The Number « 2 » in Nature
Alan Turing: why are there Numbers in the Nature?
Example of the MENDELEIEV PERIODIC TABLE

In 2009, We proposed in the book CODEX BIOGENESIS a very simple numerical formula computing the number of elements within every period then, finally, within the whole structure:

$$c(p) = 2 \left[Int\left((p+2)/2 \right) \right]^{**2}$$

(where p is the period number, c(p) is the number of Elements within the period layer and Int(x) is the integer whole value of real number x). Examples :

If p=1 ➜ c(1)=2

If p=2 ➜ c(2)=8   If p=3 ➜ c(3)=8

If p=4 ➜ c(4)=18   If p=5 ➜ c(5)=18

If p=6 ➜ c(6)=32   If p=7 ➜ c(7)=32

If p=8 ➜ c(8)=50   If p=9 ➜ c(9)=50

…/…   If p=16 ➜ c(16)=162

Ref: Jean-claude Perez, CODEX BIOGENESIS (2009) Marco Pietteur publishing (Resurgence collection) Embourg Belgium, ISBN 2874340448 pages 47-70 (in french)

$$c(p) = 2 \cdot \left[Int\left(\frac{p+2}{2} \right) \right]^2$$

The Predictive Formula of Mendeleiev's PERIODIC TABLE by J.C. Perez
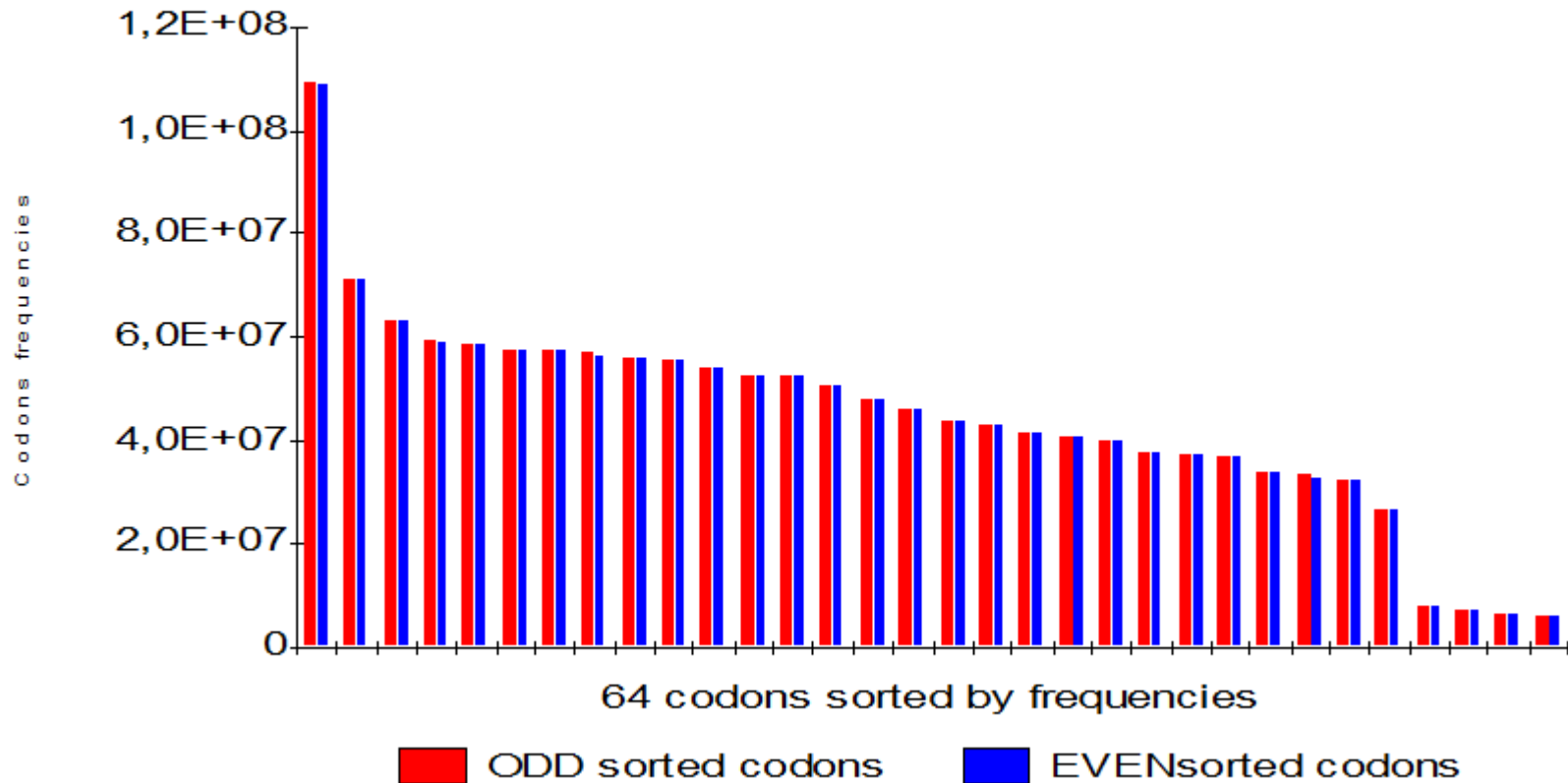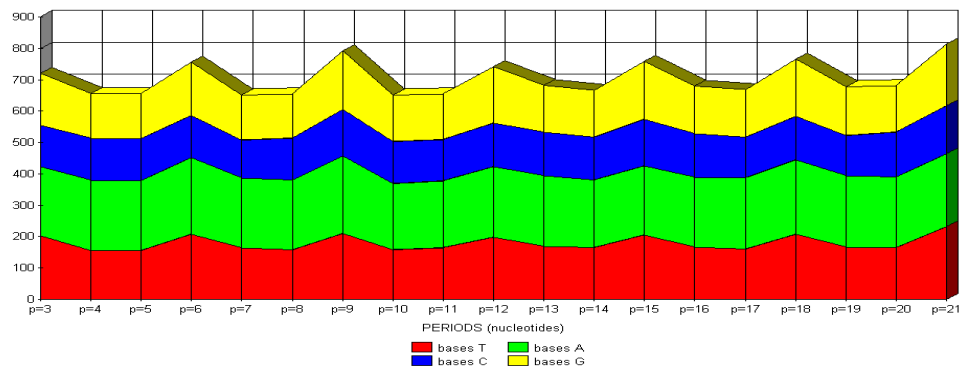
The Number « 2 » in DNA

