

Figure S1. Precision of hydrogen exchange monitored by HX-MS in Parkin is high. Distribution of deviations of the fitted m/z centroid positions between two independently measured hydrogen exchange time courses. 4966 comparisons gave a mean of -0.003 and a root mean squared error of 0.18 amu.

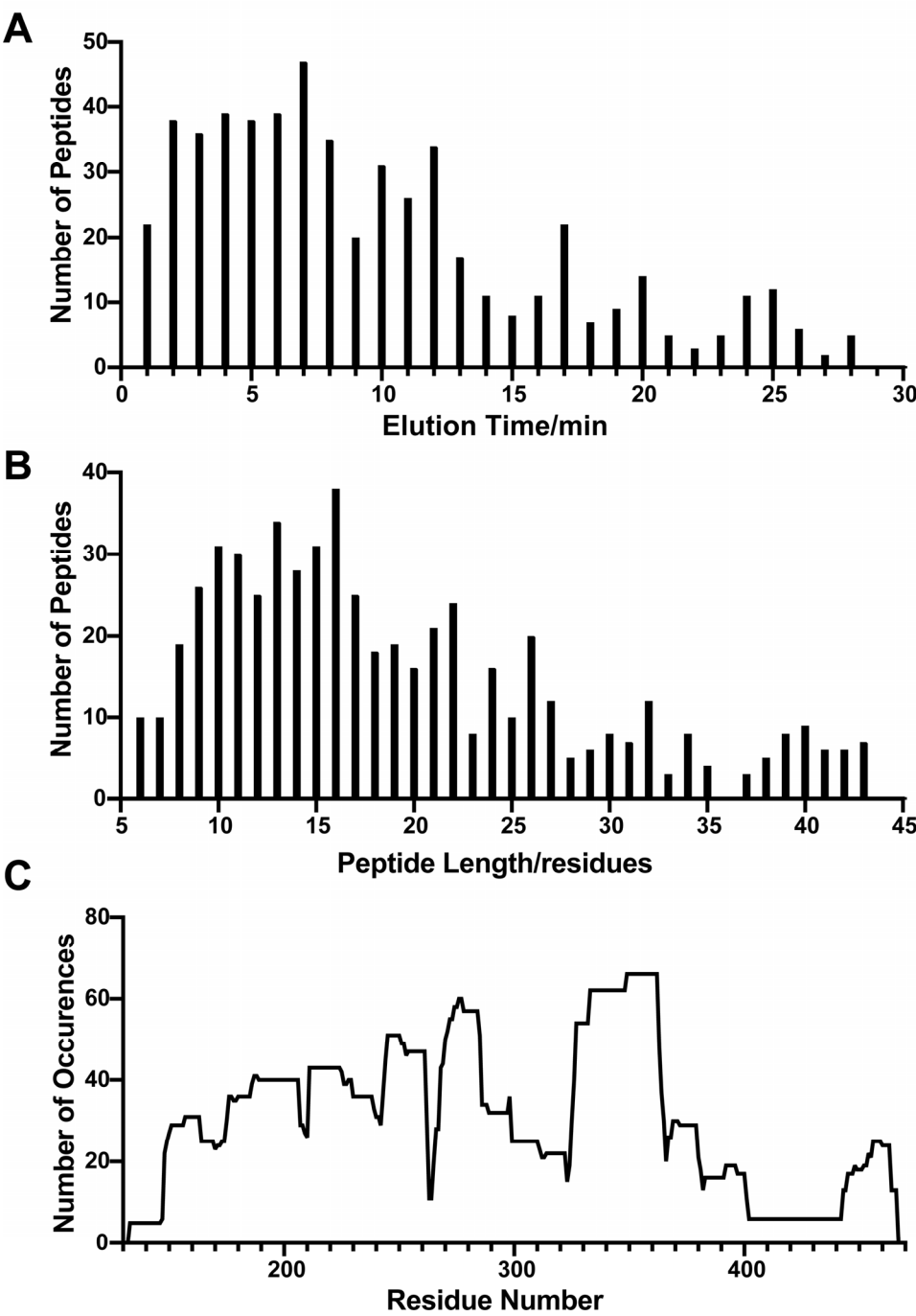


Figure S2. Summary of peptide fragmentation of free Parkin(Δ Ubl). (A) Histogram of the reverse phase chromatography elution peptide elution profile. (B) Histogram summarizing the distribution of peptide sizes. (C) Sequence coverage of the peptide coverage at each residue of the Parkin(Δ Ubl) sequence.

