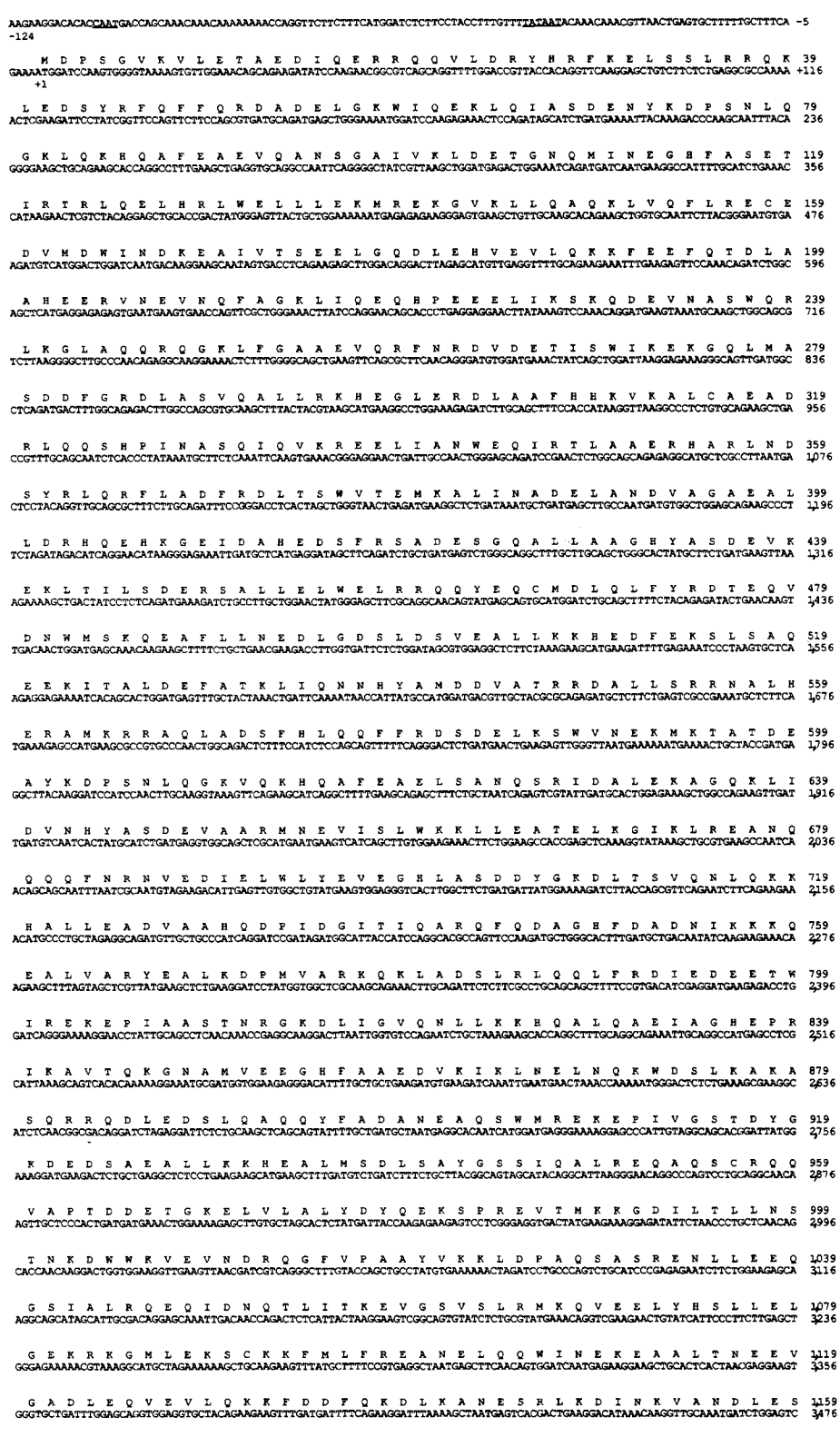
Wasenius et al., Vol. 108, No. 1, January 1989

Due to an error in production, on pages 82 and 83, the nucleotide sequence in Fig. 2 appeared out of order. The correct sequence appears below.



