Supplemental Material

Supplemental Method:

Immunoblotting. Equal amounts of cardiac proteins (40 μg) were heated with Laemmli loading buffer with 100 mM dithiothreitol at 70 °C for 10 min. The proteins were separated using sodium dodecyl-sulfate polyacrylamide gel electrophoresis on 9879a Bio-Rad Mini-Protean 10–200 kDa Tris-glycine gel, and then transferred onto a polyvinylidene difluoride membrane (Bio-Rad TransBlot Turbo). Protein loading and transfer was verified with Ponceau S stain. The blots were blocked in the blocking buffer (5% bovine serum albumin, 0.005% sodium azide, in 1× Tris-buffered saline/ Tween 20 (TBST) (Cell Signaling)), reacted with primary antibodies at 4 °C overnight, washed with 1× TBST, reacted with secondary antibodies at ambient temperature for 1 hr, washed with 16y× TBST, then detected by chemiluminescence. All antibodies were purchased from Cell Signaling, including rabbit monoclonal IgG against GAPDH (#5174), HK1 (#2024), HK2 (#2867), ANXA2 (#8235), VIM (#5741), TGM2 (#3557), PGAM1 (#12098), LDHA/C (#3558), ALDOA (#8060), PKM1/2 (#3190), PDH (#3205); and rabbit polyclonal antibodies against ANXA5 (#8555), MSN (#3146), ATP1A1 (#3010). Primary antibodies were diluted in 1:1000 in the blocking buffer. Secondary antibodies were 1:3000 goat anti-rabbit IgG conjugated to horseradish peroxidase (#7074) in the blocking buffer.

Gas chromatography. To quantify $^{2}H_2O$ enrichment levels, mouse and human plasma samples were used directly for gas chromatography MS analyses. For each sample, 20 μL of plasma was mixed with 2 μL of 10 N NaOH and 4 μL of 5% (v/v) acetone in acetonitrile. The standard curves were created by adding 0% to 20% molar ratio of $^{2}H_2O$ at 11 regular intervals in 1× PBS in place of the plasma sample to the acetone. The sample mixtures were incubated at ambient temperature overnight. Acetone was extracted by adding 500 μL of chloroform and 0.5 g of anhydrous sodium sulfate. One μL of the extracted solution was analyzed on a gas chromatography mass spectrometer (Agilent 6890/5975) with a J&W DB17-MS capillary column (Agilent, 30 m × 0.25 mm × 0.25 μm) at the UCLA Molecular Instrumentation Center. The column temperature gradient was as follows: 60 °C initial, 20 °C·min^{-1} increase to 100 °C, 50 °C·min^{-1} increase to 220 °C, 1 min hold. The mass spectrometer operated in the electron impact mode (70 eV) and selective ion monitoring at m/z 58 and 59 with 10 ms dwell time.

Protein sample preparation. The human whole blood sample was collected in lithium heparin tubes and separated into plasma and blood cells by centrifugation (800 g, 4 °C, 5 min). Erythrocytes were isolated by centrifugation on 1:1 Histopaque-1077 (400 g, 4 °C, 30 min) followed by washing twice with PBS. Plasma samples (7 μL; approximately 500 μg proteins) were depleted of the 14 top abundance proteins using an Agilent Hu14 Multiple Affinity Removal System column.

Mouse hearts were excised and homogenized by a 7-mL Dounce homogenizer (Pyrex) (20 strokes) in an extraction buffer (250 mM sucrose, 10 mM HEPES, 10 mM Tris, 1 mM EGTA, 10 mM dithiothreitol, protease and phosphatase inhibitors (Pierce Halt), pH 7.4) at 4 °C, then centrifuged (800 g, 4 °C, 7 min). The pellet was collected as the total debris fraction. The supernatant was centrifuged (4,000 g, 4 °C, 30 min) and collected as the organelle-depleted cytosolic fraction. The pellet was washed, then overlaid on a 19%/30%/60% discrete Percoll gradient, and sedimented by ultracentrifugation (12,000 g, 4 °C, 10 min). Purified mitochondria were collected from the 30%/60% interface layer and washed twice. Protein concentrations were measured by bicinchoninic acid assays (Thermo Pierce).

Mouse plasma, heart, and human erythrocyte protein samples were separately digested in-solution; 200 μg proteins were heated at 80 °C with 0.2% (w/v) Rapigest (Waters) for 5 min, then heated at 70 °C with 3 mM dithiothreitol for 5 min, followed by alkylation with 9 mM iodoacetamide in the dark at ambient temperature. Proteins were digested with 50:1 sequencing grade trypsin (Promega) for 16 h at 37 °C, then acidified with 1% trifluoroacetic acid (Thermo Pierce). Depleted human plasma samples were digested on-filter using 10,000 Da polyethersulfone filters (Nanosep; Pall Life Sciences) (1). Sample buffer was exchanged on-filter with 100 mM ammonium bicarbonate. The samples were then heated at 70 °C with 3 mM dithiothreitol for 5 min, followed by alkylation with 9 mM iodoacetamide in the dark at ambient temperature. Proteins were digested with 50:1 sequencing grade trypsin (Promega) on-filter for 16 h at 37 °C.

Two-dimensional liquid chromatography peptide separation. High-performance liquid chromatography-grade water (J.T.Baker) was used for all analytical solvent preparations. First-dimension (high-pH) separation for mouse (heart cytosol and mitochondria, plasma) and human (subject 4 and 6) samples was conducted on a Phenomenex C18 column (Jupiter Proteo C12, 4 μm particle, 90 Å pore, 100 mm × 1 mm dimension) at high pH using a Finnigan Surveyor liquid chromatography system. The solvent gradient was as follows: 0-2 min, 0-5% B; 3-32 min, 5-35% B; 32-37min, 80% B; 50 $\mu L \cdot min^{-1}$; A: 20 mM ammonium formate, pH 10; B: 20 mM ammonium formate, 90% acetonitrile, pH 10. Fifty μg of

proteolytic peptides were injected with a syringe into a manual 6-port/2-position switch valve. Twelve fractions from 16–40 min were collected, lyophilized and re-dissolved in 20 μL 0.5% formic acid with 2% acetonitrile prior to low-pH reversed-phase separation.

On-line second-dimension (low-pH) reversed-phase chromatography was performed on all samples using an Easy-nLC 1000 nano-UPLC system (Thermo Scientific) on an EasySpray C18 column (PepMap, 3-μm particle, 100-Å pore; 75 μm × 150 mm dimension; Thermo Scientific) held at 50 °C. The solvent gradient was 0–110 min: 0–40% B; 110–117 min: 40–80% B; 117–120 min: 80% B; 300 $nL \cdot min^{-1}$; A: 0.1% formic acid, 2% acetonitrile; B: 0.1% formic acid, 80% acetonitrile. Ten μL of each high-pH fraction was injected by the autosampler on the Easy-nLC 1000 nano-UPLC system.

