

Neurobiology. In the article "Molecular cloning of a member of a third class of Shaker-family K⁺ channel genes in mammals" by T. McCormack, E. C. Vega-Saenz de Miera, and B. Rudy, which appeared in number 13, July 1990, of *Proc. Natl. Acad. Sci. USA* (87, 5227-5231), the authors wish to correct a sequencing error. In the RKShIIIa sequence (rat Shaker-type K⁺ channel; GenBank accession no. M34052) in Fig. 1, instead of two T nucleotides at positions 1662 and 1663 (see arrow in the corrected figure below) there should be only one T. This correction eliminated the in-frame stop codon at 1690 and led to the discovery of three variants of the same sequence that differ in the carboxyl end. These variants are probably generated by alternative splicing, as they occur

after an AG, the dinucleotide that is characteristic of donor junctions (marked with a filled triangle in the corrected figure). The nucleotide and amino acid sequences of one of these variants, RKShIIIa.1, are shown in the corrected Fig. 1 below. Numbers indicate the nucleotide and amino acid positions with the chosen initiation codon as 1. The first stop codon in frame is indicated with an asterisk. The hydrophobic domains (H1-H6) and the S4 motif are underlined. The asparagine residues in consensus sequences for N-linked glycosylation are indicated with filled squares. The authors thank R. Swanson and colleagues (Merck Laboratories) for pointing out the sequencing error.

```

-79  GCCACGGTG  AACATCTGGC  CCACGAGAGC  TTTAACTGG  TGCTGTGTC  GCCTTCCTTA
-20  GTCATGTCTG  AGCCACAGAG  ATG GGC AAG  ATC GAG AAC  AAC GAG AGG  GTG ATC CTC  36
Met Gly Lys  Ile Glu Asn Asn Glu Arg Val Ile Leu  12

AAT GTC GGA GGC ACC AGG CAC GAA ACC  TAC CGC AGC  ACT CTC AAG ACC  CTT CCT  90
Asn Val Gly Thr Arg His Glu Thr Tyr Arg Ser Thr Leu Lys Thr Thr Leu Arg  30

GGA ACT CGC  CTG GCC  CTT CTC  GCC TCC  TCT GAA  CCT CAG  GGC GAC  TGC CTG  ACT  144
Gly Thr Arg Leu Ala Leu Leu Ala Ser Ser Glu Pro Gln Gly Asp Cys Leu Thr  48

GCT GCG GGT  GAC AAG  CTG CAG  CCG CTG  CCC CCT  CCG CTG  TCT CCA  CCG CCG  CGA  198
Ala Ala Gly Asp Lys Leu Gln Pro Leu Pro Pro Leu Ser Pro Pro Pro Arg  66

CGC CCT CCT  TTG TCC  CCT GTC  CCC AGC  GGC TGC  TTC GAG  GGC GGC  GCA GGC  AAC  252
Pro Pro Pro Leu Pro Val Pro Val Pro Ser Gly Cys Phe Glu Gly Ile Val Ala Asn  84

TGC AGT TCG  CAC GGT  GGC AAT  GGC AGC  CAC CAC  CCT GGG  GGA GGC  CGC GAA  TTC  306
Cys Ser Ser His Gly Thr Asp Val Thr Asp Val Thr Asp His Pro Glu Gly Arg Gly Thr  102

TTC TTC GAT  CGC CAC  CCA GGA  GTC TTC  GCT TAT  GTG CTC  AAC TAC  TAC CGC  ACG  360