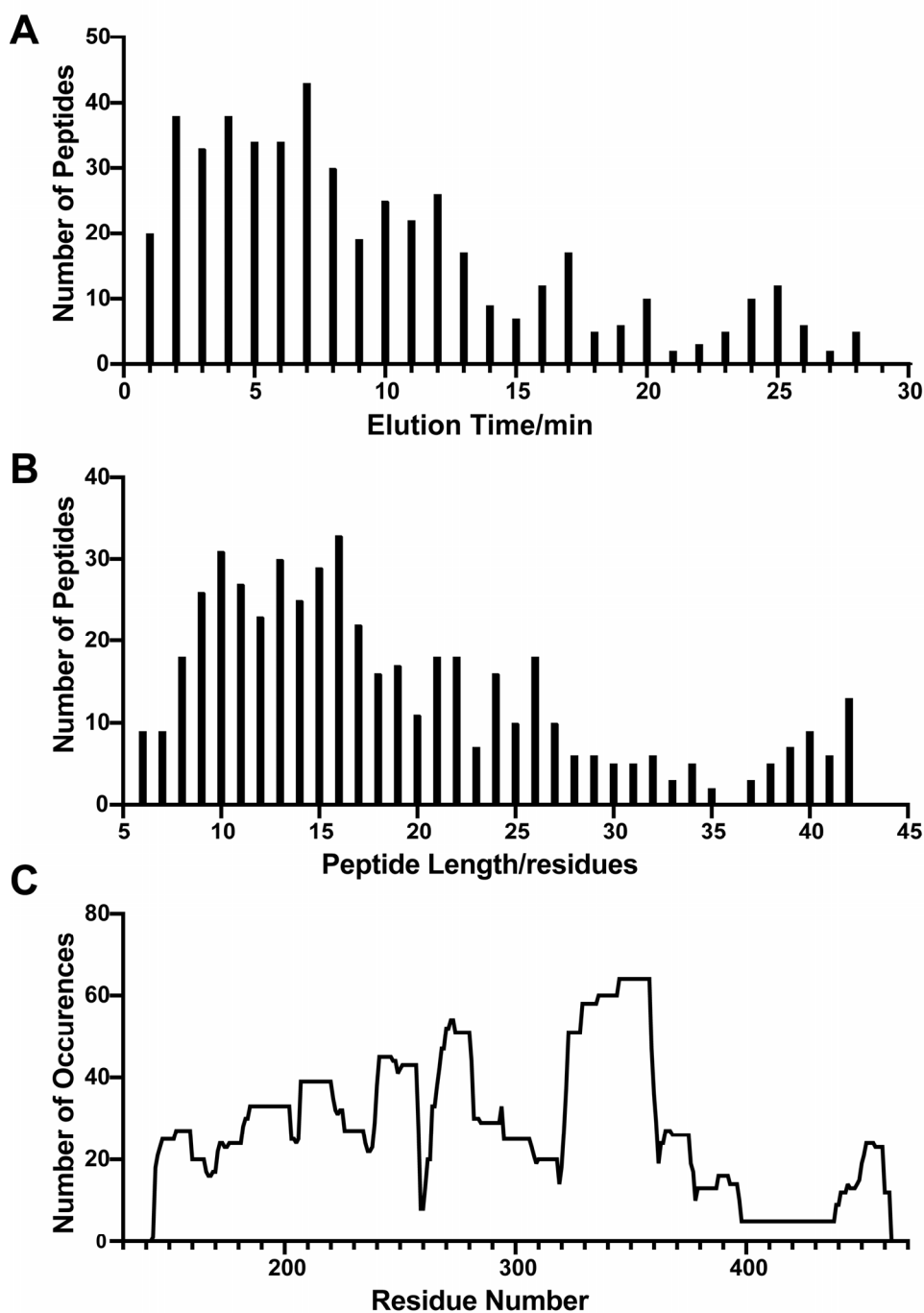


Figure S3. Summary of peptide fragmentation of Parkin(Δ Ubl) from the Parkin(Δ Ubl)•pUb complex. (A) Histogram of the reverse phase chromatography elution peptide elution profile. (B) Histogram summarizing the distribution of peptide sizes. (C) Sequence coverage of the peptide coverage at reach residue of the Parkin(Δ Ubl) sequence.

