Sequence of the flavodoxin gene from *Anabaena variabilis* 7120

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Flavodoxin is an important electron transport protein in cyanobacteria under conditions of limited iron availability (1,2). A DNA probe for the flavodoxin gene of Anacystis nidulans R2 (3) was used to localize the flavodoxin gene of Anabaena variabilis 7120 to a 5.6kb EcoRI fragment. This fragment was cloned into pUC19. From this clone a flavodoxin-encoding 0.77kb HindIII fragment was subcloned into M13mp19 in both orientations and sequenced using the chain termination method of Sanger et. al. (4). A comparison of the DNA sequences from A. nidulans R2 (3) and A. variabilis 7120 reveals that the open reading frames in both species are 513 nucleotides in length with an homology of 69.8% based on matches/length. A similar comparison of the predicted amino acid sequences also showed 69.8% homology. Twenty of the 25 residues implicated in flavin mononucleotide binding for A. nidulans R2, however, are conserved in A. variabilis 7120 (5,3).

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  3
AGATCAGGTGTCATAATGTCAAAGAAAATTGGTTTATTCTACGGTACTCAAACTGGTAAAACTGAATCAGTAGCAGAAATCATTCGAGACGAGTTTGGT
            MetSerLysLysIleGlyLeuPheTyrGlyThrGlnThrGlyLysThrGluSerValAlaGluIleIleArgAspGluPheGly
102
AATGATGTGGTGACATTACACGATGTTTCCCAGGCAGAAGTAACTGACTTGAATGATTATCAATATTTGATTATTGGCTGTCCTACTTGGAATATTGGC
AsnAspValValThrLeuHisAspValSerGlnAlaGluValThrAspLeuAsnAspTyrGlnTyrLeuIleIleGlyCysProThrTrpAsnIleGly
201
GAACTGCAAAGCGATTGGGAAGGACTCTATTCAGAACTGGATGATGTAGATTTTAATGGTAAATTGGTTGCCTACTTTGGGACTGGTGACCAAATAGGT
GluLeuGlnSerAspTrpGluGlyLeuTyrSerGluLeuAspAspValAspPheAsnGlyLysLeuValAlaTyrPheGlyThrGlyAspGlnIleGly
300
TACGCAGATAATTTTCAGGATGCGATCGGTATTTTGGAAGAAAAAATTTCTCAACGTGGTGGTAAAACTGTCGGCTATTGGTCAACTGATGGATATGAT
TyrAlaAspAsnPheGlnAspAlaIleGlyIleLeuGluGluLysIleSerGlnArgGlyGlyLysThrValGlyTyrTrpSerThrAspGlyTyrAsp
399
TTTAATGATTCCAAGGCACTAAGAAATGGCAAGTTTGTAGGACTAGCTCTTGATGAAGATAATCAATCTGACTTAACAGACGATCGCATCAAAAGTTGG
PheAsnAspSerLysAlaLeuArgAsnGlyLysPheValGlyLeuAlaLeuAspGluAspAsnGlnSerAspLeuThrAspAspArgIleLysSerTrp
498
GTTGCTCAATTAAAGTCTGAATTTGGTTTGTAAAAATTTTTCAGTTGACAGATTT
ValAlaGlnLeuLysSerGluPheGlyLeu---
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