Erratum

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Erratum to: **Prion protein structural features indicate possible relations to signal peptidases** (FEBS 20139)

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The legend of Figure 2 contained some mistakes. The figure and its legend are republished below.

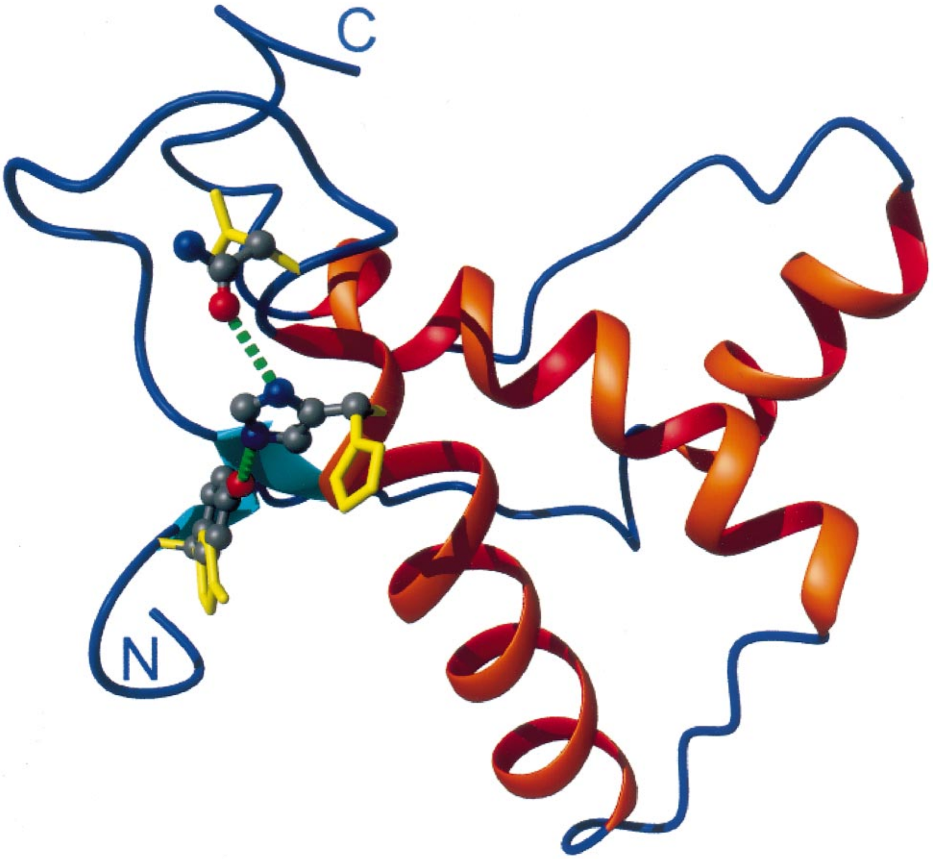

Fig. 2. Location of the PrP residues which align with the active-site residues of signal peptidases in the refined NMR structure of mouse PrP(121–231). A ribbon drawing of the energy-minimized mean solution structure of murine PrP(121–231) [22] is shown with the α-helices in red, the β-strands in light blue and the loop regions in dark blue. The side chains of Tyr-128, His-177 and Asn-174 in the energy-minimized mean structure are shown as yellow stick drawings. A hydrogen bond network reminiscent of the catalytic triad in thiol proteases was generated by rotation of these side chains about the χ^1 and χ^2 angles. The resulting positions of the side chains are shown as ball and stick models with functional colors, and the hydrogen bonds are shown in green. The figure was generated with the program MOLMOL [48].

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