Alan Turing: why are there Numbers in the Nature? Example of the discovery of « TWIN MIRROR-CODONS » in simple stranded whole Human Genome DNA

HUMAN GENOME "ARCHAIC CODE" Evidence
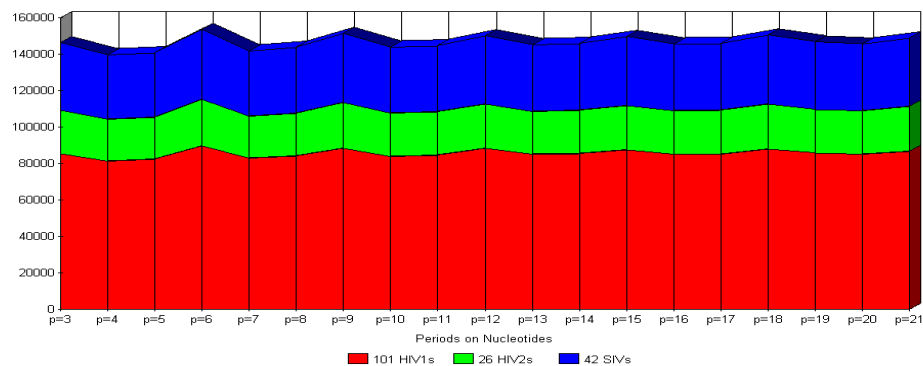
codons frequencies (1st reading frame)

- ODD sorted codons
- EVENsorted codons

64 codons sorted by frequencies

Codons frequencies

BRCA1rna splicingA BreastOvarian CANCER
CODONS EVIDENCE: 3xn Nucleotides PERIOD

169 HIV1-HIV2-SIV genomes INVARIANTS
jc Perez CODONS Emergence Periodic Law

The LAWS of CODONS Emergence: periods=3
DMD gene (Duchenne Muscular Distrophy)

The Number « 3 »

