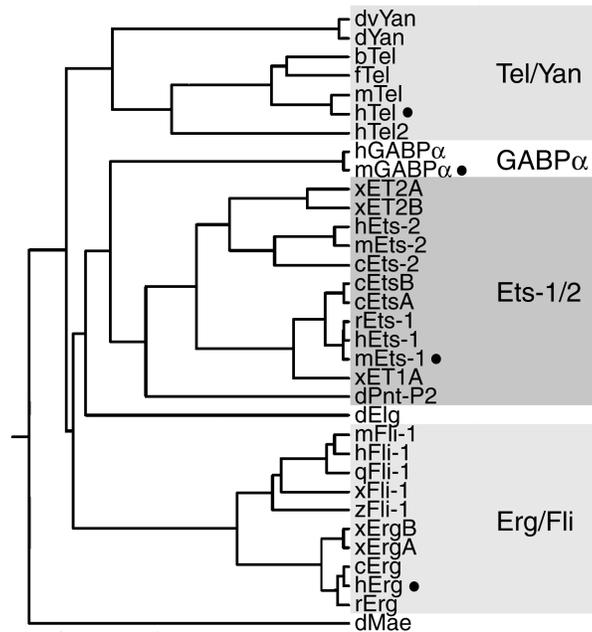


"Diversity in structure and function of the Ets family PNT domains"

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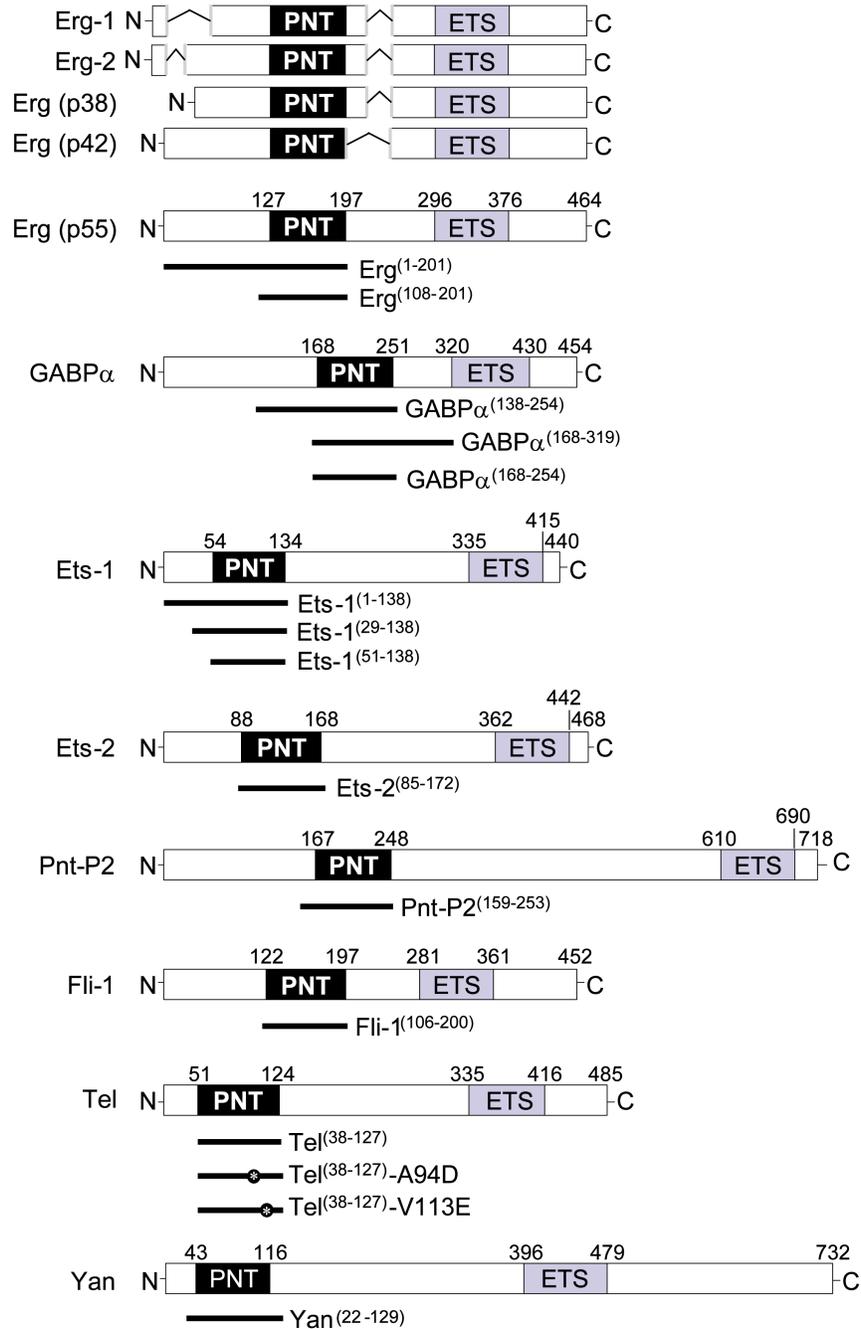
Supplementary Figure S1. Phylogenetic alignment of Ets family PNT domains. Thirty-three PNT domain sequences were clustered according to sequence similarity using the TRACE server (<http://www-cryst.bioc.cam.ac.uk/~jiye/evoltrace/evoltrace.html>).^{1,2} The sequences were grouped into sub-families based on phylogenetic similarity, with the exception of Yan, which was included with the Tel sub-family since there are no other Tel orthologues in *Drosophila*. The protein dElg may be an additional member in the GABP α sub-family based on a similar positioning of domains within the full-length transcription factors, as well as protein sequence identity outside of the PNT domain. dMae is included as an outlier, since it contains a PNT domain yet is not a member of the Ets family due to the lack of a DNA-binding ETS domain. A black dot indicates the PNT domains with known tertiary structures. The following sequences were used in the alignment (with SwissProt accession numbers): dvYan (O96416), dYan (Q01842), bTel (Q90ZS9), fTel (Q90ZS8), mTel (P97360), hTel (P41212), hTel2 (Q9Y603), hGABP α (Q06546), mGABP α (Q00422), xET2A (P19102), xET2B (Q91712), hEts-2 (P15036), mEts-2 (P15037), cEts-2 (P10157), cEtsB (P15062), cEtsA (P13474), rEts-1 (P41156), hEts-1 (P14921), mEts-1 (P27577), xET1A (P18755), dPnt-P2 (P51023), dElg (Q04688), mFli-1 (P26323), hFli-1 (AAH01670), qFli-1 (O93425), xFli-1 (P41157), zFli-1 (Q9PU61), xErgB (Q9W6Z9), xErgA (Q9W700), cErg (Q90837), hErg (P11308), rErg (BAB62744), dMae (NP_523786). The organism abbreviations are: b, bovine (*Bos taurus*); c, chicken (*Gallus gallus*); d, *Drosophila melanogaster*; dv, *Drosophila virilis*; f, *Fugu rubripes*; h, human (*Homo sapiens*); m, murine (*Mus musculus*); q, quail (*Coturnix coturnix*); r, rat (*Rattus norvegicus*); x, *Xenopus laevis*; and z, zebrafish (*Danio rerio*).

