

## Human mannose-binding protein carbohydrate recognition domain trimerizes through a triple $\alpha$ -helical coiled-coil

S. Sheriff, C.Y. Chang and R.A.B. Ezekowitz  
*Nature Structural Biology* **1**, 789–794 (1994).

The following errors have been noted by the authors since publication:

p. 790, second column, third line from the bottom should read:  
In rat MBP, Trp 105 and Phe 138 are replaced by Leu 98 and Leu 131,...

p. 792, Table 1, under Refinement, second line, should read:  
Number of reflections                      6244      6318

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## The not-so-great escape

J. Erickson  
*Nature Structural Biology* **2**, 523–529 (1995)

The section under the subheading **Cleavage-site mutants** (p. 526, starting the sixth line from the bottom of the page) should read:

This may be especially important where a mutant HIV PR becomes rate-limiting for virus replication. Recent evidence from *in vitro* studies reveals that mutations in *gag* polyprotein cleavage sites can synergize with I84V or A mutations in the protease to produce a virus with  $10^2$ – $10^3$ -fold decreased sensitivity to an inhibitor (D. Lamarre *et al.*, pers. comm.). One such *gag* mutation was identified as a change in the P1 residue of the P1/P6 cleavage site from a Leu to a Phe, which alters the cleavage site from Phe–Leu to Phe–Phe. A synthetic peptide containing the Phe–Phe cleavage site is cleaved at a higher catalytic efficiency by both mutant and wild-type HIV PR than the corresponding peptide with the wild-type sequence.

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## Structure of the $\text{Ca}^{2+}$ -free GLA domain sheds light on membrane binding of blood coagulation proteins

M. Sunnerhagen, S. Forsén, A-M Hoffrén, T Drakenberg, O. Teleman and J. Stenflo  
*Nature Structural Biology* **2**, 504–509.

The following errors have been noted:

Page 505, Fig. 1. **h-factor X**, residues 34–40 should read: S D K T N  $\gamma$  F

Page 505, Fig. 1. **h-Factor IX**, residues 34–40 should read: T  $\gamma$  R T T  $\gamma$  F

Page 506, first column, line 10 should read: Mutating any of Gla residues 7, 16, 20, 26 or 29 to Asp results in loss of membrane binding and/or biological activity<sup>22,25</sup>.