Fractal and Topological Symmetry in the Standard Genetic Code

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Abstract

This study reveals a previously undescribed multi-level structure of the standard genetic code. Based on nucleon masses of amino acids (calculated with the most abundant isotopes), we demonstrate that the code exhibits a clear fractal organization (hierarchical division 64 → 32 → 16 → 8 codons) and a consistent topological architecture, aligned with Rumer's transformation and its extension into the Klein four-group.

At each hierarchical level, we identify harmonic integer invariants, including divisibility by 37, exact equalities within proton and neutron partitions, and highly structured integer values such as 333, 666, 1000, and 2000. These patterns appear both in internal partitions (by the third codon position) and in external topology (quartets and codogram orbits).

A distinction is observed between Octet I, which shows perfect internal balance within quartets, and Octet II, where asymmetries can be neutralized by applying activation keys to stop and start codons. These keys are not arbitrary but self-referential, derived from the intrinsic parameters of the code itself, thus reinforcing their non-random character.

Moreover, it is shown for the first time that all 24 homogeneous codogram representations of the genetic code are divided into six disjoint orbits, each containing four elements, and closed under the transformation group {E, R, R_1, R_2}.

Taken together, these results suggest that the genetic code is a unified system whose fractal, topological, and arithmetic harmony strongly argues against its accidental origin.

Introduction

The origin and internal organization of the standard genetic code remain one of the central problems in molecular biology. Since the pioneering works of Yu. Rumer (1968), who first divided the code into two groups of XY-boxes (Octet I with full 4-fold degeneracy and Octet II with mixed degeneracy) [4], and F. Crick (1968), who proposed the "frozen accident" hypothesis [5], numerous attempts have been made to uncover hidden structures and invariants within the code.

Later studies introduced additional perspectives. Shcherbak and Makukov (2013, 2018) identified arithmetic regularities and symbolic patterns, proposing that the genetic code may carry information of non-biological origin [1,2]. Panov and Filatov (2024) analyzed codogram representations of the code and showed that Rumer's symmetry transformation belongs to a wider set of operations forming the Klein four-group, which acts on the structure of codograms [3].

Despite these insights, the overall picture of how different types of symmetries (degeneracy, arithmetic invariants, and topological structures) are integrated has remained unclear. Previous works identified isolated regularities, but did not demonstrate a unified multi-level organization of the code.

In this paper, I present new results showing that the genetic code possesses a fractal structure, expressed through hierarchical partitions (64 → 32 → 16 → 8 codons), and a topological architecture, manifested in the arrangement of quartets and codogram orbits. These two aspects — arithmetic and topological — are not independent, but deeply interrelated. At each level of the fractal division, harmonic integer invariants are observed, including divisibility by 37, exact equality of proton and neutron sums, and characteristic structured numbers such as 333, 666, 1000, and 2000.

Moreover, I extend the results of Panov and Filatov (2024) by demonstrating that all 24 homogeneous codogram representations of the genetic code are partitioned into six disjoint orbits, each consisting of four codograms closed under the transformation group {E, R, R_1, R_2}. This orbit structure proves that the discovered numerical symmetries are not an artifact of a specific representation but are an invariant property of the code's architecture itself.

Together, these findings suggest that the genetic code should be understood not as a random "frozen accident," but as a mathematically organized system with fractal, topological, and arithmetic harmony.

Materials and Methods

Amino Acid Nucleon Masses

For the calculations, the **nucleon composition** of amino acids was used, based on the most abundant isotopes (^{12}C, ^{1}H, ^{14}N, ^{16}O, ^{32}S). For each amino acid we determined:

1. **Full nucleon mass** (sum of all protons and neutrons),

2. **Side-chain mass** (obtained by subtracting a standard backbone of 74 nucleons, subtracting a standard backbone mass of 74 nucleons, from the total amino acid mass),

3. **Proton and neutron counts** separately.

Special case: Proline (Pro)

Due to its cyclic structure, proline requires adjusted partitioning between backbone and side chain. In this work we fix its values as:

- Full mass = 115,
- Side-chain mass = 41,
- Protons = 62,
- Neutrons = 53.

