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## Structure and variability of recently inserted alu family members

M. A. Batzer

G. E. Kilroy

P. E. Richard

T. H. Shaikh

T. D. Desselle

*See next page for additional authors*

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**Authors**

M. A. Batzer, G. E. Kilroy, P. E. Richard, T. H. Shaikh, T. D. Desselle, C. L. Hoppens, and P. L. Deininger

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## Addendum

### Factor IX<sub>Basel</sub>: a Swiss family with severe haemophilia B having a point mutation in EGF type B domain

by M.Alkan, M.Rodriguez Ponte, N.T.Malik, S.Hofmann, N.Bösch-Al Jadoo, Hj.Müller and E.M.Bühler

*Nucleic Acids Research*, **19**, p. 409 (1991)

D.D.Koeberl *et al.* recently reported FIX<sub>Toronto 2</sub> mutation which Cys 56 within the EGF type B domain is substituted by thymosine resulting also in severe haemophilia B (*Am.J.Hum.Genet.*, **47**, 202–217, 1990).

## Corrigendum

### Optimization of the annealing temperature for DNA amplification *in vitro*

by W.Rychlik, W.J.Spencer and R.E.Rhoads

*Nucleic Acids Research*, **18**, pp. 6409–6412 (1990)

Equation (iii) from the above article is published below in complete form

$$T_m^{\text{product}} = 81.5 + 0.41 (\%G + \%C) + 16.6 \log[K^+] - 675/l$$

## Erratum

### Structure and variability of recently inserted Alu family members

by M.A.Batzer, G.E.Kilroy, P.E.Richard, T.H.Shaikh, T.D.Desselle, C.L.Hoppens and P.L.Deininger

*Nucleic Acids Research*, **18**, pp. 6793–6798 (1990)

The publishers wish to apologize for an error which occurred during printing of the above article. Figure 1 appeared with an incorrect figure legend. The correct figure and legend are published below.

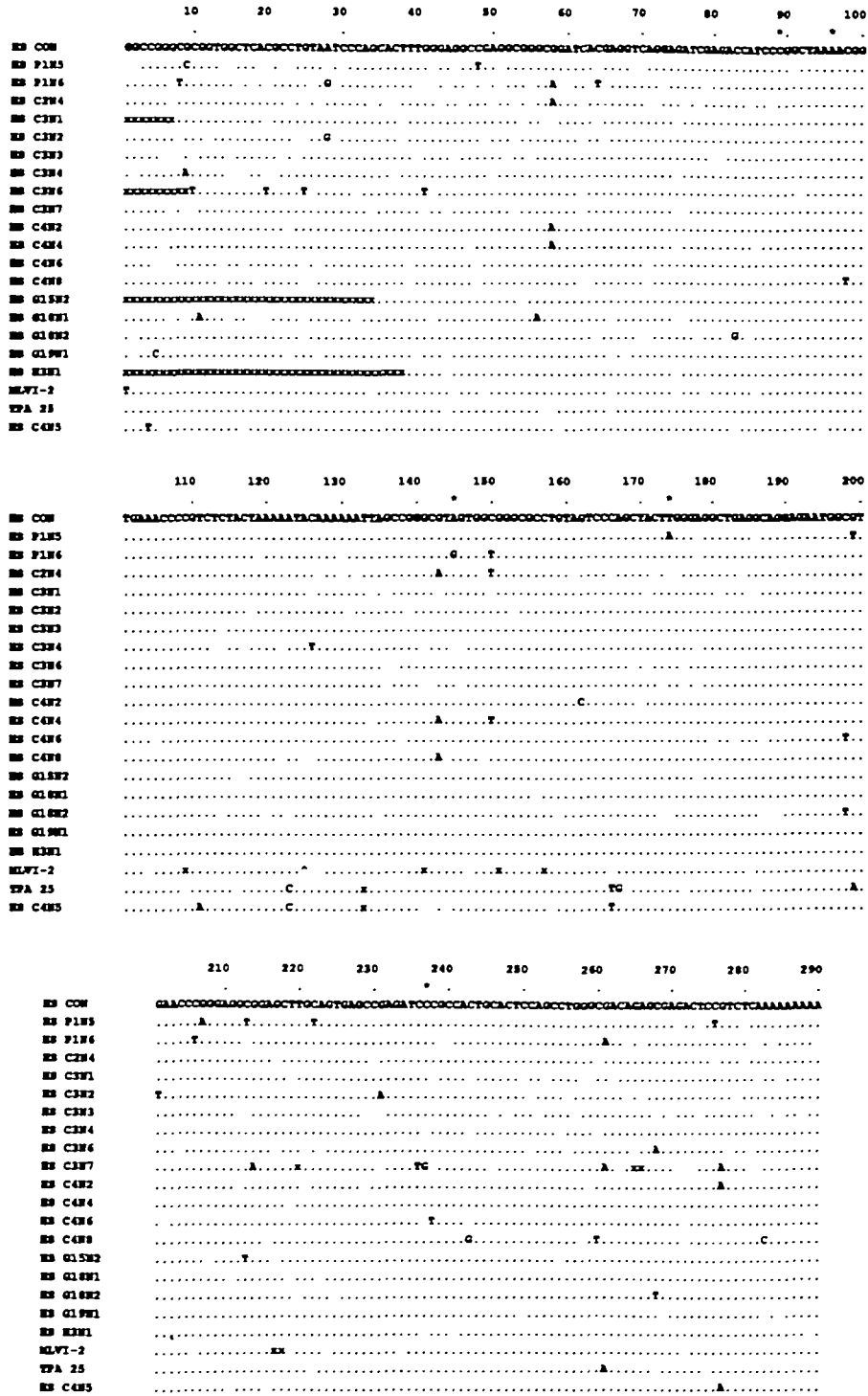


Figure 1. Alignment of HS subfamily members. Alignment of TPA 25 (19), MLVI-2 (20), HS C2N4, C3N1, C4N4, C4N5, C4N6, and C4N8 (18), as well as several other sequences reported here. The HS-I subfamily consensus (con) is derived from the most common nucleotide found at each position within the subfamily members. The HS-I consensus differs from the consensus for older Alu sequences (shown as a star above the consensus) as previously reported (18). Nucleotide substitutions at each position are indicated with the appropriate nucleotide. Insertions are indicated with an ^ . Deletions are marked by an X.