0+7+6+3+2+3+3=68. Just like as in Adenine (A): 70

The thirteenth fifteen groups of Euler's numbers after the comma:
8+2+9+8+8+0+7+5+3+1+9+5+2+5+1=73. Just like as in Adenine (A): 70

The fourteenth fifteen groups of Euler's numbers after the comma:
0+1+9+0+1+1+5+7+3+8+3+4+1+8+7=58. Just like as in Adenine (U): 58

The fifteenth fifteen groups of Euler's numbers after the comma:
9+3+0+7+0+2+1+5+4+0+8+9+1+4+9=62. Just like as in Uracil (C): 64

The sixteenth fifteen groups of Euler's numbers after the comma:
9+3+4+8+8+4+1+6+7+5+0+9+2+4+4=74. Just like as in Adenine (A): 70

The seventeenth fifteen groups of Euler's numbers after the comma:
7+6+1+4+6+0+6+6+8+0+8+2+2+6+4=66. Just like as in Thymine (T): 66

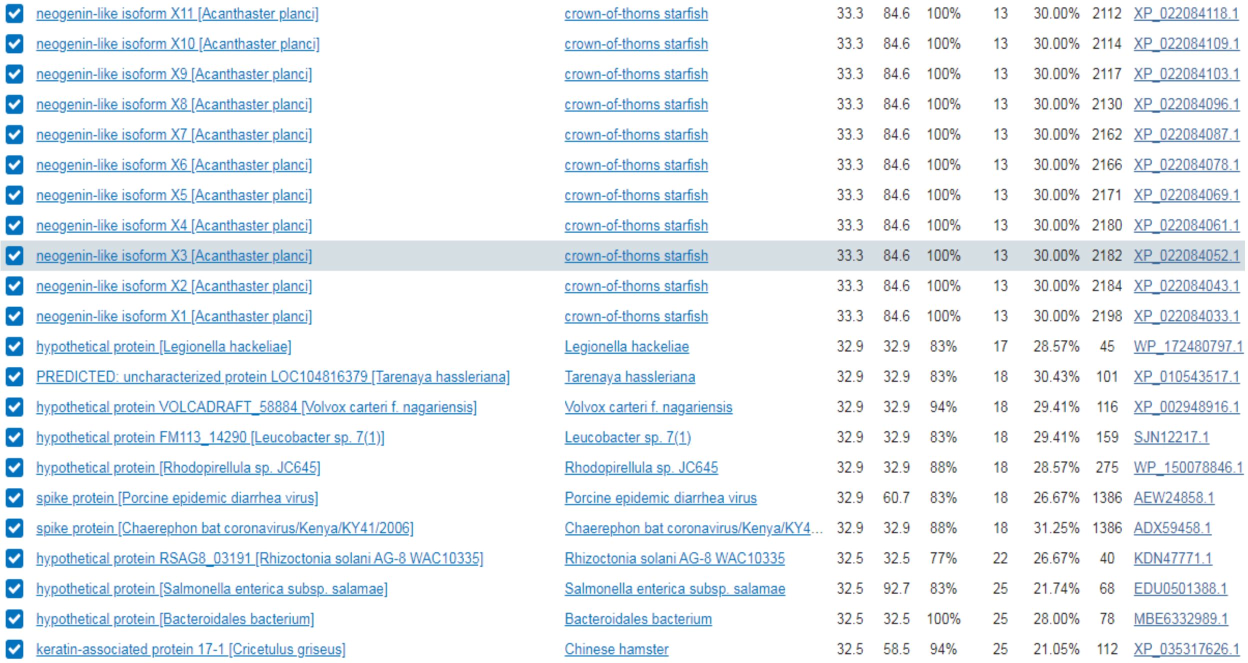
The eighteenth fifteen groups of Euler's numbers after the comma:
8+0+0+1+6+8+4+7+7+4+1+1+8+5+3=63. Just like as in Cytosine(C): 64