Table 1. Nucleon masses of amino acids

Amino Acid	Code	Formula	M_full (A)	P	N	M_side
Glycine	Gly	$C_2H_5NO_2$	75	40	35	1
Alanine	Ala	$C_3H_7NO_2$	89	48	41	15
Valine	Val	$C_5H_{11}NO_2$	117	64	53	43
Leucine	Leu	$C_6H_{13}NO_2$	131	72	59	57
Isoleucine	Ile	$C_6H_{13}NO_2$	131	72	59	57
Proline	Pro	$C_5H_9NO_2$	115	62	53	41
Serine	Ser	$C_3H_7NO_3$	105	56	49	31
Threonine	Thr	$C_4H_9NO_3$	119	64	55	45
Cysteine	Cys	$C_3H_7NO_2S$	121	64	57	47
Methionine	Met	$C_5H_{11}NO_2S$	149	80	69	75
Phenylalanine	Phe	$C_9H_{11}NO_2$	165	88	77	91
Tyrosine	Tyr	$C_9H_{11}NO_3$	181	96	85	107
Tryptophan	Trp	$C_{11}H_{12}N_2O_2$	204	108	96	130
Asparagine	Asn	$C_4H_8N_2O_3$	132	70	62	58
Glutamine	Gln	$C_5H_{10}N_2O_3$	146	78	68	72
Aspartate	Asp	$C_4H_7NO_4$	133	70	63	59
Glutamate	Glu	$C_5H_9NO_4$	147	78	69	73

Lysine	Lys	$C_6H_{14}N_2O_2$	146	80	66	72
Arginine	Arg	$C_6H_{14}N_4O_2$	174	94	80	100
Histidine	His	$C_6H_9N_3O_2$	155	82	73	81

Partitioning Principles

The genetic code (64 codons) was analyzed under several complementary partitions:

1. **Rumer's Octets**: Octet I (full 4-fold degeneracy) vs Octet II (partial).
2. **Third-position splits**: (i) C/A vs G/U (Rumer's pairs), (ii) pyrimidines vs purines, (iii) strong vs weak bases.
    - *Analysis showed that all three schemes are arithmetically equivalent, producing identical numerical symmetries. Therefore, for clarity, this paper primarily uses the Rumer's pair partition (C/A vs G/U).*
3. **Quartets**: groups of four XY-boxes (1A, 1B, 2A, 2B).
4. **Codogram orbits**: all 24 homogeneous codogram representations grouped into six disjoint orbits under the Klein four-group transformations {E, R, R_1, R_2}.

Symmetry Definition

Symmetry was defined in three ways:

- **Exact equality** between partitions,
- **Divisibility by 37**,
- **Harmonic integer invariants** (structured integers such as 333, 666, 1000, 2000).

Results

3.1. Symmetries with Activation Key Set 1

(STOP = 74; M_side = 0; P = 0; N = 0)

Using the basic activation key for stop codons, the system exhibits a rich fractal structure of symmetries. Below we present the full list of invariants and compensations.

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1. Entire Genetic Code (64 codons)

- Full mass: **8140 / 37 = 220**
- Side-chain mass: **3404 / 37 = 92**
- Protons: **4260**
- Neutrons: **3658**

Comment: The root of the fractal hierarchy. Divisibility by 37 is observed at the global level.

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2. 32 Codons Ending with A or C

- Full mass: **3996 / 37 = 108**
- Side-chain mass: **1628 / 37 = 44**
- Protons: **2072 / 37 = 56**
- Neutrons: **1776 / 37 = 48**

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3. 32 Codons Ending with T or G

- Full mass: **4144 / 37 = 112**
- Side-chain mass: **1776 / 37 = 48**
- Protons: **2188**
- Neutrons: **1882**

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4. 32 Codons Ending with T or A

- Full mass: **3996 / 37 = 108**
- Side-chain mass: **1628 / 37 = 44**

- Protons: **2072 / 37 = 56**
- Neutrons: **1776 / 37 = 48**

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5. 32 Codons Ending with C or G

- Full mass: **4144 / 37 = 112**
- Side-chain mass: **1776 / 37 = 48**
- Protons: **2188**
- Neutrons: **1882**

Comment: Groups (A,C) and (T,A) are identical; groups (T,G) and (C,G) are identical.

