Erratum

In the September 2002 issue of CMLS, a printing error occurred concerning figure 1A in the Review Article "Copines: a ubiquitous family of Ca^{2+}-dependent phospholipid-binding proteins", by J. L. Tomsig and C. E. Creutz (CMLS 59:1467–1477). The correct figure is as follows:

Figure 1A. Sequence alignment of the human copines. (A) The predicted amino acid sequences of the seven human copines were aligned using the PRETTY program of the Genetics Computer Group Wisconsin Package. The Consensus sequence represents residues that appear in the same position in at least four of the seven copines. Asterisks mark the positions of residues conserved in all seven copines. The positions of the C2 and A domains are marked by underlining. The residues in the C2 domains that are thought to coordinate calcium are marked with a C. The residues in the A domain that are thought to coordinate magnesium are marked with an M. The sequences for copines I, III, VI and VII were obtained from current GenBank entries for full-length proteins. The sequences for copines II, IV and V were inferred from current GenBank EST entries.

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            1                                   *          *  *   *  50
   copineI   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~MAHCVT LVQLSISCDH LIDKDIGSKS
 copineIII   ~~~~~~~~~~ ~~~~~~~~~~ ~~~MAAQCVT KVALNVSCAN LLDKDIGSKS
  copineII   ~~~~~~~~~~ ~~~~~~~~~~ ~~MGPQYCVC KVELSVSGQN LLDRDVTSKS
  copineIV   MKKMSNIYE. SAANTLGIFN SP.....CLT KVELRVACKG ISDRDALSKP
 copineVII   ~~~MSAGSER GAAATPGGLP AP.....CAS KVELRLSCRH LLDRDPLTKS
   copineVI  ~~~~~~~~~~ MSDPEMGWVP EPPTMTLGAS RVELRVSCHG LLDRDTLTKP
    copineV  ~~~~~~~MEQ PEDMASLSEF DSLAGSIPAT KVEITVSCRN LLDKDMFSKS
 Consensus   ---------- ---------- -------C-T KVEL-VSC-- LLDRD—SKS
                                                         C

            51 *    *              *    ***       *           **   * *  100
   copineI   DPLCVLLQD. VGGGSWAELG RTERVRNCSS PEFSKTLQLE YRFETVQKLR
 copineIII   DPLCVLFLN. TSGQQWYEVE RTERIKNCLN PQFSKTFIID YYFEVVQKLK
  copineII   DPFCVLFTE. NNG.RWIEYD RTETAINNLN PAFSKKFVLD YHFEEVQKLK
  copineIV   DP.CVILKM. QSHGQWFEVD RTEVIRTCIN PVYSKLFTVD FYFEEVQRLR
 copineVII   DP.SVALLQ. QAQGQWVQVG RTEVVRSSLH PVFSKVFTVD YYFEEVQRLR
   copineVI  HP.CVLLKL. YSDEQWVEVE RTEVLRSCSS PVFSRVLALE YFFEEKQPLQ
    copineV  DPLCVMYTQG MENKQWREFG RTEVIDNTLN PDFVRKFIVD YFFEEKQNLR
 Consensus   DP-CVLL--- ----QW-EV- RTEV-RNCLN P-FSK-F--D Y-FEEVQ-LR
                C

                              C2 DOMAIN

            101*    *                ** *   * ** * *                150
   copineI   FGIYDID.NK TPELRDDDFL GGAECSLGQI VSS..QVLTL PLMLKPGKPA
 copineIII   FGVYDID.NK TIELSDDDFL GECECTLGQI VSS..KKLTR PLVMKTGRPA
  copineII   FALFDQD.KS SMRLDEHDFL GQFSCSLGTI VSS..KKITR PLLLLNDKPA
  copineIV   FEVHDISSNH N.GLKEADFL GGMECTLGQI VSQ..RKLSK S.LLKHGNTA
 copineVII   FEVYDTHGPS GFSCQEDDFL GGMECTLGQI VAQ..KKVTR PLLLKFGRNA
   copineVI  FHVFDAE.DG ATSPRNDTFL GSTECTLGQI VSQ..TKVTK PLLLKNGKTA
    copineV  FDLYDVDS.K SPDLSKHDFL GQAFCTLGEI VGSPGSRLEK PIVGIPGKKC
 Consensus   F-VYD-D--- ---L--DDFL G--ECTLGQI VSS---KLT- PLLLK-GK-A
                C C           C
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              151*    *    *                                    **    **    ****              * 200
    copineI   GRGTITVSAQ ELK.DNRVVT MEVEARNLDK KDFLGKSDPF LEFFRQ.GDG
  copineIII   GKGSITISAE EIK.DNRVVL FEMEARKLDN KDLFGKSDPY LEFHKQTSDG
   copineII   GKGLITIAAQ ELS.DNRVIT LSLAGRRLDK KDLFGKSDPF LEFYKPGDDG
   copineIV   GKSSITVIAE ELSGNDDYVE LAFNARKLDD KDFFSKSDPF LEIFRMNDDA
  copineVII   GKSTITVIAE DISGNNGYVE LSFRARKLDD KDLFSKSDPF LELYRVNDDQ
   copineVI   GKSTITIVAE EVSGTNDYVQ LTFRAYKLDN KDLFSKSDPF MEIYKTNEDQ
    copineV   G..TIILSAE ELSNCRDVAT MQFCANKLDK KDFFGKSDPF LVFYRSNEDG
  Consensus   GK-TIT--AE ELS--N-VV- L-F-ARKLD- KDLFGKSDPF LEFYR-N-DG
                                                    C         C
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_____   _____