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  E  G  L  M  A  E  E  V  Q  A  V  E  H  Q  E  V  Y  G  M  M  P  R  D  E  T  D  S  K  T  V  S  P  W  K  S  A  R  M  M  V  1,199
TGAAGGGCTGATGGCAGAGGAAGTGCAAGCAGTAGAGCACCAGGAAGTCTATGGAATGATGCCCAGAGATGAAACTGATTCTAAGACAGTCTCTCCTTGGAAGTCTGCACGTATGATGGT  3596

  H  T  V  A  T  F  N  S  I  K  E  L  N  E  R  W  R  S  L  Q  Q  L  A  E  E  R  S  Q  L  L  G  S  A  D  E  V  Q  R  F  H  1,239
ACACACGGTGGCAACATTTAACTCAATTAAGGAACTGAATGAACGCTGGAGATCCCTGCAGCAGTTGGCAGAGGAGCGAAGCCAGCTGTTGGGCAGCGCTGATGAAGTCCAGAGGTTCCA  3716

  R  D  A  D  E  T  K  E  W  I  E  E  K  N  Q  A  L  N  T  D  N  Y  G  H  D  L  A  S  V  Q  A  L  Q  R  N  D  E  G  F  E  1,279
CAGAGATGCTGATGAAACAAAAGAATGGATAGAAGAGAAGAATCAAGCATTAAATACCGACAACTATGGACATGACTTGGCCAGTGTGCAGGCTCTGCAGCGCAACGATGAAGGCTTTGA  3836

  R  D  L  A  A  L  G  D  K  V  N  S  L  G  E  T  A  Q  R  L  I  Q  S  H  P  E  L  A  E  D  L  Q  E  K  C  T  E  L  N  Q  1,319
GAGAGACTTGGCAGCTCTTGGAGACAAGGTGAATTCTCTTGGTGAAACTGCCCAGCGTCTGATCCAGTCACATCCAGAACTAGCTGAAGATCTTCAAGAAAAATGTACTGAGTTGAACCA  3956

  A  W  S  S  L  G  K  R  A  D  Q  R  K  E  K  L  G  D  S  H  D  L  Q  R  F  L  S  D  F  R  D  L  M  S  W  I  N  G  I  R  1,359
AGCCTGGAGTAGTCTGGGAAAACGTGCTGACCAACGCAAAGAGAAGCTTGGAGATTCTCATGACCTGCAGCGTTTCCTCAGTGATTTTAGAGACCTTATGTCTTGGATCAATGGAATCCG  4076

  G  L  V  S  S  D  E  L  A  K  D  V  T  G  A  E  A  L  L  E  R  H  Q  E  H  R  T  E  I  D  A  R  A  G  T  F  Q  A  F  E  1,399
GGGTCTGGTCTCCTCAGATGAACTTGCAAAAGATGTGACTGGAGCTGAAGCTCTGTTGGAAAGGCATCAGGAGCACCGTACTGAAATAGATGCACGGGCTGGCACTTTTCAGGCATTTGA  4196

  Q  F  G  Q  Q  L  L  A  R  G  H  Y  A  S  P  E  I  K  E  K  L  D  I  L  D  Q  E  R  T  D  L  E  K  A  W  V  Q  R  R  M  1,439
ACAGTTTGGACAGCAGCTTCTGGCTCGTGGACACTATGCCAGCCCAGAGATTAAGGAGAAACTGGATATTCTAGATCAAGAACGGACAGACCTAGAGAAGGCCTGGGTCCAGCGCAGAAT  4289

  M  L  D  Q  C  L  E  L  Q  L  F  H  R  D  C  E  Q  A  E  N  W  M  A  A  R  E  A  F  L  N  T  E  D  K  G  D  S  L  D  S  1,479
GATGCTAGACCAGTGCTTAGAACTACAGCTGTTTCATCGGGATTGTGAACAAGCTGAAAACTGGATGGCTGCCCGAGAGGCGTTCCTAAATACAGAAGACAAAGGAGACTCCTTAGACAG  4409