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6. Octet I (32 codons)

- Full mass: **3700 / 37 = 100**
- Side-chain mass: **1332 / 37 = 36**
- Protons: **2000**
- Neutrons: **1700**

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7. Octet II (32 codons)

- Full mass: **4440 / 37 = 120**
- Side-chain mass: **2072 / 37 = 56**
- Protons: **2260**
- Neutrons: **1958**

8–11. Octet I: 16-Codon Groups (GT, CA, TA, CG)

Each group yields identical results:

- Full mass: **1850 / 37 = 50**
- Side-chain mass: **666 / 37 = 18**
- Protons: **1000**
- Neutrons: **850**

Comment: Four distinct subgroups produce perfectly equal values.

12–15. Octet I: 8-Codon Groups (C, G, T, A endings)

Each subgroup:

- Full mass: **925 / 37 = 25**
- Side-chain mass: **333 / 37 = 9**
- Protons: **500**
- Neutrons: **425**

Comment: Perfect equality across all four groups, including harmonic invariants 500 and 425.

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16. Octet II: 16 Codons Ending with GT

- Full mass: **2294 / 37 = 62**
- Side-chain mass: **1110 / 37 = 30**
- Protons: **1188**
- Neutrons: **1032**

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17. Octet II: 16 Codons Ending with CA

- Full mass: **2146 / 37 = 58**
- Side-chain mass: **962 / 37 = 26**
- Protons: **1072**
- Neutrons: **926**

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18. Octet II: 16 Codons Ending with TA

- Full mass: **2146 / 37 = 58**
- Side-chain mass: **962 / 37 = 26**
- Protons: **1072**
- Neutrons: **926**

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19. Octet II: 16 Codons Ending with CG

- Full mass: **2294 / 37 = 62**
- Side-chain mass: **1110 / 37 = 30**
- Protons: **1188**
- Neutrons: **1032**

Comment: Groups (GT) and (CG) are equal; groups (CA) and (TA) are equal.

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20. Octet II: 8 Codons Ending with C

- Full mass: **1123**
- Side-chain mass: **531**
- Protons: **598**

- Neutrons: **525**

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21. Octet II: 8 Codons Ending with G

- Full mass: **1171**
- Side-chain mass: **579**
- Protons: **590**
- Neutrons: **507**

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22. Octet II: 8 Codons Ending with T

- Full mass: **1123**
- Side-chain mass: **531**
- Protons: **598**
- Neutrons: **525**

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23. Octet II: 8 Codons Ending with A

- Full mass: **1023**
- Side-chain mass: **431**
- Protons: **474**
- Neutrons: **401**

Comment: Differences at the 8-codon level are compensated at higher partitions.

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24. Octet I: 16 Codons Ending with A/G (Purines)

- Full mass: **1850 / 37 = 50**
- Side-chain mass: **666 / 37 = 18**
- Protons: **1000**
- Neutrons: **850**

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25. Octet I: 16 Codons Ending with C/T (Pyrimidines)

- Full mass: **1850 / 37 = 50**
- Side-chain mass: **666 / 37 = 18**
- Protons: **1000**
- Neutrons: **850**

Comment: Purine and pyrimidine halves of Octet I are strictly identical.

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26. Octet II: 16 Codons Ending with A/G (Purines)

- Full mass: **1972**
- Side-chain mass: **1010**
- Protons: **1064**
- Neutrons: **908**

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27. Octet II: 16 Codons Ending with C/T (Pyrimidines)

- Full mass: **2246**
- Side-chain mass: **1062**
- Protons: **1196**

- Neutrons: **1050**

Comment: In Octet II, purine/pyrimidine asymmetry is visible, but their differences are compensated across other partitions.

Compensatory Equalities

1. **C + G (8 codons each):**
   Side-chain = 531 + 579 = **1110 = 30×37**, identical to 16-codon GT and CG groups.

2. **T + A (8 codons each):**
   Side-chain = 531 + 431 = **962 = 26×37**, identical to 16-codon CA and TA groups.

3. **Invariant 1776:**

   - Neutrons {A,C} = **1776 / 37 = 48** (see point 2),
   - Neutrons {T,A} = **1776 / 37 = 48** (see point 4),
   - Side-chain {T,G} = **1776 / 37 = 48** (see point 3).

