

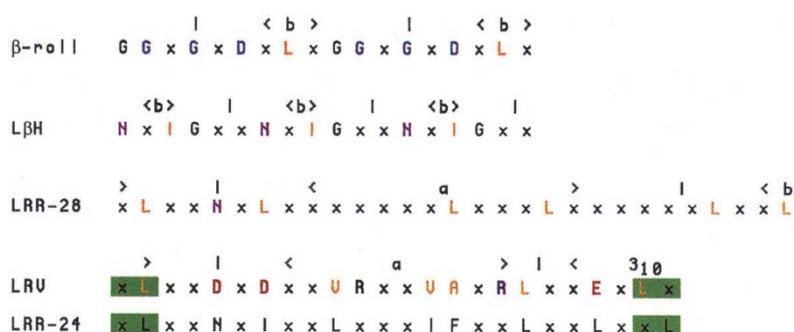
## Leucines on a roll

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977–980 (1996).

Figure 3 was inadvertently misprinted. The version to the right is as it should have appeared in the December issue of *Nature Structural Biology*.

**Fig. 3** Consensus sequences of repeats in proteins with coiled folds. Structural units in  $\alpha/\alpha$  coiled folds and right-handed  $\beta$ -helices do not shown any identifiable sequence repeat, although attempts have been made to define a structural profile for the latter<sup>33</sup>. L $\beta$ H, left-handed  $\beta$ -helix. The approximate locations of the elements of secondary structure are shown above the sequence: "a",  $\alpha$ -helix; "b",  $\beta$ -strand; "3<sub>10</sub>", 3<sub>10</sub>-helix; "l", loop. Some consensus residues that perform similar roles in different coiled folds are coloured: yellow, hydrophobic residues that form the hydrophobic core of the coil; magenta, polar residues that form hydrogen bonds with neighbouring repeats, such as in asparagine ladders<sup>7</sup>; red and blue, Asp and Arg residues that form a ladder in LRV; cyan, residues that coordinate Ca<sup>2+</sup> ion in the  $\beta$ -roll structures. Two consensus sequences are shown for LRR proteins corresponding to two subfamilies identified by sequence-profile searching<sup>30</sup>: the longer ~28-residue LRRs found in RI (LRR-28), and the "typical" shorter LRRs with ~24 residues found in >90% of LRR proteins for which no structural information is currently available (LRR-24). The important differences between LRR and LRV consensus sequences, the xLxL motif versus the LxxL motif, respectively, are highlighted with a green box. The 'phasing' of LRRs (that is, what residue corresponds to the beginning of a structural unit) has been depicted rather arbitrarily in the literature. Here I use a phasing different from that of Peters *et al.*<sup>2</sup>, not with the intention of confusing the readers, but to illustrate the unit most compatible with genetic and biochemical data such as the exon/intron boundaries and the neurotrophin binding activities of single motifs from neurotrophin receptors (refs 35,36; M.E. Lang, B.K., J.M. Windisch, R. Marksteiner, E. Schneider-Scherzer, M. Schweiger and R. Schneider, personal communication).



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