  V  E  A  L  I  K  K  H  E  D  F  D  K  A  I  N  V  Q  E  E  K  I  A  V  L  Q  S  F  A  D  Q  L  I  A  A  D  H  Y  A  K  1,519
CGTGGAGGCACTCATCAAGAAGCATGAAGATTTCGATAAAGCAATCAATGTCCAGGAAGAGAAAAATTGCTGTCTTGCAGTCTTTTGCTGACCAACTGATTGCTGCTGATCATTATGCAAA  4529

  G  V  I  A  N  R  R  N  E  V  L  D  R  W  R  R  L  K  A  Q  M  I  E  K  R  S  K  L  G  E  S  Q  T  L  Q  Q  F  S  R  D  1,559
AGGAGTCATTGCTAACAGACGCAATGAGGTTCTGGACAGGTGGCGTCGTCTGAAGGCTCAGATGATTGAGAAGAGATCTAAGCTGGGAGAATCTCAGACCCTCCAACAGTTCAGTCGTGA  4649

  V  D  E  I  E  A  W  I  S  E  K  L  Q  T  A  S  D  E  S  Y  K  D  P  T  N  I  Q  L  S  K  L  L  S  K  H  Q  K  H  Q  A  1,599
TGTTGATGAAATAGAAGCTTGGATCAGTGAAAAGCTTCAAACTGCAAGTGATGAGTCATATAAGGATCCCACAAACATCCAGCTTTCCAAACTGCTGAGCAAGCACCAGAAGCACCAAGC  4796

  F  E  A  E  L  H  A  N  A  D  R  I  R  G  V  I  E  M  G  N  P  L  I  E  R  G  A  C  A  G  S  E  D  A  V  K  A  R  L  A  1,639
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  A  L  A  D  Q  W  E  F  L  V  Q  K  S  S  E  K  S  Q  K  L  K  E  A  N  K  Q  Q  N  F  N  T  G  I  K  D  F  D  F  W  L  1,679
TGCCCTGGCTGACCAATGGGAGTTCCTGGTCCAGAAGTCATCAGAGAAGAGTCAGAAACTGAAAGAAGCAAATAAACAGCAGAATTTCAATACCGGCATCAAGGACTTTGATTTCTGGCT  5036

  S  E  V  E  A  L  L  A  S  E  D  Y  G  K  D  L  A  S  V  N  N  L  L  K  K  H  Q  L  L  E  A  D  I  S  A  H  E  D  R  L  1,719
TTCAGAGGTGGAAGCTTTGTTGGCATCTGAAGACTATGGGAAGGACTTGGCATCAGTGAACAACCTTCTGAAGAAGCACCAATTACTGGAAGCTGATATATCTGCTCATGAGGATCGGCT  5156

  K  D  L  N  S  Q  A  D  S  L  M  T  S  S  A  F  D  T  S  Q  V  K  D  K  R  E  T  I  N  G  R  F  Q  R  I  K  S  M  A  A  1,759
GAAGGACCTGAACAGCCAGGCTGACAGTTTGATGACCAGCAGTGCTTTCGATACCTCCCAAGTAAAGGATAAACGTGAAACTATAAATGGGCGCTTCCAGAGAATCAAGAGCATGGCAGC  5276

  A  R  R  A  K  L  N  E  S  H  R  L  H  Q  F  F  R  D  M  D  D  E  E  S  W  I  K  E  K  K  L  L  V  S  S  E  D  Y  G  R  1,799
TGCCGCCGTGCGAAGCTCAACGAGTCGCACCGCTTGCATCAGTTCTTCCGTGACATGGATGATGAGGAGTCCTGGATCAAAGAGAAGAAACTGTTGGTGAGCTCAGAGGACTATGGCAG  5396

