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On the cover, a three-dimensional computer model illustrating the constitutive positive charges at the quaternary amine groups of the dimethylated N-terminal Pro and trimethylated Lys-3 residues identified on the N-terminal peptide of *Arabidopsis* cytosolic ribosomal protein L12: PPKLDPSQIVDVYVR. The image was generated using the open source biomolecular modeling software BALLView v1.2 (Moll *et al.* (2005) *J. Comput. Aided Mol. Des.* **19**, 791–800). For details, see the article by Carroll *et al.*, pages 347–369.

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