1. Lichtarge, O., Bourne, H. R. & Cohen, F. E. (1996). *J. Mol. Biol.* **257**, 342-358.

2. Innis, C. A., Shi, J. & Blundell, T. L. (2000). *Protein Eng.* **13**, 839-847.

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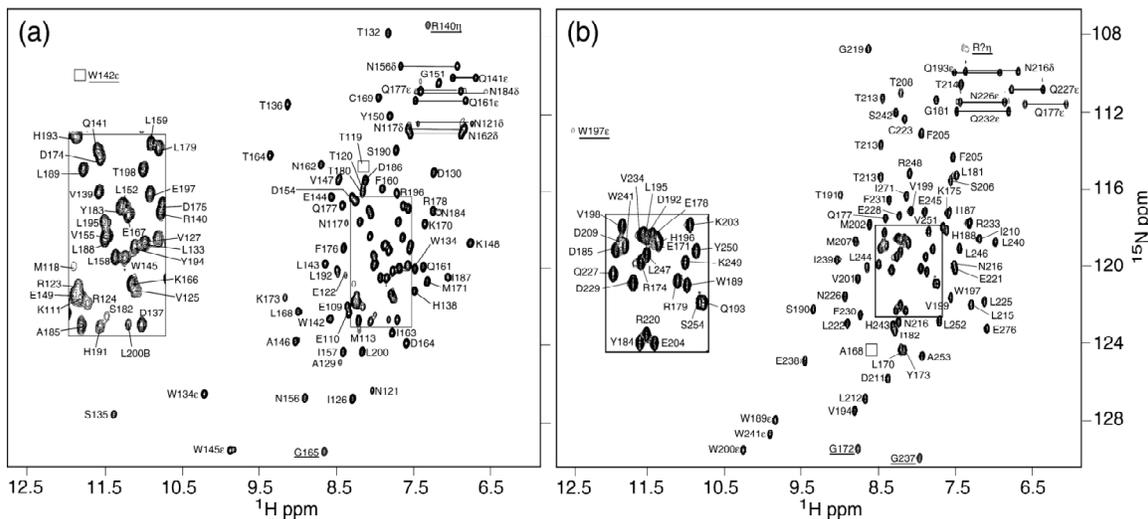
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Supplementary Figure S2. Schematic representations of full-length Erg (five isoforms), GABP α , Ets-1, Ets-2, Pnt-P2, Fli-1, Tel, and Yan. The numbered boundaries of the PNT and ETS domains are defined based upon the current structural and dynamic studies or using the SMART database (<http://smart.embl-heidelberg.de/>). The various PNT domain-containing fragments used herein are indicated by black bars. The sites of the solubilizing mutations A94D and V113E in the Tel PNT domain are shown with white asterisks. SwissProt accession numbers for the sequences are given in the legend of Figure 1.

