

Figure S11 – 50S subunits r-protein degradation kinetics (1/4)

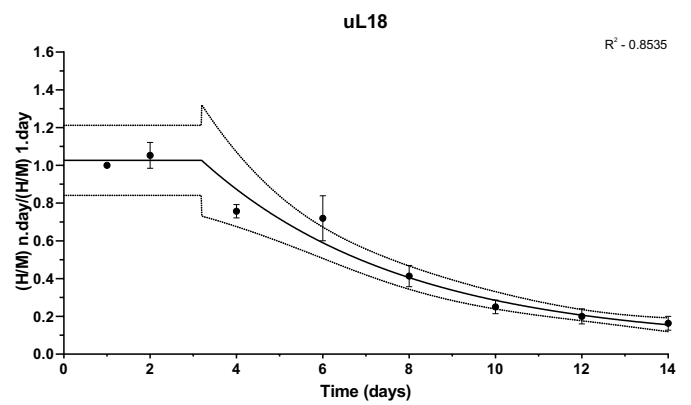
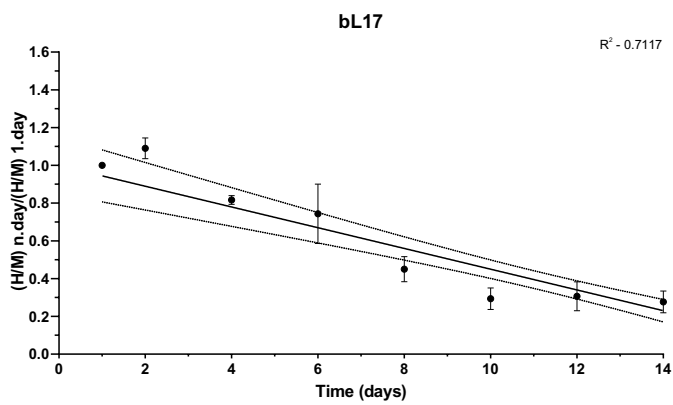
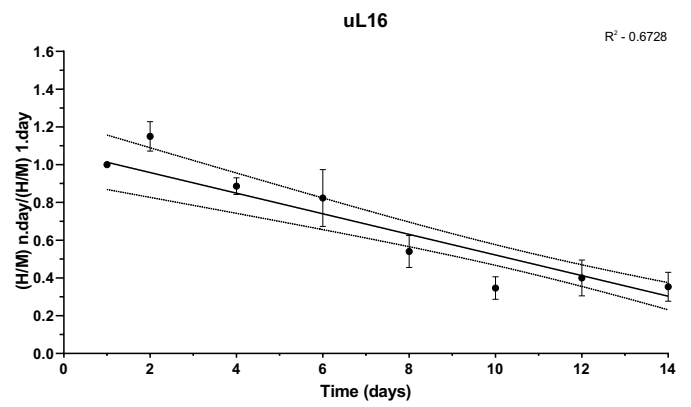
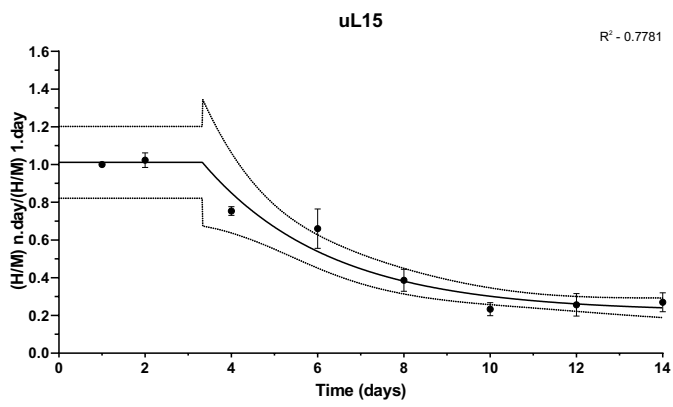
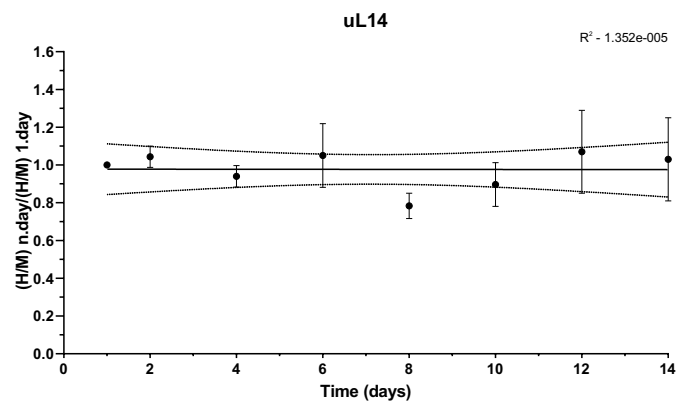
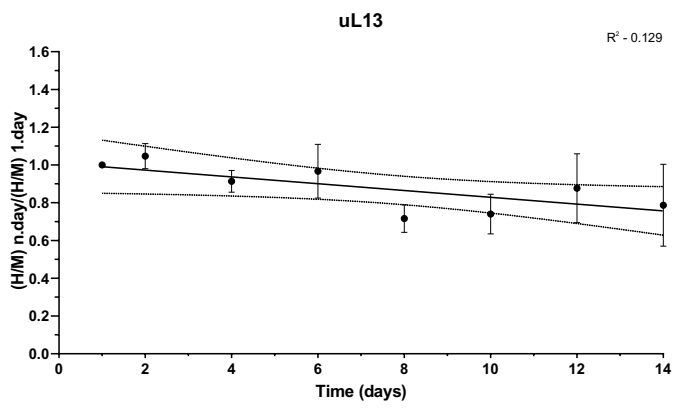
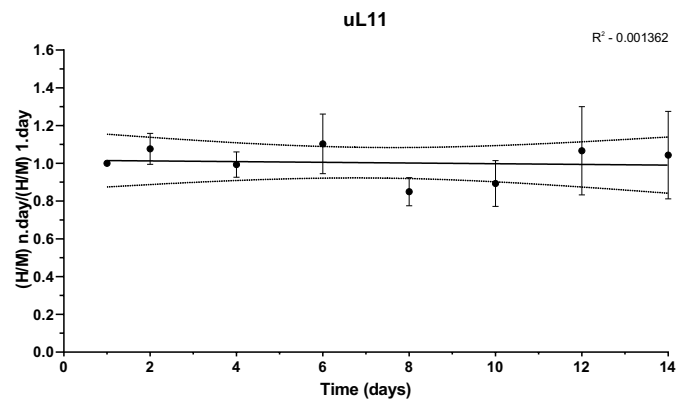
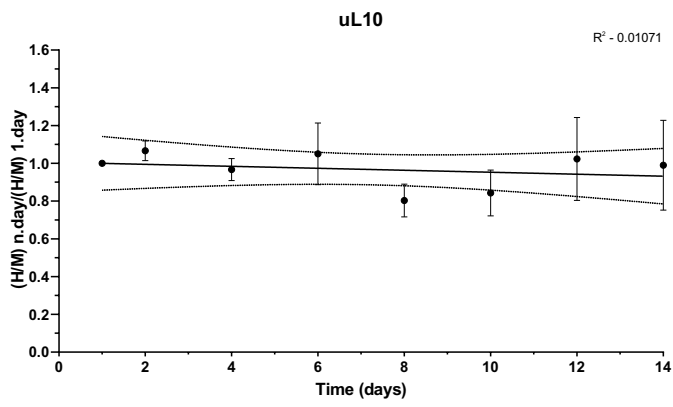