Protein identification from mass spectrometry data. Mass spectrometry was performed on an LTQ Orbitrap Elite mass spectrometer (Thermo Fisher Scientific) controlled by XCalibur (v.2.1.0) coupled to the Easy-nLC 1000 nano-UPLC system through a Thermo EasySpray interface. Each survey scan was analyzed inside the orbitrap at 60,000 resolving power in profile mode, followed by data-dependent collision-induced dissociation MS2 scans on the top 15 ions inside the ion trap. MS1 and MS2 target ion accumulations were 1×10^4 and 1×10^6, respectively. Dynamic exclusion was set to 90 s. An MS1 lock mass of m/z 425.120025 was used. Protein identification was performed with ProLuCID (2) against a reverse-decoyed database (human: Uniprot Reference Proteome Reviewed, Feb-09-2013, 20,241 entries; mouse: Uniprot Reference Proteome Reviewed, Feb-19-2013, 16,590 entries). Static cysteine carbamidomethylation (+57.02146 Da) modification and ≤3 variable methionine oxidation (+15.9949 Da), lysine acetylation (+42.0106 Da), serine/threonine/tyrosine phosphorylation (+79.9663 Da), or lysine ubiquitylation (+114.0403 Da) were allowed. Tryptic peptides within a 20-ppm mass window surrounding the candidate precursor mass were searched. Protein identifications were filtered by DTASelect (3), requiring ≤1% global peptide false discovery rate and two unique peptides per protein. Modified and unmodified peptides are subjected to separate statistical filter in DTASelect v.2.0 with the –modstat parameter. Spectral counts were calculated in DTASelect. Additional protein identification was performed using MaxQuant (4) for comparison.

Computational workflow for ^2H_2O-labeling data analysis. The nonlinear fitting parameters utilized to deduce protein turnover rate were as follows. Orbitrap spectra were input to ProTurn after conversion

into [.mzML] format using MSConvert (5). ProTurn was instructed to select confidently identified peptides that were uniquely assigned to proteins, and to integrate the areas-under-curves within 60 ppm of the peptide mass at the retention time in the MS1 extracted ion chromatograph, as indicated by the scan number in the protein identification result. Savitzky-Golay filters were applied to the MS1 chromatographs prior to integration (6). Peptides shared by multiple proteins as indicated by the search engine (ProLuCID or MaxQuant) were discarded. In the mouse experiments, we accepted only peptides explicitly identified in at least 4 time points for kinetics calculation as a filter against false positive identifications and to minimize the effect of errors in isotope ratio measurements. Although more proteins may be quantified if the time-point requirement is relaxed, in our experience the statistics of low-abundance proteins does not contribute substantially to overall comparative analyses.

The integrated mass isotopomer fractional abundance information from every time point was fitted using the Nelder-Mead method (7) by ProTurn to optimize for k. The optimization results were independently verified by two data-fitting scripts, written in R and in MATLAB. Peptide isotopomer time-series were accepted if they fit to the model with $r \geq 0.9$, or alternatively with standard error of estimate ≤10% in the mouse or a variable threshold ≤5–9% in human, which permits a small proportion (<10%) of well-fitted peptide isotopomers with low turnover rates. The error range of fitting for k at the isotopomer level is measured by $dk/dA_0 \times \sigma_A$, where σ_A is the residual sum of squares after optimization (vide infra). The turnover rate of a protein is reported as the median and the median absolute deviation of the turnover rates of all its constituent peptide isotopomers.

For the single-time-point analyses, the peptide isotopomer data were filtered without a priori knowledge of the true turnover rates from the full experimental dataset. For a fitting to be considered valid: **(1)** the coefficient of variance of the measured peptide isotopomer fractional abundance in the triplicate mass spectrometry experiments must be ≤10%; **(2)** the residual sum of squares of fitting must be ≤1.5%; and **(3)** the fitted turnover must lie within 0.5–3 half-lives at the sampling time.

For iBAQ label-free quantification in ProTurn, the integrated isotopomer peak areas were summed up as the peptide cluster area. Protein areas were defined as the sum of all peptide areas normalized to the total spectral intensity, then normalized to the potential number of tryptic peptides (six or more amino acids in length) that may be produced from the protein sequence (8).

Nonlinear model of ProTurn. The nonlinear model in ProTurn allows for large-scale proteome dynamics analysis in human as well as diverse animal models. Under gradual ^2H_2O enrichment, label

incorporation into proteins deviates from the first-order exponential decay function. We therefore derived a nonlinear function that resolves isotopomer shifts by accounting for both the rate constants of ^2H_2O enrichment and protein turnover. The gradual incorporation of isotope labels in a proteolytic peptide can be represented by the decrease in the fractional abundance of the 0th isotopomer, A_0, i.e., the fraction of peptides devoid of any heavy isotopes. We followed the assumption that the decrease in fractional abundance of the unlabeled (0th) peptide isotopomer (dA_0/dt) upon ^2H incorporation follows the kinetics of protein pool replacement (9, 10). Thus the rate of decrease is strictly the result of protein turnover and follows first-order kinetics, where k is the protein turnover rate constant and $A_{0,max}$ is the fractional abundance of the 0th isotopomer in the newly-synthesized, labeled peptide, i.e., the amount of label that is entering the peptide pool. The component ($A_{0,max} - A_0$) therefore represents the difference between the steady-state label and the protein label at a particular time.

$$\frac{dA_0}{dt} = k\left(A_{0,max} - A_0\right) \quad \textbf{(S1)}$$

The amount of label entering the protein is governed by the number of labeling sites on the peptide, N, the precursor enrichment level, p, and the natural fractional abundance of the 0th isotopomer prior to labeling, a:

$$A_{0,max} = a\,(1-p)^N \quad \textbf{(S2)}$$

In a simplified scenario where fast and constant precursor label enrichment can be achieved (e.g., in cell cultures following change of medium), $A_{0,max}$ is constant and represents the fractional abundance of the 0th isotopomer when the peptide is fully labeled as dictated by the precursor level, i.e., the fractional abundance when the peptide has reached the plateau and undergoes no additional changes. The resulting exponential decay equation reflects first-order kinetics:

$$A_0 = a + \left(A_{0,max} - a\right)(1 - e^{-kt}) \quad \textbf{(S3)}$$

However, in most realistic labeling situations, p and therefore $A_{0,max}$ are time-dependent and a simple exponential decay equation no longer adequately describes the changes of A_0. This is due to the fact that when an organism intakes ^2H_2O, the pre-existing unlabeled H_2O predominates in molar ratio, and relative isotope abundance of ^2H rises slowly. We further reasoned that the time-dependent change of relative isotope abundance itself follows first-order kinetics with the steady-state level p_{ss} and the rate constant of k_p.

$$p = p_{ss}\left(1 - e^{-k_p t}\right) \quad \textbf{(S4)}$$

Substituting **Equation S4** into **Equation S2**:

$$A_{0,max} = a\ \left(1 - p_{ss}\left(1 - e^{-k_p t}\right)\right)^N \quad \textbf{(S5)}$$