  D  L  T  G  V  Q  N  L  R  K  K  H  K  R  L  E  A  E  L  A  A  H  E  P  A  I  Q  G  V  L  D  T  G  K  K  L  S  D  D  N  1,839
AGACCTGACTGGTGTGCAGAACCTGAGGAAGAAACATAAGCGCTTGGAAGCAGAATTAGCTGCCCATGAACCTGCTATCCAGGGTGTTCTAGACACTGGCAAGAAGCTTTCAGATGATAA  5516

  T  I  G  K  E  E  I  Q  Q  R  L  A  Q  F  V  D  H  W  K  E  L  K  Q  L  A  A  A  R  G  Q  R  L  E  E  S  L  E  Y  Q  Q  1,879
CACAATTGGGAAGGAGGAGATACAGCAAAGACTGGCTCAGTTTGTGGACCACTGGAAAGAGTTAAAACAGCTGGCAGCTGCTCGGGGGCAACGTCTGGAGGAGTCCCTGGAGTACCAACA  5636

  F  V  A  N  V  E  E  E  E  A  W  I  N  E  K  M  T  L  V  A  S  E  D  Y  G  D  T  L  A  A  I  Q  G  L  L  K  K  H  E  A  1,919
GTTTGTAGCAAATGTTGAGGAAGAGGAGGCATGGATCAACGAGAAAATGACATTGGTAGCCAGTGAGGATTATGGAGACACACTTGCTGCTATCCAGGGCTTGCTGAAGAAGCATGAAGC  5756

  F  E  T  D  F  T  V  H  K  D  R  V  N  D  V  C  A  N  G  E  D  L  I  K  K  N  N  H  H  V  E  N  I  T  A  K  M  K  G  L  1,959
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  K  G  K  V  S  D  L  E  K  A  A  A  Q  R  K  A  K  L  D  E  N  S  A  F  L  Q  F  N  W  K  A  D  V  V  E  S  W  I  G  E  1,999
CAAGGGCAAGGTATCAGATCTGGAGAAAGCCGCAGCTCAGAGGAAAGCCAAACTGGATGAGAACTCTGCCTTCCTCCAGTTCAACTGGAAAGCAGATGTGGTGGAGTCATGGATAGGTGA  5996

  K  E  N  S  L  K  T  D  D  Y  G  R  D  L  S  S  V  Q  T  L  L  T  K  Q  E  T  F  D  A  G  L  Q  A  F  Q  Q  E  G  I  A  2039
GAAGGAAAACAGCCTGAAGACAGATGATTATGGCCGTGACCTCTCCTCTGTGCAAACACTACTCACCAAACAGGAAACCTTTGATGCTGGACTTCAGGCTTTCCAGCAGGAGGGAATTGC  6116

  N  I  T  A  L  K  D  Q  L  L  A  A  K  H  I  Q  S  K  A  I  E  V  R  H  A  S  L  M  K  R  W  N  Q  L  L  A  N  S  A  A  2079
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  R  K  K  K  L  L  E  A  Q  E  H  F  R  K  V  E  D  L  F  L  T  F  A  K  K  A  S  A  F  N  S  W  F  E  N  A  E  E  D  L  2119
CAGGAAAAAGAAACTCTTGGAGGCTCAGGAGCACTTCAGAAAGGTTGAAGATCTCTTCTTGACTTTTGCCAAGAAGGCCTCTGCCTTCAACAGTTGGTTTGAGAATGCTGAGGAGGACCT  6356

  T  D  P  V  R  C  N  S  L  E  E  I  K  A  L  R  E  A  H  D  A  F  R  S  S  L  S  S  A  Q  A  D  F  N  Q  L  A  E  L  D  2159
GACGGATCCCGTGCGCTGCAATTCCCTGGAAGAAATCAAAGCACTGCGAGAAGCCCACGATGCCTTCCGTTCCTCACTTAGCTCTGCCCAAGCTGACTTCAACCAGCTGGCAGAGCTTGA  6476

