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Sequence of a 3.18 kb tandem repeat of *Xenopus laevis* DNA containing 8 tRNA genes

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SEQUENCE ORIGIN & CONTENT: Complete sequence of a tandemly-repeated 3183 bp *Hin*dIII fragment of *Xenopus laevis* DNA (clone t210, Refs. 1 & 2) containing 8 tRNA genes, all without 3'-CCA: on upper strand, gene for tyrosine tRNA (GUA) from 393-478 (split by 13 bp intron from 430-442), methionine tRNA (CAU) from 957-1028 (Met-A), variant methionine tRNA (CAU) from 1373-1444 (Met-B), leucine tRNA (CAG) from 2609-2691, and variant lysine tRNA (UUU) from 2992-3064; on lower strand, gene for phenylalanine tRNA (GAA) from 320-248, asparagine tRNA (GUU) from 1945-1872, and alanine tRNA (UGC) from 2429-2358.

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AGCTTTTCCCAAGGGCAACCCAGGAAATCAGAAACCGCAGGCATGCTTCCGAGTGCCTTTTTGCTCTTCTGGAAGTGAGGTCGGTCCCATTGGTTCCCAAAAGCGGCCCGGGAGGAAGAT  120
CTTTCTCAGTCGGAGCCCTGCTTAGCAGGGCCGATCTTCCGTATAGCGCCTTCGCCAACGTGTGGCTACATTCGTGTCCCCTACTTAAATTGGTCCCAAAAGCCACCGACGGCTCCGTGG  240
CCCCACCTGCCGAAACCCGGGATCGAACCAGGGACCTTTAGATCTTCAGTCTAACGCTCTCCCAACTGAGCTATTTCGGCACCGGGTGCGCCACCCTGTAGCAGCTGAACAATTGAAGTC  360
CACCAAGTCACGGGCGATGGGTGCCCCACCGGCCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGGTGTGATCGAGCAATCCTTAGGTCGCTGGTTCGATTCCGGCTCGAAGGACG  480
CTTTGTTTTCCAATGCGAGCCTAAGAAGGAGATGAGTGGCATTTCAGGAAAGCTCTTTCTGCACCATGTGGCTGAGGACGAATGCTGAGGACACCACACCCCGTCAAGCGCTAAGCGCGA  600
TTAGACGCTTCCTTCTTTTCTGGCCCATTATCCAACCACGACACCACATGAGCCACTCACGTGCCTCCCAACAAATGGATACTATTGCAGGTTTGGGCCACCTTTCATTACGACTAACAA  720
GAATGGTGACAACCAATGGCACCCCCCCACACACACACGAACACACGCACTGTTGAGGGCACCACACTTCGAGGGTGTAGCTTCTGCCCTCTAAAAGGAGACACTATGCATCCGATTCTT  840
TGCAGTCAGTCAATTGCAGGGACCTTTCTTGTCCCTTTGCTACCTTATGTTGGAAACATTAGCTGCATGTCTTAGAAGCAACGTAAAGGAAGAGAATCACCCAAAGGACGGCAATCAGCA  960
GAGTGGCGCAGCGGAAGCGTGCTGGGCCCATAACCCAGAGGTCGATGGATCGAAACCATCCTCTGCTAAAACTTTTTGCCAGGCAGAAGAAGAAAAAAAAAACCCACAATGTGGGGTCTA 1080
TGTCCATTGTCAAGAACGAAGAAGGGAGAGTTTTGAGTCAAATGGGTTTGCGGCCGTAGGATGCATTTCTCAAAAAAATGTGTTATTCCCCAAGGATTGCCTCCACAAATGAGGCCTCTA 1200
ATTTTAGCTACTTAAGACATAAGGGAAGATGTATTTTTCCGGCGAGGCAGCCACCCCCCCTCACCTCCGAAGGCTGACAGGACATAAACCATGTTGGGAAAAGTTATTGCCCACCCCCAC 1320
CCCCATACAATGCACAGCGCAGCAAGAATACCTGCGCGTGCCAGCTGCGATTAGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCCATAACCCAGAGGTCGATGGATCGAAACCATTCTCT 1440
GCTAGATTTTCTTTTTTTGGGAGGGGGGCAGGCCGGGAAAAAAAAAAAAACGCCCTCGAAACTGGGTTTAAATCCTTTGTCTAGAGCAAATGAAGGAGGTTTTCAGTCAAAGGGTGGCAGG 1560
