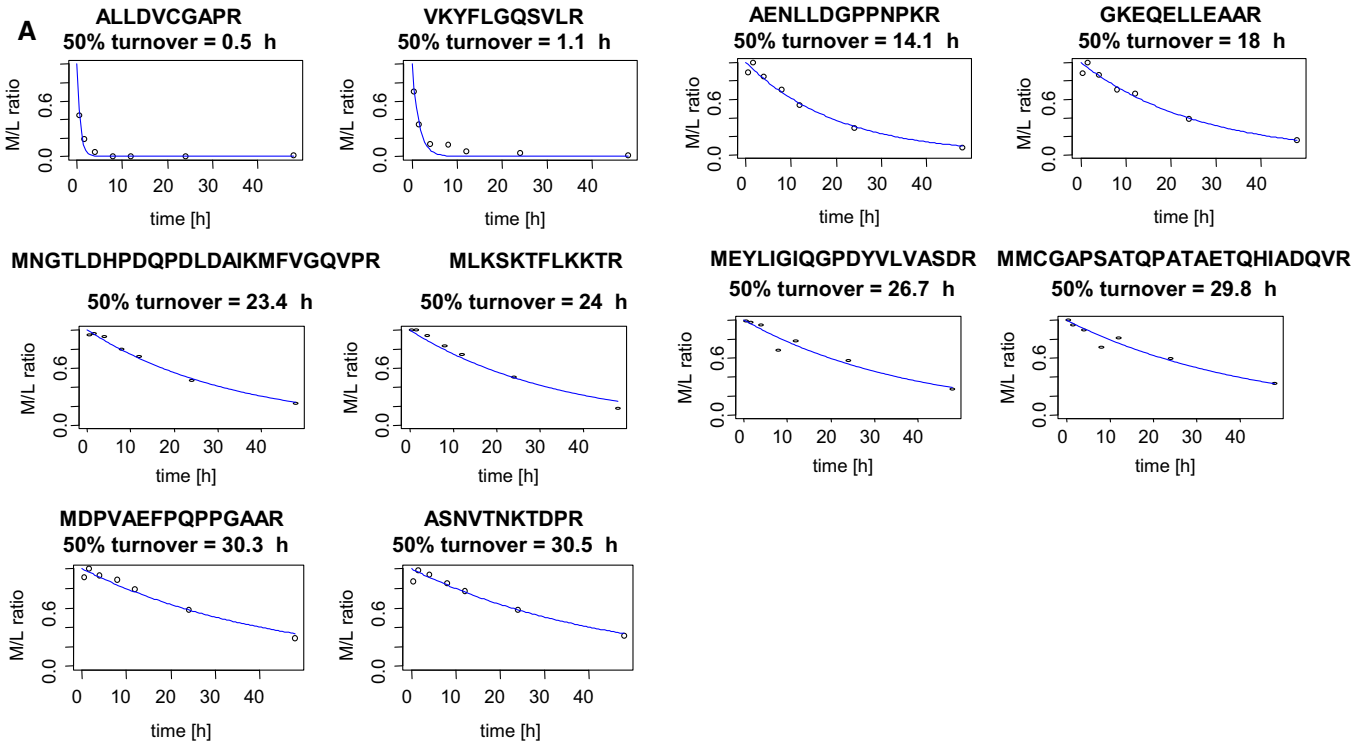
Expanded View Figures



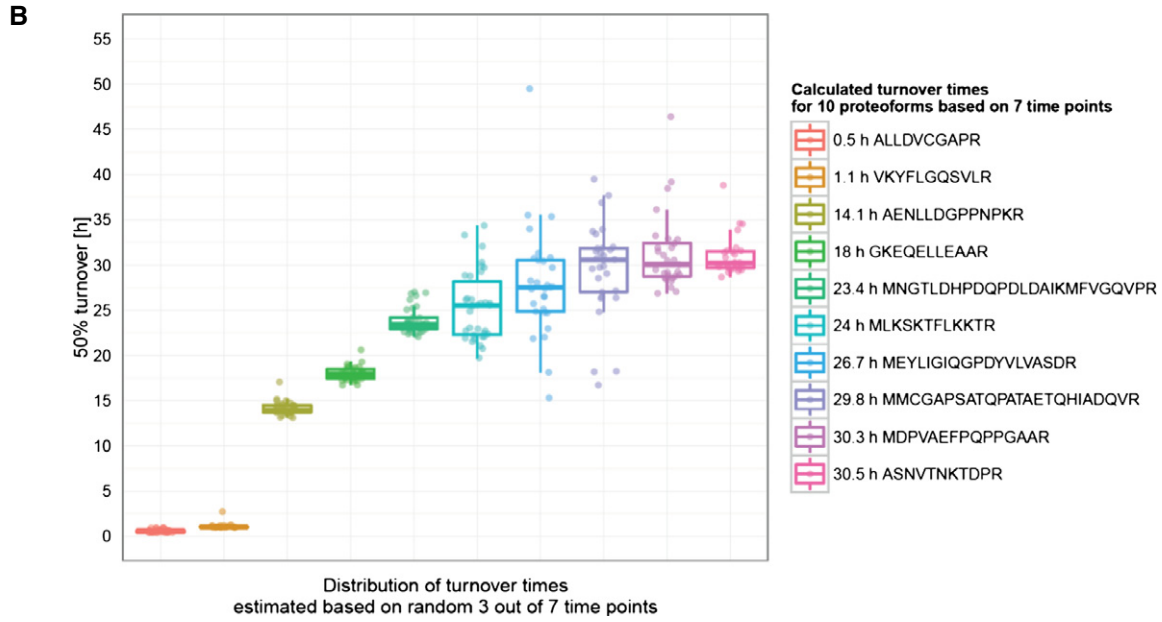


Figure EV1. Turnover time calculations using a subset of available data points.