3.2. Symmetries in the Informationally Activated State

Applying the extended, self-referential activation keys (STOP = {M_side:222, P:116, N:106}; START = {M_side:+74}) causes the system to undergo a qualitative transition. Compensatory relationships evolve into exact equalities, and large blocks of codons align into states of perfect symmetry. Importantly, these keys are not arbitrary: they are informationally self-referential, derived from within the structure of the code itself. Below is the full enumeration of invariants in this activated state.

1. Full Genetic Code (64 codons)

- Side-chain mass: 4144 (= 112 × 37)
- Protons: 4608
- Neutrons: 3976

2–5. 32-Codon Partitions (A/C vs G/T; T/A vs C/G)
All four major 32-codon partitions become strictly identical across all three metrics:

- Side-chain mass: 2072 (= 56 × 37)
- Protons: 2304
- Neutrons: 1988

Comment: The activation keys induce a state of perfect global balance.

6–7. Octet Partition (32 codons)

- Octet I: M_side = 1332 (= 36 × 37), P = 2000, N = 1700
- Octet II: M_side = 2812 (= 76 × 37), P = 2608, N = 2276

Comment: The fundamental distinction between the code's core (Octet I) and periphery (Octet II) is preserved, even in the activated state.

8–15. Octet I Partitions (16 and 8 codons)
All symmetries within Octet I remain unchanged, confirming its status as the invariant core of the system.

- 16-codon groups (GT, CA, TA, CG): identical at M_side = 666 (= 18 × 37), P = 1000, N = 850.
- 8-codon “quanta” (C, G, T, A): identical at M_side = 333 (= 9 × 37), P = 500, N = 425.

Comment: Octet I continues to exhibit ideal balance at every fractal level.

16–19. Octet II: 16-Codon Partitions

- Groups (G/T) and (C/G): M_side = 1406 (= 38 × 37), P = 1304, N = 1140.
- Groups (C/A) and (T/A): M_side = 1406 (= 38 × 37), P = 1304, N = 1136.

Comment: The activation keys create perfect equality in side-chain mass and proton sums for all four 16-codon partitions of Octet II. The only remaining asymmetry is a minimal difference of 4 neutrons between the pairs.

20–23. Octet II: 8-Codon “Quanta”

- Group C: M_side = 531, P = 598, N = 525.
- Group U (T): M_side = 531, P = 598, N = 525.
- Group A (includes 2 STOP codons): M_side = 875, P = 706, N = 613.
- Group G (includes 1 STOP and 1 START codons): M_side = 875, P = 706, N = 613.

Comment: This is the culmination of the analysis. The activation keys create perfect paired equality at the quantal level: the pyrimidine pair (C = U) is identical, and the purine pair (A = G) also becomes identical across all three fundamental metrics, despite inclusion of START and STOP codons.

24–27. Purine/Pyrimidine Partitions

- Octet I: Purine and pyrimidine halves remain identical (M_side = 666, P = 1000, N = 850).
- Octet II: Purine and pyrimidine halves become equal in side-chain mass (1406) and protons (1304), differing only by 4 neutrons (1140 vs 1136).

4. Topological Architecture and Group Structure of Codograms

4.1 Rumer’s Octets

The foundation of the topological analysis of the genetic code was established by Yu. B. Rumer, who demonstrated that the 16 XY-boxes (codon families defined by the first two nucleotide positions) can be divided into two sets of eight columns, or **Octets**.

- **Octet I** consists of XY-boxes with complete four-fold degeneracy, where all four codons code for the same amino acid.
- **Octet II** contains the remaining XY-boxes, where degeneracy is incomplete.
  This partition has since been recognized as one of the most fundamental structural symmetries of the genetic code【4】.

4.2 Rumer’s Transformations

Rumer also discovered that Octet I and Octet II are not independent but connected through a simple substitution rule:
R-transformation: U ↔ G, C ↔ A.
This symmetry links the two halves of the code, showing that the degeneracy pattern is structured rather than random.

4.3 The Extended Transformation Group {E, R, R1, R2}

Building on this, Panov and Filatov (2024) analyzed *codograms*—4×4 arrangements of the genetic code with different permutations of nucleotides along the axes. They identified a set of four transformations that preserve the overall partitioning of the code:

- **E**: Identity.
- **R**: Full Rumer transformation (U ↔ G, C ↔ A).
- **R1**: Purine-only transformation (U ↔ G, A and C unchanged).
- **R2**: Pyrimidine-only transformation (C ↔ A, U and G unchanged).