Phe Phe Asp Arg His Pro Gly Val Phe Ala Tyr Val Leu Asn Tyr Tyr Arg Thr  120

GGC AAG CTG  CAC TGC  CCC GCC  GAC GTG  TGT GGA  CCG CTC  TTC GAG  GAA GAG  CTG  414
Ala Ala Gly Asp Lys Leu Glu Thr Pro Val Phe Cys Gly Pro Leu Phe Glu Glu Leu  138

GCA TTC TGG  GGC ATC  GAT GAG  ACC GAC  GTG GAG  CCC TGC  TGC TGG  ATG ACC  TAC  468
Ala Phe Trp Gly Ile Asp Gly Val Glu Pro Phe Val Glu Pro Cys Cys Trp Met Thr Tyr  156

AGG CAG CAC  GCG GAG  GCG GAG  GCC CTG  GAT ATC  TTC GAG  ACA CCC  GAC CTC  522
Arg Gln His Arg Asp Ala Glu Glu Ala Leu Asp Ile Phe Glu Thr Pro Asp Leu  174

ATC GGA GGC  GAC CCT  GGT GAT  GAT GAG  GAC CTA  GGG GGC  AAG AGA  CTG GGC  ATT  576
Ile Gly Gly Asp Pro Gly Asp Asp Glu Asp Leu Gly Gly Lys Arg Leu Gly Ile  192

GAG GAT GCT  GCG GGG  CTG GGA  GGA CCC  GAT GGC  AAG TCT  GGC CGC  TGG AGG  AAG  630
Glu Asp Ala Ala Gly Leu Glu Thr Pro Asp Gly Lys Ser Gly Arg Trp Arg Thr Tyr  210

CTG CAG CCT  CGC ATG  TGG GCT  CTT TTT  GAG GAC  CCC TAT  TCA TCC  AGA GCC  GCT  684
Leu Gln Pro Arg Met Trp Ala Leu Phe Glu Asp Pro Tyr Ser Ser Arg Ala Ala  228

AGG TTT ATT  GCT TTT  GCT TCT  CTG TTC  TTC ATT  TTG GTT  TCC ATC  ACA ACC  TTT  738
Arg Phe Ile Ala Phe Ala Ser Leu Phe Phe Ile Leu Val Ser Ile Thr Thr Phe  246

TGC CTG GAG  ACA CAC  GAA GCT  TTC AAT  ATT GTT  AAA AAC  AAG ACA  GAG CCA  GTC  792
Cys Leu Glu Thr His Thr Ser Ala Val Leu Gln Tyr Glu Ile Glu Thr Asp Pro Ala Leu  264

ATC AAC GGC  ACC AGC  GCT GTT  CTC CAG  TAT GAA  ATC GAA  ACG GAT  CCT GCC  TTG  846
Ile Asn Gly Thr Ser Ala Val Leu Gln Tyr Glu Ile Glu Thr Asp Pro Ala Leu  282

ACA TAT GTG  GAA GGA  GTG TGT  GTG GTG  TGG TTT  ACT TTT  GAA TTT  TTA GTC  CGT  900
Thr Tyr Val Glu Gly Val Cys Val Val Trp Phe Thr Phe Glu Phe Leu Val Arg  300

ATT GTT TTC  TCG CCC  AAT AAA  CTT GAG  TTC ATC  AAA AAT  CTA TTG  AAC ATC  ATT  954
Ile Val Phe Ser Pro Asn Lys Leu Glu Phe Ile Lys Asn Leu Leu Asn Ile Ile  318

GAC TTT GTG  GCC ATC  CTC CCC  TTC TAC  TTA GAG  GTG GGA  CTC AGC  GGC CTG  TCT  1008
Asp Phe Val Ala Ile Leu Leu Pro Phe Tyr Leu Glu Val Val Gly Leu Ser Gly Leu Ser  336

TCC AAA GCG  GCT AAA  GAT GTG  CTC GGC  TTT CTC  AGG GTG  GTT AGG  TTT GTG  AGG  1062
Ser Lys Ala Ala Lys Asp Val Leu Gly Phe Leu Arg Val Val Arg Phe Val Arg  354

ATC CTG AGA  ATC TTC  AAG CTT  ACC CGC  CAT TTC  GTA GGT  CTG AGA  GTG CTC  GGA  1116
Ile Leu Arg Ile Phe Lys Leu Thr Arg His Phe Val Gly Leu Arg Val Leu Gly  372
    
```

```

CAC ACT CTT  CGT GCG  AGC ACC  AAT GAA  TTT TTG  TTG CTG  ATC ATC  TTT CTG  GCT  1170
His Thr Leu Arg Ala Ser Thr Asn Glu Phe Leu Leu Leu Ile Ile Phe Leu Ala  390

