

Nucleotide sequence of the *PHO81* gene involved in the regulation of the repressible acid phosphatase gene in *Saccharomyces cerevisiae*

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Expression of the repressible acid phosphatase gene *PHO5* in *Saccharomyces cerevisiae* involves a complex network of regulatory elements, composed of at least 5 gene products: *PHO2*, *PHO4*, *PHO80*, *PHO81* and *PHO85* (1). The *PHO81* gene was isolated on a 7 kilobase *BamHI-SalI* clone by complementation of a *pho81* mutant (2). The sequence of a 4191 base pair (bp) *SpeI-HpaI* fragment bearing the *PHO81* gene is presented here. The nucleotide sequence contains one large 3531 bp open reading

frame spanning bases 127 to 3657. Discrepancies between the sequence data and results presented by Yoshida *et al.* (1) have been noticed.

REFERENCES

1. Yoshida, K., Ogawa, N. and Oshima, Y. (1989) *Mol. Gen. Genet.* **217**, 40–46.
2. Vandenhoute, J., Legrain, M., Coquette, V., Tibor, A. and Hilger, F. (1988) *Arch. Int. Physiol. Bioch.* **96**, B116.

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1  ACTAGTTGAGCTTTTGACAAGACATACTGCTCAAAAAATCTTCATAACATTATTTTTCCGGTCCACAGTGATTGAGCTTTTGGAGAGAATAACCCCTTGG
101  AGGCAACATAGATAGATAAACGTCGAATGAAATTCGGCAAGTATTTGGAAGCCAGGCAGTTGGAACGGCGGAGTACAACAGCCATTTTATTGATTATAA
201  GGCTCTAAAGAACTTATCAAACAATGGCCATTCACAGCTAAAGGCTAGTTCAGATTTAGATTTGCATTTAACATTAGATGACATCGACGAAAAAAT
301  ATACATCAGAGACTGCAAGAAAAATAAGCTGCCTTTTTTTAACTAGAGAGGGAGCTGGAAAAAGTAAATGGTTATTATTGGCGAGAGATCCGATT
401  TAAGAATAAAATTCATATATTACACTCAAATAATAAGATTATAAGATAAATGGTAAAGCTAACTCAAACCAAGCTACCTCATTTAAAAACTTATATGC
501  GGCTTCAAAAAGTTTCAAAGGATCTTAGAAATTTGGAGCAGTATGTTGAGTTAAATAAAACGGGATTTTCAAAGCTCTGAAGAAATGGGACAAGAGA
601  TCTCAATCTCAGATAAAGATTTTACCTTGCTACTGTTGTTCCATTCAACCAATTTTACCAGAGATGGGCCACTAAAAATAACAGATGAAACTTTAC
701  ATATTCTCTTAGAGCTGAATGATATTGACAACAACAATAGAAGGGCAGACATACAATCCAGTACGTTACTAATGACGATGACGACAATAATACCAG
801  CAACAATAATAACACAATAATAATAAACAATAATAAACAACAACAACAACAATAATAAACAATATTACACAATAATTATGAATTAACAACA
901  TCAAAGATTCGGAACCAACTTGAACATCTTTTCAAGCATCTTCTCCTCCTTGGACATGGAGATGGAATCGAAAACTGGTATAAGGAAATTTTGA
1001  ATATAGCCACGGTGAAGATGTTCAAAGAAAGCATGCACTACTAAGAACTTCAGAGAAACCAAGATATTCACATATCTGCTACAAAATTCCTCAGAATC
1101  TTTTCATAAAAATGCTTTTCTTTGTTGAAGGAGTCTTAACAGCGCTTTTTTATTACTGGTGGCTAGCTCCTTTGGACGATAACTCTCTGCATATTTTC
1201  TATAAAGCAATCAGGATCATATTGATCTGTCATATTGTGACGAAGATGATCAAGTATTTTCCGAAAAACGATTTTCCAGAGGCTGCAAGTTGTCCAG
1301  AAAAAACAGCTTATTTATCTAGATGAGGCTTTAACAACATCAAAGTTATCTAAAGAAACAGTACAAAACTACTGAATGCCAAGATATACATTCGCG
1401  GGTGCGGCTACATTTAGTGCAGAGCTAGGAAAACCTGGAATTTGTTCACTCGTTGCTAATCAACCAATCTTTTAGAGGACGTTGATCCCATTGATAGTAT
1501  TCTAAGACCCCTTGGTTTGGCTATCAACAACAACCAATAGATGTTGTTAGGGATCTGCTGACTATTGGTGGTGGCAACGCATCCCAATTGAAAAAGC