Figure S11 – 50S subunits r-protein degradation kinetics (2/4)

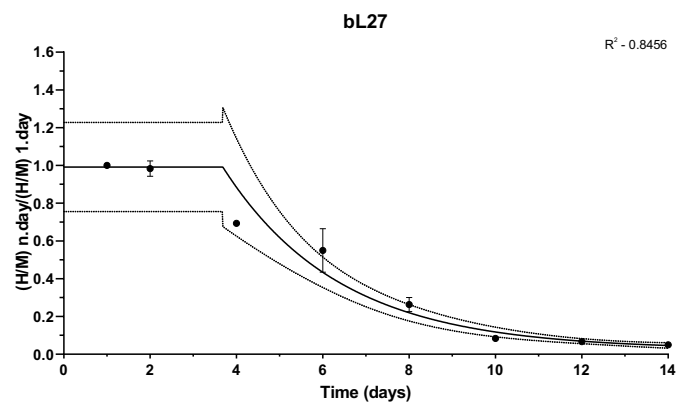
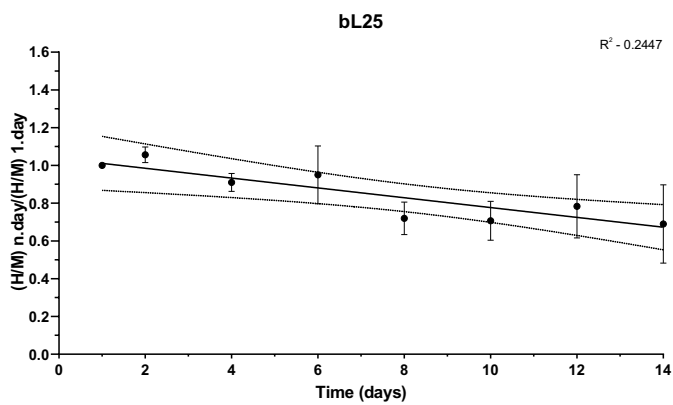
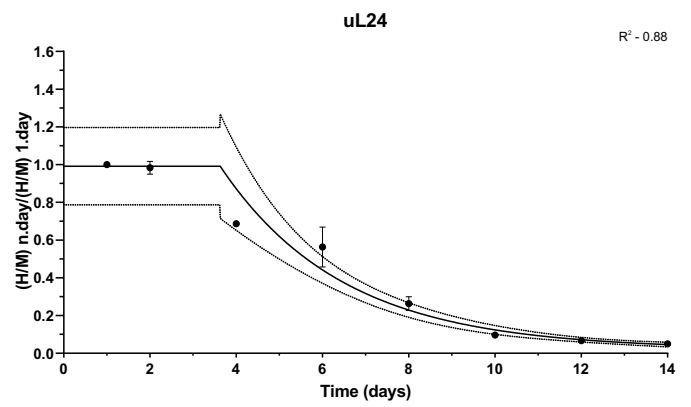
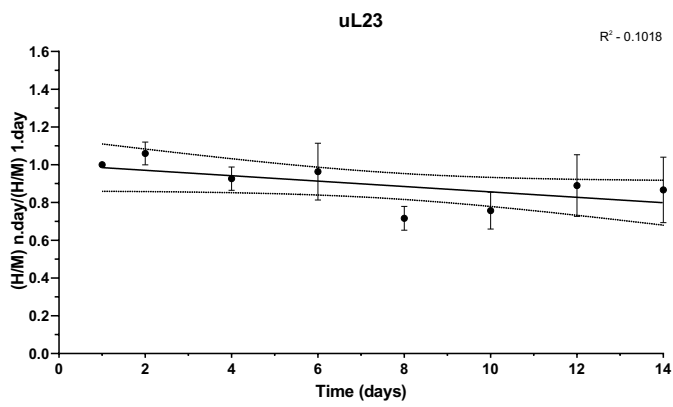
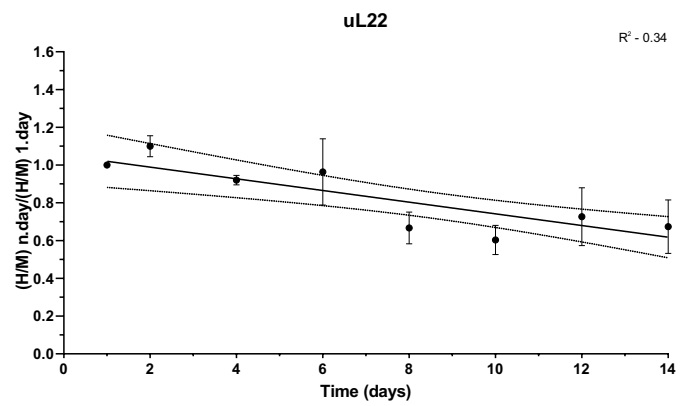
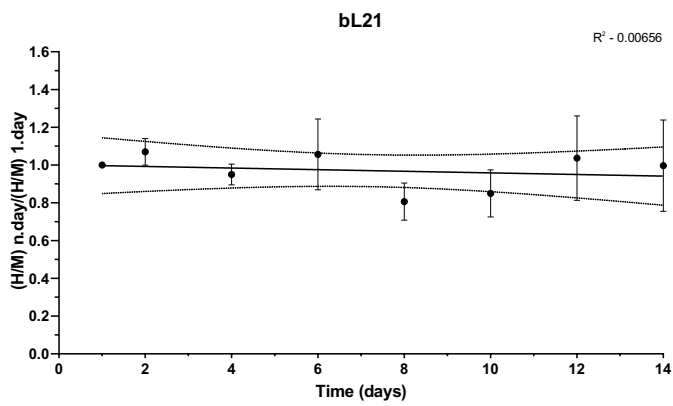
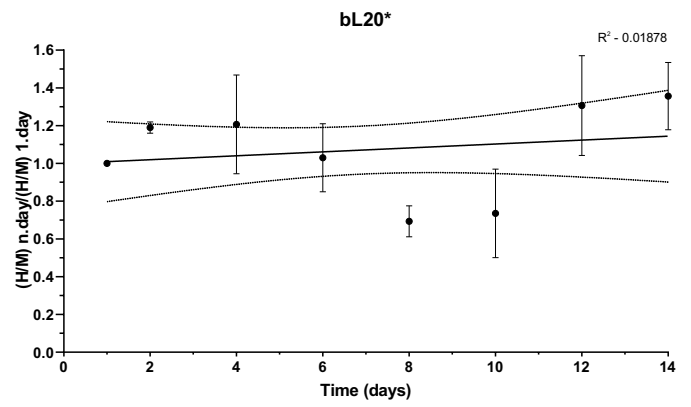
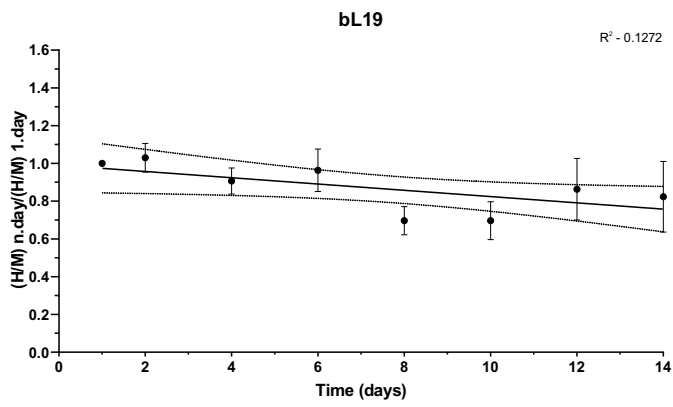


