CORRECTION

Involvement of proteasomal subunits zeta and iota in RNA degradation

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The top panel in Figure 2 is incorrect as printed. The correct figure appears below:

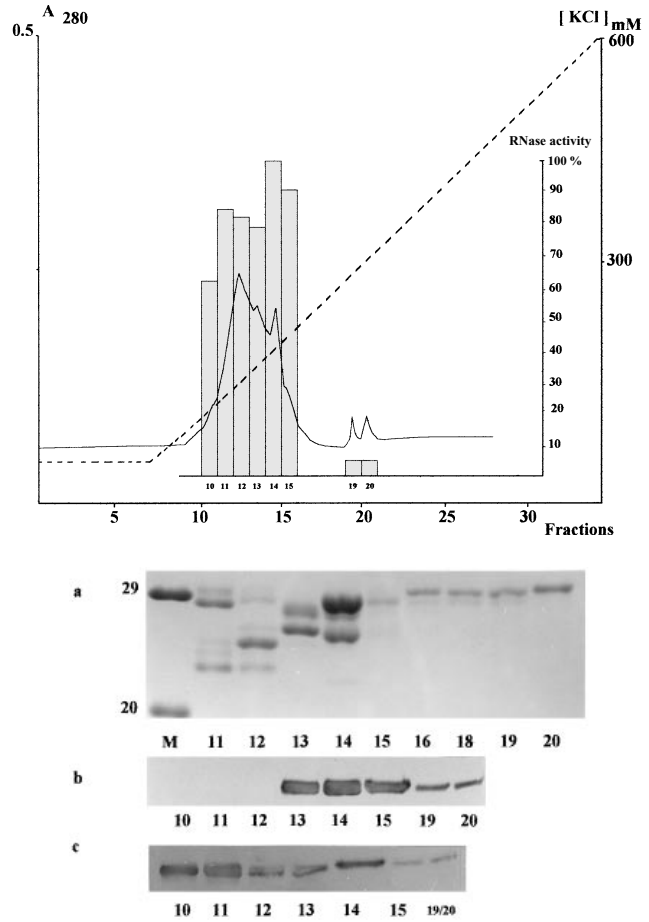

Figure 2 Co-elution of RNase activity with proteasomal subunits

Top panel: 2 mg of highly purified proteasomes eluted from Superose 6 columns was dialysed against TBK 0, and then incubated for 10 min at 37 °C with 6 M urea (final concentration). The suspension was loaded on to an FPLC Mono Q HR 5/5 column equilibrated in TBK 0 containing 6 M urea. Proteasomal subunits were eluted with a linear salt gradient containing 6 M urea from TBK 0 to TBK 600. Eluted fractions were dialysed against TBK 120, and 200 μl aliquots were incubated with 4 μg of TMV RNA for 20 min at 37 °C to analyse RNase activity, as described in the Experimental section. RNase activity is shown by the bar diagram, the solid line indicates A_{280}, and the broken line indicates KCl concentration. (**a**–**c**) Distribution of subunits zeta and iota in fractions eluted from FPLC Mono Q columns. Portions of 800 μl of fractions 11–20 (top panel) were incubated with 10% trichloroacetic acid (final concentration) to precipitate the proteins. Sedimented proteins were analysed by PAGE. After gel electrophoresis, proteins were transferred to nitrocellulose filters and probed with the monoclonal antibodies MCP196 and IB5. Mouse IgG was detected as described in the Experimental section. (**a**) Proteasome subunits visualized by Coomassie Blue staining (lane M contains molecular mass markers; kDa); (**b**) subunit zeta detected by MCP196; (**c**) subunit iota detected by IB5.