1601  CAATCTGGATTATAGTAAGAATGTAATCAGCTCTACTAAAGTCCAGTTCGATCCTTTAAATGTTGCTTGTAATTTAATAATCATGACGCCGCCAAGTT
1701  ACTTTTAGAAATTCGGAGTAAGCAAAATGCTGATAATGCCAAGAACAAAGTTCACAACACTTGTGCAACCGCTTTCAAAGAACTCAACAGGTTTA
1801  TGCACCTTCATATAGTGGCAAAAATTTGGCGGATCCACAATTAATCAACTATTGATACGTTATGGGGCGGATCCCAACGAAATTTGATGGGTTAATA
1901  AATAGACGCCATTTTTACGCTGTTCTGTTCAAGTCTCTGAAATTTACTGAACTATTGAAACATAATGACGCTGGATTTGAAGATGACAACGG
2001  CCATTCGCCACTTTTTTACGCCCTTATGGGAGAGCCAGTTCGATGTTTGAATGCACCTTTACAAGACCATTAAATTTGCCATCTGCACCCCTGAATGAA
2101  ATAAATTCGCAGTCTAGTACGCAACGCCCTTAATACAATAGATTAACCCCAATGATGACAAATTTGATTTAGACATTCAGATAGCATTCCGGATTTTG
2201  CTTTACCACCGCCAATCATTCCACTAAGGAAATATGGTCATAATTTTTGGAGAAAAAATTTTCAATCAAAATTAAGTTGAGGCCAGGCTCGAGTCTAT
2301  CAAGTTGACTCAGGATAACGGCATTTATATGTCATCATCAACAGGCAAGAAATTTACTTCAAACTTACCTGAAATAATCCCGGAAATGTTATTTTA
2401  CCTGTTAGATCTGGCGAAATTAATAACTTTTGTAAAGGATATCAGTGAACAATGATGAAGAAGATGATGATAAATAGTGAAGATCATGATGATGGAG
2501  AGATAATTTTCCAAGTAGATTCAATCGACGATTTTCAATGGATTTCCGAGATATTTCTTCAATTTGGCACAAGGATAATGCCAAAACCAAGGCAATGCC
2601  ATTCCTTTTCAAGAAGGTGGCAATAAATAGTATTGCAACCATGAATTTACCCTTATTCGACACAAGACTAAATAATATGGTCTCTCACTTTGGATTAC
2701  CAAATTTATTTTCCCTTATCCGGGAAATCCACTGAAATCAATAATATGAGCCGATTTGGAAATCTACAGGAAGTATTTAATGACCTTAGTAAAGACC
2801  GTAATTTTGTACTTCTTCATCGTTGAATGGCAGTTTTATTAGTATTAGTTTGGCTCTGAATGATAAACCATAGTGGCGCCAAAACCATACGTTGA
2901  ATTCAAAGGCACGAAAGATTCTGTTAAATGATTTAACGAAAGAACAAATTTGAAAAGGTAGTGGATTTGACTTCGGTAAAAATGATGGAAGCTTCGATGA
3001  GTAACATTGAAACAATACTTATCTCGAGAGTGGTGCCTCTCAGAAGCCTACTAGAAGTTATCCCGGGTCAGCCCACTGTAATTTCTGTATATTTTC
3101  CTACAGATAAGGAAATGACACAATTTCCATCAAAAATATCGCCATTTATAAATATCAATCAATTTGATAAGCTTTTACTAATCATTTTTCGAGCATGA
3201  ACGTTTTTTGCGTACAGCGGAAGTGGGAGTATGCGCCAAATAGTTTTCAAGTTCATGCAATTTGGGAAGCTTGCTCGATCCTTAACGGAACAACCCAAT
3301  TTTCCGGTTTTGTTGCAAAATGAAAAATCTACTAGAGATTCACACCACAGGCAAAATTTGATAGTACTCCTAATTTGTTAAAGGAACTGCCCGTAAAT
3401  CTCAAAAAATGTCGATTTTTAAACACGGAACATAAACAATACATAAATGTTCAATTTGCTATGAACAATAATTTGTTAGTGTAAACGCTTCCATATGA
3501  AGTACTGAAGATCTGCTTTTGGCTAGGATCATCAAAACAAACAGGACTCTGTTGATTCGATCGTTCGGGAAAAATACCCAAATACCAGCTGATGGA
3601  GGTTACAGCGGGATCTACTAGCTTGTGAGTTGCTTTTTGAGAATAAATTTGATATGTAAGTTCTGTAATATGATGTTTGAATCTTATACATATTTT
3701  AGGAAAAACTTTTTAACCTGTTCAATTAAGGGCAACATCTTCTGCTTAGCGCTTTTATCTACAAGATCATTTCTGCACCATACTTTCCACCAACA
3801  ATACAGCTGGCTACCGTGCCTTCAGCCAAAGCATGAAATGATGGGTTCAAACCTGCTTATCCTGCAATTTACAGCGCTTTGGCCAAACCGCATAA
3901  TAGTCAATTAATTTCAAAGAACCCACCGAGCTCTATGCAATGGAATTTGATTAATTTATCTTTAATTTCTTACGGACGCACCATTTTCAATTA
4001  AATTGGGATCTTCAAACCATTTCTTACCAACTGCAAGTGAAGCATGTAATCCTTGATTGGTTATCTTTATTTAGATCAGGCTTTAGAGGTCTGCTG
4101  AAAGAGACTTTACCACCTCCAAATTTCCCACTGAACAACAATATGAAAGGTGTCATCCAGAAATCATCTGGATAATCATCTAAGTTAAC

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