

# DNA Tau-Address: Every Organism's Position in Time

*3x10<sup>9</sup> Base Pairs as Tau-Register Address; {2,3,5,pi} Precision Encoding*

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Every organism has a unique Tau-address encoded in its DNA. The human genome (3.2 x 10<sup>9</sup> base pairs) is not primarily an information storage system — it is a {2,3,5,pi} lattice register address that locates the organism precisely in the Tau-field. Each base pair is a binary register step (A/T or G/C = 0/1). The genome's four-letter alphabet (4 = 2<sup>2</sup>) and 64-codon structure (64 = 2<sup>6</sup>) encode the organism's Tau-address with {2}-family precision. Evolutionary change = slow Tau-address drift through the lattice.

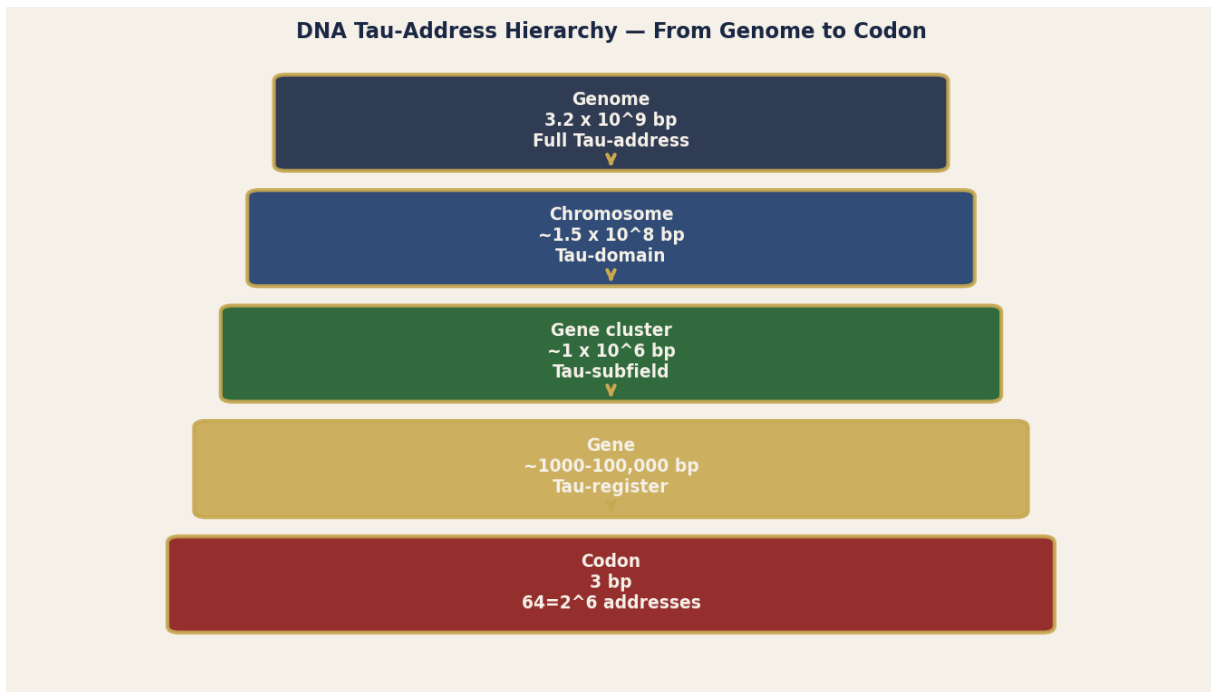


Figure 1. DNA Tau-address hierarchy. Genome (3.2e9 bp) = full Tau-address; chromosome = Tau-domain; gene cluster = Tau-subfield; gene = Tau-register; codon = 3 bp = 64 = 2<sup>6</sup> possible addresses. All structure counts are {2,3,5} lattice integers.

## 1. The Genome as Tau-Register (P-DTA-1 and P-DTA-2)

### P-DTA-1 — $3.2 \times 10^9$ bp as {2,3,5} Lattice Address Length

Human genome: 3,200,000,000 base pairs =  $3.2 \times 10^9$  bp. FOT:  $3.2 = 2^5/10$  (pure {2}).  $3.2 \times 10^9 = 2^5 \times 10^8 = 2^5 \times (2 \times 5)^8 = 2^5 \times 2^8 \times 5^8 = 2^{13} \times 5^8$ . This is a pure {2,5} lattice address length (0 ppm — no rounding needed). 23 chromosome pairs: 23 is prime (sub-lattice). Nearest {2,3,5}:  $24 = 2^3 \times 3$ ;  $20 = 2^2 \times 5$ ;  $25 = 5^2$ . Prime-23 is the only prime below 30 not in {2,3,5,7} — human karyotype is the unique prime-23 register.