- *« Why a Triplet ?*

We have argued that the code must have been basically a triplet code from a very early stage, so that one is not entitled to use sophisticated arguments which would apply only to a later stage, although one could argue that early organisms with doublet or quadruplet codes actually existed but became extinct, only the triplet code surviving. … / … It must have, to some extent, a definite structure and this is likely to be based on stretches of double-helix. Thus,the diameter of a double.helix (since two may have to lie side by side) may have dictated the size of the codon, in that a doublet-code (moving along two bases at a time) would present an impossible recognition problem. »
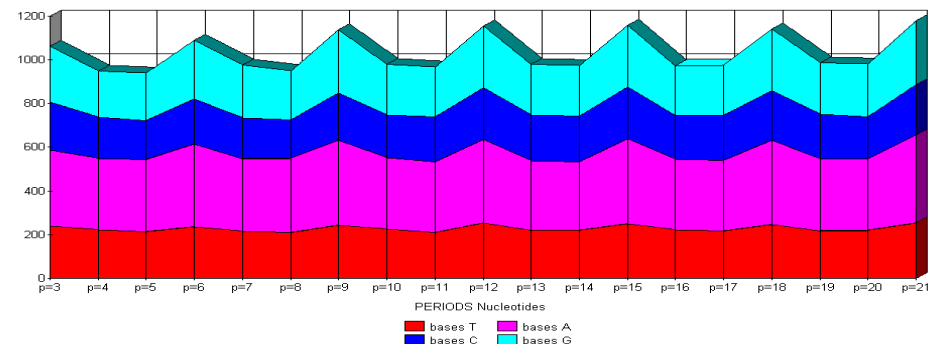
F. H. C. CRICK in « The Origin of the Genetic Code », published in 1968, *J. Mol. Biol.* (1968) 38, 367-379.

OUR RESPONSE: Doing DNA sequence reshapings: modulo2 (2 columns array), modulo3 (3 columns array), modulo »n » (« n » columns array)... We discovered typical tops for modulo3 multiples numbers (3 6 9 12 15...).

THEN:

there is an evidence of DNA sequences shaded organization in triplets (coding and uncoding DNA)!

Decoding non-coding Dna Codes: Human Genome Meta-Chromosomes Architecture *Dr. Jean-Claude Perez*

The Number « 4 »: Doing a 4-partition of single-stranded whole Human Genome DNA Codon populations

ODD range sorted codons		EVEN range Sorted codons	
QUARTILE 1 : 316027664		QUARTILE 2 : 315402427	
36530115	TTT	AAA	36381293
23669701	ATT	AAT	23634011
20990387	TCT	AGA	20948987
19750578	TTA	TAA	19721149
19568343	TAT	ATA	19548709
19195946	CTG	CAG	19176935
19152113	TGT	ACA	19073189
18944797	CTT	AAG	18894716
18708048	TTC	GAA	18678084
18565027	TCA	TGA	18562015
18005020	TTG	CAA	17927956
17480496	TGG	CCA	17444649
17423117	CAT	ATG	17409063
16835177	CCT	AGG	16810797
15942742	CTC	GAG	15939419
15266057	AGT	ACT	15251455
QUARTILE 3: 158309529		QUARTILE 4 : 158064247	
14619310	GGA	TCC	14614789
14252868	GTG	CAC	14214421
13852086	GTT	AAC	13794251
13649076	TGC	GCA	13635427
13252828	GCT	AGC	13242724
12658530	GAT	ATC	12650299
12446600	GGG	CCC	12428986
12240281	TAG	CTA	12217331
11268094	GCC	GGC	11258126
11026602	GGT	ACC	11007307
10766854	GTA	TAC	10755607
8955434	GTC	GAC	8938833
2606672	CCG	CGG	2604253
2379612	CGT	ACG	2372235
2247440	GCG	CGC	2244432
2087242	TCG	CGA	2085226
Cumulated ODD codons		Cumulated EVEN codons	
474337193			473466674

The 4 « quartiles »:

Q1= 316027664 bases Q2= 315402427 bases

Q3= 158309529 bases Q4= 158064247 bases

if we consider 2 clusters of 32 codon populations each, the most frequent (Q1+Q2) is exactly 2X as numerous as the least frequent of the 32 codons (Q3+Q4) . Exact ratio is 1.995859355

