Nucleotide sequence of the *Penicillium chrysogenum* pyrG (orotidine-5'-phosphate decarboxylase) gene

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We have cloned a gene that encodes a functional orotidine-5'-phosphate decarboxylase and is similar to the equivalent genes from *Saccharomyces cerevisiae* (1), *Neurospora crassa* (2), *Aspergillus nidulans* (3) and *Aspergillus niger* (4). This gene complements *pyrG* mutants of *P. chrysogenum* after transformation (5,6). The *P. chrysogenum* *pyrG* gene has a 68% nucleotide homology with the sequence of *A. nidulans* and 74% with the sequence of *A. niger*. The deduced amino acid sequence has a 73% and 84% homology with the amino acid sequences of the *A. nidulans* and *A. niger* genes respectively. A single intron found in the *pyrG* gene of *A. nidulans* and *A. niger* is also present in the *pyrG* of *P. chrysogenum*.

ATG TCC TCC AAG TCG CAA TTG ACC TAC ACG GCC CCG GCC CAA TCG CAC CCC AAT CCC CTC GCG CCG AAG CTA TTC CAA GTC
Met Ser Ser Lys Ser Gln Leu Thr Tyr Thr Ala Arg Ala Gln Ser His Pro Asn Pro Leu Ala Arg Lys Leu Phe Gln Val

GCC GAA GAG AAG AAG AGC AAT GTT ACT GTC TCC GCT GAC GTG ACC ACA ACA AAG GAG CTC CTG GAC CTC GCC GAC C GTAAG
Ala Glu Glu Lys Lys Ser Asn Val Thr Val Ser Ala Asp Val Thr Thr Thr Lys Glu Leu Leu Asp Leu Ala Asp A

TGAAC CCAGC TCCCC CCACT CCAAA GGAAC AAGCC ACTAA CCATC CACAG GC CTT GGC CCC TAC ATC GCC GTG ATT AAA ACA CAC
rg Leu Gly Pro Tyr Ile Ala Val Ile Lys Thr His

ATC GAC ATC CTC TCC GAC TTC AGC CAA GAA ACA ATC GAT GGC CTG AAC GCC CTA GCG CAA AAG CAC AAC TTC CTT ATC TTC
Ile Asp Ile Leu Ser Asp Phe Ser Gln Glu Thr Ile Asp Gly Leu Asn Ala Leu Ala Gln Lys His Asn Phe Leu Ile Phe

GAA GAC CCG AAA TTC ATC GAC ATC GGC AAC ACA GTC CAG AAA CAG TAC CAC AAT GGC ACC CTC CCG ATC TCC GAA TGG GCG
Glu Asp Arg Lys Phe Ile Asp Ile Gly Asn Thr Val Gln Lys Gln Tyr His Asn Gly Thr Leu Arg Ile Ser Glu Trp Ala

CAC ATA ATC AAC TGC TCC ATC CTA CCC GGC GAG GGC ATT GTC GAG GCC CTC GCT CAA ACC GCC CAG GCC ACT GAT TTC CCC
His Ile Ile Asn Cys Ser Ile Leu Pro Gly Glu Gly Ile Val Glu Ala Leu Ala Gln Thr Ala Gln Ala Thr Asp Phe Pro

TAC GGC TCC GAG CGT GGC CTC CTC ATC CTC GCC GAG ATG ACC TCG AAG GGA TCC CTC GCA ACA GGC GCC TAC ACC TCC GCC
Tyr Gly Ser Glu Arg Gly Leu Leu Ile Leu Ala Glu Met Thr Ser Lys Gly Ser Leu Ala Thr Gly Ala Tyr Thr Ser Ala

TCC GTC GAC ATC GCG CCG AAG TAC CCC AGC TTC GTG CTT GGC TTT GTC TCG ACC CCG TCT CTC GGC GAG GTC GAG TCT ACA
Ser Val Asp Ile Ala Arg Lys Tyr Pro Ser Phe Val Leu Gly Phe Val Ser Thr Arg Ser Leu Gly Glu Val Glu Ser Thr

GAG GCG CCC GCG AGC GAG GAT TTC GTC GTC TTC ACC ACT GGC GTC AAC CTC TCG TCT AAG GGC GAT AAG CTC GGT CAG CAG
Glu Ala Pro Ala Ser Glu Asp Phe Val Val Phe Thr Thr Gly Val Asn Leu Ser Ser Lys Gly Asp Lys Leu Gly Gln Gln

TAC CAG ACG CCG CAG TCG GCT GTT GGC CCG GGT GCT GAC TTT ATT ATC TCT GGT CGT GGT ATC TAT GCC GCT GCC GAT CCT
Tyr Gln Thr Pro Gln Ser Ala Val Gly Arg Gly Ala Asp Phe Ile Ile Ser Gly Arg Gly Ile Tyr Ala Ala Ala Asp Pro

GTT GAG GCC GCT AAG CAG TAC CAG CAG CAG GGC TGG GAG GCG TAT CTG GCC CCG GTG GGT GCG CAA TAG GAGCGTGCST
Val Glu Ala Ala Lys Gln Tyr Gln Gln Gln Gly Trp Glu Ala Tyr Leu Ala Arg Val Gly Ala Gln *

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