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

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

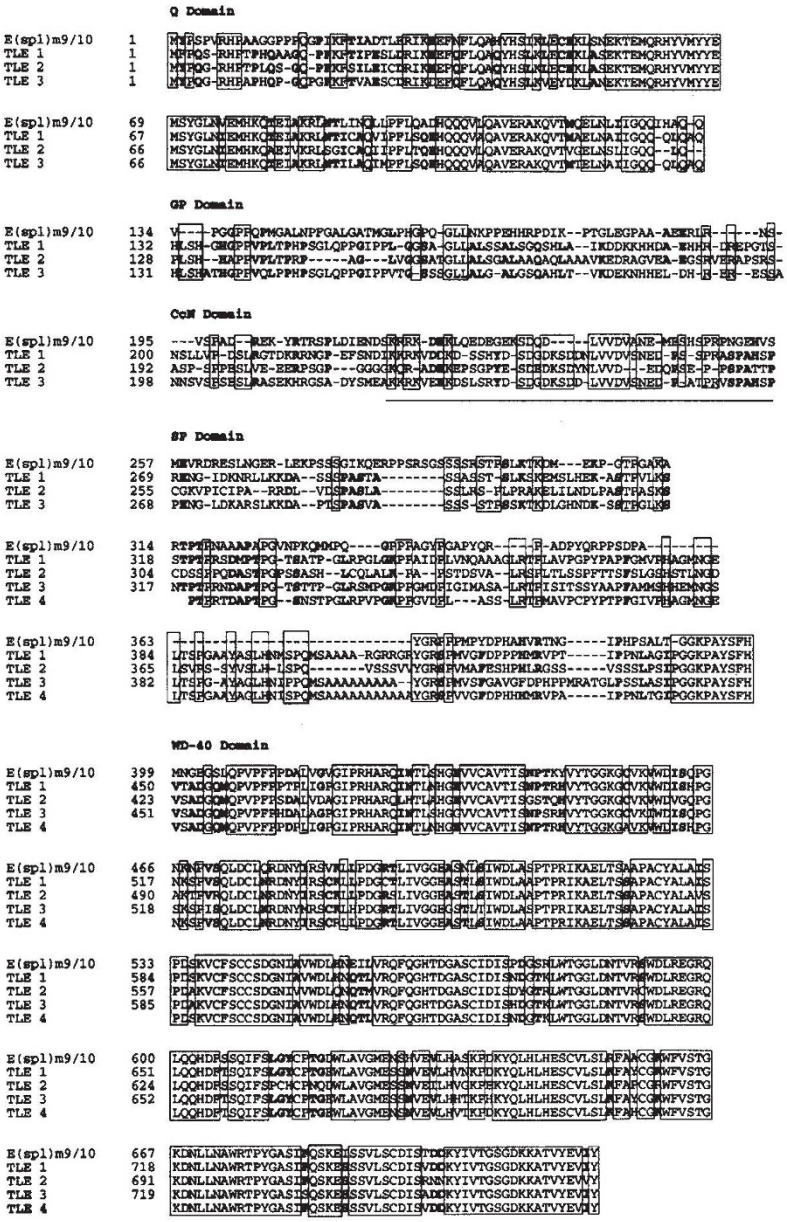

Fig. 1 Comparison of the amino acid sequence of *Drosophila* E(spl) m9/10 and human TLE proteins. Amino acids are numbered on the left side. Identical residues in all compared sequences are boxed, while residues identical in either three out of four or four out of five sequences are indicated in boldface 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.

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	^{231}SDQD	^{247}SPRP
TLE 1	^{239}SDGD	^{259}SPRA^{263}SPAH^{267}SPR
TLE 2	^{228}SDED	^{249}SPAT^{253}TPCGK
TLE 3	^{239}SDGD	^{258}TPRV^{262}SPAH^{266}SPP
SV 40 T antigen	^{111}S^{112}SDDE	S^{124}TPPK
human c-myc	S^{384}SDTE	T^{344}SPRS
human p53	^{284}TEEE	S^{315}SPQP
human A-myb	^{467}SLND	^{479}TRLK
dorsal[b]	^{312}SDGV^{316}TSEA	^{290}TPRY

[a]Phosphorylatable Ser/Thr residues are numbered.
[b]The *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

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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 $N = N_t C$ and $\sigma' = (\mathrm{var}_r)/(\overline{C})$. With regard to the second substitution, our standard deviation σ' is smaller by a factor $(\overline{C})$ than Luria-Delbrück's standard deviation (var_r) 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 γE-crystallin gene of the Elo mouse

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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		