This sequence is" [AUGUUGAUAUTAAUCATC]. Let me try to explain this sequence with the "Quantum Perspective Model."For example, The first fifteen groups of Euler's numbers after comma equal to Adenine (A):68 with the lack of two"2" Hydrogen bonds(H:1).(Remember, See Table-1; (A)Adenine:70) This result could be the meaning of Euler's numbers sequence in fifteen groups. [AUGUUGAUAUTAAUCATC]. The fourth fifteen groups of Euler's numbers after the comma is regarded as Uracil (U). Because Phosphate group "PO4"(P:15*1+O:8*4=47) and Uracil (U): 58 and one

Hydrogen (H). Totally,47+58+1:106*[5]. The fifth, sixth and seventh fifteen groups of Euler's numbers after the comma is UGA [Uracil, Guanine and Adenine] which also means STOP codon [13]. So, the deviations in the calculation of Euler's numbers can be derived from the Adenine (A) - Thymine (T) Hydrogen bonds because of Adenine (A) pairs with Thymine (T) by *two* hydrogen bonds. Cytosine(C) - Guanine (G) pairs with by *three* hydrogen bonds [3]. The reason for the lack of hydrogen bonds: Hydrogen bonding is a very versatile attraction. (Ölmez T, 2020) Hydrogen bonds are relatively *weak and easily broken* by increasing hardness (Farrell R E, 2010).

a) The National Center for Biotechnology Information (NCBI) results for Euler's numbers

After searching Euler's numbers result [AUGUUGAUAUTAAUCATC] in NCBI databases, some conceptual relationships can be found with bony fish. Types of bony fish are based on Zebra fish(DANIO RERIO) (See FIGURE -4), European star fish, blunt-snouted clingfish, pinecone soldierfish, orbiculate cardinal fish and crown of thorns star fish (See FIGURE -1). Types of other living creatures are human chromoseme18, domestic cat, European eel, domestic cat, American alligator, common sunflower, wine grape, golden and black snub-nosed monkey, green monkey, Rhesus monkey, house fly, giant panda, fall armyworm, Porcine epidemic diarrhea virusan, and chinese hamster[4] (See FIGURE -2). The most interesting result of this research result is bat coronavirus(spike protein –chaerephon bat coronavirus ADX59458.1) [11] (See FIGURE -3).