Ratios Integer Numbers

The Number « 1 » (Q1+Q3)÷(Q2+Q4) =1.001838607

The Number « 2 » (Q1+Q2)÷(Q3+Q4) =1.995835745

The Number « 3 » (Q1+Q2+Q3+Q4)÷Q1 =2.99911677

(Q1+Q2+Q3+Q4)÷Q2=3.00506206

(Q1+Q2+Q3+Q4)÷(Q3+Q4)=2.995835745

The Number « 4 » (Q1+Q2)÷(Q4) =3.994768602

The Number « 5 » (Q1+Q2+Q3)÷(Q4) =4.996320389

The Number « 6 » (Q1+Q2+Q3+Q4)÷(Q4)=5.996320389
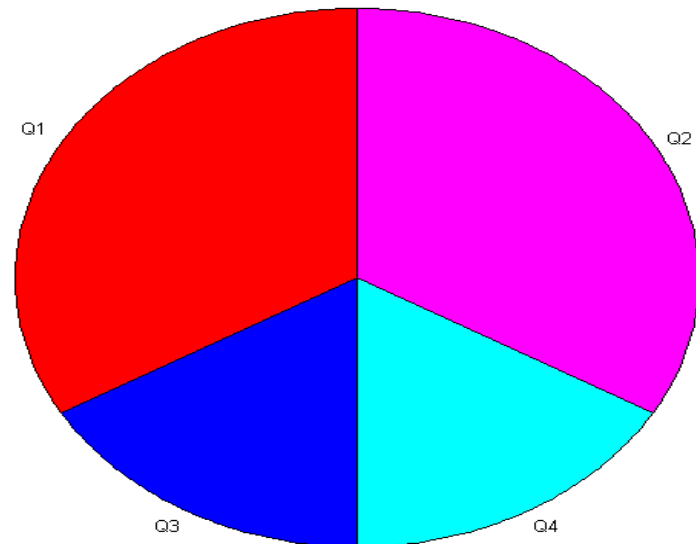
Other ratios : « 3/2 » etc.

(Q1+Q2+Q3+Q4)÷(Q1+Q2) =1.501043236

Number « 4 »...1 2 3 5 6...

HUMAN GENOME "ARCHAIC CODE" Evidence
codons frequencies (1st reading frame)

64 codons sorted by frequencies

■ ODD sorted codons   ■ EVENsorted codons

The NUMERICAL Code of the Human Genome
4-folding by QUARTILES

The perfect Whole Human Genome ATOMIC WEIGHTS BALANCING...

A consequence of the « TWIN CODONS mirror symmetry » between codons is the PERFECT BALANCE between ATOMIC MASS of the 2 DNA STRANDS:

We prove that total atomic weights of each of the 2 simple DNA strands exhibit the same perfect symmetry: For the whole human genome, the balance ratio between both DNA strands is exactly = 1.000000456. Also, we noticed that this equilibrium has increased as the whole human genome sequence has grown in precision (successive releases of the draft human genomes sequences of April 2001, November 2002 and finally August 2003):

Balance mass strand1 / mass strand 2 evolution:

First Human Genome release April 2001: *1.000039049*
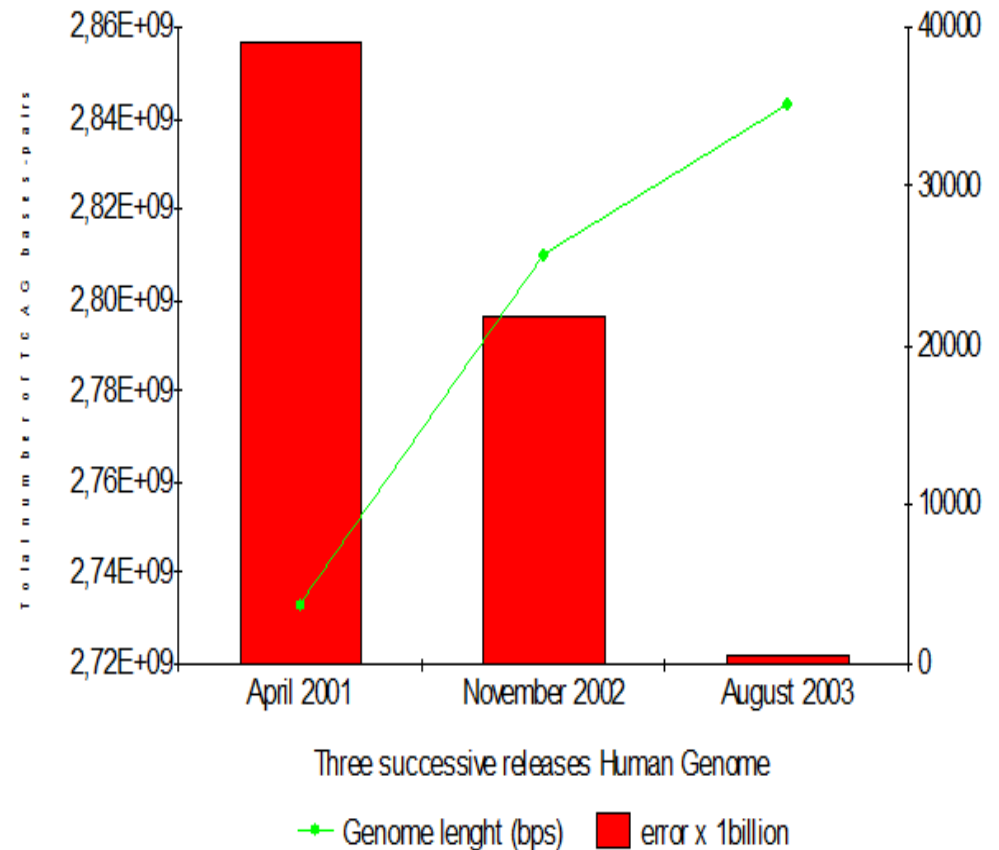
Intermediary release November 2002: *1.000021780*

Finalized « BUILD34 » August 2003: *1.000000456*

2 strands XX female whole genome: **1.000000599**

2 strands XY male whole genome: **1.000000309**

2 strands Hypothtical YY HumGMO genome: **1.000000005**

Optimal BALANCE of Human DNA 2 strands
2 Strands mass Balance Evidence

Three successive releases Human Genome

- Genome lenght (bps)   error x 1billion

Perfect Whole Human Genome DNA CODON POPULATIONS, « Phi » the golden ratio and ATOMIC WEIGHTS BALANCING...

If we consider 2 clusters of 32 codon populations each, the most frequent (Q1+Q2) is exactly 2X as numerous as the least frequent of the 32 codons (Q3+Q4) . Exact ratio is 1.995859355...Then, what about TA versus CG quartiles composition?

Majors CG and TA: • T 1985989068 • C 857106311

  • A 1982488350 • G 857309551

MAJOR CG = C+G = 1714415862 MAJOR TA = T+A = 3968477418

Minors CG and TA • T 537655334 • C 885972717

  • A 536994232 • G 886719273

MINOR CG = C+G = 1772691990 MINOR TA = T+A = 1074649566

(MAJOR CG / MINOR CG) /'(MAJOR TA / MINOR TA) =

(MAJR CG x MINOR TA) / (MINOR CG x MAJOR TA) = **0.2618941805**

• (PHI*2) / 10 = 0.2618033989   **Error = 0.00009078157758**

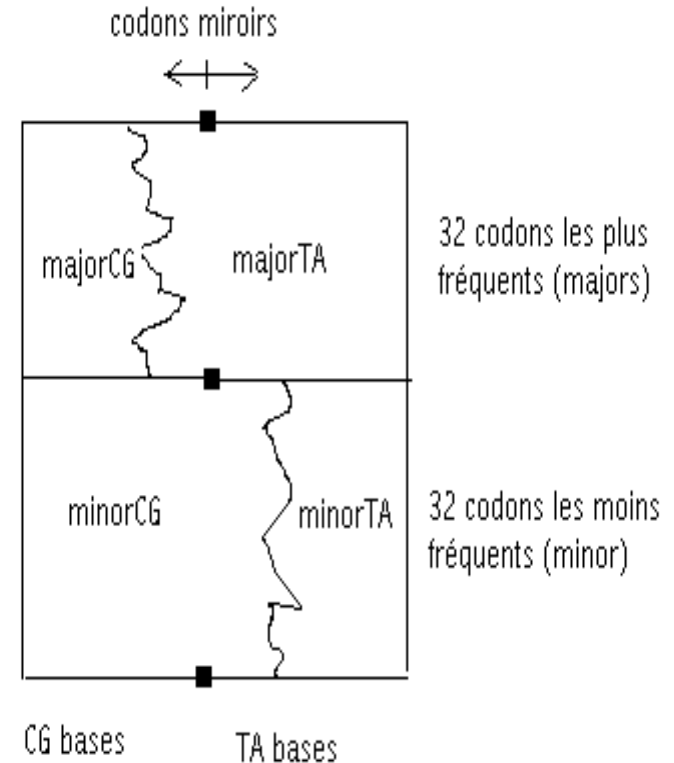OTHERS RATIOS/ NUMBER « 3 »: (Major CG / Major TA) + (Major CG / minor TA)