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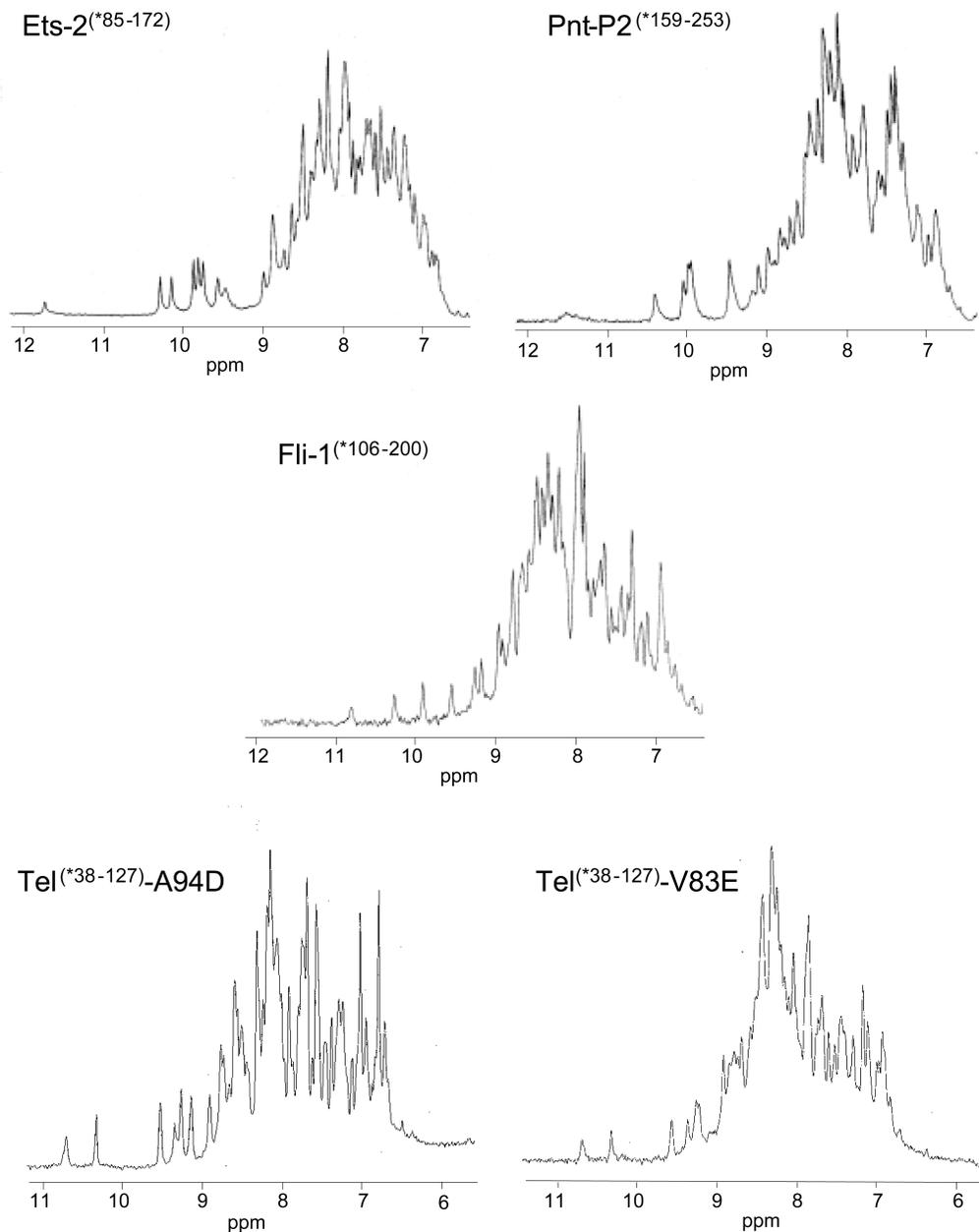
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Supplementary Figure S3. Annotated ^1H - ^{15}N HSQC spectra of (a) Erg^(*108-201) and (b) GABP α ^(*168-254). Peaks with underlined labels are aliased in the ^{15}N dimension. Boxes denote weak peaks not seen at the contour levels of the spectra. Signals from the NH_2 groups of Asn and Gln sidechains are connected by a horizontal line. Crowded regions are labeled in the corresponding expanded regions of each spectrum. The signal at 13.2 ppm and 167.5 ppm from the protected $\text{N}^{\text{e}2}\text{H}$ of His243 in GABP α ^(*168-254) is not shown.

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Supplementary Figure S4. The dispersion and linewidths of the amide resonances in the ¹H-NMR jump-return echo spectra of Ets-2^(*85-172), Pnt-P2^(*159-253), Fli-1^(*106-200), and Tel^(*38-127) indicate that these isolated PNT domains are monomeric and folded in solution (20 mM potassium phosphate, pH 7.0, and 50 mM NaCl at 30 °C). In the case of Tel^(*38-127), two separate solubilizing mutants, A94D and V113E, were used in order to prevent oligomerization.