The differential equation for dA_0/dt could now be solved, after substituting **Equation S5** into **Equation S1** and performing binomial expansion on the resulting expression (11):

$$\frac{dA_0}{dt} = k\left(a\ \left(1 - p_{ss}\left(1 - e^{-k_p t}\right)\right)^N - A_0\right) \quad \textbf{(S6)}$$

$$\frac{dA_0}{dt} = k\left(a\ \left((1 - p_{ss}) + p_{ss}e^{-nk_p t}\right)^N - A_0\right)$$

$$\frac{dA_0}{dt} = k\left(\mathrm{a}\sum_{n=0}^{N}\left(\binom{N}{n}(1 - p_{ss})^{N-n}\left(p_{ss}\mathrm{e}^{-\mathrm{k}_p \mathrm{t}}\right)^n - \mathrm{A}_0\right)\right.$$

$$\frac{dA_0}{dt} = ka\left(\sum_{n=0}^{N} b_n e^{-nk_p t}\right) - A_0$$

$$b_n = \binom{N}{n}(1 - p_{ss})^{N-n}{p_{ss}}^n$$

Solving the differential equation:

$$A_0 = a\sum_{n=0}^{N}\left(\frac{k}{k - nk_p}\ b_n\ e^{-nk_p t} + \left(\frac{1}{N+1} - \frac{k}{k - nk_p}\ b_n\right)e^{-kt}\right) \quad \textbf{(S7)}$$

Equation S7 fully describes the time-dependent change in A_0 as the result of labeling, and is a nonlinear function of five parameters:

i. k, the turnover rate of the protein to which the peptide belongs. This is the parameter of interest.

ii. p_{ss}, the plateau level of enrichment of ^2H_2O in the biological system. This parameter was readily measured from body fluid samples with gas chromatography-mass spectrometry.

iii. k_p, the rate constant of the rise-to-plateau kinetics of body water ^2H_2O enrichment. This parameter could be acquired from fitting gas chromatography measurements of body fluid samples at regular time points following the initiation of labeling to **Equation S4**.

iv. a, which represents the unlabeled fractional abundance of the 0^{th} isotopomer of the particular peptide. The value of a could be readily calculated from the peptide sequence and the natural biological abundance of heavy isotopes of carbon, nitrogen, oxygen, and sulfur, using the formula:

$$a = (1 - 0.011)^{N_C}(1 - 0.00366)^{N_N}(1 - 0.00238)^{N_O}(1 - 0.0498)^{N_S}$$

N_C, N_N, N_O, N_S denote the number of carbon, nitrogen, oxygen, and sulfur atoms in the peptide, respectively.

v. N, which represents the number of deuterium-accessible labeling sites on the peptide sequence. N could then be calculated as the sum of the known average accessible deuterium/tritium labeling sites on individual amino acids (N_{aa}) in mice, as has been reported in the literature (12). It may be seen from experimental data (**Supplemental Data 2**) that the values of a and N accurately predict the plateau values of A_0 of identified peptides, which is given by $a \cdot (1 - p_{ss})^N$. The values of a and N may be further adjusted in cases of methionine oxidation, serine/threonine/tyrosine phosphorylation, lysine acetylation, and the lysine ubiquitination remnant diglycine, based on their respective atomic compositions.

The values for p_{ss} and k_p, for an experiment, together with the values of a and N for each individual peptide, were then substituted into **Equation S7**, which could now be fitted using the Nelder-Mead method (7) for the optimal value of k that minimizes the residual values between the model and the experimental data points. In systems where the target enrichment levels are quickly achieved ($k_p \gg k$) such as in mouse models, $A_{0,max}$ is effectively constant and the nonlinear model approaches a simple first-order exponential decay function. The nonlinear model is therefore applicable to both gradual and fast labeling experiments and can be used in both the mouse and human labeling studies.

In all cases of fitting, the standard error of fitting for each peptide time-series was estimated by:

$$\frac{dk}{dA_0}\ \sigma_A = \sigma_k$$

$$\frac{dk}{dA_0} = \frac{1}{a\ \sum_{n=0}^{N}\left(\frac{nk_p}{k(k-nk_p)}\ \frac{k}{k-nk_p}b_n\left(e^{-kt}-e^{-nk_pt}\right)-t\left(\frac{1}{N+1}-\frac{k}{k-nk_p}\,b_n\right)e^{-kt}\right)}$$

$$\sigma_k = \frac{\sigma_A}{a\ \sum_{n=0}^{N}\left(\frac{nk_p}{k(k-nk_p)}\ \frac{k}{k-nk_p}b_n\left(e^{-kt}-e^{-nk_pt}\right)-t\left(\frac{1}{N+1}-\frac{k}{k-nk_p}\,b_n\right)e^{-kt}\right)} \qquad \textbf{(S8)}$$

Since **Equation S8** is a function of time, we estimated error for each fitting where A_0 was most sensitive to the change of k among the time points where experimental data exist. The upper limit and the lower limit of k were defined as $k + \sigma_k$ and $k^2/(k + \sigma_k)$, respectively. The minimized sum of residual squares (σ_A) also allowed for an evaluation of the goodness-of-fit of the function. Fitting accuracy in the nonlinear regression used was not in some cases reflected by the coefficient of determination alone. Slow turnover peptides with relatively gentle curves had low coefficients of determination even when residuals from the curve were minimal and the kinetics curve trajectory was apparent. This is because the residual variance approached the data point variance. To ensure reliable data points are retained and at the same time filter out unreliable data, we additionally calculated the standard error of estimate (SE) of the fitted data:

$$r = \sqrt{1-\frac{\sigma_A}{(\sum_i(A_{0,t=i}-\bar{A}))^2}}$$

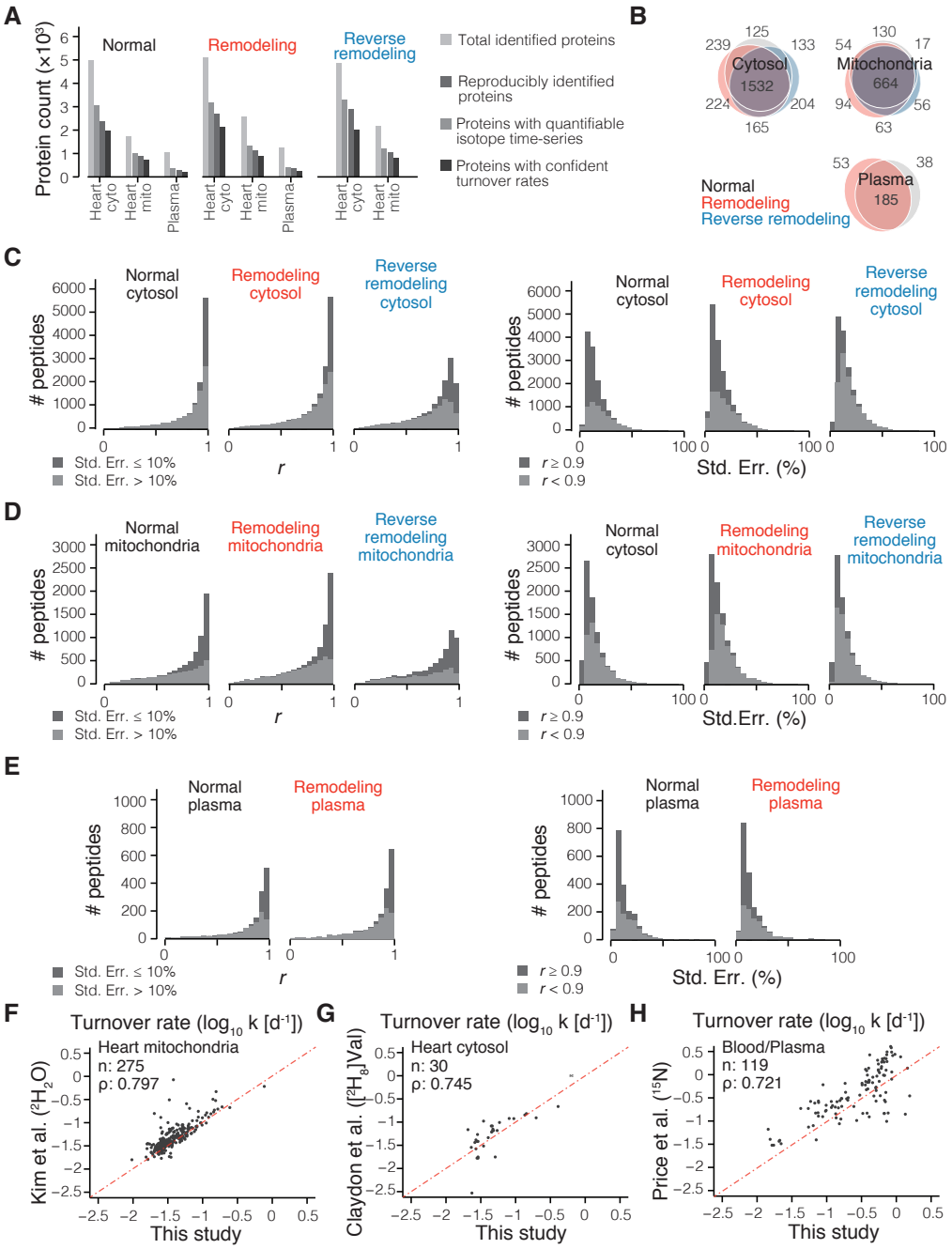
$$SE = \sqrt{\frac{\sigma_A}{\nu}}$$

For fitted curves with the quasi-constant enrichment scheme in the mouse experiments, peptides that showed $r \geq 0.9$ or $SE \leq 10\%$ were accepted. In human labeling, enrichment levels reached different plateaux in each subject, causing intrinsic spectral abundance variability to affect fitting to various degrees especially for the low-turnover curves that were permitted by standard errors, i.e., data from individuals with lower p_{ss} values were more variable because on average less ^{2}H atoms were incorporated into proteins. We therefore used a variable standard error filter that varied between 4 to 9% for each subject. These values were empirically determined to maximize the number of retained well-fitted peptides while minimizing peptide-to-peptide variability within a given protein.

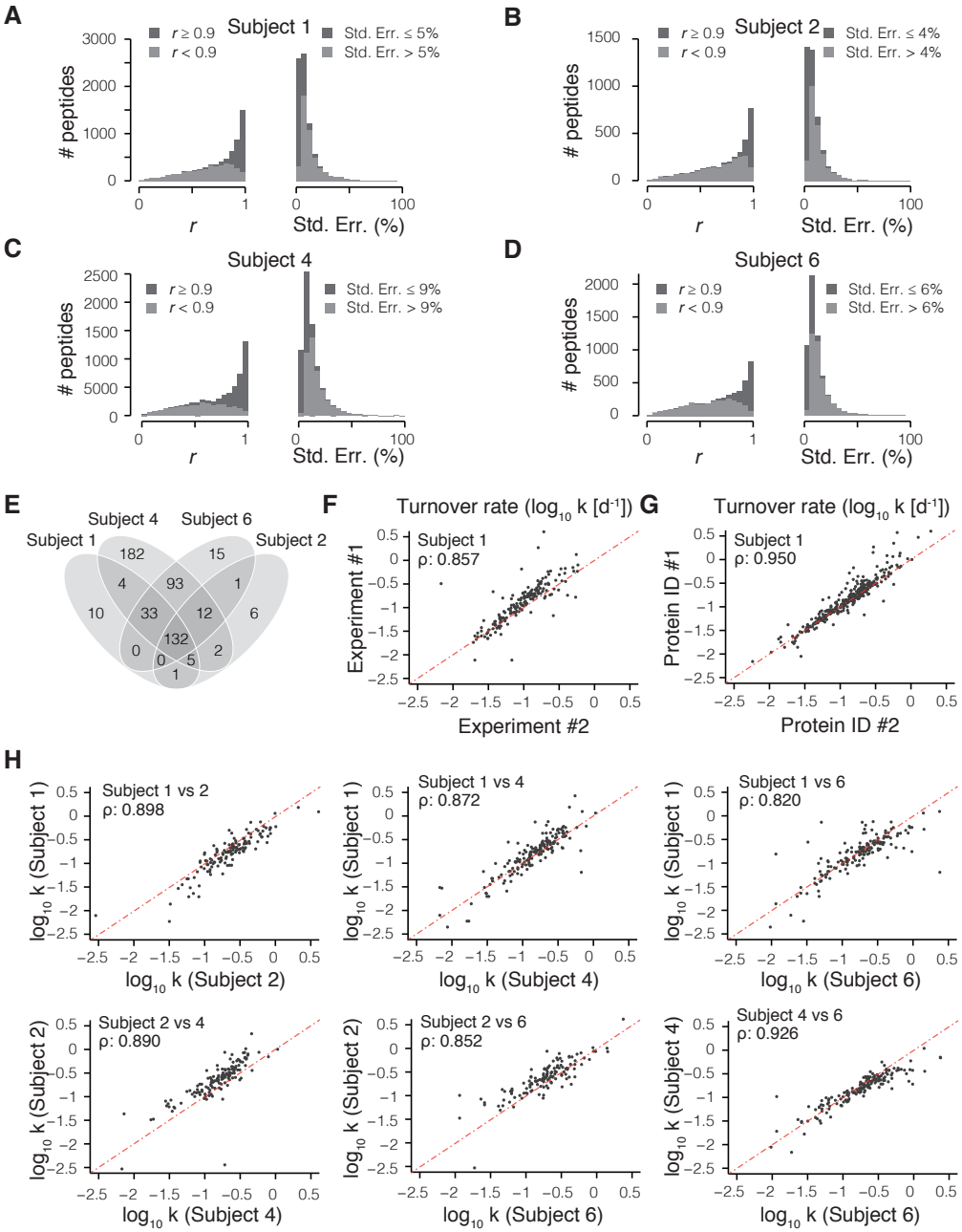
The significance of protein kinetics comparison between two samples was evaluated on multiple levels. On the peptide isotopomer abundance level, every non-zero time point-fractional label coordinate between proteins from two samples was compared using Kolmogorov-Smirnov and Mann-Whitney-

Wilcoxon statistics. On the isotopomer time-series level, we compared the value (optimized k) and deviation (optimized σ_k) of each peptide-sequence pair between proteins of two samples using the Welch's t test. The minimal pairwise fitting error significance (maximal P) among all peptide-sequence pairs were reported as its P value (P_{MPFE}). Lastly on the peptide distribution level, the Mann-Whitney-Wilcoxon test was performed on every protein pair in any two samples each with three or more confidently fitted peptides and reported as its P value (P_{PD}).

