Supporting Information

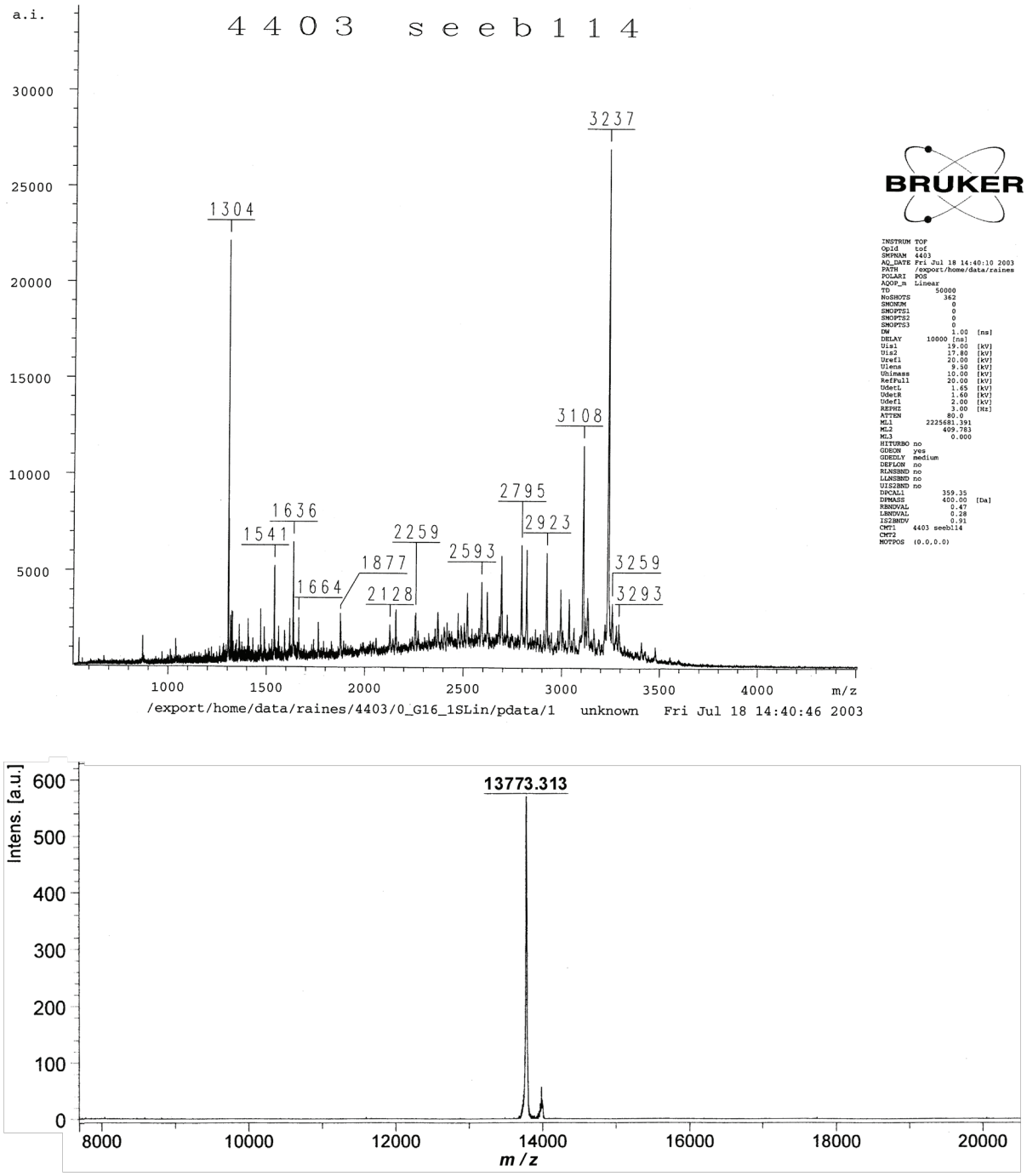

Figure S1. Mass spectra of peptide CAYKTTQANKHIIVACEG–β^2-hAla–β^3-hAla–YVPVHFDASV, which corresponds to residues 95–124 of RNase A (top; *m*/*z* 3237; expected for $C_{145}H_{224}N_{38}O_{42}S_2$: 3236), and $\beta^3\beta^2$hAla RNase A (bottom; *m*/*z*, 13,773; expected: 13,772).