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              201           **        *   *   *      *          *        *  *    * 250
    copineI   KWHLVYRSEV IKNNLNPTWK RFSVPVQHFC GGNPSTPIQV QCSDYDSDGS
  copineIII   NWLMVHRTEV VKNNLNPVWR PFKISLNSLC YGDMDKTIKV ECYDYDNDGS
   copineII   KWMLVHRTEV IKYTLDPVWK PFTVPLVSLC DGDMEKPIQV MCYDYDNDGG
   copineIV   TQQLVHRTEV VMNNLSPAWK SFKVSVNSLC SGDPDRRLKC IVWDWDSNGK
  copineVII   GLQLVYRTEV VKNNLNPVWE AFKVSLSSLC SCEETRPLKC LVWDYDSRGK
   copineVI   SDQLVWRTEV VKNNLNPSWE PFRLSLHSLC SCDVHRPLKF LVYDYDSSGK
    copineV   TFTICHKTEV MKNTLNPVWQ TFSIPVRALC NGDYDRTIKV EVYDWDRDGS
  Consensus   ---LVHRTEV VKNNLNPVW- -F-VSL-SLC -GD--RPIKV -VYDYDSDG-
                                                             C  C
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_____   **C2 DOMAIN**_____

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              251** **                                  *      *   **        300
    copineI   HDLIGTFHTS LAQL...... QAVPAEFECI HPEKQQKKKS YKNSGTIRVK
  copineIII   HDLIGTFQTT MTKLKE..AS RSSPVEFECI NEKKRQKKKS YKNSGVISVK
   copineII   HDFIGEFQTS VSQMCE..AR DSVPLEFECI NPKKQRKKKN YKNSGIIILR
   copineIV   HDFIGEFTST FKEMRG..AM EGKQVQWECI NPKYKAKKKN YKNSGTVILN
  copineVII   HDFIGEFSTT FEEMQK..AF EEGQAQWDCV NPKYKQKRRS YKNSGVVVLA
   copineVI   HDFIGEFTST FQEMQEGTAN PGQEMQWDCI NPKYRDKKKN YKSSGTVVLA
    copineV   HDFIGEFTTS YRELARGQSQ FNI...YEVV NPKKKMKKKK YVNSGTVTLL
  Consensus   HDFIGEF-TT --EM----A- -------ECI NPKK--KKK- YKNSGTV-L-
                 C
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              301          *  ***    **  *    ***   ***   *** *      *  **    *  350
    copineI   ICRVETEYSF LDYVMGGCQI NFTVGVDFTG SNGDPSSPDS LHYLSPTGVN
  copineIII   QCEITVECTF LDYIMGGCQL NFTVGVDFTG SNGDPRSPDS LHYISPNGVN
   copineII   SCKINRDYSF LDYILGGCQL MFTVGIDFTA SNGNPLDPSS LHYINPMGTN
   copineIV   LCKIHKMHSF LDYIMGGCQI QFTVAIDFTA SNGDPRNSCS LHYIHPYQPN
  copineVII   DLKFHRVYSF LDYIMGGCQI HFTVAIDFTA SNGDPRNSCS LHYINPYQPN
   copineVI   QCTVEKVHTF LDYIMGGCQI SFTVAIDFTA SNGDPRSSQS LHCLSPRQPN
    copineV   SFAVESECTF LDYIKGGTQI NFTVAIDFTA SNGNPSQSTS LHYMSPYQLN
  Consensus   -C------SF LDYIMGGCQI -FTVAIDFTA SNGDPR-S-S LHYISP-Q-N
                                    M   M     M
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              351 *    *    **      *  ** **       ****    **    ***   *   * 400
    copineI   EYLMALWSVG SVVQDYDSDK LFPAFGFGAQ VPPDWQVSHE FALNFNPSNP
  copineIII   EYLTALWSVG LVIQDYDADK MFPAFGFGAQ IPPQWQVSHE FPMNFNPSNP
   copineII   EYLSAIWAVG QIIQDYDSDK MFPALGFGAQ LPPDWKVSHE FAINFNPTNP
   copineIV   EYLKALVAVG EICQDYDSDK MFPAFGFGAR IPPEYTVSHD FAINFNEDNP
  copineVII   EYLKALVSVG EICQDYDSDK RFSALGFGAR IPPKYEVSHD FAINFNPEDD
   copineVI   HYLQALRAVG GICQDYDSDK RFPAFGFGAR IPPNFEVSHD FAINFDPENP
    copineV   AYALALTAVG EIIQHYDSDK MFPALGFGAK LPPDGRVSHE FPLNGNQENP
  Consensus   EYL-AL-AVG -I-QDYDSDK MFPAFGFGA- IPP---VSHE FAINFNP-NP
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Figure 1A (continued)