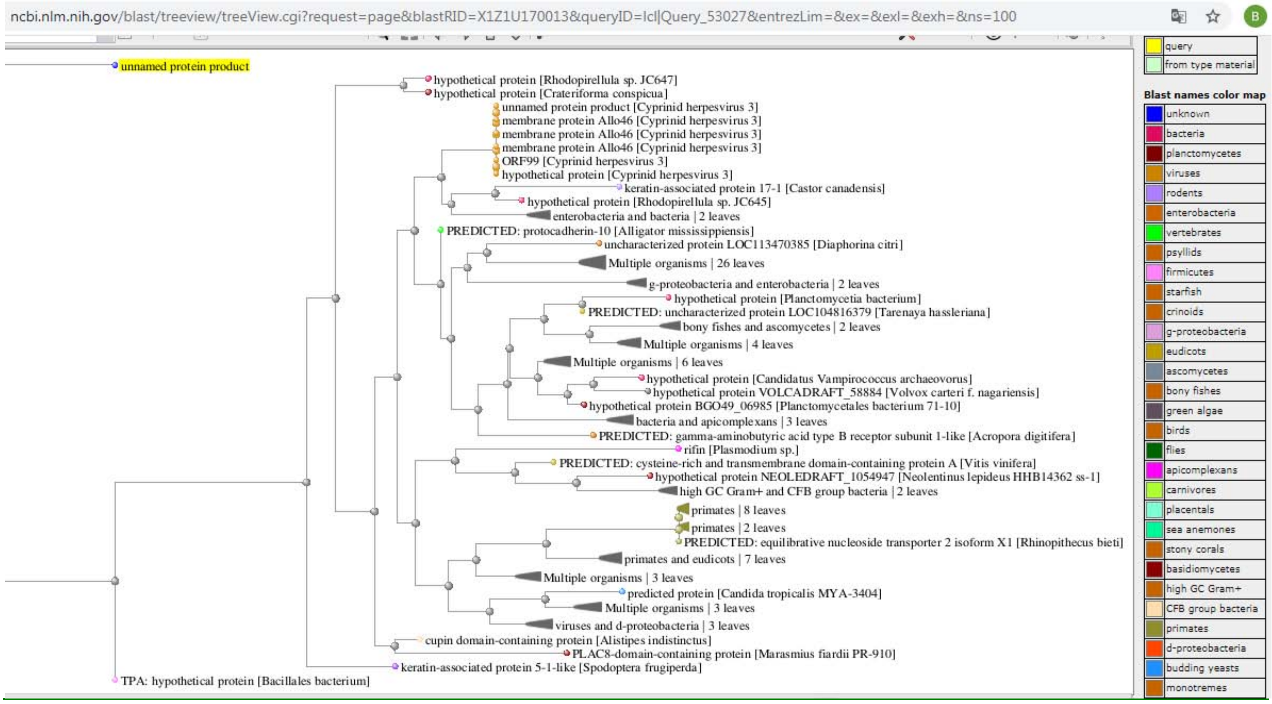


☑	neogenin-like isoform X11 [Acanthaster planci]	crown-of-thorns starfish	33.3	84.6	100%	13	30.00%	2112	XP_022084118.1
☑	neogenin-like isoform X10 [Acanthaster planci]	crown-of-thorns starfish	33.3	84.6	100%	13	30.00%	2114	XP_022084109.1
☑	neogenin-like isoform X9 [Acanthaster planci]	crown-of-thorns starfish	33.3	84.6	100%	13	30.00%	2117	XP_022084103.1
☑	neogenin-like isoform X8 [Acanthaster planci]	crown-of-thorns starfish	33.3	84.6	100%	13	30.00%	2130	XP_022084096.1
☑	neogenin-like isoform X7 [Acanthaster planci]	crown-of-thorns starfish	33.3	84.6	100%	13	30.00%	2162	XP_022084087.1
☑	neogenin-like isoform X6 [Acanthaster planci]	crown-of-thorns starfish	33.3	84.6	100%	13	30.00%	2166	XP_022084078.1
☑	neogenin-like isoform X5 [Acanthaster planci]	crown-of-thorns starfish	33.3	84.6	100%	13	30.00%	2171	XP_022084069.1
☑	neogenin-like isoform X4 [Acanthaster planci]	crown-of-thorns starfish	33.3	84.6	100%	13	30.00%	2180	XP_022084061.1
☑	neogenin-like isoform X3 [Acanthaster planci]	crown-of-thorns starfish	33.3	84.6	100%	13	30.00%	2182	XP_022084052.1
☑	neogenin-like isoform X2 [Acanthaster planci]	crown-of-thorns starfish	33.3	84.6	100%	13	30.00%	2184	XP_022084043.1
☑	neogenin-like isoform X1 [Acanthaster planci]	crown-of-thorns starfish	33.3	84.6	100%	13	30.00%	2198	XP_022084033.1
☑	hypothetical protein [Legionella hackeliae]	Legionella hackeliae	32.9	32.9	83%	17	28.57%	45	WP_172480797.1
☑	PREDICTED: uncharacterized protein LOC104816379 [Tarenaya hassleriana]	Tarenaya hassleriana	32.9	32.9	83%	18	30.43%	101	XP_010543517.1
☑	hypothetical protein VOLCADRAFT_58884 [Volvox carteri f. nagariensis]	Volvox carteri f. nagariensis	32.9	32.9	94%	18	29.41%	116	XP_002948916.1
☑	hypothetical protein FM113_14290 [Leucobacter sp. 7(1)]	Leucobacter sp. 7(1)	32.9	32.9	83%	18	29.41%	159	SJN12217.1
☑	hypothetical protein [Rhodopirellula sp. JC645]	Rhodopirellula sp. JC645	32.9	32.9	88%	18	28.57%	275	WP_150078846.1
☑	spike protein [Porcine epidemic diarrhea virus]	Porcine epidemic diarrhea virus	32.9	60.7	83%	18	26.67%	1386	AEW24858.1
☑	spike protein [Chaerephon bat coronavirus/Kenya/KY41/2006]	Chaerephon bat coronavirus/Kenya/KY4...	32.9	32.9	88%	18	31.25%	1386	ADX59458.1
☑	hypothetical protein RSAG8_03191 [Rhizoctonia solani AG-8 WAC10335]	Rhizoctonia solani AG-8 WAC10335	32.5	32.5	77%	22	26.67%	40	KDN47771.1
☑	hypothetical protein [Salmonella enterica subsp. salamae]	Salmonella enterica subsp. salamae	32.5	92.7	83%	25	21.74%	68	EDU0501388.1
☑	hypothetical protein [Bacteroidales bacterium]	Bacteroidales bacterium	32.5	32.5	100%	25	28.00%	78	MBE6332989.1
☑	keratin-associated protein 17-1 [Cricetulus griseus]	Chinese hamster	32.5	58.5	94%	25	21.05%	112	XP_035317626.1

