The nucleotide sequence of the *luxD* gene of *Xenorhabdus luminescens* Hm

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The sequence of the *luxD* gene of *Xenorhabdus luminescens* and the translated amino acid sequence of the acyl-transferase is given below. The acyl-transferase frees fatty acids from the fatty acid biosynthetic machinery for conversion to the aldehyde substrate of the luciferase-catalyzed, luminescent reaction. DNA fragments were subcloned from pCGLS1 (1) and sequenced on both strands by the dideoxynucleotide, chain-termination method (2). The open-reading-frame was identified as the *luxD* gene by homology of the encoded protein with the acyl-transferase of *Vibrio harveyi* (66%) (3) and *V. fischeri* (64%) (4). The protein is comprised of 307 amino acids and has a molecular weight of 34,705 Da. The sequence below also shows the 3′ end of the *luxC* gene of *X. luminescens* as determined by homology of the encoded amino acids with the carboxyl-terminus of the fatty acid reductase of *V. harveyi*. This confirms the gene order to be *luxC-luxD-luxA-luxB-luxE* in *X. luminescens*, as reported (5), which is the same as it is in *V. harveyi* and *V. fischeri*.

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TATATTTCTCATGAAAGGCCATCTAACTATACGGCTAAGGATGTTGCGGTTGAAATAGAACAGACTCGATTCCTGGAAGAAGATAAG
TyrIleSerHisGluArgProSerAsnTyrThrAlaLysAspValAlaValGluIleGluGlnThrArgPheLeuGluGluAspLys
TTCCTTGTATTTGTCCCATAATAGGTAAAAAGTATGGAAAATGAATCAAAATATAAAACCATCGACCACGTTATTTGTGTTGAAGGA
PheLeuValPheValProEnd                MetGluAsnGluSerLysTyrLysThrIleAspHisValIleCysValGluGly
AATAAAAAAATTCATGTTTGGGAAACGCTGCCAGAAGAAAACAGCCCAAAGAGAAAGAATGCCATTATTATTGCGTCTGGTTTTGCC
AsnLysLysIleHisValTrpGluThrLeuProGluGluAsnSerProLysArgLysAsnAlaIleIleIleAlaSerGlyPheAla
CGCAGGATGGATCATTTTGCTGGTCTGGCGGAATATTTATCGCGGAATGGATTTCATGTGATCCGCTATGATTCGCTTCACCACGTT
ArgArgMetAspHisPheAlaGlyLeuAlaGluTyrLeuSerArgAsnGlyPheHisValIleArgTyrAspSerLeuHisHisVal
GGATTGAGTTCAGGGACAATTGATGAATTTACAATGTCTATAGGAAAGCAGAGCTTGTTAGCAGTGGTTGATTGGTTAACTACACGA
GlyLeuSerSerGlyThrIleAspGluPheThrMetSerIleGlyLysGlnSerLeuLeuAlaValValAspTrpLeuThrThrArg
AAAATAAATAACTTCGGTATGTTGGCTTCAAGCTTATCTGCGCGGATAGCTTATGCAAGCCTATCTGAAATCAATGCTTCGTTTTTA
LysIleAsnAsnPheGlyMetLeuAlaSerSerLeuSerAlaArgIleAlaTyrAlaSerLeuSerGluIleAsnAlaSerPheLeu
ATCACCGCAGTCGGGTTTGTTAACTTAAGATATTCTCTTGAAAGAGCTTTAGGGTTTGATTATCTCAGTCTACCCATTAATGAATTG
IleThrAlaValGlyPheValAsnLeuArgTyrSerLeuGluArgAlaLeuGlyPheAspTyrLeuSerLeuProIleAsnGluLeu
CCGAATAATCTAGATTTTGAAGGCCATAAATTGGGTGCTGAAGTCTTTGCGAGAGATTGTCTTGATTTTGGTTGGGAAGATTTAGCT
ProAsnAsnLeuAspPheGluGlyHisLysLeuGlyAlaGluValPheAlaArgAspCysLeuAspPheGlyTrpGluAspLeuAla
TCTACAATTAATAACATGATGTATCTTGATATACCGTTTATTGCTTTTACTGCAAATAACGATAATTGGGTCAAGCAAGATGAAGTT
SerThrIleAsnAsnMetMetTyrLeuAspIleProPheIleAlaPheThrAlaAsnAsnAspAsnTrpValLysGlnAspGluVal
ATCACATTGTTATCAAATATTCGTAGTAATCGATGCAAGATATATTCTTTGTTAGGAAGTTCGCATGACTTGAGTGAAAATTTAGTG
IleThrLeuLeuSerAsnIleArgSerAsnArgCysLysIleTyrSerLeuLeuGlySerSerHisAspLeuSerGluAsnLeuVal
GTCCTGCGCAATTTTTATCAATCGGTTACGAAAGCCGCTATCGCGATGGATAATGATCATCTGGATATTGATGTTGATATTACTGAA
ValLeuArgAsnPheTyrGlnSerValThrLysAlaAlaIleAlaMetAspAsnAspHisLeuAspIleAspValAspIleThrGlu
CCGTCATTTGAACATTTAACTATTGCGACAGTCAATGAACGCCGAATGAGAATTGAGATTGAAAATCAAGCAATTTCTCTGTCTTAA
ProSerPheGluHisLeuThrIleAlaThrValAsnGluArgArgMetArgIleGluIleGluAsnGlnAlaIleSerLeuSerEnd
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