

Sequence of the *Kluyveromyces lactis* URA3 gene

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We report here the sequence of the *Kluyveromyces lactis* URA3 gene (orotidine-5-phosphate decarboxylase). The gene was isolated from a Sau3A *K. lactis* genomic library by complementation of a pyrF::Tn5 mutation in *E. coli* strain MH5 (gift from Michael Hall). The isolated sequence was able to complement a *ura3* mutation of *K. lactis* as well as the *ura3-52* mutation in *S. cerevisiae*. The *K. lactis* protein is 81 percent homologous to its *S. cerevisiae* analog (1) and the DNA sequences are 71 percent homologous. These levels of homology and those of other *K. lactis* cloned genes (unpublished data) mark *K. lactis* as the yeast most related to the *Saccharomyces* genus to date. The *K. lactis* protein is about 30 percent homologous to the analogous *Neurospora crassa* PYR4 protein and the DNA sequences are about 24 percent homologous (2).

ACGTGATTTGCTTAAGAAATTGTCGTTTCAATGGTGACACTTTTAGCTTTGACATGATTAAGCTCATCT
CAATTGATGTTATCTAAAAGTCATTTCAACTATCTAAGATGTGGTTGTGATTTGGGCCATTTTGTGAA
AGCCAGTACGCCAGCGTCAATACACTCCCGTCAATTAGTTGCACC
MetSerThrLysSerTyrThrSerArgAlaGluThrHisAlaSerProValAlaSerLysLeuLeu
ATGTCCACAAAATCATATACCAGTAGAGCTGAGACTCATGCAAGTCCGGTTGCATCGAAACTTTTA
ArgLeuMetAspGluLysLysThrAsnLeuCysAlaSerLeuAspValArgSerThrAspGluLeu
CGTTTAATGGATGAAAAGAAGACCAATTGTGTGCTTCTCTTGACGTTTCGTTGACTGATGAGCTA
LeuLysLeuValGluThrLeuGlyProTyrIleCysLeuLeuLysThrHisValAspIleLeuAsp
TTGAAACTTGTGAAACGTTGGGTCCATACATTTGCCTTTTGAAAACACACGTTGATATCTTGGAT
AspPheSerTyrGluGlyThrValValProLeuLysAlaLeuAlaGluLysTyrLysPheLeuIle
GATTTCAAGTTATGAGGTTACTGTCGTTCCATTGAAAGCATTGGCAGAGAAAATACAAGTTCTTGATA
PheGluAspArgLysPheAlaAspIleGlyAsnThrValLysLeuGlnTyrThrSerGlyValTyr
TTTGAGGACAGAAAATTCGCGATATCGGTAACACAGTCAAATTACAATATACATCGGGCGTTTAC
ArgIleAlaGluTrpSerAspIleThrAsnAlaHisGlyValThrGlyAlaGlyIleValAlaGly
CGTATCGCAGAAATGGTCTGATATCACCAACGCCACGGGGTTACTGGTGCTGGTATTTGTTGCTGGC
LeuLysGlnGlyAlaGlnGluValThrLysGluProArgGlyLeuLeuMetLeuAlaGluLeuSer
TTGAAAACAAGGTGCGCAAGGTTCAACAAAGAACCAAGGGGATTTATGATGCTTGTGAAATTTGCT
SerLysGlySerLeuAlaHisGlyGluTyrThrLysGlyThrValAspIleAlaLysSerAspLys
TCCAAGGGTCTCTAGCACACGGTGAATATACTAAGGGTACCGTTGATTTGCAAAGAGTGATAAA
AspPheValIleGlyPheIleAlaGlnAsnAspMetGlyGlyArgGluGluGlyPheAspTrpLeu
GATTTGCTTATTGGGTTTATTGCTCAGAACGATATGGGAGGAAGAGAAGAAGGGTTTGAATTGGCTA
IleMetThrProGlyValGlyLeuAspAspLysGlyAspAlaLeuGlyGlnGlnTyrArgThrVal
ATCATGACCCCAAGGTGTAGGTTTAGACGACAAAGGCGATGCAATGGGTGAGCAGTACAGAACCGTC
AspGluValValSerGlyGlySerAspIleIleIleValGlyArgGlyLeuPheAlaLysGlyArg
GACGAAGTTGTAAGTGGTGGATCAGATATCATTTGTTGGCAGAGGACTTTTCGCCAAGGGTAGA
AspProLysValGluGlyGluArgTyrArgAsnAlaGlyTrpGluAlaTyrGlnLysArgIleSer
GATCCTAAGGTTGAAGGTGAAAGATACAGAAATGCTGGATGGGAAGCGTACAAAAGAGAATCAGC
AlaProHisOC
GCTCCCCATTAA
TTATACAGGAACTTAATAGAACAAATCACATATTTAATCTAATAGCCACCTGCATTGGCACGGTG
CAACACTACTTCAACTTCATCTTACAAAAGATCACGTGATCTGTTGTATTGAACTGAAAATTTTT
TGTTGCTTCTCTCTCTTTCATTATGTGAGATTTAAAAACCAGAAACTAC

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