Figure 1: The NCBI (National Biotechnology Information Center) Result for Nucleotide Sequence "AUGUUGAUAUTAAUCATC" [4]

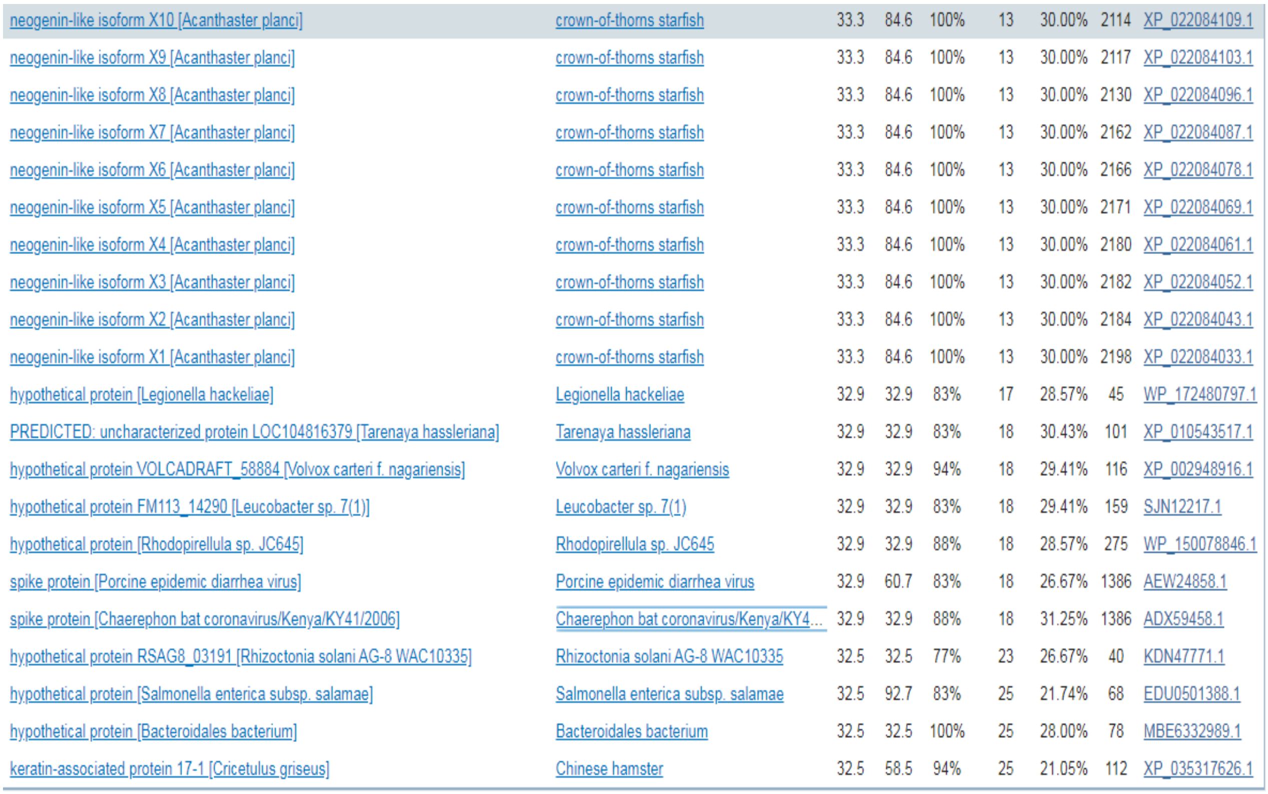
Ref

13. CM Yang - arXiv preprint q-bio/0309014, 2003 - arxiv.org December 26, 2020.



ncbi.nlm.nih.gov/blast/treeview/treeView.cgi?request=page&blastRID=X1Z1U170013&queryID=lcl|Query_53027&entrezLim=&ex=&exl=&exh=&ns=100

Figure 2: The NCBI (National Biotechnology Information Center) Result Blast Tree View Widget for "AUGUUGAUAUTAAUCATC" Nucleotide Sequence [4]