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         401  *       *      *    *      *****  *       **   *          *450
   copineI   YCAGIQGIVD AYRQALPQVR LYGPTNFAPI INHVARFAAQ AAHQGTASQY
 copineIII   YCNGIQGIVE AYRSCLPQIK LYGPTNFSPI INHVARFAAA ATQQQTASQY
  copineII   FCSGVDGIAQ AYSACLPHIR FYGPTNFSPI VNHVARFAAQ ATQQRTATQY
  copineIV   ECAGIQGVVE AYQSCLPKLQ LYGPTNIAPI IQKVAKSASE ETNTKEASQY
 copineVII   ECEGIQGVVE AYQNCLPRVQ LYGPTNVAPI ISKVARVAAA EESTGKASQY
  copineVI   ECEEISGVIA SYRRCLPQIQ LYGPTNVAPI INRVAEPAQR EQSTGQATKY
   copineV   SCCGIDGILE AYHRSLRTVQ LYGPTNFAPV VTHVARNAAA VQD...GSQY
 Consensus   -C-GIQGIVE AY--CLP--Q LYGPTNFAPI INHVAR-AA- ------ASQY
                                     M
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A DOMAIN

```
         451  **   ***    *    *    *    * *   ****  ****** *   *   *  ** *500
   copineI   FMLLLLTDGA VTDVEATREA VVRASNLPMS VIIVGVGGAD FEAMEQLDAD
 copineIII   FVLLIITDGV ITDLDETRQA IVNASRLPMS IIIVGVGGAD FSAMEFLDGD
  copineII   FILLIITDGV ISDMEETRHA VVQASKLPMS IIIVGVGNAD FAAMEFLDGD
  copineIV   FILLILTDGV ITDMADTREA IVHASHLPMS VIIVGVGNAD FSDMQMLDGD
 copineVII   YILLILTDGV VTDMADTREA IVRASRLPMS IIIVGVGNAD FTDMQVLDGD
  copineVI   SVLLVLTDGV VSDMAETRTA IVRASRLPMS IIIVGVGNAD FSDMRLLDGD
   copineV   SVLLIITDGV ISDMAQTKEA IVNAAKLPMS IIIVGVGQAE FDAMVELDGD
 Consensus   F-LLILTDGV ITDMA-TREA IV-AS-LPMS IIIVGVGNAD F-AM--LDGD
                M
```

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         501          *    *******  * *                  **   ****  * *550
   copineI   GGPLHTRSGQ AAARDIVQFV PYRRFQN... ...APREALA QTVLAEVPTQ
 copineIII   GGSLRSPLGE VAIRDIVQFV PFRQFQN... ...APKEALA QCVLAEIPQQ
  copineII   SRMLRSHTGE EAARDIVQFV PFREFRN... ...AAKETLA KAVLAELPQQ
  copineIV   DGILRSPKGE PVLRDIVQFV PFRNFKH... ...ASPAALA KSVLAEVPNQ
 copineVII   DGVLRSPRGE PALRDIVQFV PFRELKN... ...ASPAALA KCVLAEVPKQ
  copineVI   DGPLRCPRGV PAARDIVQFV PFRDFKD... ...AAPSALA KCVLAEVPRQ
   copineV   DVRI.SSRGK LAERDIVQFV PFRDYVDRTG NHVLSMARLA RDVLAEIPDQ
 Consensus   DG-LRSP-GE -A-RDIVQFV PFR-F-N--- ---A---ALA K-VLAEVP-Q
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         551 * *            *                       590
   copineI   LVSYFRAQGW APLKPLP..P SAKDPAQAPQ A~~~~~~~~~
 copineIII   VVGYFNT..Y KLLPPKN..P ATKQQKQ~~~ ~~~~~~~~~~
  copineII   VVQYFK...H KNLPPTNSEP A~~~~~~~~~ ~~~~~~~~~~
  copineIV   VVDYYNGKG. ..IKPK.CSS EMYESSRTLA P~~~~~~~~~
 copineVII   VVEYYSHRG. ..LPPRSLGV PAGEASPGCT P~~~~~~~~~
  copineVI   VVEYYASQG. ..ISPGAPRP CTLATTPSPS P~~~~~~~~~
   copineV   LVSYMKAQGI RPRPPPAAPT HSPSQSPART PPASPLHTHI
 Consensus   VV-Y----G- --LPP----P ---------- P---------
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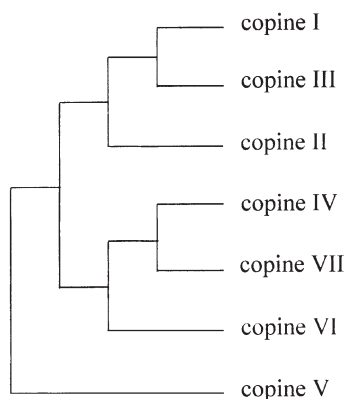
Figure 1 A (continued)

Figure 1 B. Multiple sequence alignment dendrogram for the seven human copines, as generated by the PILEUP program of the Genetics Computer Group Wisconsin Package.