Supplemental Figures:



Supplemental Figure S1. **Nonlinear fitting of $^{2}H_2O$ labeling data in mouse.** **(A)** The number of proteins that were identified and quantified in each sample. **(B)** The overlap of proteins with confident turnover in normal and disease mice. **(C–E)** The goodness-of-fit (*r*) and standard error of estimate (Std. Err.) of the turnover rate fitting by the nonlinear model implemented in ProTurn, for each quantified peptide isotopomer in **(C)** mouse heart cytosol, **(D)** mouse heart mitochondria, and **(E)** mouse plasma. The method modeled the time-evolution of 35–50% of all peptide isotopomer series precisely. **(F–H)** The correlation between the turnover rates of common proteins analyzed in this study and three previous studies using $^{2}H_2O$, [$^{2}H_8$]-valine and ^{15}N tracers (9, 13, 14).



Supplemental Figure S2. ^2H_2O-labeling and data fitting in four healthy human subjects. (A-D) Histograms of goodness-of-fit of the nonlinear fitting model in healthy human subject 1, 2, 4, and 6. Only peptides explicitly identified in ≥ 4 time points and containing quantifiable mass isotopomer information are included. In these subjects, the nonlinear fitting method implemented in ProTurn modeled at least 35% of peptides closely ($r \geq 0.9$ or standard error of estimate of 4 to 9%). **(E)** Venn diagram of the overlap of protein species with confident turnover rates. **(F)** Scatter plot and Spearman's correlation coefficient of turnover rates, showing the reproducibility of protein turnover rates in two labeling procedures and MS experiments conducted on the same subject (Subject 1) six months apart. Each data point represents a commonly quantified individual protein. **(G)** Scatter plot and Spearman's correlation coefficient of turnover rates from the same sample (Subject 1) when processed using two different protein identification workflows (ProLuCID and MaxQuant). **(H)** Scatter plots and Spearman's correlation coefficient of turnover rates of proteins commonly identified in any pairwise combination of the four subjects.

Supplemental Data

Supplemental Data 1 [.xslx] | Protein turnover rates in each sample.

Supplemental Data 2 [.pdf] | Example fitting evidence for peptide isotopomers in human. All fitting data can be found at [http://www.heartproteome.org/proturn/supplemental].

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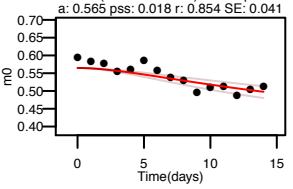
Supplemental Data 2:

This file contains the data fitting evidence of 120 peptides from each of Human Subject 1, 2, 4, and 6.

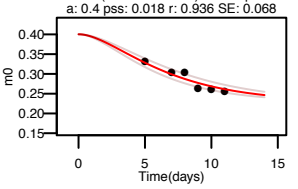
All fitting evidences can be downloaded at:

[http://www.heartproteome.org/proturn/supplemental]

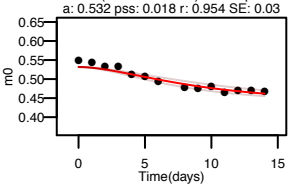
Q14624 SPEHVVVTR 2 +
k: 0.059 (0.042 – 0.084) N: 17 kp: 0.258
a: 0.565 pss: 0.018 r: 0.854 SE: 0.041



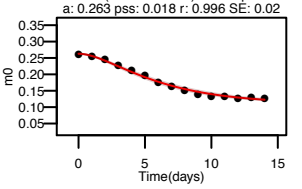
Q14624 SPEQQETVLDGNLII 2 +
k: 0.268 (0.208 – 0.347) N: 31 kp: 0.258
a: 0.4 pss: 0.018 r: 0.936 SE: 0.068



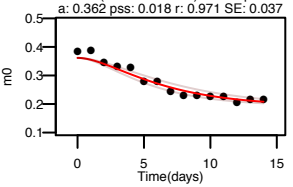
Q14624 LGVYELLLK 2 +
k: 0.177 (0.128 – 0.246) N: 10 kp: 0.258
a: 0.532 pss: 0.018 r: 0.954 SE: 0.03



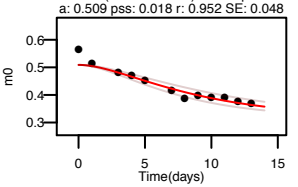
Q14624 QGPVNLLSDPEQGVEVTGQYER 3 +
k: 0.297 (0.267 – 0.33) N: 48 kp: 0.258
a: 0.263 pss: 0.018 r: 0.996 SE: 0.02



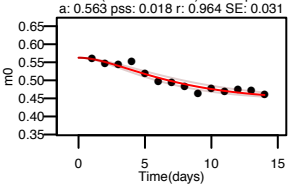
Q14624 NMEQFQVSVSVAPNAK 3 +
k: 0.284 (0.209 – 0.385) N: 35 kp: 0.258
a: 0.362 pss: 0.018 r: 0.971 SE: 0.037



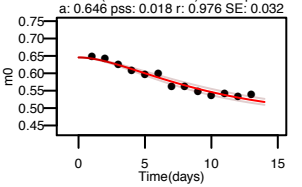
Q14624 SLVPASAENVNK 2 +
k: 0.169 (0.125 – 0.23) N: 26 kp: 0.258
a: 0.509 pss: 0.018 r: 0.952 SE: 0.048



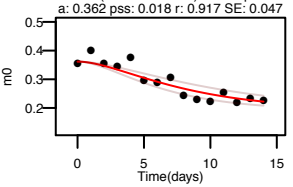
Q14624 NVHSGSTFF 2 +
k: 0.256 (0.193 – 0.339) N: 13 kp: 0.258
a: 0.563 pss: 0.018 r: 0.964 SE: 0.031



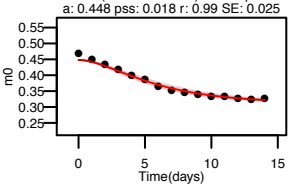
Q14624 LDNGGLAR 2 +
k: 0.149 (0.126 – 0.176) N: 17 kp: 0.258
a: 0.646 pss: 0.018 r: 0.976 SE: 0.032



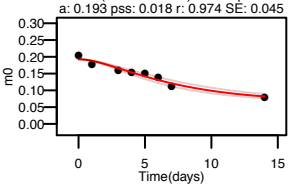
Q14624 NMEQFQVSVSVAPNAK 2 +
k: 0.185 (0.122 – 0.281) N: 35 kp: 0.258
a: 0.362 pss: 0.018 r: 0.917 SE: 0.047