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neogenin-like isoform X5 [Acanthaster planci]	crown-of-thorns starfish	33.3	84.6	100%	13	30.00%	2171	XP_022084069.1
neogenin-like isoform X4 [Acanthaster planci]	crown-of-thorns starfish	33.3	84.6	100%	13	30.00%	2180	XP_022084061.1
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keratin-associated protein 17-1 [Cricetulus griseus]	Chinese hamster	32.5	58.5	94%	25	21.05%	112	XP_035317626.1

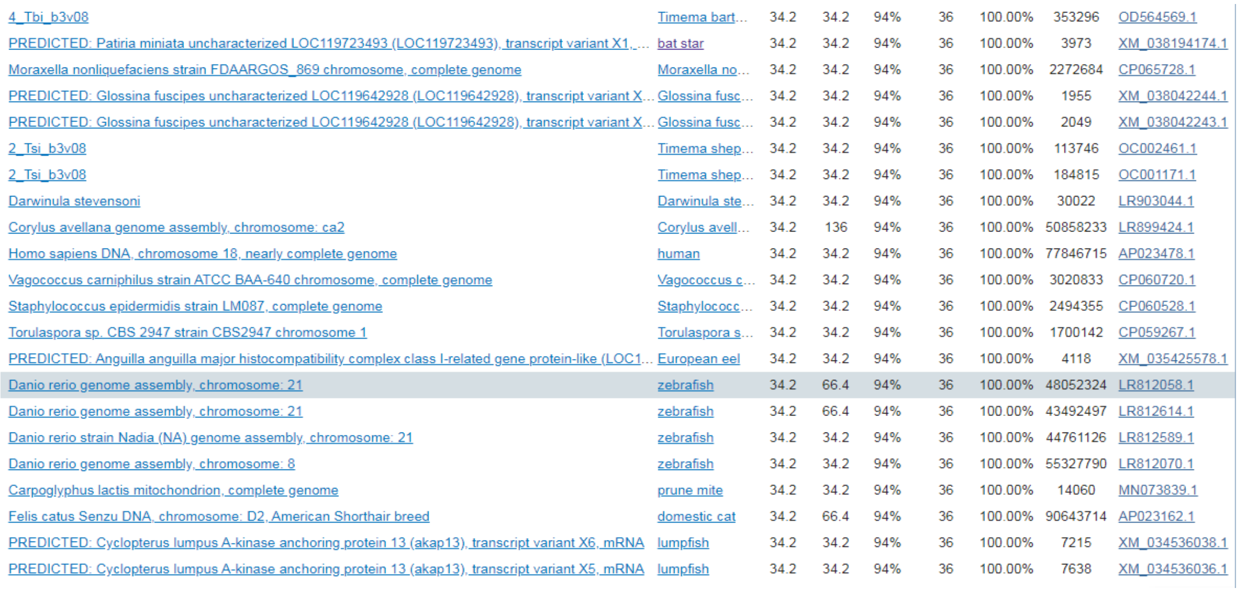
Figure 3: The NCBI (National Biotechnology Information Center) Result for bat coronavirus [4]

