Nucleotide sequence of *S. pombe* inorganic pyrophosphatase

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The gene coding for *Schizosaccharomyces pombe* inorganic pyrophosphatase (PPA) (E C 3.6.1) has been isolated by hybridization of an oligonucleotide probe originally designed for the purpose of detecting histone H1 homologue (1) with *S. pombe* genomic library which was constructed in pUC118 from the genomic DNA digested with *EcoRI*. The nucleotide sequence of 1366 base pairs (bp) from the isolated subclone includes 5' (150 bp) and 3' (349 bp) noncoding regions with a 867 bp open reading frame (ORF). The deduced amino acid (aa) sequence is 289 residues with a molecular weight of 32466 daltons. The amino acid sequence is 68.3% identical in 284 aa overlap (194/284) to *Saccharomyces cerevisiae* PPA sequence (285 aa)

(2). Also, the nucleotide sequence is 73.5% identical in 603 bp overlap (443/603) to *S. cerevisiae* PPA gene within the coding region (3). Because of the extensive homology with *S. cerevisiae* PPA, we concluded that the ORF is identical to *S. pombe* PPA gene.

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CATGCGATATTAAAAATATAAACCTGTTCCCTTAGAAAATTTATAAATTAATATAAGATT    60
TTTTGTATACATTGAGTTACAAATTTGTAGCAGATGTTGCGAATTAGTGACATTGCAACCTGTAACCAAAAAACACTTTTCAGTC    150
ATGAGTGAATACACTACCCGTAAGTTGGCGCTTTGAACACATTGGACTACCAAGTCTATGTTGAGAAAAATGGTACTCCTATCTCTTCT    240
M S E Y T T R E V G A L N T L D Y Q V Y V E K N G T P I S S
TGGCACGATATCCCTTGTATGCCAATGCTGAGAAGACCATCTTGAACATGGTTCGTTGAGATCCCTCGTTGGACTCAGGCTAAGCTTGAA    330
W H D I P L Y A N A E K T I L N M V V E I P R W T Q A K L E
ATTACCAAGGAAGCTACCTTGAACCTATCAAGCAAGATACTAAGAAGGGTAAGCTTCGTTTCGTTTCGTAAGCTTTCCTCACCACGGT    420
I T K E A T L N P I K Q D T K K G K L R F V R N C F P H H G
TACATTTGGAACACGGTGCTTTTCCTCAAACCTATGAGGATCCTAATGTTGTTTCATCCTGAAACCAAGGCCAAGGGTGATAGCGATCCT    510
Y I W N Y G A F P Q T Y E D P N V V H P E T K A K G D S D P
CTCGATGTTTGTGAGATCGGTGAAGCTCGTGGCTACACCGGCCAAGTCAAGCAAGTTAAGGTCTTGGGTGTTATGGCCCTTCTTGACGAG    600
L D V C E I G E A R G Y T G Q V K Q V K V L G V M A L L D E
GGTGAGACTGACTGGAAGGTTATTGTCATCGACGTTAATGACCCCTTAGCTCCTAAGCTTAATGATATTGAGGATGTTGAACGTCATATG    690
G E T D W K V I V I D V N D P L A P K L N D I E D V E R H M
CCTGGCTTAATCCGTGCTACTAACGAGTGGTTCCGCATTTACAAGATCCCCGATGGCAAGCCTGAAAATTCCTTTGCTTTTCAGTGGTGAA    780
P G L I R A T N E W F R I Y K I P D G K P E N S F A F S G E
TGCAAGAACCGTAAGTATGCTGAAGAAGTTGTTGCTGAGTGAATGAAGCTTGGGAGCGCCTTATTACCGGTAAGACTGATGCAAGTCT    870
C K N R K Y A E E V V R E C N E A W E R L I T G K T D A K S
GACTTTTCTTTGGTCAATGTTTCAGTCACTGGATCTGTTGCCAATGACCCCTTCCGTTTCCAGCACTATTCTCTCTGCTCAAGAGCTCGCT    960
D F S L V N V S V T G S V A N D P S V S S T I P P A Q E L A
CCTGCTCCTGTTGATCCAGCGTTCACAAATGGTTCTACATTTCTGGCTCTCTCTTTAAGTAGTAGTATCACACTATAATATAGAATAT    1050
P A P V D P S V H K W F Y I S G S P L *
AGACTATATCTGCGACACTACATTTTTGACCGAAACAGGACTATATGCGATTATCGTAGTCAGTAAATATGTGAATAATGCTACATTTTC    1140
AAATAAATGGTAAAGCGACGTAACATAAATCAAGCAGTAAACCTCATGGCATACTTAAATAACCTACAATCGTTACACACATAAATATA    1230
CAAATTACCGGTCCTTAAACATCGACATAAAACAAAAATATCATTTAACTAAGCATTAAGAGTCATTGCTCCTAATTGGGCCACCA    1320
CCGTATATACTCTCCAAACGTTTCATAATTAATCACCACCATCATC    1366

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