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Sequence of the glyceraldehyde-3-phosphate dehydrogenase gene from *Bacillus subtilis*

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The Bacillus subtilis gap gene, encoding the glycolytic enzyme glyceraldehyde-3-phosphate dehydrogenase (GADPH; EC 1.2.1.12), was isolated from a genomic library of strain BR151 established in the vector pUC18 [1]. The figure shows the nucleotide sequence of gap and the derived amino-acid sequence. The polypeptide is 80% homologous (267 identical residues on a total of 334) with GAPDH from the related thermophilic species Bacillus stearothermophilus [2].

Homologies with eukaryotic GAPDH subunits range from 44% (yeast TDH1) [3] to 50% (rat) [4].

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                                                                  PvuII
                                                                 CAGCTGGATGACATAGACGCCATCCCCGATATTATTGCGGTAGCGGGCGGATCATCAAAAGCCGAAGC
  PvuI          DraI           100                                                                                DraI
  GATCGAGGCTTACTTTAAAAAGCCACGCAACACGGTTCTCGTCACAGACGAAGGAGCCGCAAAGAAGTTATTAAGGGATGAATAATCCCTCAATATAAATATCTCTCACTTATTTAAAGGAGGAAACAATC
200                                                                                                                             HpaI
  ATG GCA GTA AAA GTC GGT ATT AAC GGT TTT GGT CGT ATT GGA CGT AAC GTA TTC CGC GCA GCA TTA AAC AAT CCT GAA GTT GAG GTA GTA GCG GTT AAC
  Met Ala Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Asn Val Phe Arg Ala Ala Leu Asn Asn Pro Glu Val Glu Val Val Ala Val Asn  33
 300
  GAT TTA ACA GAT GCT AAC ATG CTG GCT CAC CTT TTA CAA TAT GAT TCT GTA CAC GGA AAA TTA GAC GCT GAA GTT TCA GTT GAC GGT AAC AAC CTT GTT
  Asp Leu Thr Asp Ala Asn Met Leu Ala His Leu Leu Gln Tyr Asp Ser Val His Gly Lys Leu Asp Ala Glu Val Ser Val Asp Gly Asn Asn Leu Val  66
  400                                 PstI
  GTT AAC GGC AAA ACA ATT GAA GTT TCT GCA GAA CGC GAT CCT GCT AAA CTT AGC TGG GGC AAA CAA GGC GTT GAA ATC GTA GTT GAA TCT ACT GGT TTC
  Val Asn Gly Lys Thr Ile Glu Val Ser Ala Glu Arg Asp Pro Ala Lys Leu Ser Trp Gly Lys Gln Gly Val Glu Ile Val Val Glu Ser Thr Gly Phe  99
    500                                                                                                        EcoRV
  TTC ACA AAA CGC GCA GAC GCT GCG AAA CAC TTA GAA GCT GGC GCG AAA AAA GTA ATC ATC TCT GCT CCT GCT AAC GAA GAA GAT ATC ACA ATT GTT ATG
  Phe Thr Lys Arg Ala Asp Ala Ala Lys His Leu Glu Ala Gly Ala Lys Lys Val Ile Ile Ser Ala Pro Ala Asn Glu Glu Asp Ile Thr Ile Val Met 135
     600
  GGT GTT AAC GAA GAT AAA TAC GAT GCG GCT AAC CAC GAT GTT ATC TCT AAC GCA TCT TGC ACA ACA AAC TGC CTT GCG CCG TTT GCA AAA GTA CTT AAC
  Gly Val Asn Glu Asp Lys Tyr Asp Ala Ala Asn His Asp Val Ile Ser Asn Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Phe Ala Lys Val Leu Asn 168
      700                                                                                     Sau3A
  GAT AAA TTC GGC ATC AAA CGC GGT ATG ATG ACA ACT GTT CAC TCT TAC ACA AAC GAT CAG CAA ATC CTT GAT CTT CCG CAC AAA GAC TAC CGT CGT GCG
  Asp Lys Phe Gly Ile Lys Arg Gly Met Met Thr Thr Val His Ser Tyr Thr Asn Asp Gln Gln Ile Leu Asp Leu Pro His Lys Asp Tyr Arg Arg Ala 201
        800  PvuII
  CGT GCA GCA GCT GAA AAC ATC ATC CCA ACA TCA ACT GGT GCT GCT AAA GCA GTT TCT CTA GTT CTT CCT GAA CTA AAA GGC AAA CTG AAC GGT GGA GCA
  Arg Ala Ala Ala Glu Asn Ile Ile Pro Thr Ser Thr Gly Ala Ala Lys Ala Val Ser Leu Val Leu Pro Glu Leu Lys Gly Lys Leu Asn Gly Gly Ala 234
         900                                                                             PvuII
  ATG CGT GTT CCA ACT CCA AAC GTT TCT CTA GTT GAC TTG GTT GCT GAA CTG AAC CAA GAA GTA ACA GCT GAA GAA GTA AAC GCA GCT CTT AAA GAA GCG
  Met Arg Val Pro Thr Pro Asn Val Ser Leu Val Asp Leu Val Ala Glu Leu Asn Gln Glu Val Thr Ala Glu Glu Val Asn Ala Ala Leu Lys Glu Ala 267
         1000                                                                                                           ClaI
  GCT GAA GGC GAC CTT AAA GGA ATC CTT GGC TAC AGC GAA GAG CCA TTA GTT TCT GGC GAC TAC AAC GGA AAC AAA AAC TCT TCT ACA ATC GAT GCT CTT
  Ala Glu Gly Asp Leu Lys Gly Ile Leu Gly Tyr Ser Glu Glu Pro Leu Val Ser Gly Asp Tyr Asn Gly Asn Lys Asn Ser Ser Thr Ile Asp Ala Leu 300
           1100
  TCT ACA ATG GTT ATG GAA GGC AGC ATG GTA AAA GTA ATC TCT TGG TAC GAT AAC GAA AGC GGC TAC TCT AAC CGC GTT GTT GAC CTT GCA GCT TAC ATC
  Ser Thr Met Val Met Glu Gly Ser Met Val Lys Val Ile Ser Trp Tyr Asp Asn Glu Ser Gly Tyr Ser Asn Arg Val Val Asp Leu Ala Ala Tyr Ile 333
            1200                         AvaII                                                                     1300
  GCA AAA AAA GGT CTT TAA TTTATAGCTGAAAAAGGACCTGACTTGGTTCTTTCGAATAGAAGCGCTATAATGAAAGCGGACAAGGGAAGGGGACGGACTCCCTTTCCCTTTTTCCATGAAGACCG
  Ala Lys Lys Gly Leu                                                                                                              338
                                                                                    1400                            Sau3A
  GCTTTCAGAAAACGCTCTGTGATAGAGAAACGACCGCGTTTTAAGCAGCTTTGCCGGCGCTTTCGCCTAAGGCCGCTGCCTGGCTTTTAGACGAACTGCCCTGTGCCGAAAAAGACTGCGATC
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