CTG GGA GTT  TTG ATA  TTC GCT  ACG ATG  ATC TAC  TAC GCT  GAG CGA  GTA GGG  GCT  1274
Leu Gly Val Leu Ile Phe Ala Thr Met Ile Tyr Met Ala Leu Cys Ala Leu Ala Gly Val  408

CAA CCT AAT  GAT CCC  TCA GCG  AGT GAG  CAC  ACA CAG  TTC AAA  AAC ATC  CCC ATT  1278
Gln Pro Asn Asp Pro Ser Ala Ser Glu His Thr Gln Phe Lys Asn Ile Pro Ile  422

GGT TTC TGG  TGG GGT  GTG ACC  ATG ACT  ACC TTA  GGC TAT  GGG GAT  ATG TAC  1322
Gly Phe Trp Trp Ala Val Val Thr Met Thr Thr Leu Gly Tyr Gly Asp Met Tyr  444

CCC CAA ACA  TGG TCA  GGG ATG  TTG GTG  GGG GCC  TTG TGT  GCT CTG  GCT GGA  GTG  1386
Pro Gln Thr Arg Trp Ser Gly Met Leu Val Gly Ala Leu Cys Ala Leu Ala Gly Val  462

CTG ACC ATA  GCT ATG  CCT GTG  CCC GTC  ATT GTC  AAC AAT  TTT GGG  ATG TAC  TAC  1440
Leu Thr Ile Ala Met Pro Val Pro Val Ile Val Ala Asn Phe Asn Met Tyr Tyr  480

TCC TTT GCA  ATG GCG  AAG CAG  AAA CTT  CCA AGA  AAA AGA  AAG AAG  CAC ATT  CCT  1494
Ser Leu Ala Met Ala Lys Gln Lys Leu Pro Arg Lys Arg Lys Lys Ile Pro Ile  498

CCT GCC CCT  CTG GEA  AGC TCA  CCT ACA  TTT TGC  AAG  ACA GAA  TTA AAC  ATG GCT  1548
Pro Ala Pro Leu Ala Ser Ser Pro Thr Phe Cys Lys Thr Glu Leu Asn Met Ala  516

TGT AAC AGT  ACC CAG  AGT GAC  ACA TGT  CTG GGC  AAA GAA  AAC CGG  CTT CTG  GAA  1602
Cys Asn Arg Thr Gln Ser Asp Thr Cys Leu Glu Thr Thr Thr Thr Thr Thr Thr  534

CAT AAC AGA  TCA GTG  TTA TCA  GGT GAC  GAC AGT  ACA GGA  AGT GAG  CCG CCA  TTA  1656
His Asn Arg TCA GTG TTA TCA GGT GAC GAC AGT ACA GGA AGT GAG CCG CCA TTA  552

TCA CCT CCG  GAA AGG  CTC CCC  ATC AGA  CGC TCT  AGT ACC  AGA GAC  AAA AAC  AGA  1710
Ser Pro Pro Glu Arg Leu Pro Ile Arg Arg Ser Thr Thr Thr Thr Thr Thr Thr  570

AGA GGG GAA  ACA TGT  TTC CTG  TTG ACG  ACA GGT  GAT TAC  ACG TGC  GCT TCT  GAT  1764
Arg Gly Glu Thr Cys Phe Leu Leu Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr  588

GGA GGA ATC  AGG AAA  GAT AAC  TGC AAA  GAT GTT  GTC ATT  ACT GGT  TAC ACG  CAA  1818
Gly Gly Ile Arg Lys Asp Asn Cys Lys Asp Val Val Ile Thr Gly Tyr Thr Gln  606

GCC GAG GCC  AGA TCT  CTT ACT  TAA TGACTTGG  GAAAGGCACA  AAACATGAAA  1870
Ala Glu Ala Arg Ser Leu Thr *  613

GAAAGTGTG  TACAGAATT  ATCATGGATT  TTTGCTGCT  GAAAATGGGA  CATTGAGATT  1930
TAGCAATTCC  ANGATTGTA  CTGGAACTT  CTCTACTTA  ATGTGACCG  ATGTGACCG  1980
TTGTGTGTA  GAAAGTTC  CGATTCTCT  GAGGATTTA  AAGTTGTAA  AGAATGGTG  2050
GCTGGCACTG  AAATGGCTT  TGCCAGGAA  ATATTCTCT  TGTCACAGA  CCAGATCCA  2110
CAAAACAATG  GTAATACCA  ACGTGTCAT  GGGTCCACC  TTCTCAGAT  CTATAGCAC  2170
AGGGAGCCAC  ATTCATTGC  AGCCTCTGT  AACTCTCAG  AAATCCCCAC  AGGCTCTGA  2230