These four transformations form a closed algebraic structure isomorphic to the **Klein four-group V_4**. Panov and Filatov further showed that certain codograms (the "simply-connected" ones) exhibit especially clear and continuous partitions into Octet I and Octet II【3】.

4.4 Extension: Six Codogram Orbits

In this work, we extend the group-theoretical analysis further. By systematic computation, we established that the full set of 24 homogeneous codograms (corresponding to the 24 permutations of {U, C, A, G}) does not form a single family but decomposes into **six disjoint orbits**, each containing four codograms:

1. {TCAG, GACT, GCAT, TACG}
2. {TCGA, GATC, GCTA, TAGC}
3. {CTAG, AGCT, CGAT, ATCG}
4. {CTGA, AGTC, CGTA, ATGC}
5. {TGCA, GTAC, TGAC, GTCA}
6. {ACGT, CATG, ACTG, CAGT}

Each orbit is closed under the transformation group {E, R, R1, R2}. This shows that the codogram representation is not arbitrary but highly constrained by the algebraic symmetry of the code.

4.5 Quartets as Fundamental Topological Units

The XY-boxes can also be grouped into four **Quartets**, each containing four boxes (16 codons). These quartets (1A, 1B, 2A, 2B) map naturally onto the two Octets:

- **Octet I = Quartets 1A + 1B** (stable “core” of the code).
- **Octet II = Quartets 2A + 2B** (variable “periphery”).

Analysis of numerical invariants within quartets shows two distinct design principles:

- In **Octet I**, quartets are internally balanced: splitting codons by third-position pairs (C/A vs G/U) yields perfect equality.
- In **Octet II**, quartets are internally asymmetric, but these asymmetries compensate each other across quartets, producing global balance at the Octet level.

4.6 Integration of Topology and Arithmetic Symmetry

A central result of this study is that **arithmetic invariants of the third codon position (C/A vs G/U)** align perfectly with the **topological quartets** of the code. Two orthogonal “cuts” of the genetic code—one topological (by XY-boxes), the other arithmetic (by third position)—turn out to be synchronized.

Thus:

- Octet I follows the principle of **ideal balance** (internal equality).
- Octet II follows the principle of **compensatory harmony** (asymmetries neutralized across blocks).

When activation keys are applied, even Octet II transitions toward ideal balance, showing that both arithmetic and topological dimensions of the code form a unified, fractal, self-referential structure.

5. Discussion

The results presented here reveal that the genetic code is not a random mapping of codons to amino acids but a **fractal, topological, and arithmetical structure**, where multiple layers of symmetry interact.

5.1 Fractal Architecture

At the arithmetic level, the code unfolds as a fractal hierarchy:
64 codons → 32 → 16 → 8.
At each level, masses, proton and neutron counts, and side-chain partitions produce **harmonic integer invariants**, frequently divisible by 37. In Octet I these invariants appear as strict equalities; in Octet II they manifest as compensatory balances.

5.2 Integer Invariants and Harmonic Symmetries

Across all scales, the system exhibits integer-based invariants:

- Divisibility by 37 (37, 74, 111, 222, 333, 666, etc.).

- Proton/Neutron sums aligning to structured values (500, 1000, 2000; 425, 850, 1700).
  These invariants persist regardless of the chosen key set, showing that the arithmetic harmony of the code is robust.

5.3 Role of Activation Keys

A central discovery is the role of **activation keys**: parameterizations of STOP and START codons.

- In the **biochemical state**, Octet I displays strict internal balance, while Octet II displays compensatory harmony.

- Under **informational activation** (STOP = {222,116,106}, START = +74), Octet II undergoes a transformation: compensatory asymmetries collapse into exact equalities. At this stage, both Octets demonstrate near-identical levels of structural purity.
  This shows that the symmetries of the code are **self-referential**—they can be selectively “unlocked” depending on how informational elements (STOP/START) are represented.

5.4 Integration of Arithmetic and Topology

The most striking finding is that **arithmetical invariants of the third codon position (C/A vs G/U partitions)** align perfectly with the **topological quartets** defined by the first two positions.

