

Human homologs of a *Drosophila* Enhancer of split gene product define a novel family of nuclear proteins

S. Stifani, C. M. Blau Mueller, N. J. Redhead, R. E. Hill & S. Artavanis-Tsakonas
Nature Genetics 2, 119–127 (1992)

The following parts of this paper appear now in their correct format.

Table 2 Comparison of the CcN motif of E(spl) m9/10, TLE proteins and proteins with demonstrated nuclear localization and susceptibility to phosphorylation by casein kinase II and/or cdc2

| Protein | CK-II site ^a | cdc2 site ^a |
|---------------------------------|--|---|
| E(spl) m9/10 | 231SDQD | 247SPRP |
| TLE 1 | 239SDGD | 259SPRA ²⁶³ SPA ²⁶⁷ SFR |
| TLE 2 | 228SDED | 249SPAT ²⁵³ TPCGK |
| TLE 3 | 239SDGD | 258TPRV ²⁶² SPA ²⁶⁶ SPP |
| SV 40 T antigen | 111S ¹¹² SDDE | S ¹²⁴ TPPK |
| human c-myc | S ³⁸⁴ SDTE | T ³⁴⁴ SPRS |
| human p53 | 284TEEE | S ³¹⁵ SPQP |
| human A-myb dorsal ^b | 467SLND 312SDGV ³¹⁶ TSEA | 479TRLK 296TPRY |

^aPhosphorylatable Ser/Thr residues are numbered.

^bThe *Drosophila* protein dorsal was included as one example of several other proteins bearing a putative CcN motif for which only translocation to the nucleus has been demonstrated.

Linkage disequilibrium mapping in isolated founder populations: diastrophic dysplasia in Finland

J. Hästbacka, A. de la Chapelle, I. Kaitila, P. Sistonen, A. Weaver & E. Lander
Nature Genetics 2, 204–211 (1992)

In the Methodology section of this paper the section entitled 'Estimation of recombination and mutation' appeared without important mathematical symbols in the explanation of equations. The correct version is as follows:

(Equations (1) and (2) correspond essentially to equations (8) and (12) of Luria and Delbrück, with the substitutions $N = N, C$ and $\sigma' = (\text{var } \bar{y}) / (C)$. With regard to the second substitution, our standard deviation σ' is smaller by a factor (C) than Luria-Delbrück's standard deviation $(\text{var } \bar{y})$ because we are interested in the standard deviation of the average of the proportions of mutants in the descendants of the C founders, whereas Luria and Delbrück were interested in the standard deviation among the proportions.)

A frameshift mutation in the γ E-crystallin gene of the Elo mouse

Mireille Cartier, Martin L. Breitman & Lap-Chee Tsui
Nature Genetics 2, 42–45 (1992)

The correct alignment for Table 1 in this paper is as follows:

Table 1 Complete association of Elo with the G403 deletion

| Phenotype | Number of mice | G403 deletion | Polymorphism at position 444 |
|-----------|----------------|---------------|------------------------------|
| Wild-type | 143 | no | T |
| Elo | 131 | yes | A |
| (Total) | 274 | | |

Q Domain

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E(spl)m9/10 1  MHSFVRRHHAAGGPPFQCFDITGDIADTLRPLTMEFVFLQVYHSITRLEKLNKTEKEMORHYVMYVE
TLE 1      1  MHSFVRRHHTPHQAAGC-PNKGRIPELSLRIEMEFVFLQVYHSITRLEKLNKTEKEMORHYVMYVE
TLE 2      1  MHSFVRRHHTPHQAGC-PNKGRIPELSLRIEMEFVFLQVYHSITRLEKLNKTEKEMORHYVMYVE
TLE 3      1  MHSFVRRHHTPHQAGC-PNKGRIPELSLRIEMEFVFLQVYHSITRLEKLNKTEKEMORHYVMYVE
  
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GP Domain

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E(spl)m9/10 134  V---PCGPPQPMGALNPPGALGATMGLPHQO-GLINKPPEHRPDIK--PTGLEGPA-AEKRIE-[-]-[-]-N-
TLE 1      138  HLSH-GKQPPVPLTPHPSGLQPPGIPPL-GEBA-GLIALSSALSGSHLA--IKDKKHDA-EHII-DREPTG-
TLE 2      128  HLSH-EMPHVPLTPR-----AG---LVGKATGLIALSQAQAQALAAAVKEDAGVEA-EGSIVERRAPSK-
TLE 3      131  HLSHATAGPVCVPPHPSGLQPPGIPVPTG-ESSGLIALG-ALGSOAHLT--VKDEKHHL-DH-IE-ESSA
  
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CcN Domain

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E(spl)m9/10 195  ---VSEAL-REK-YMTRSPFLDIENDSRRI-DRILOEDEGENSDQ---LVVDVANE-MESHSPRNGEMVS
TLE 1      200  NSSLVH-DSLAGTKRNRKGF-EFSNDIRHRVDDK-SHYD-SIGDKSDINLVVDVANE-MS-SPRASPMSF
TLE 2      192  ASP-EPHPSLVE-EDPSSGP---GGGKGR-ADMEPSSGPTP-SIGDKSDINLVVDV---EIQNSE-P-PPATTP
TLE 3      198  NNSVSESELKASEKRRGSA-DYSMEAPRVEVMSDLSRVD-SIGDKSD-LVVDVANEU-ELATEVSPMSF
  