Figure S11 – 50S subunits r-protein degradation kinetics (3/4)

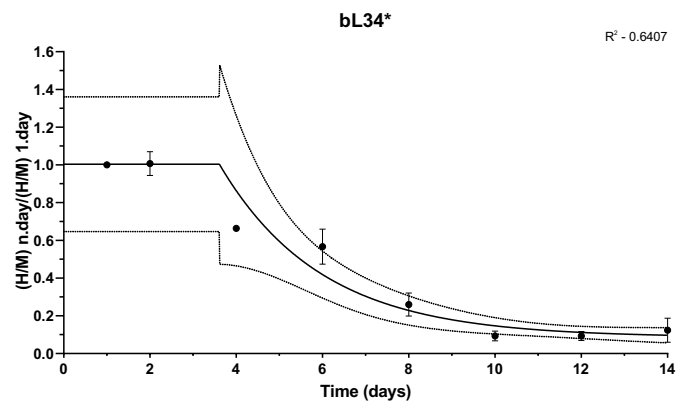
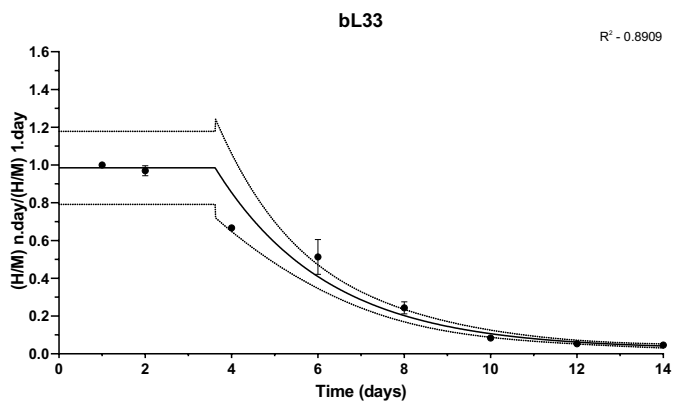
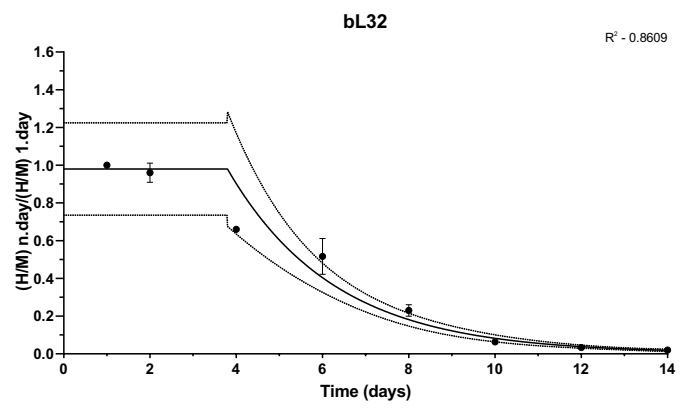
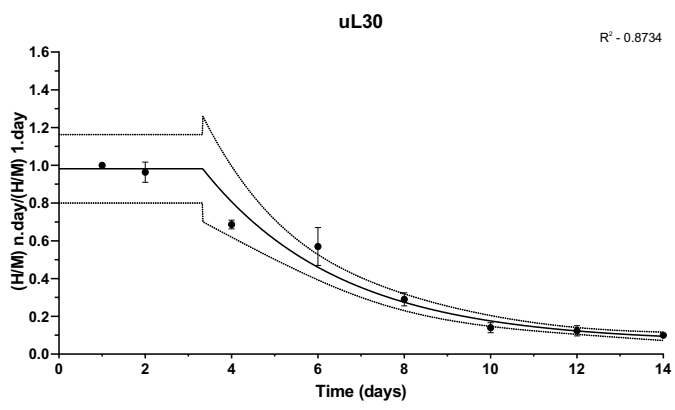
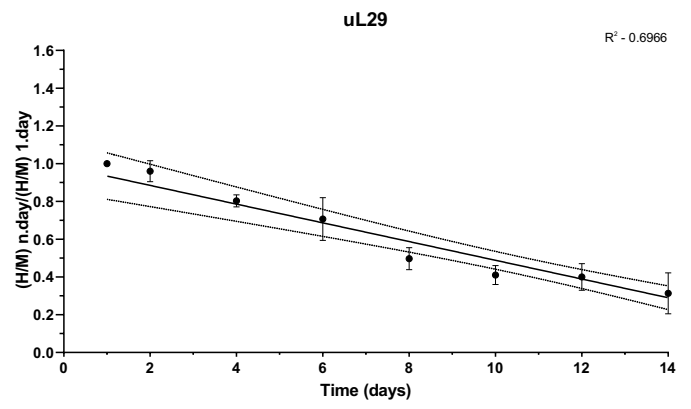
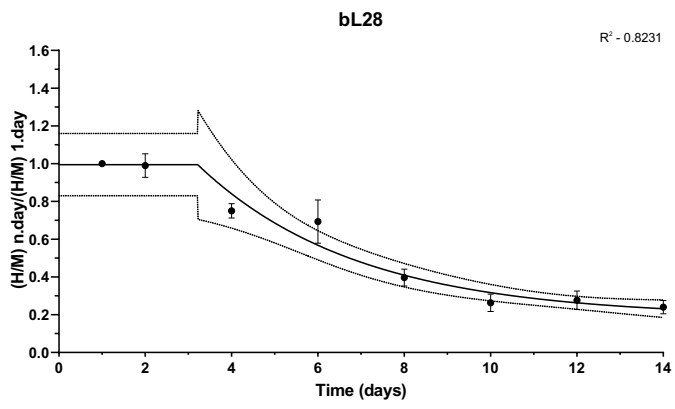


Figure S11 – 50S subunits r-protein degradation kinetics (4/4)

Figure S11 – 50S subunits r-protein degradation kinetics. This figure is related to Figure 7 in the main text. Normalized H/M ratio values measured over 14 days were analyzed using non-linear regression. Data was fitted into two models: plateau followed by one phase decay and straight line. The fit of models was compared using Akaike's information criteria (2). Statistics of the analysis are presented in table S6. Shown on the figure are r-proteins with best-fitting models. On Y-axis is the normalized H/M ratio and on X-axis is time in days. The black line represents best-fit values and the dotted line represents confidence bands (90%). All calculations were based on data obtained from 3 individual biological experiments (n=3). Black circles with error bars shown in the figure are the means of three independent biological experiments with standard deviation (n=3; mean \pm SD).