seizures, and an elevated blood lactate with normal hearing.

The incidence of renal involvement in the MELAS syndrome is unknown, and the reported frequency of hearing loss is 75%. The *MTTL1* gene mutations should be considered in patients presenting with renal insufficiency and hearing loss.

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Gene expression analysis in microdissected renal biopsy

To the Editor: Microdissection of renal biopsy may be necessary to analyze gene expression in glomeruli and tubulointerstitium [1], but this procedure is delicate because RNA degradation may occur. The Munich group [2, 3, 4] recently reported the possibility of microdissecting biopsies stored in *RNA later*®, a commercial RNase inhibitor. We completely agree that control of RNAase activity is crucial during microdissection; nevertheless, we obtained different results that may be worthy of discussion.

The cortical tissue from five kidney biopsies taken from sites remote from tumor-bearing tissue was immediately divided under the stereomicroscope into three randomly allocated pieces: A and B were stored in *RNA later* following the protocol instructions to investigate microdissection feasibility and evaluate RNA extraction, respectively; C was kept in saline containing 100 U of *RNAsin*® at 4°C. After 1 hour of storing in *RNA later*, pieces A were microdissected; but although our experience includes over 150 renal biopsies, we had trouble separating glomeruli from the tubulointerstitium. Indeed, fragments of a homogeneous yellowish color appeared at the stereomicroscope, glomeruli could be hardly recognized, and specimens appeared compact and stiff, resembling fixed tissues. On the contrary, from pieces C it was possible to collect easily 10 to 20 glomeruli each.

We agree with the authors in reference to the quality (yield and purity) of extracted RNA from the cortical tissue of pieces B. Thus, in our experience storing tissues in *RNA later* represents an optimal mean to preserve RNA from degradation, but does not warrant microdissection of the biopsy.

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Can error in GFR formulas explain their poor performance in transplant patients?

To the Editor: In a recent paper by Mariat et al [1], the performance of several glomerular filtration rate (GFR) equations was assessed against inulin clearance in renal transplant patients. One of the GFR estimate equations used was the Nankivell formula, which was printed as the following:

GFR (mL/minute) = 6.7/serum creatinine + 0.25 × weight – 0.5 × urea – 0.01 × height^2 + 35(25 for woman).

However, on review of Dr. Nankivell's original article [2], the original formula derived was:

GFR (mL/minute) = 6.7/creatinine (mmol/L) + BW(kg)/4 – urea(mmol/L)/2 – 100/height(m)^2 + 35 (25 for woman).

If this was not a printing error and this formula was applied to the data, this may account for the relative decreased accuracy of the Nankivell formula when compared with the other GFR calculation equations.

In addition, the Levey formula (Mariat et al [1]) was printed as:

GFR (mL/minute) = 170 × serum creatinine$^{-0.999}$ × age$^{-0.1}$ × 0.762 (if woman) × 1.180 (if patient is black)