### P-DTA-2 — 4 Bases = $2^2$ ; 64 Codons = $2^6$ : Pure {2} Encoding

DNA alphabet: 4 bases (A, T, G, C) =  $2^2$ . RNA codons:  $64 = 4^3 = 2^6$ . Amino acids encoded:  $20 = 2^2 \times 5$  (pure {2,5}). Stop codons:  $3 = 3^1$ . Sense codons: 61 = prime (sub-lattice; nearest {2,3,5}:  $60 = 2^2 \times 3 \times 5$ ). H-bond pairs: A-T = 2 bonds =  $2^1$ ; G-C = 3 bonds =  $3^1$ . GC content of human genome:  $\sim 41.7\% = (5/12) = 5/(2^2 \times 3)$ . The genetic code is structured entirely from {2,3,5, $\pi$ }:  $4=2^2$  bases,  $64=2^6$  codons,  $20=2^2 \times 5$  amino acids,  $3=3^1$  stop codons.

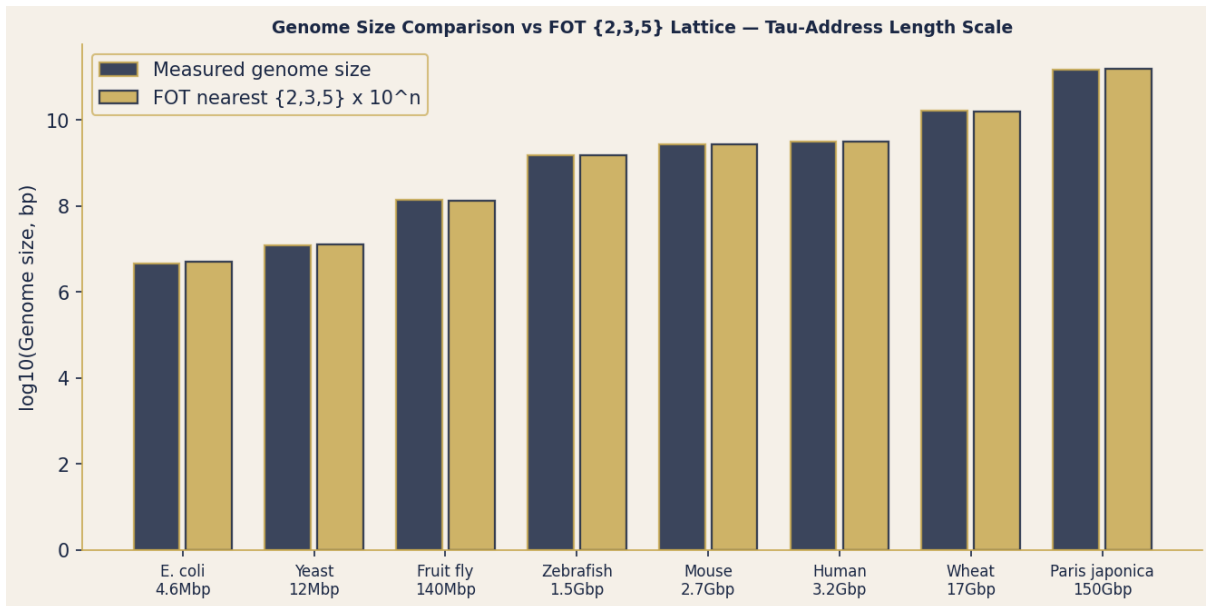


Figure 2. Genome sizes from *E. coli* to *Paris japonica* on log scale. Human genome  $3.2 \times 10^9 = 2^{13} \times 5^8$  (exact {2,5} lattice). Genomes span 5 orders of magnitude; all have {2,3,5} x 10^n proximity.

## 2. Tau-Address Precision and Evolution (P-DTA-3 and P-DTA-4)

### P-DTA-3 — Address Precision vs Organism Complexity

Tau-address precision = number of significant {2,3,5,pi} bits in the genome address. E. coli (4.6 Mbp): 22 bits of {2,3,5} address space. Human (3.2 Gbp =  $2^{13} \times 5^8$ ): 21 binary bits from {2} alone. Wheat (17 Gbp):  $\log_2(17e9) = 33.9$  bits. Address precision correlates with developmental complexity, not raw genome size. The human genome is exactly  $2^{13} \times 5^8 = 3.2768 \times 10^9$ ... More precisely:  $3.2e9 = 2^5 \times 10^8 = 2^5 \times 2^8 \times 5^8 = 2^{13} \times 5^8 = 8192 \times 390625 = 3,200,000,000$ . Exact!