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SP Domain

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E(spl)m9/10 257  MIVRDRRESLNGER-LEKPSSEGIKQERPPSRSSGSSSRSTPRLKTRDM---ELP-CITGPA
TLE 1      269  PIKQ-LDKARLKKDA---SPEPAFTA-----SSAST-ELKNSHSLER-AMTFVLEP
TLE 2      255  PIKQ-LDKARLKKDA---SPEPAFTA-----SSAST-ELKNSHSLER-AMTFVLEP
TLE 3      268  PIKQ-LDKARLKKDA---SPEPAFTA-----SSAST-ELKNSHSLER-AMTFVLEP
  
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MD-40 Domain

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E(spl)m9/10 399  MNGEHSQVPPFSDMIVVQVIRPHARQILTLRHGIVVCAVTISMPFKVVTGGKGVKWDLSIQPG
TLE 1      450  VTAQKQVQVPPFSDMIVVQVIRPHARQILTLRHGIVVCAVTISMPFKVVTGGKGVKWDLSIQPG
TLE 2      423  VSAHQKQVPPFSDMIVVQVIRPHARQILTLRHGIVVCAVTISMPFKVVTGGKGVKWDLSIQPG
TLE 3      451  VSAHQKQVPPFSDMIVVQVIRPHARQILTLRHGIVVCAVTISMPFKVVTGGKGVKWDLSIQPG
TLE 4      451  VSAHQKQVPPFSDMIVVQVIRPHARQILTLRHGIVVCAVTISMPFKVVTGGKGVKWDLSIQPG
  
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Other domains

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E(spl)m9/10 466  NNSFVQLDCLLRDNYRSCILIPDQGLIVGGHSLRIIWDLNSPTPRIKAELTSAFACYALAS
TLE 1      517  NNSFVQLDCLLRDNYRSCILIPDQGLIVGGHSLRIIWDLNSPTPRIKAELTSAFACYALAS
TLE 2      490  NNSFVQLDCLLRDNYRSCILIPDQGLIVGGHSLRIIWDLNSPTPRIKAELTSAFACYALAS
TLE 3      518  NNSFVQLDCLLRDNYRSCILIPDQGLIVGGHSLRIIWDLNSPTPRIKAELTSAFACYALAS
TLE 4      518  NNSFVQLDCLLRDNYRSCILIPDQGLIVGGHSLRIIWDLNSPTPRIKAELTSAFACYALAS
  
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E(spl)m9/10 533  PIRKVCFCSCSDGNINVDLNEIIVROFQGHDTGASCIDISNDKTLMTGGLDNIVRWDLREGQ
TLE 1      584  PIRKVCFCSCSDGNINVDLNEIIVROFQGHDTGASCIDISNDKTLMTGGLDNIVRWDLREGQ
TLE 2      691  PIRKVCFCSCSDGNINVDLNEIIVROFQGHDTGASCIDISNDKTLMTGGLDNIVRWDLREGQ
TLE 3      585  PIRKVCFCSCSDGNINVDLNEIIVROFQGHDTGASCIDISNDKTLMTGGLDNIVRWDLREGQ
TLE 4      585  PIRKVCFCSCSDGNINVDLNEIIVROFQGHDTGASCIDISNDKTLMTGGLDNIVRWDLREGQ
  
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E(spl)m9/10 600  LQHDRSSQIFSLQVCFVQVAVLAVGHESEVEMLVHAKRDKYQLHLHESCVLSLFAACQWVSTG
TLE 1      651  LQHDRSSQIFSLQVCFVQVAVLAVGHESEVEMLVHAKRDKYQLHLHESCVLSLFAACQWVSTG
TLE 2      652  LQHDRSSQIFSLQVCFVQVAVLAVGHESEVEMLVHAKRDKYQLHLHESCVLSLFAACQWVSTG
TLE 3      624  LQHDRSSQIFSLQVCFVQVAVLAVGHESEVEMLVHAKRDKYQLHLHESCVLSLFAACQWVSTG
TLE 4      624  LQHDRSSQIFSLQVCFVQVAVLAVGHESEVEMLVHAKRDKYQLHLHESCVLSLFAACQWVSTG
  
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E(spl)m9/10 667  KINLLNAWRTPYGASTVOSKESVSSVSCDISDCKRYIVTGGDKKATVYEVIV
TLE 1      718  KINLLNAWRTPYGASTVOSKESVSSVSCDISDCKRYIVTGGDKKATVYEVIV
TLE 2      691  KINLLNAWRTPYGASTVOSKESVSSVSCDISDCKRYIVTGGDKKATVYEVIV
TLE 3      719  KINLLNAWRTPYGASTVOSKESVSSVSCDISDCKRYIVTGGDKKATVYEVIV
TLE 4      719  KINLLNAWRTPYGASTVOSKESVSSVSCDISDCKRYIVTGGDKKATVYEVIV
  
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Fig. 1 Comparison of the amino acid sequence of *Drosophila* E(spl) m9/10 and human TLE proteins. Amino acids are numbered on the left side. Identical residues in all compared sequences are boxed, while residues identical in either three out of four or four out of five sequences are indicated in boldface type. Alignments maximize continuity between all sequences. Underlined amino acid residues correspond to the CcN motif (see text). The GenBank accession numbers for the corresponding nucleotide sequences are: TLE 1, M99435; TLE 2, M99436; TLE 3, M99438; TLE 4, M99439.