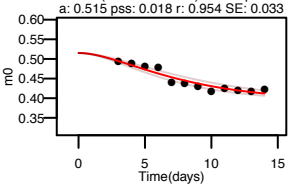
Q14624 NGIDIYSLTVDSR 2 +
k: 0.367 (0.299 – 0.451) N: 20 kp: 0.258
a: 0.448 pss: 0.018 r: 0.99 SE: 0.025



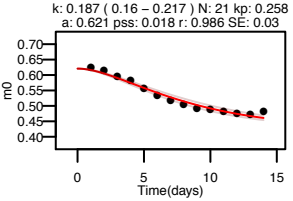
Q14624 TSM(15.9949)VVTKPDDQEQSQVAEKPMEGESR 4 +
k: 0.22 (0.173 – 0.28) N: 59 kp: 0.258
a: 0.193 pss: 0.018 r: 0.974 SE: 0.045



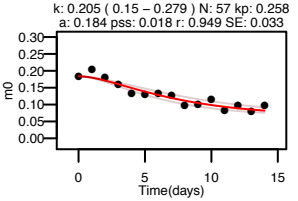
Q14624 ELVYEELLK 2 +
k: 0.215 (0.167 – 0.276) N: 15 kp: 0.258
a: 0.515 pss: 0.018 r: 0.954 SE: 0.033



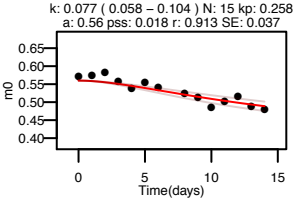
Q14624 ALDNGGLAR 2 +
k: 0.187 (0.16 – 0.217) N: 21 kp: 0.258
a: 0.621 pss: 0.018 r: 0.986 SE: 0.03



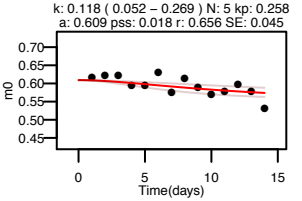
Q14624 FSSHVGGTLGQFYQEVLWGSPAASDDGR 3 +
k: 0.205 (0.15 – 0.279) N: 57 kp: 0.258
a: 0.184 pss: 0.018 r: 0.949 SE: 0.033



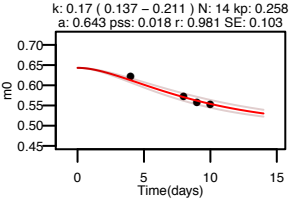
Q14624 FAHTVVTSR 2 +
k: 0.077 (0.058 – 0.104) N: 15 kp: 0.258
a: 0.56 pss: 0.018 r: 0.913 SE: 0.037



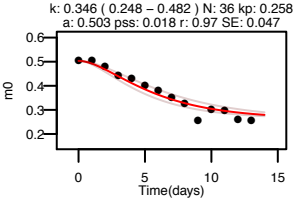
Q14624 VVFVIDK 2 +
k: 0.118 (0.052 – 0.269) N: 5 kp: 0.258
a: 0.609 pss: 0.018 r: 0.656 SE: 0.045



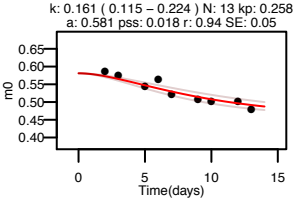
Q14624 KPTLSQQ 2 +
k: 0.17 (0.137 – 0.211) N: 14 kp: 0.258
a: 0.643 pss: 0.018 r: 0.981 SE: 0.103



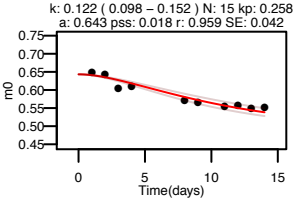
Q14624 EAQAQYSAAVAK 2 +
k: 0.346 (0.248 – 0.482) N: 36 kp: 0.258
a: 0.503 pss: 0.018 r: 0.97 SE: 0.047



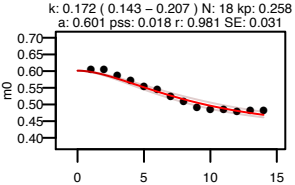
Q14624 DVLTATVSGK 2 +
k: 0.161 (0.115 – 0.224) N: 13 kp: 0.258
a: 0.581 pss: 0.018 r: 0.94 SE: 0.05



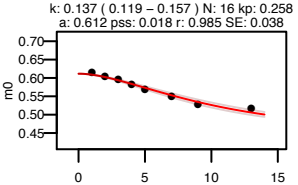
Q14624 SIQNNVR 2 +
k: 0.122 (0.098 – 0.152) N: 15 kp: 0.258
a: 0.643 pss: 0.018 r: 0.959 SE: 0.042



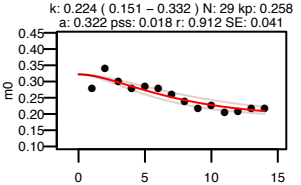
Q14624 KPTLSQQQ 2 +
k: 0.172 (0.143 – 0.207) N: 18 kp: 0.258
a: 0.601 pss: 0.018 r: 0.981 SE: 0.031



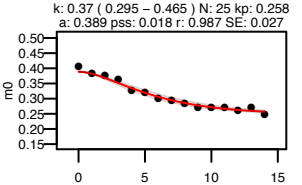
Q14624 RPQQLVK 2 +
k: 0.137 (0.119 – 0.157) N: 16 kp: 0.258
a: 0.612 pss: 0.018 r: 0.985 SE: 0.038

