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Sequence of the ferredoxin-NADP$^+$-reductase gene from *Anabaena* PCC 7119

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Ferredoxin-NADP$^+$-reductase (FNR, E.C.1.18.1.2) is a flavoenzyme that plays a key role in the metabolism of photosynthetic organisms. Besides catalyzing photoreduction of NADP$^+$ using ferredoxin or flavodoxin as electron donors, it has also been implicated in the reverse electron transfer from NADPH to nitrogenase via ferredoxin or flavodoxin, and in light-dependent modulation of linear and cyclic electron transport (1, 2). Cloning of the FNR gene has been performed by low-stringency hybridization with the c-DNA from pea FNR (3) and a mixed oligonucleotide probe derived from the N-terminal amino acid sequence of FNR from *Anabaena variabilis* (4). The FNR gene was localised in a 3.5 kb HindIII fragment and cloned into pEMBL8. From this clone, a 2 kb HindIII-HincII fragment containing the whole coding region for FNR was subcloned into pEMBL8 and pEMBL19 and sequenced in both directions using the method of Sanger (5). The predicted amino acid sequence shows about 50% homology with the proteins isolated from pea and spinach (3, 6) and it increases to 65% when it is compared to the FNR from the cyanobacteria *Spirulina platensis* (7).

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1
ACACCATGACTCAAGCGAAAGCCAAACACGCTGATGTTCCTGTTAATCTTTACCGTCCCAATGCTCCATTT
     MetThrGlnAlaLysAlaLysHisAlaAspValProValAsnLeuTyrArgProAsnAlaProPhe
72
ATTGGTAAGGTAATCTCTAATGAACCACTGGTAAAAGAAGGCGGGATAGGTATTGTTCAGCACATTAAATTT
IleGlyLysValIleSerAsnGluProLeuValLysGluGlyGlyIleGlyIleValGlnHisIleLysPhe
144
GATCTAACTGGTGGTAACTTAAAGTACATCGAAGGTCAAAGTATTGGTATCATTCCACCAGGAGTGGACAAG
AspLeuThrGlyGlyAsnLeuLysTyrIleGluGlyGlnSerIleGlyIleIleProProGlyValAspLys
216
AACGGCAAGCCGGAAAAATTGAGACTCTACTCCATTGCCTCGACCCGTCACGGCGATGATGTGGATGATAAA
AsnGlyLysProGluLysLeuArgLeuTyrSerIleAlaSerThrArgHisGlyAspAspValAspAspLys
288
ACCATCTCACTGTGCGTCCGTCAATTAGAGTACAAACATCCAGAAAGCGGCGAAACAGTTTACGGTGTTTGT
ThrIleSerLeuCysValArgGlnLeuGluTyrLysHisProGluSerGlyGluThrValTyrGlyValCys
360
TCTACTTACTTGACTCACATTGAACCAGGTTCAGAAGTGAAAATCACTGGGCCTGTGGGTAAAGAAATGCTG
SerThrTyrLeuThrHisIleGluProGlySerGluValLysIleThrGlyProValGlyLysGluMetLeu
432
TTACCCGATGATCCTGAAGCTAATGTCATCATGTTGGCAACAGGTACTGGTATTGCGCCTATGCGGACTTAC
LeuProAspAspProGluAlaAsnValIleMetLeuAlaThrGlyThrGlyIleAlaProMetArgThrTyr
504
CTGTGGCGGATGTTCAAGGATGCAGAAAGAGCTGCTAACCCAGAATATCAATTCAAAGGATTCTCTTGGTTA
LeuTrpArgMetPheLysAspAlaGluArgAlaAlaAsnProGluTyrGlnPheLysGlyPheSerTrpLeu
576
GTCTTTGGTGTTCCTACAACTCCTAACATTCTTTATAAAGAAGAACTGGAAGAAATCCAACAAAAATATCCC
ValPheGlyValProThrThrProAsnIleLeuTyrLysGluGluLeuGluGluIleGlnGlnLysTyrPro
648
GATAACTTCCGCCTAACTTACGCTATCAGCCGGGAGCAAAAGAATCCCCAAGGTGGCAGAATGTACATCCAA
AspAsnPheArgLeuThrTyrAlaIleSerArgGluGlnLysAsnProGlnGlyGlyArgMetTyrIleGln
720
GACCGTGTGGCAGAACACGCTGATGAACTGTGGCAATTAATCAAGAATCAAAAAACCCACACCTACATCTGT
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792
GGTTTGCGCGGTATGGAAGAGGGCATTGATGCTGCTTTAAGTGCTGCGGCTGCGAAAGAAGGTGTTACCTGG
GlyLeuArgGlyMetGluGluGlyIleAspAlaAlaLeuSerAlaAlaAlaAlaLysGluGlyValThrTrp
864
AGTGATTACCAAAAAGACCTCAAGAAAGCTGGTCGCTGGCACGTAGAAACATACTAAGTTGGTTAT
SerAspTyrGlnLysAspLeuLysLysAlaGlyArgTrpHisValGluThrTyr
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