A Representative proteoforms (10) identified in seven time points displaying a large variety of turnover rates.

B For each peptide, all possible combinations of 3 random points were fitted with an exponential model and used for calculating 50% turnover time. Next, models with R^2 coefficient below 0.8 were rejected. The remaining valid models were grouped per peptide and represented as box plots.

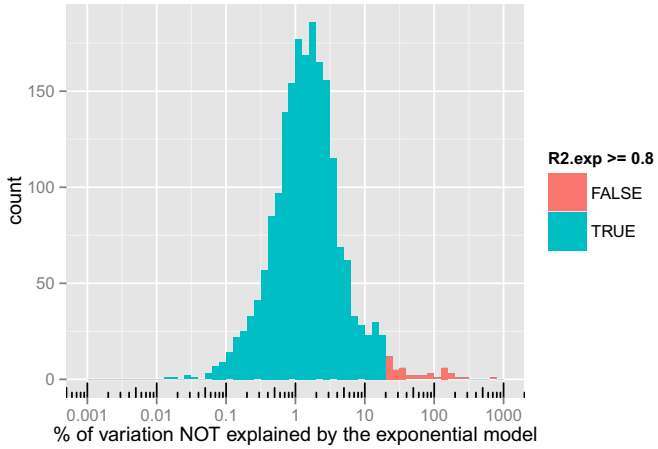


Figure EV2. For each proteoform quantified in at least three time points (1,972), variation of data unexplained by the exponential model was calculated as ($1 - R^2$) and represented in %.
The distribution of the unexplained variations is tightly centred around 2% (corresponding to a median $R^2 = 0.98$) while only a minority of exponential models fitted insufficiently ($R^2 < 0.8$) and were rejected.

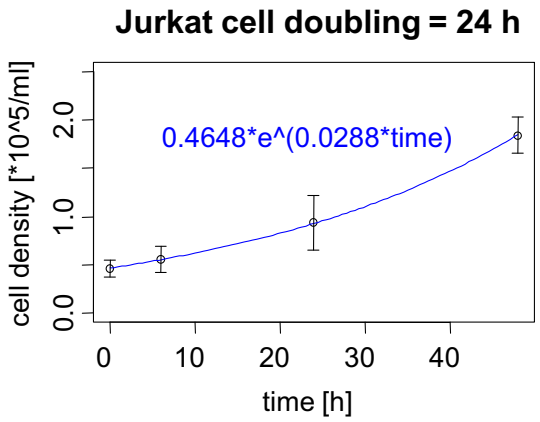


Figure EV3. Experimental assignment of Jurkat cell doubling time.
Density of cell culture was monitored in triplicate over the course of 48 h and fitted with an exponential model using the Doubling Time Online Calculator (http://www.doubling-time.com/compute.php). Cell doubling time was calculated from the assigned growth rate (0.0288) as follows: ln(2)/0.0288 and represented in hours.

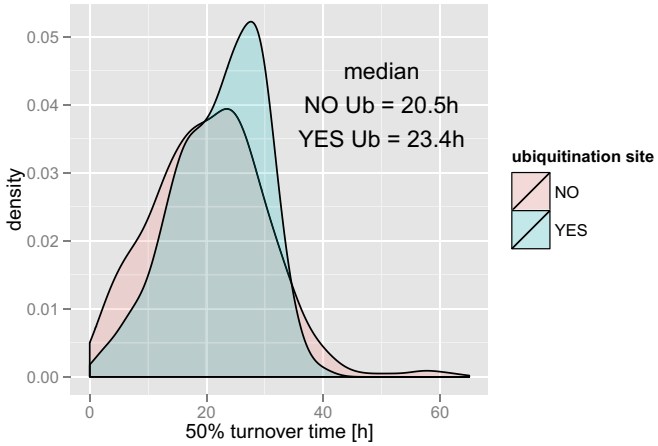


Figure EV4. Distribution of turnover values for lysine containing ubiquitinated (N = 348) and non-ubiquitinated dbTIS indicative N-termini (N = 388).

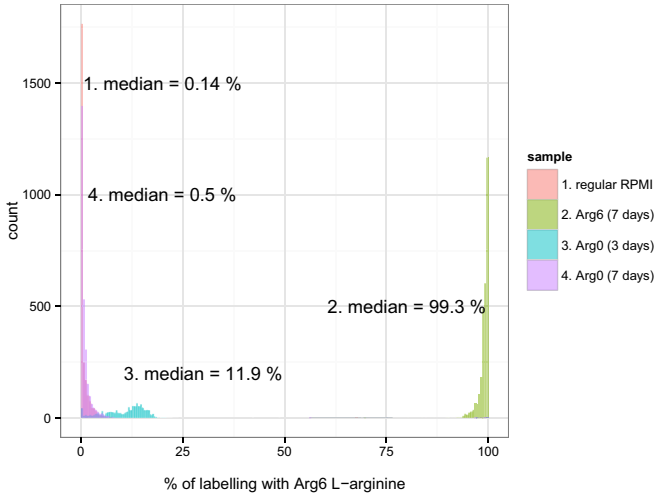


Figure EV5. SILAC labelling of Jurkat cells.
Jurkat cells cultured in regular RPMI medium were transferred to RPMI SILAC medium containing Arg^6 L-arginine and cultured for 7 days. Subsequently, cells were transferred to a RPMI SILAC medium containing Arg^0 L-arginine for next 7 days, to achieve complete unlabelling. The isotope replacement was monitored by quantifying the identified MS spectra using Mascot Distiller.