IV. Results

The relationships between the numerical value of the numbers of light velocities against genetic codes were researched based on the quantum perspective model (Köklü K, 2019b). Further, after the manual division of Twenty-Two (22) to seven (7) numbers, each of the *fourteen (14) number sequences* obtained after the comma was followed by approximately continuously same nucleotide base codes (Köklü K, 2019a). If you take Pi numbers as fourteen sequences a hundred times, The output of the genetic code is [ATU]. this result is similar to ZEBRAFISH- DANIO RERIO in NCBI Blast. (See FIGURE -4). [4] (NCBI: The National Center for Biotechnology).This fish is a perfect favorite example of many experiments related to biology and gene sequences. [2] The square of the speed of light is written just like those gene sequences: [UUATACCTC] or [UUAUACCTC].After searching three times this sequence (27), the output of this nucleotide blast is similar to Zebrafish-Danio Rerio. (Köklü K, 2019b). In other words, the output of this nucleotide blast is common to Zebra fish in groups of fourteen pi numbers and Euler numbers in groups of fifteen. In sum, the common feature of the square of the speed of light and pi numbers and Euler numbers is Zebra fish. Insulin receptor (IR) signaling is thought to be important in growth and development. The role of insulin receptor signaling in Zebrafish embryogenesis has vital roles in vertebrate embryogenesis and growth [9].Also, new genetic models have been produced to study resistance to the thyroid hormone receptor in Zebrafish [10].Besides, even both the CAAT Box and TATA Box NCBI results in consist of bony fishes(Denticle Herring).In other words, CAAT Box and TATA Box are also related to the golden ratio. Remember, the NCBI result of Euler's numbers also consist of bony fishes (Zebrafish) ,too. (Ölmez T, 2020). Denticle Herring is the most primitive living clupeiform. [6].Interestingly, it also consists of "phosphoserine phosphatase" protein -coding [7].Let alone, the length of it's *15(fifteen)*cm.[8]Remember, this research is taken Euler's numbers as *fifteen* groups, too. Monkeys and humans have a different number of chromosomes, but they probably have the same number of genes. [12] This similarity can be regarded as a Quantum Perspective Model. In summary, this similarity may be the beginning of the mutual relations of the sciences based on the Quantum Perspective Model at minor level systems. Namely, atoms with the smallest base structure can be taken as a small unit of analysis from the same point of view as mathematical numbers. As a result, with this quantum perspective model, the relationships between chemical formulas and numbers have introduced different *paradigms* to obtain new clues.

Ref

4. Lodish H, Berk A, Zipursky S L, Matsudaira P, Baltimore D and Darnell J. Molecular Cell Biology, 6th edition, Translation: Geçkil H, Özmen M, Yeşilada Ö, Palme Publishing, New York, 2018, 294-302.