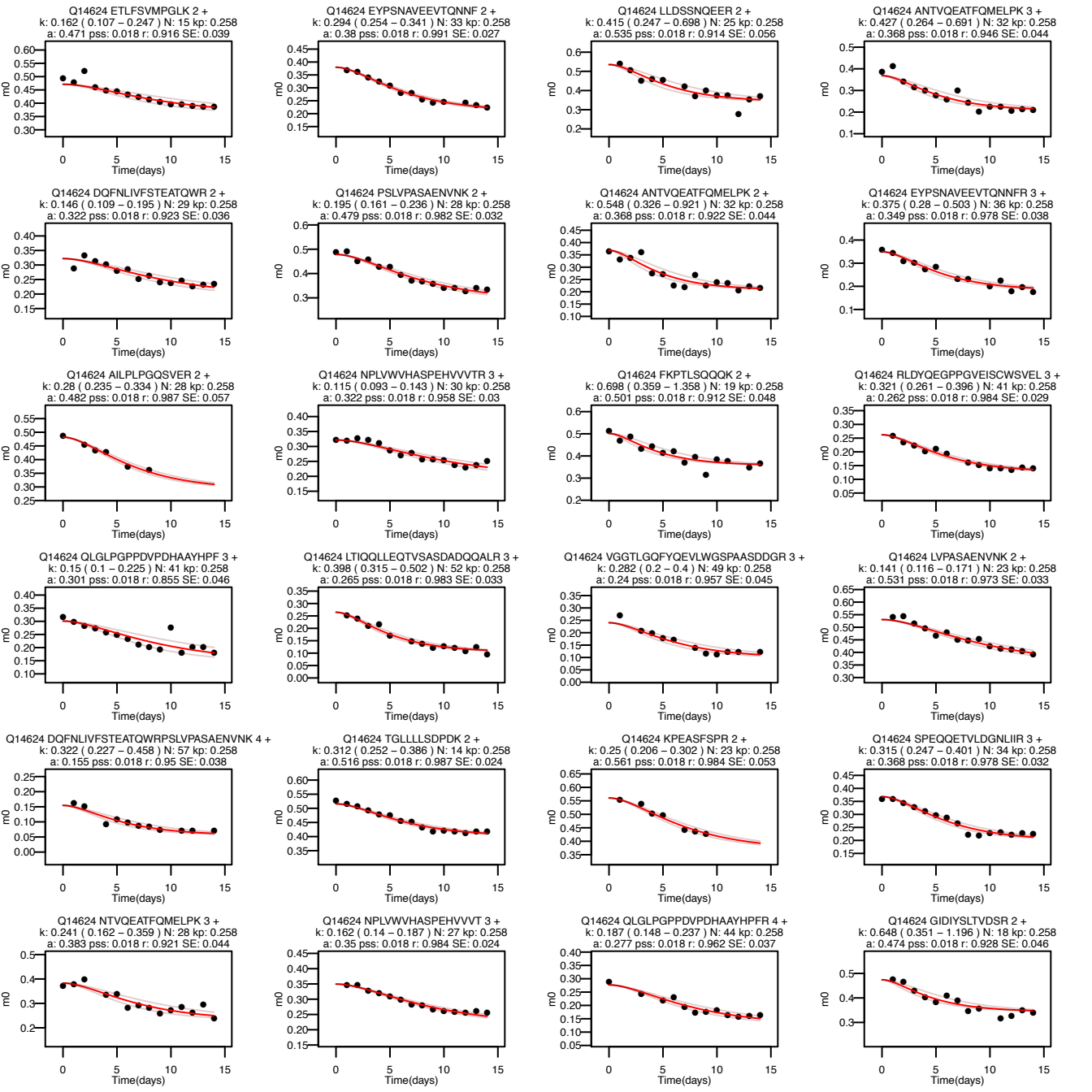


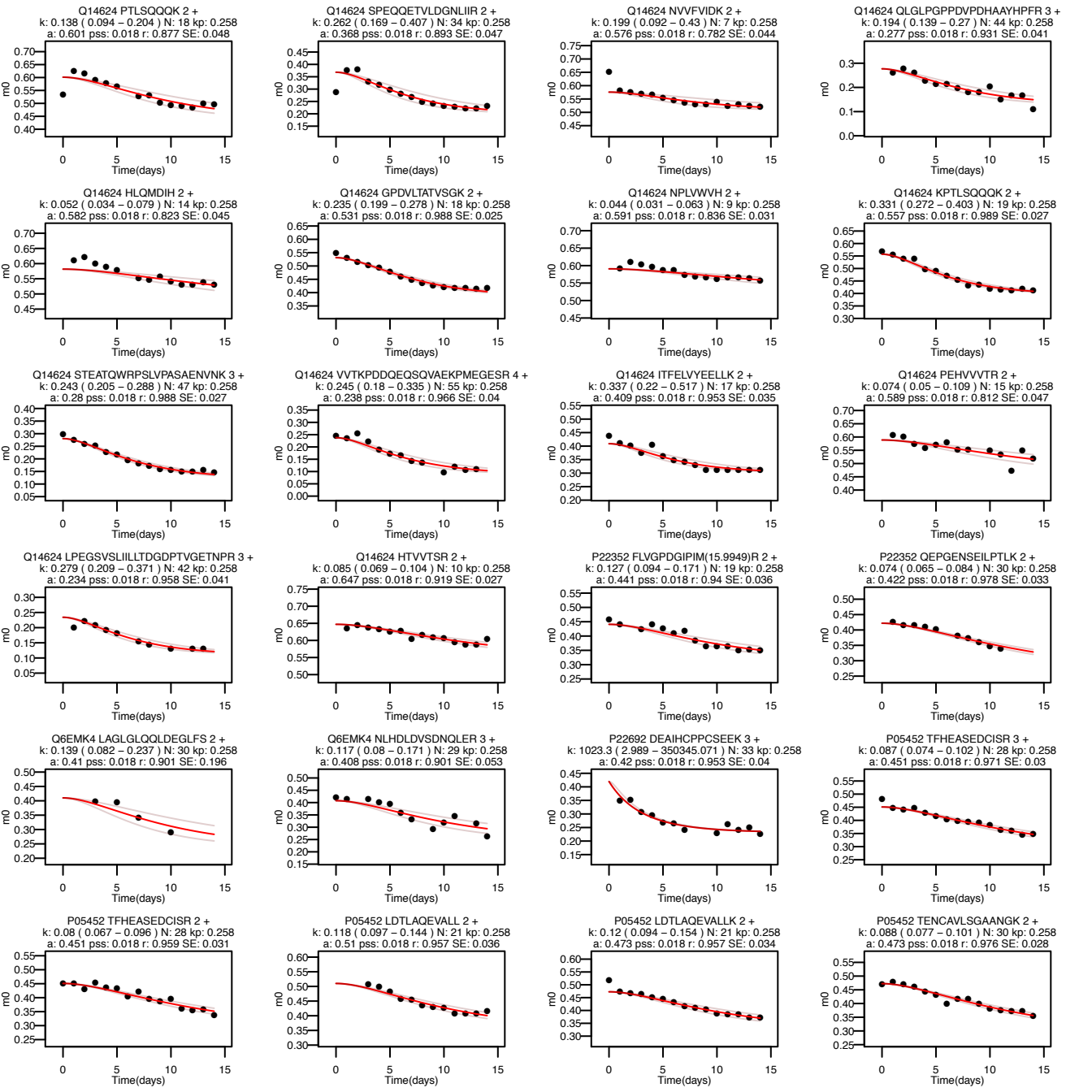
Q14624 DQFNLIVFSTEATQWR 3 +
k: 0.224 (0.151 – 0.332) N: 29 kp: 0.258
a: 0.322 pss: 0.018 r: 0.912 SE: 0.041