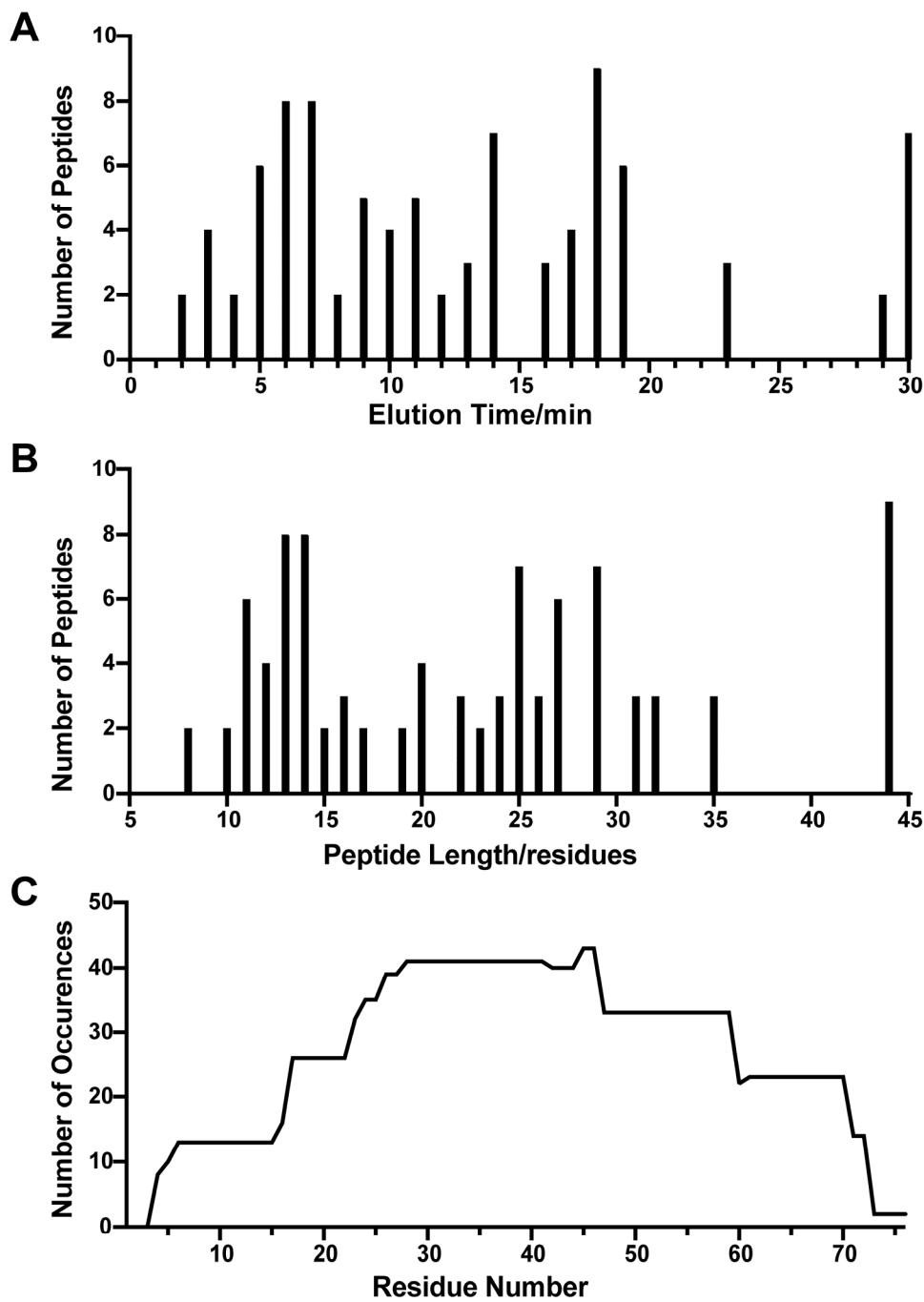


Figure S4. Summary of peptide fragmentation of pUb from the Parkin(Δ Ubl)•pUb complex. (A) Histogram of the reverse phase chromatography elution peptide elution profile. (B) Histogram summarizing the distribution of peptide sizes. (C) Sequence coverage of the peptide coverage at each residue of the Parkin(Δ Ubl) sequence.