- In Octet I, both decompositions (by quartets and by 3rd-position partitions) converge to perfect balance.

- In Octet II, both decompositions are individually asymmetric, but they **compensate each other**, restoring balance at higher scales.

Thus, the arithmetic and topological “cuts” of the code are not independent: they are synchronized.

5.5 Group-Theoretical Constraints and Six Orbits

Extending the work of Panov and Filatov (2024), who identified the Klein four-group {E, R, R1, R2} as the governing symmetry of codograms, we demonstrated that the 24 homogeneous codograms split into **six closed orbits** under this group. This discovery shows that the codogram representation space itself is highly structured, further constraining the genetic code’s architecture.

5.6 Implications

Taken together, these findings support the view that the genetic code embodies **a designed mathematical structure**:

- Fractal organization across multiple scales.
- Integer invariants (nucleon masses, protons, neutrons).
- Harmonic balances and compensations.
- Group-theoretical closure of codogram permutations.

This unification of arithmetic, topology, and group theory suggests that the genetic code is not merely a biochemical artifact but a **self-referential information structure**, capable of representing both biological function and mathematical harmony.

6. Conclusion

This study demonstrates that the standard genetic code exhibits a **fractal, topological, and arithmetical organization** that cannot be explained by chance. The main results can be summarized as follows:

1. **Fractal hierarchy**: The code decomposes into balanced partitions at every scale (64 → 32 → 16 → 8 codons), producing integer invariants consistently divisible by 37.
2. **Octet distinction**: Octet I functions as an invariant *core*, displaying perfect internal balance, while Octet II operates under the principle of *compensatory harmony*.
3. **Activation keys**: When STOP and START codons are represented by self-referential values, compensatory asymmetries in Octet II collapse into exact equalities, raising its structure to the same level of purity as Octet I.
4. **Topological architecture**: Quartets (1A, 1B, 2A, 2B) act as fundamental building blocks, and the arithmetic symmetries of the third codon position align seamlessly

with these topological partitions.

5. **Group-theoretical closure**: The 24 codogram representations of the code fall into six closed orbits under the Klein four-group {E, R, R1, R2}, extending the work of Rumer and Panov–Filatov.

Together, these findings reveal that the genetic code is not a flat biochemical mapping but a **deeply structured information system**, unifying arithmetic invariants, topological design, and group-theoretical order.

Future research should focus on:

- Identifying whether additional activation keys exist that could fully restore Octet II to the same degree of perfection as Octet I.
- Extending the analysis to variant genetic codes in mitochondria and some unicellular organisms.
- Exploring whether the observed integer invariants and orbit structures have functional or evolutionary implications.

Supplementary Material

Additional data, including detailed numerical tables and visualizations for all discovered symmetries, are provided in the supplementary documents. An interactive online tool is also available for independent verification and further research.

Supplementary Online Tool: An interactive analyzer used for this study is available at:

https://github.com/RuslanKhafizov/genetic-code-analyzer

(The tool allows for the replication of all calculations by selecting the corresponding demonstration sets and activation keys.)

Supplementary Document 1: Key Set 1.

This document contains a full, detailed enumeration of the 27 hierarchical partitions of the genetic code where M_side(STOP) = 0. It provides the complete numerical data (Full Mass, Side-Chain Mass, Protons, Neutrons) for each partition, demonstrating the principles of fractal hierarchy, the cross-symmetry of the invariant 1776, and the compensatory harmony within Octet II.

Supplementary Document 2: Key Set 2.

This document presents the full numerical data for the same 27 partitions but with the self-referential activation keys applied (STOP = {M_side:222, P:116, N:106}; START = {M_side:+74}). It demonstrates the emergence of perfect direct balances and paired equalities across the code's structure.

Supplementary Document 3: Topological and Structural Symmetries.

This document provides visualizations and further details on the topological architecture of the code, including:

Quartets of XY-boxes: Visual representation of the four topological blocks (1A, 1B, 2A, 2B) and their relationship to the Octets.

Codogram Orbits: Screenshots illustrating the complete classification of the 24 homogeneous codograms into six disjoint orbits under the Klein four-group transformations.

Additional Symmetries: Visualizations of other partitioning principles, such as the Purine/Pyrimidine splits, confirming their arithmetical equivalence to the main Rumer's pair partition.

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