Supporting Information

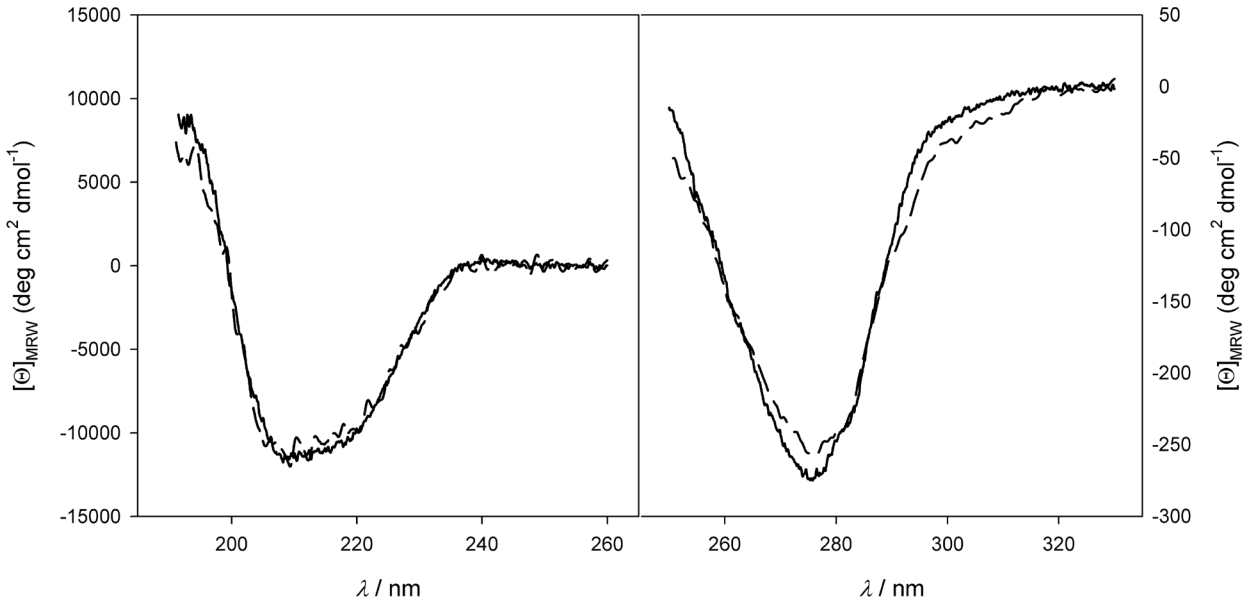

Figure S2. Far-UV (left) and near-UV CD spectra (right) of $\beta^2\beta^3$hAla RNase A (dashed lines) and wild-type RNase A (solid lines). CD spectra were recorded at pH 8.0 and 25 °C, as described in the Materials and Methods section.

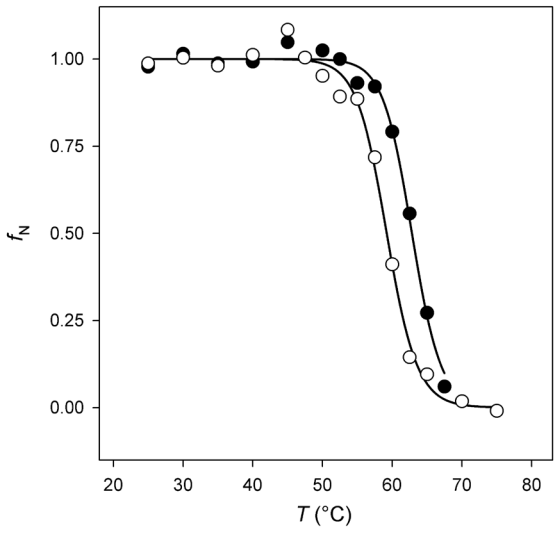

Figure S3. Thermally induced transition of $\beta^2\beta^3$hAla RNase A (open symbols) and wild-type RNase A (closed symbols). Unfolding was monitored by pulse proteolysis with thermolysin. Protein solutions (0.1 mg mL^{-1}) were equilibrated at the respective temperature. One-tenth volume of thermolysin was added to 0.5 mg mL^{-1}, and the reaction was stopped by the addition of EDTA to 10 mM and transfer of the samples to ice. Samples were analyzed by SDS–PAGE followed by staining with Coomassie Brilliant Blue G-250 and densitometric evaluation.