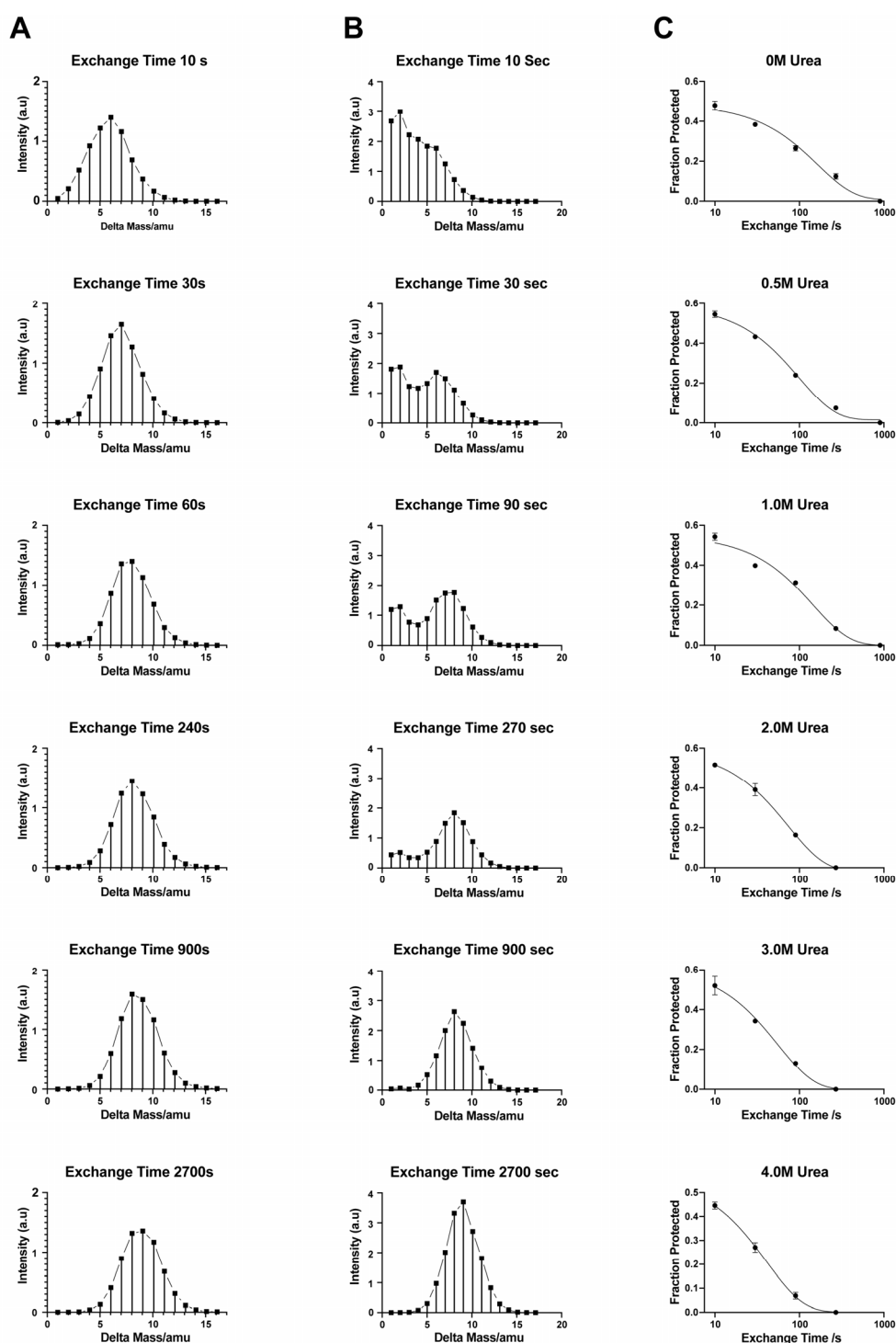


Figure S5. Hydrogen exchange in free and complexed pUb. Individual m/z distributions during hydrogen exchange derived from residues 60-72 in free (A) and complexed (B) pUb. Free pUb shows a smooth transition to higher mass indicative of EX2-type hydrogen exchange. pUb complexed to Parkin(Δ Ubl) shows two distinct populations, one exchanging as free pUb and a slower exchanging population corresponding to complexed pUb. Note that pUb and Parkin(Δ Ubl) were in a 2:1 molar ratio. (C) The fractional protection of the average of eight separate peptides derived from residues 60-72 of pUb were fitted to simple single exponential decays. Fitting of these data gave average R^2 and $Sy.x$ values of 0.99 ± 0.01 and 0.02 ± 0.01 , respectively.