CCTCTTGATTTCTAGCGACACAGATTGTCAATGCTTTGAAAGACACCATTATGAAGTGGCAAAGGAAATGAATAGGAAGCAAGGGCAGAAATCATGTGCGCTTCTTTCGCGGTGGGGTGA 1680
CCGCCATCAGAGCAGGGGTTGCAAAGAAATTCAAACAACAGCACAGCAGGCCCCATGTATTCAATTGGCAGATGGAGCTCCCAGCCAGCACTTAATCCTCCTGGTATTGCTAGAACCTTT 1800
GCTTGCAGAAGAACAGTCGCCATGTATACTTGTTCGAGTCTTGGATTGCACAGAAGCAGCAGGGAAAAAGACGTCCCTGGGTGGGCTCGAACCACCAACCTTTCGGTTAACAGCCGAACG 1920
CGCTAACCGATTGCGCCACAGAGACGACGCTTGCCACCGGCCACCAGGTGTCGCCTTAAGCGCGTGGAAACGCCAGAGTTTTCCATCTTCAGGCATTTGTCTGCTCTAAACATGGAACCA 2040
TATATTAGTCACCGAGGATTGCCACTACAAATGAGGCCTCTAAAAGCCTCTTTGTATTCTTAGCGTCTTTGGATTCCAGAGAGCCGGAAGGGAGAGGACTTCTGTTGCCCCTTCGCTCCC 2160
TTGTATCGGAAACCCAAGCTGTATGTTAGAAGTAAGCTATCGACGTCTTTTTTTTTTCAGATGGTAGAGCGTGCTACCTAGACATTCCCCCTCTATACTTAACGCCGCCAGTGTCCGCAT 2280
ACATTATTTGAAGGGAAACATTCTGCTCCAAAATACGTGACCTGCACGTTAAAGCAGCGGCCTTAAAGACCCGCCGGTGGAGATGCTGGGGATTGAACCCAAGACCTCATACATGCAAAG 2400
CATGCGCTCTACCACTGAGCTACACCCCCACCGCCGACGTTTGAGCCCCGTTTTGCTTATGGCCTCAAACATGAGAACAATCTCTGCGGCTCACTCTTCAAAAGAGCCGGGGAAGCCTAA 2520
GTCATTATGATCCATCTATCTGTCAGAAGCAGACGGCAGAGGCGCTTATGAAGGCTGGCCTCCACCCTCACAACGGCTGGCTTTCACAGTCAGGATGGCCGAGCGGTCTAAGGCGCTGCG 2640
TTCAGGTCGCAGTCTCCCCTGGAGGCGTGGGTTCGAATCCCACTTCTGACACTGAACTTCTTTGCTGCCAAACACGAATCTGGACTTTCAGACCAAATGAATTCCTTACAATCAAAGAGG 2760
AGACTTGCGCTTTCCCGTCCATCGATCCAAGCGCGACTCCTTTTGCGATATTGCCATTCCTCCCAGATAACGGATACCGTTGTAAATTCGGGCGAGCCTTCGTAATTCCTGGTGCCCAAA 2880
TGTGAATTTCCAAGAATGGTTAAAAAAACCCTTACCCCCCCCCTCTACCGCATGCTTCCTGTGGCCTAACGGAAAGGCCATTAAAAGCGGCGGAGGAACGAGCGACGCAGTGCCCGCATA 3000
GCTCAGTCGGTAGAGCATCAGACTTTTAATCTGAGGGTCCAGGGTTCAAGTCCCTGTTCGGGCGACGCGGCCTTCTCTGAAGTGACGTGTAAAGCCTTAAGTTAGGTTGAAAATAAACAC 3120
ACGTCCGTCAAGTTTAACCTTTTAACTCTTTTTCACCTGCCTAACTGCCAGTGTGTTCCGGGA(AGCTT) 3183
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COMMENTS: The entire sequence of both strands was determined by the chemical method. The 5' flanking regions of 7 of the genes can be placed in two groups; the Met-B gene seems most related to Group II but some single point changes yield a 9 bp alternating RY tract (underlined) that inhibits transcription *in vitro* (3):

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Group I:   R-ARR--R--R---AA--R-CGRCR--Mature tRNA
   Ala:    GcAAAacGggGctcAAacGtCGGCGgt
   Lys:    AaAAGcgGcgGaggAAcgAgCGACGcagt
   Met-A:  GaAGAgaAtcAcccAAagGaCGGCAatc

Group II:  -----CTG-YR--GGGTGGC---C---Mature tRNA
   Asn:    gacacCTGgTGgccGGTGGCaagCgtc
   Leu:    ccaccCTcaCAacGGcTGGCtttCaca
   Phe:    ttcagCTGcTAcaGGGTGGCgcaCccggt
   Tyr:    agtcaCgGgCGatGGGTGcCccaCcgg

   Met-B:  caagaaTacCtgcGcGTGcCagctgcgatt
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