+ (Major CG / minor CG) = **3.002226104**

NUMBER « 3/2 »: (minor TA / Major TA) + (minor TA / Major CG)

+ (minor TA / minor CG) = **1.499096404**

NUMBER « 1 »:

(Major TA / Major CG) / minor CG = **0.9997090771**

codons miroirs

32 codons les plus fréquents (majors)

majorCG   majorTA

minorCG   minorTA

32 codons les moins fréquents (minor)

CG bases   TA bases

(majorCG / minorCG) / (majorTA / minorTA) = Phi2/10

The perfect Whole Human Genome DNA CODON POPULATIONS, « Phi » the golden ratio and ATOMIC WEIGHTS BALANCING...

2- ATOMIC WEIGHTS CODON POPULATIONS PERFECT
BALANCING = Phi*2 / 10:

• *Base T : 125.105935*   • *Base A : 134.119288*

• *Base C : 110.094498*   • *Base G : 150.118718*

• *Majors 1 2*

MASSESTRAND1majCG 2.230608998E11

MASSESTRAND1majTA 5.143489452E11

• *minors 3 4*

MASSESTRAND1minCG 2.30653882E11

MASSESTRAND1minTA 1.392851573E11

• *(MASSESTRAND1majCG / MASSESTRAND1minCG)=0.9670806224*

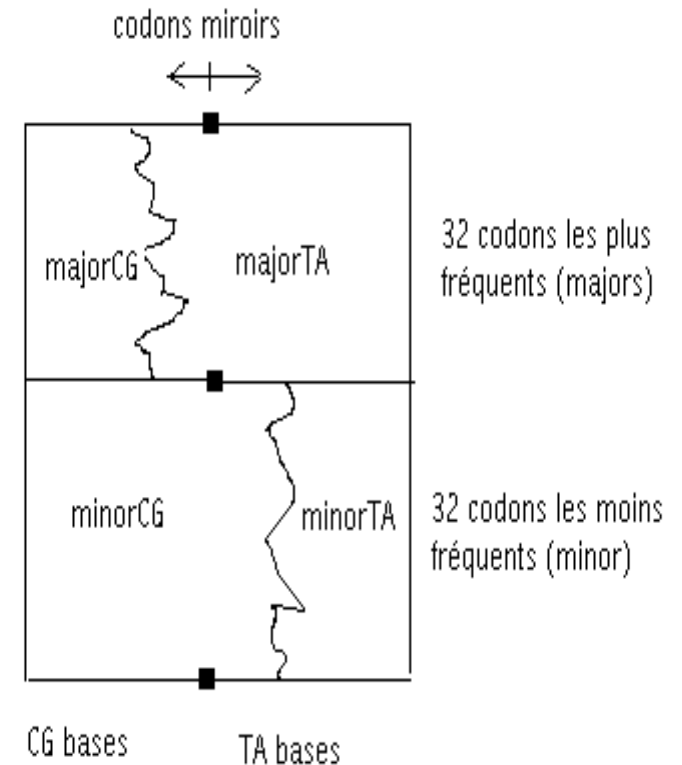• *(MASSESTRAND1majTA / MASSESTRAND1minTA)=3.692776424*

(MASSESTRAND1majCG/ MASSESTRAND1minCG) /
(MASSESTRAND1majTA / MASSESTRAND1minTA)

=0.2618844228

Error : 0.2618844228-(PHI2÷10) = 0.00008102388274.

Then an error of 81 millionths at whole human genome
TCAG atomic weights balance

codons miroirs

majorCG   majorTA   32 codons les plus fréquents (majors)

minorCG   minorTA   32 codons les moins fréquents (minor)

CG bases   TA bases

(majorCG / minorCG) / (majorTA / minorTA) = Phi2/10