4_Tbi_b3v08	Timema bart…	34.2	34.2	94%	36	100.00%	353296	OD564569.1
PREDICTED: Patiria miniata uncharacterized LOC119723493 (LOC119723493), transcript variant X1,…	bat star	34.2	34.2	94%	36	100.00%	3973	XM_038194174.1
Moraxella nonliquefaciens strain FDAARGOS_869 chromosome, complete genome	Moraxella no…	34.2	34.2	94%	36	100.00%	2272684	CP065728.1
PREDICTED: Glossina fuscipes uncharacterized LOC119642928 (LOC119642928), transcript variant X…	Glossina fusc…	34.2	34.2	94%	36	100.00%	1955	XM_038042244.1
PREDICTED: Glossina fuscipes uncharacterized LOC119642928 (LOC119642928), transcript variant X…	Glossina fusc…	34.2	34.2	94%	36	100.00%	2049	XM_038042243.1
2_Tsi_b3v08	Timema shep…	34.2	34.2	94%	36	100.00%	113746	OC002461.1
2_Tsi_b3v08	Timema shep…	34.2	34.2	94%	36	100.00%	184815	OC001171.1
Darwinula stevensoni	Darwinula ste…	34.2	34.2	94%	36	100.00%	30022	LR903044.1
Corylus avellana genome assembly, chromosome: ca2	Corylus avell…	34.2	136	94%	36	100.00%	50858233	LR899424.1
Homo sapiens DNA, chromosome 18, nearly complete genome	human	34.2	34.2	94%	36	100.00%	77846715	AP023478.1
Vagococcus carniphilus strain ATCC BAA-640 chromosome, complete genome	Vagococcus c…	34.2	34.2	94%	36	100.00%	3020833	CP060720.1
Staphylococcus epidermidis strain LM087, complete genome	Staphylococc…	34.2	34.2	94%	36	100.00%	2494355	CP060528.1
Torulaspora sp. CBS 2947 strain CBS2947 chromosome 1	Torulaspora s…	34.2	34.2	94%	36	100.00%	1700142	CP059267.1
PREDICTED: Anguilla anguilla major histocompatibility complex class I-related gene protein-like (LOC1…	European eel	34.2	34.2	94%	36	100.00%	4118	XM_035425578.1
Danio rerio genome assembly, chromosome: 21	zebrafish	34.2	66.4	94%	36	100.00%	48052324	LR812058.1
Danio rerio genome assembly, chromosome: 21	zebrafish	34.2	66.4	94%	36	100.00%	43492497	LR812614.1
Danio rerio strain Nadia (NA) genome assembly, chromosome: 21	zebrafish	34.2	34.2	94%	36	100.00%	44761126	LR812589.1
Danio rerio genome assembly, chromosome: 8	zebrafish	34.2	34.2	94%	36	100.00%	55327790	LR812070.1
Carpoglyphus lactis mitochondrion, complete genome	prune mite	34.2	34.2	94%	36	100.00%	14060	MN073839.1
Felis catus Senzu DNA, chromosome: D2, American Shorthair breed	domestic cat	34.2	66.4	94%	36	100.00%	90643714	AP023162.1
PREDICTED: Cyclopterus lumpus A-kinase anchoring protein 13 (akap13), transcript variant X6, mRNA	lumpfish	34.2	34.2	94%	36	100.00%	7215	XM_034536038.1
PREDICTED: Cyclopterus lumpus A-kinase anchoring protein 13 (akap13), transcript variant X5, mRNA	lumpfish	34.2	34.2	94%	36	100.00%	7638	XM_034536036.1

Figure 4: The NCBI (National Biotechnology Information Center) Result for Zebra fish [4]

V. CONCLUSION

First, the results of this research can be summarized by obtaining Euler's numbers through the chemical structure of chemical elements. At a minor level, Euler's numbers can be thought of as an indicator of chemical formulas. One of the results of both Biochemistry and Mathematics common feature is NCBI blast results. Because these are bony fishes especially DANIO RERIO. Even not only the NCBI result of pi and square number of light is DANIO RERIO, but also NCBI result of Euler's numbers is DANIO RERIO. Since fish are one of the vertebrates that make the most eggs, this is similar to Euler's numbers in terms of multifunctional. This may be an indicator of the Euler's numbers for living things, especially fish.

Finally, at a macro level, the calculation results of Euler's numbers with chemical structures (especially A, T, C, G, and U) are related to both Biochemistry and Mathematics. Briefly, Euler's numbers are not only attributed to numbers in Mathematics but also attributed to chemical formulas of Biochemistry (Carbon(C), Nitrogen (N), Oxygen (O), and Hydrogen (H)). In summary, this similarity may be the beginning of the mutual relations of the sciences on based on Quantum Perspective Model at minor level systems. Namely, atoms with the smallest base structure can be taken as a small *unit of analysis* from the same point of view as mathematical numbers.

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