  R  Q  I  K  S  F  R  V  A  S  N  P  Y  T  W  F  T  M  E  A  L  E  E  T  W  R  N  L  Q  K  I  I  K  E  R  E  L  E  L  Q  2199
TCGGCAGATCAAGAGCTTCCGTGTAGCCTCCAACCCGTACACTTGGTTTACTATGGAGGCTCTTGAAGAAACTTGGAGGAATCTGCAGAAAATTATCAAGGAGCGTGAATTGGAGTTGCA  6596

  K  E  Q  R  R  Q  E  E  N  D  K  L  R  Q  E  F  A  Q  H  A  N  A  F  H  Q  W  I  Q  E  T  R  T  Y  L  L  D  G  S  C  M  2239
GAAGGAGCAGCGGAGGCAGGAAGAAAATGACAAGTTGCGCCAGGAGTTTGCTCAGCATGCTAATGCCTTCCACCAGTGGATTCAGGAGACAAGGACTTACCTGCTAGATGGGTCCTGTAT  6716

  V  E  E  S  G  T  L  E  S  Q  L  E  A  T  K  R  K  H  Q  E  I  R  A  M  R  S  Q  L  K  K  I  E  D  L  G  A  A  M  E  E  2279
GGTGGAGGAGTCGGGAACACTGGAATCCCAGCTGGAAGCTACTAAACGCAAGCACCAGGAGATCCGGGCTATGAGGAGCCAGCTGAAGAAGATTGAGGACCTTGGAGCAGCCATGGAAGA  6836

  A  L  I  L  D  N  K  Y  T  E  H  S  T  V  G  L  A  Q  Q  W  D  Q  L  D  Q  L  G  M  R  M  Q  H  N  L  E  Q  Q  I  Q  A  2319
GGCACTTATCTTGGACAACAAATACACAGAGCACAGCACCGTGGGGCTGGCGCAGCAGTGGGACCAGCTTGACCAGCTGGGAATGAGAATGCAGCACAATCTGGAACAGCAGATTCAAGC  6956

  R  N  T  T  G  V  T  E  E  A  L  K  E  F  S  M  M  F  K  H  F  D  K  D  K  S  G  R  L  N  H  Q  E  F  K  S  C  L  R  S  2359
TCGAAACACAACTGGAGTCACAGAGGAGGCCCTGAAGGAGTTCAGCATGATGTTCAAGCACTTTGACAAGGACAAATCTGGACGTCTTAATCACCAGGAGTTTAAGTCTTGCTTGCGCTC  7076

  L  G  Y  D  L  P  M  V  E  E  G  E  P  D  P  E  F  E  S  I  L  D  T  V  D  P  N  R  D  G  H  V  S  L  Q  E  Y  M  A  F  2399
CCTTGGCTATGACCTGCCCATGGTTGAGGAAGGAGAGCCTGACCCCGAATTTGAGTCTATTCTTGACACTGTTGATCCCAACAGGGATGGCCACGTCTCGCTGCAGGAGTACATGGCGTT  7196

  M  I  S  R  E  T  E  N  V  K  S  S  E  E  I  E  S  A  F  R  A  L  S  S  E  R  K  P  Y  V  T  K  E  E  L  Y  Q  N  L  T  2439
CATGATCAGCAGGGAAACAGAGAACGTGAAATCCAGCGAGGAGATTGAGAGTGCTTTCCGTGCCCTCAGCTCGGAGAGGAAGCCTTACGTGACCAAGGAGGAGCTCTACCAGAACCTGAC  7316

  R  E  Q  A  D  Y  C  I  S  H  M  K  P  Y  M  D  G  K  G  R  E  L  P  S  A  Y  D  Y  I  E  F  T  R  S  L  F  V  N  *  2479
CCGGGAGCAGGCCGACTACTGCATTTCTCACATGAAGCCCTACATGGATGGCAAGGGCAGAGAACTTCCTTCTGCCTACGACTACATAGAATTTACACGTTCACTCTTTGTGAATTGATA  7436

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