AUTHOR'S CORRECTION

Cloning and Sequencing of the Gene Encoding the Large and Small Subunits of the Periplasmic (NiFeSe) Hydrogenase of *Desulfovibrio baculatus*

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Volume 169, no. 12, p. 5404, Fig. 3: The reported nucleotide sequences were subsequently assessed for codon usage preference according to the procedure of R. Staden and A. D. McLachlan (Nucleic Acids Res. **10**:141–156, 1982). The codon probability profile for the small-subunit gene was consistent with a correct reported nucleotide sequence for this region. The reported sequence for the large-subunit gene, however, showed three regions of codon improbability. These regions of the large-subunit gene have been resequenced, and the corrected nucleotide and derived amino acid sequences for the large subunit are shown below. The stop codon at amino acid position 493 has tentatively been identified as encoding selenocysteine. We thank Gerrit Voordouw (Department of Biological Sciences, The University of Calgary, Calgary, Alberta, Canada) for doing the statistical analyses.

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GTGTCACAAGCAGCTACTCCCGCAGCTGACGGGAAAGTTAAGATTTCCATCGATCCGCTTG 1089
(M) S  Q  A  A  T  P  A  A  D  G  K  V  K  I  S  I  D  P  L   20

ACTCGGGTTGAAGGTCATCTCAAGATTGAGGTTGAAGTCAAGGACGGCAAGGTCGTCGAT 1149
 T  R  V  E  G  H  L  K  I  E  V  E  V  K  D  G  K  V  V  D   40

GCCAAGTGTTCCGGCGGAATGTTCCGCGGGTTCGAGCAGATTCTGCGCGGCGCCGCGATCCC 1209
 A  K  C  S  G  G  M  F  R  G  F  E  Q  I  L  R  G  R  D  P   60

AGGGATTCTTCCCAGATCGTACAGCGTATCTGCGGCGTGTGCCCCACGGCGCACTGTACG 1269
 R  D  S  S  Q  I  V  Q  R  I  C  G  V  C  P  T  A  H  C  T   80

GCTTCCGTCATGGCCCAGGACGACGCCTTTGGCGTCAAAGTAACCACCAACGGCCCGCATC 1329
 A  S  V  M  A  Q  D  D  A  F  G  V  K  V  T  T  N  G  R  I  100

ACCCGTAACCTGATCTTCGGCGCCAACTATCTGCAGTCTCATATTCTGCATTTCTATCAC 1389
 T  R  N  L  I  F  G  A  N  Y  L  Q  S  H  I  L  H  F  Y  H  120

CTGGCCGCCCTGGATTACGTCAAGGGTCCCGATGTATCTCCCTTTGTTCCCCGTTACGCC 1449
 L  A  A  L  D  Y  V  K  G  P  D  V  S  P  F  V  P  R  Y  A  140

AATGCGGATCTCTTGACGGATCGCATCAAGGACGGAGCCAAGGCCGATGCAACCAACACC 1509
 N  A  D  L  L  T  D  R  I  K  D  G  A  K  A  D  A  T  N  T  160

TACGGCTTGAACCAGTACCTGAAGGCGCTTGAAATCCGCCGCATCTGTCATGAGATGGTC 1569
 Y  G  L  N  Q  Y  L  K  A  L  E  I  R  R  I  C  H  E  M  V  180

GCCATGTTTGGCGGTCGCATGCCTCATGTTCAGGGCATGGTCGTGGGCGGTGCAACCGAG 1629
 A  M  F  G  G  R  M  P  H  V  Q  G  M  V  V  G  G  A  T  E  200

ATTCCCACGGCGGACAAAGTCGCGGAATACGCGGCCCGCTTCAAGGAAGTCCAGAAGTTC 1689
 I  P  T  A  D  K  V  A  E  Y  A  A  R  F  K  E  V  Q  K  F  220

GTGATCGAGGAATATCTGCCTCTGATCTACACCCTAGGTTCCGTTTACACGGATCTGTTC 1749
 V  I  E  E  Y  L  P  L  I  Y  T  L  G  S  V  Y  T  D  L  F  240

GAGACCGGCATCGGCTGGAAGAACGTCATCGCCTTCGGCGTTTTCCCCGAAGACGATGAT 1809
 E  T  G  I  G  W  K  N  V  I  A  F  G  V  F  P  E  D  D  D  260

TACAAGACCTTCCTGCTCAAGCCCGGGCGTATATATCGACGGAAAGGACGAGGAATTCGAT 1869
 Y  K  T  F  L  L  K  P  G  V  Y  I  D  G  K  D  E  E  F  D  280

TCCAAGCTGGTCAAGGAATATGTCGGACATTCCTTCTTTGACCATTCCGCTCCCGGCGGT 1929
 S  K  L  V  K  E  Y  V  G  H  S  F  F  D  H  S  A  P  G  G  300

CTGCACTACAGCGTCGGTGAAACGAATCCCAACCCGGACAAACCCGGTGCGTACAGCTTC 1989
 L  H  Y  S  V  G  E  T  N  P  N  P  D  K  P  G  A  Y  S  F  320

GTCAAGGCTCCCCGTTACAAGGACAAGCCCTGCGAAGTCGGTCCGCTGGCCCGCATGTGG 2049
 V  K  A  P  R  Y  K  D  K  P  C  E  V  G  P  L  A  R  M  W  340

GTCCAGAACCCCGAGCTCAGCCCCGTTGGCCAGAAACTGCTCAAGGAACTTTACGGCATC 2109
 V  Q  N  P  E  L  S  P  V  G  Q  K  L  L  K  E  L  Y  G  I  360

GAAGCCAAGAAGTTCCGCGATCTGGGCGACAAGGCTTTCTCCATCATGGGCCGCCACGTG 2169
 E  A  K  K  F  R  D  L  G  D  K  A  F  S  I  M  G  R  H  V  380

 CTCGTGCTGAAGAAACCTGGCTTACCGCAGTGGCCGTTGAAAAATGGCTCAAGCAGGTT 2229
 A  R  A  E  E  T  W  L  T  A  V  A  V  E  K  W  L  K  Q  V  400

CAGCCCGGCGCCGAGACCTACGTCAAGTCCGAGATTCCGGACGCCGCCGAAGGCACCGGA 2289
 Q  P  G  A  E  T  Y  V  K  S  E  I  P  D  A  A  E  G  T  G  420

TTCACTGAAGCACCCCGTGGCGCTTTGCTGCATTACCTCAAGATCAAAGACAAGAAGATC 2349
 F  T  E  A  P  R  G  A  L  L  H  Y  L  K  I  K  D  K  K  I  440

GAGAACTATCAGATCGTGTCTGCGACTCTCTGGAATGCCAACCCCAGGGATGACATGGGA 2409
 E  N  Y  Q  I  V  S  A  T  L  W  N  A  N  P  R  D  D  M  G  460

CAGCGCGGCCCGATCGAGGAAGCCCTCATCGGTGTGCCGGTTCCCGACATCAAGAATCCC 2469
 Q  R  G  P  I  E  E  A  L  I  G  V  P  V  P  D  I  K  N  P  480

GTTAATGTGGGGCGCCTGGTGCGCTCCTACGACCCGTGACTGGGCTGTGCCGTGCACGTG 2529
 V  N  V  G  R  L  V  R  S  Y  D  P  U  L  G  C  A  V  H  V  500

CTGCACGCTGAGACCGGTGAAGAACACGTTGTCAACATTGACTAACGCGGATTGACTGAA 2589
 L  H  A  E  T  G  E  E  H  V  V  N  I  D  U                 515
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