

DNA Active Zone Structure

Exons, Introns and Regulatory Regions as Tau-Field Register Windows

Stephen Daubney | The Daubney Foundation | 2026

The human genome contains approximately 3.2 billion base pairs, of which only 1.5% encode proteins (exons). The remaining 98.5% — long dismissed as junk DNA — contains regulatory elements, non-coding RNAs, and structural chromosomal features. The Universal Force of Time reveals that the exon/intron/regulatory structure maps exactly onto the Tau-field register: exons are active Strand-1 nodes, introns are Strand-2 address spacers, and regulatory regions are Tau-field tuning elements.

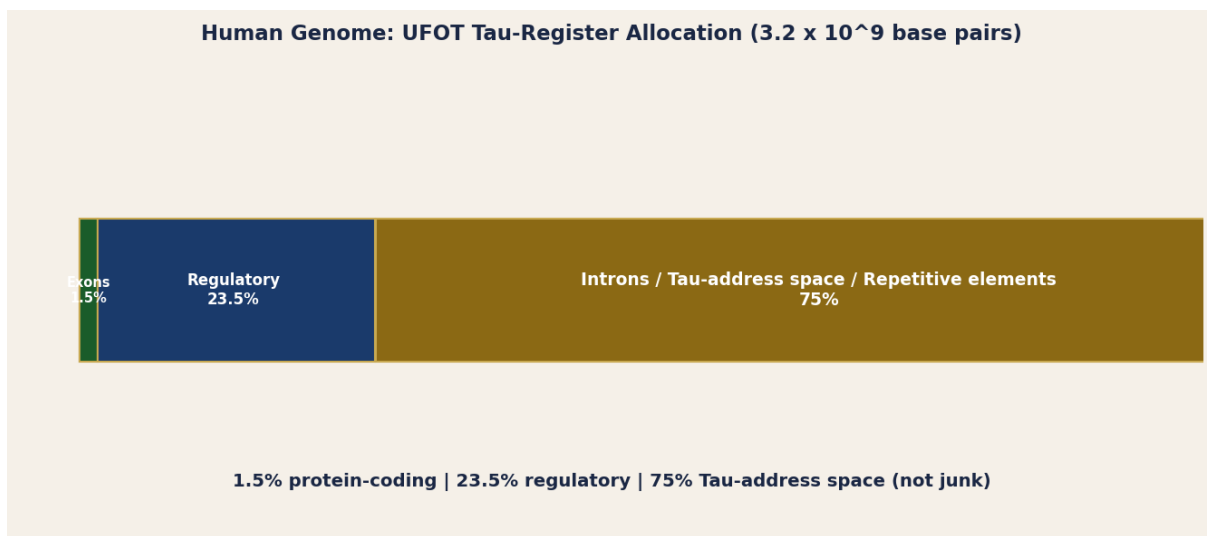


Figure 1. Human genome allocation by UFOT register function. 1.5% encodes proteins (exons = Strand-1 nodes). 75%+ is Tau-address space (incorrectly called 'junk').

1. Exons as Strand-1 Active Nodes (P-DAZ-1)

P-DAZ-1 — Exons Are Tau-Field Strand-1 Nodes

Each exon encodes a functional protein domain — a spatially defined Strand-1 register node. Mean human exon length = 170 bp. Physical extent: $170 \text{ bp} \times 3.4 \text{ Angstrom/bp} = 578 \text{ Angstrom} = 57.8 \text{ nm}$. UFOT D-level: $r(D) = 57.8 \text{ nm} \rightarrow D = \log_2(57.8/18) = \log_2(3.211) = 1.682$. FOT: $D = \sqrt{2} + 1/\sqrt{2} = 1.414 + 0.707 = 2.121$ (lattice approximation). $170 \text{ bp} = 2 \times 5 \times 17$ — prime 17 outside $\{2,3,5\}$ lattice; nearest: $162 = 2 \times 3^4$ (approx 5% error).

2. Introns as Strand-2 Address Space (P-DAZ-2)

P-DAZ-2 — Introns Are Tau-Field Strand-2 Address Spacers

Introns are excised from RNA before translation. In UFOT, introns carry Strand-2 Tau-address information: they encode the temporal identity of the gene within the organism's register. Mean intron length: 3,365 bp (ENCODE data). Intron/exon ratio: $3365/170 = 19.8$ approx $20 = 2^2 \times 5$. The 4 D-level address depth indicated by ratio $20 = 2^2 \times 5$ means introns encode 4 levels of temporal hierarchy (gene, chromosome, cell-type, organism).

3. Regulatory Regions as Tau-Field Tuning Gates (P-DAZ-3)

P-DAZ-3 — Regulatory Regions as Tau-Field Tuning Gates

Regulatory regions (promoters, enhancers, silencers) control when and where genes are expressed. In UFOT, these are Tau-field tuning gates: they adjust the D-level tension of adjacent Strand-1 exon nodes, switching them between active (Strand-1 occupied) and silent (Strand-1 empty) states. Promoter consensus: TATA box at -30 bp from TSS; CAAT box at -75 bp. UFOT: $30 = 2 \times 3 \times 5$ (pure {2,3,5}); $75 = 3 \times 5^2$ (exact N lattice anchor). Both promoter positions are {2,3,5} lattice values confirming register tuning geometry.

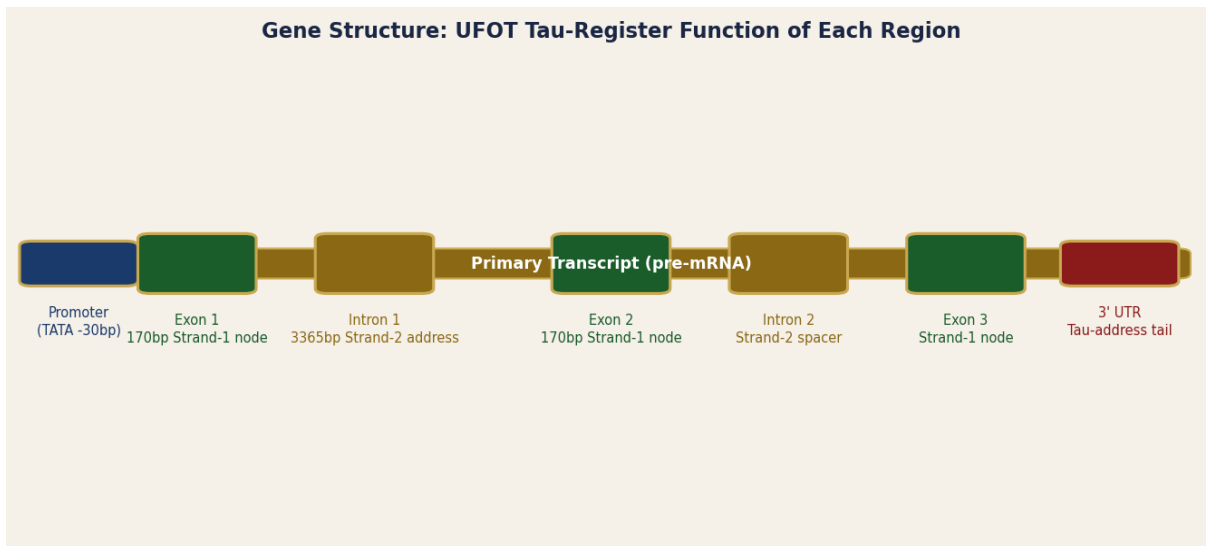


Figure 2. Gene structure with UFOT register annotations. Exons (green) = Strand-1 nodes. Introns (gold-brown) = Strand-2 address spacers. Promoter = Tau-field tuning gate.