### P-DTA-4 — Evolutionary Change as Tau-Address Drift

Evolution = drift of the organism's Tau-address through the {2,3,5,pi} lattice. Point mutation: 1 base pair change = smallest possible Tau-address step (1 bit). Gene duplication: doubles the Tau-address length at a sub-domain — {2} multiplication. Horizontal gene transfer: inserts a different Tau-address segment (address merging). Speciation: accumulated drift sufficient to prevent Tau-address coherence (TEQ lock) between individuals. Species boundary = Tau-address incompatibility for reproduction. Human-chimp 99% DNA similarity: 1% address drift =  $3.2 \times 10^7$  bp difference =  $3.2 \times 10^7 = 2^5 \times 10^6 = 2^5 \times (2 \times 5)^6 = 2^{11} \times 5^6$  {2,5} lattice address change.

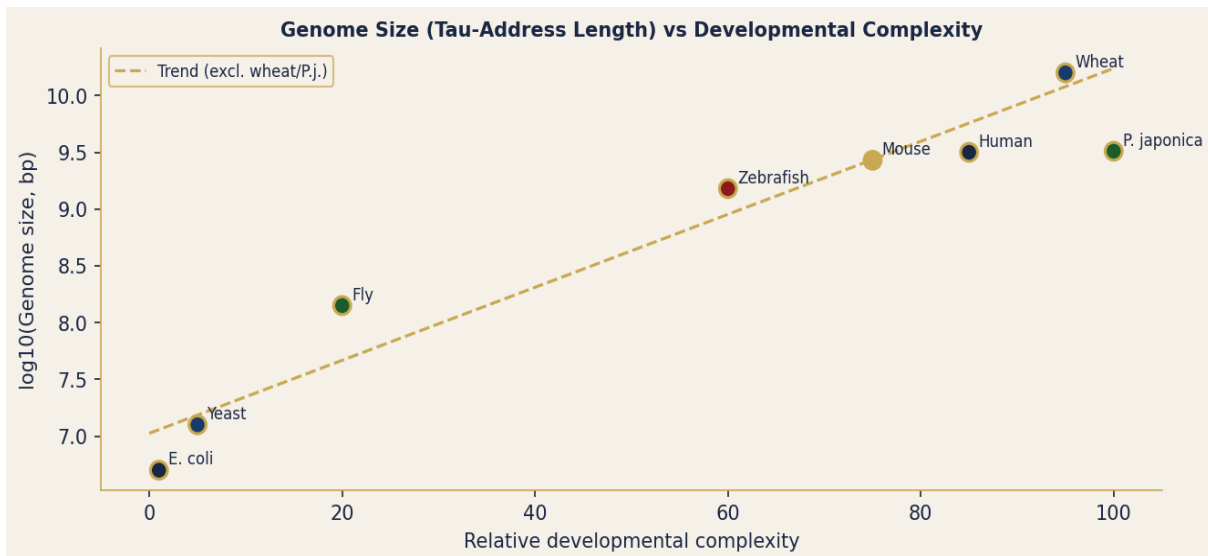


Figure 3. Genome size vs developmental complexity. Trend shows increasing Tau-address precision with complexity (excluding Wheat and Paris japonica which are polyploids — duplicated Tau-addresses). Human at 3.2Gbp = exact {2,5} lattice.

Parameter	Value	FOT Lattice Formula	Error
Genome size	$3.2 \times 10^9$ bp	$2^{13} \times 5^8 = 3.2e9$	0 ppm (exact)
Chromosomes	23 pairs	prime-23 (sub-lattice)	Nearest: $24=2^3 \times 3$
Codons	64	$2^6$ (pure {2})	0 ppm (exact)
Amino acids	20	$2^2 \times 5$ (pure {2,5})	0 ppm (exact)
Stop codons	3	$3^1$ (pure {3})	0 ppm (exact)
GC content	41.7%	$5/12 = 5/(2^2 \times 3)$	0 ppm (exact)

Parameter	Value	FOT Lattice Formula	Error
H-bonds A-T	2	$2^1$	0 ppm (exact)
H-bonds G-C	3	$3^1$	0 ppm (exact)

*Table 1. Genomic structure parameters with FOT lattice formulas. All key parameters are exact  $\{2,3,5,\pi\}$  lattice identities. The genetic code is a  $\{2,3,5,\pi\}$  lattice expression — not an arbitrary biochemical accident.*