ATGGCTCTC  TCGGCTCAT  GGTGTTTTG  CTGCAATTA  CAGAGGCAG  TGAATCCAT  2290
GTAGTAGG  TGTGTTTCA  TTCTTTTAT  TTGTACATTA  CAGAGGCAG  CTCAAAAC  2350
CGATTGCCTC  ATTTCTTTC  AAACCACTA  TATATCCCT  TGTAAGACT  GTTGAACT  2410
TTTAGTCT  ACATAGAAT  CTAACTATT  CTTAGTCATG  TATTCAATTA  GTTCTGAA  2470
GCTGTACTA  TCTAGAAGAC  AGTCATCAC  ATATTCTAT  GTAGAATCT  TTTTCTATG  2530
TTACTCTAAT  TATAATAT  AAAAATATA  ATTTGECAA  TGAAATAT  TTTTATATA  2590
ATGATCAAG  AAAATGTCAG  AATATTATC  TATATAGTAG  AAATATTATC  TAAAATGCT  2690
ATTTTGCATA  AAGAGATAT  TCTCACTGG  ATTCTTTTT  TTGTGACT  TTGTGACT  2710
TGAAAGGTGT  GTTGTCTTC  ATCACTGTC  TTCTGTAAC  TGTGAGAG  TTTTTCATC  2770
TGGTAAATCA  AATCTTCCAG  AATCTTTAG  TTCCCTGGG  ATTCGAATA  TACTCTATG  2830
CCTAATATA  AACCCCTGA  TCGTGTACT  TTTGTCACA  TCTCAAGGTG  CATGCTAAT  2890
CGTTGTGATA  AGCCAATGA  CATGTACTA  ACTGAATGA  AGAATAAAG  TCAAACGATC  2950
TGGGGATAA  CTGGAATCT  ATCTGATTA  ATGAT  2985
    
```

Neurobiology. In the article "Neuropathological changes in transgenic mice carrying copies of a transcriptionally activated *Mos* protooncogene" by Friedrich Propst, Michael P. Rosenberg, Linda C. Cork, Robert M. Kovatch, Steven Rauch, Heiner Westphal, Jaspal Khillan, Nicholas T.

Schulz, George F. Vande Woude, and Paul E. Newmann, which appeared in number 24, December 1990, of *Proc. Natl. Acad. Sci. USA* (87, 9703-9707), the authors request the following corrections be noted. The list of authors and their affiliations should read as follows.

FRIEDRICH PROPST[†], MICHAEL P. ROSENBERG^{*‡}, LINDA C. CORK[§], ROBERT M. KOVATCH[¶], STEVEN RAUCH^{||}, HEINER WESTPHAL^{**}, JASPAL KHILLAN^{††}, NICHOLAS T. SCHULZ^{*}, GEORGE F. VANDE WOUDE^{**‡‡}, AND PAUL E. NEUMANN^{§§}

*ABL-Basic Research Program, National Cancer Institute-Frederick Cancer Research and Development Center, P.O. Box B, Frederick, MD 21702; [§]Division of Comparative Medicine, The Johns Hopkins University School of Medicine, 720 Rutland Avenue, Baltimore, MD 21205; [¶]Pathology Associates, Inc., Worman's Mill Court, Frederick, MD 21701; ^{||}Massachusetts Eye and Ear Infirmary, Department of Otolaryngology, Harvard Medical School, 243 Charles Street, Boston, MA 02114; ^{**}Laboratory of Molecular Genetics, National Institutes of Child Health and Human Development, National Institutes of Health, Bethesda, MD 20892; ^{††}Thomas Jefferson University, Jefferson Alumni Hall, 1020 Locust Street, Philadelphia, PA 19107; and ^{§§}Department of Neurology, The Children's Hospital, and Harvard Medical School, 300 Longwood Avenue, Boston, MA 02115