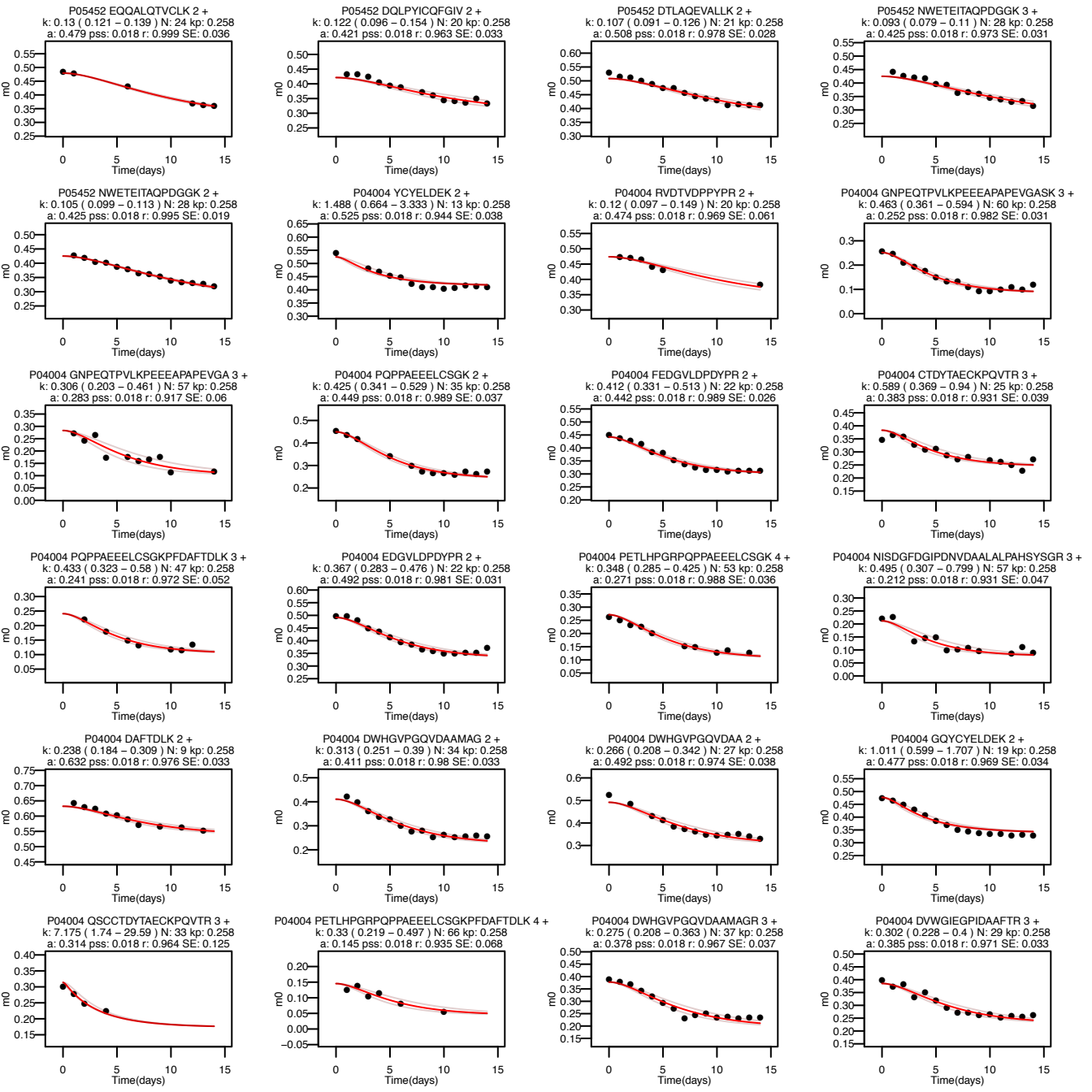


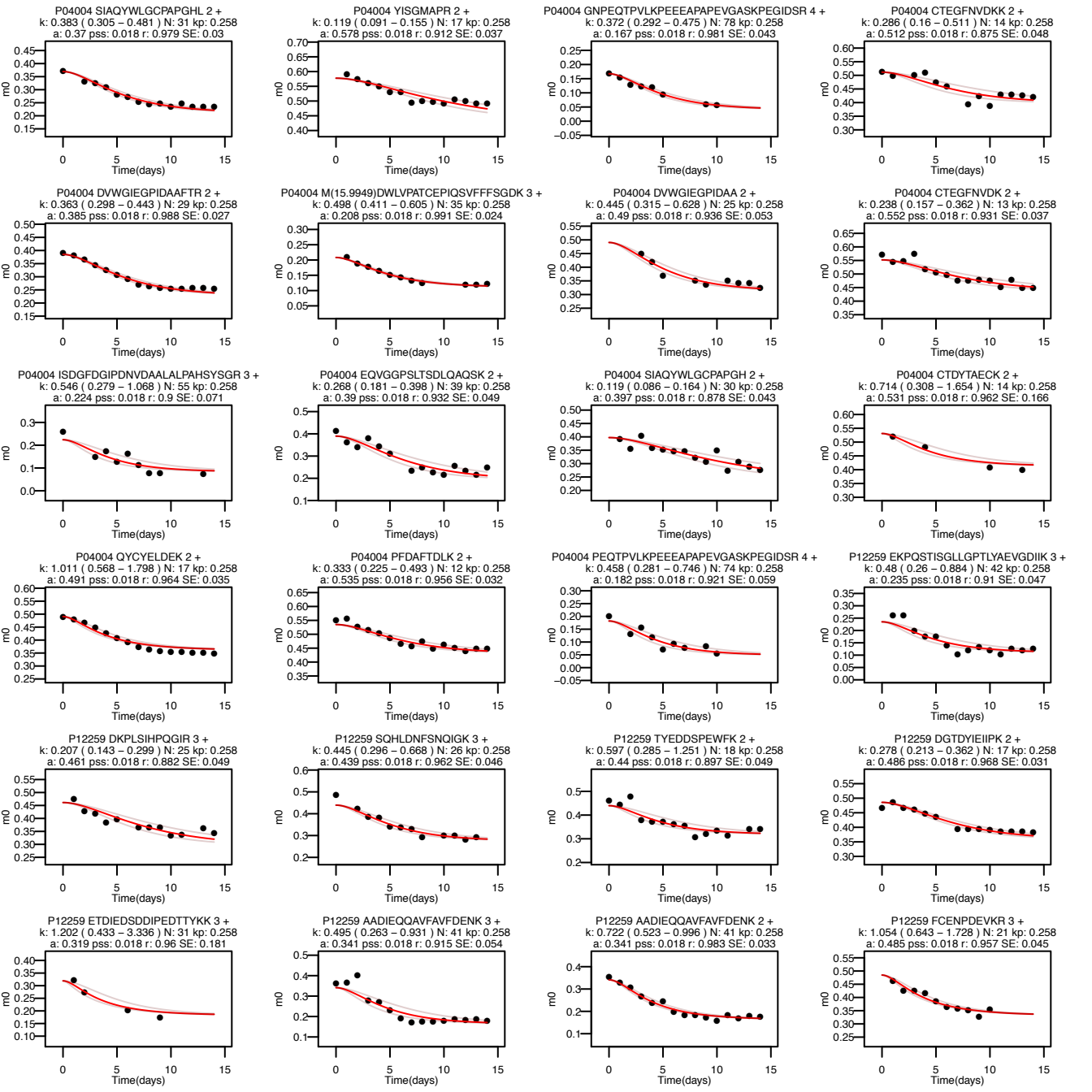
Q14624 EKNGIDIYSLTVDSR 3 +
k: 0.37 (0.295 – 0.465) N: 25 kp: 0.258
a: 0.389 pss: 0.018 r: 0.987 SE: 0.027

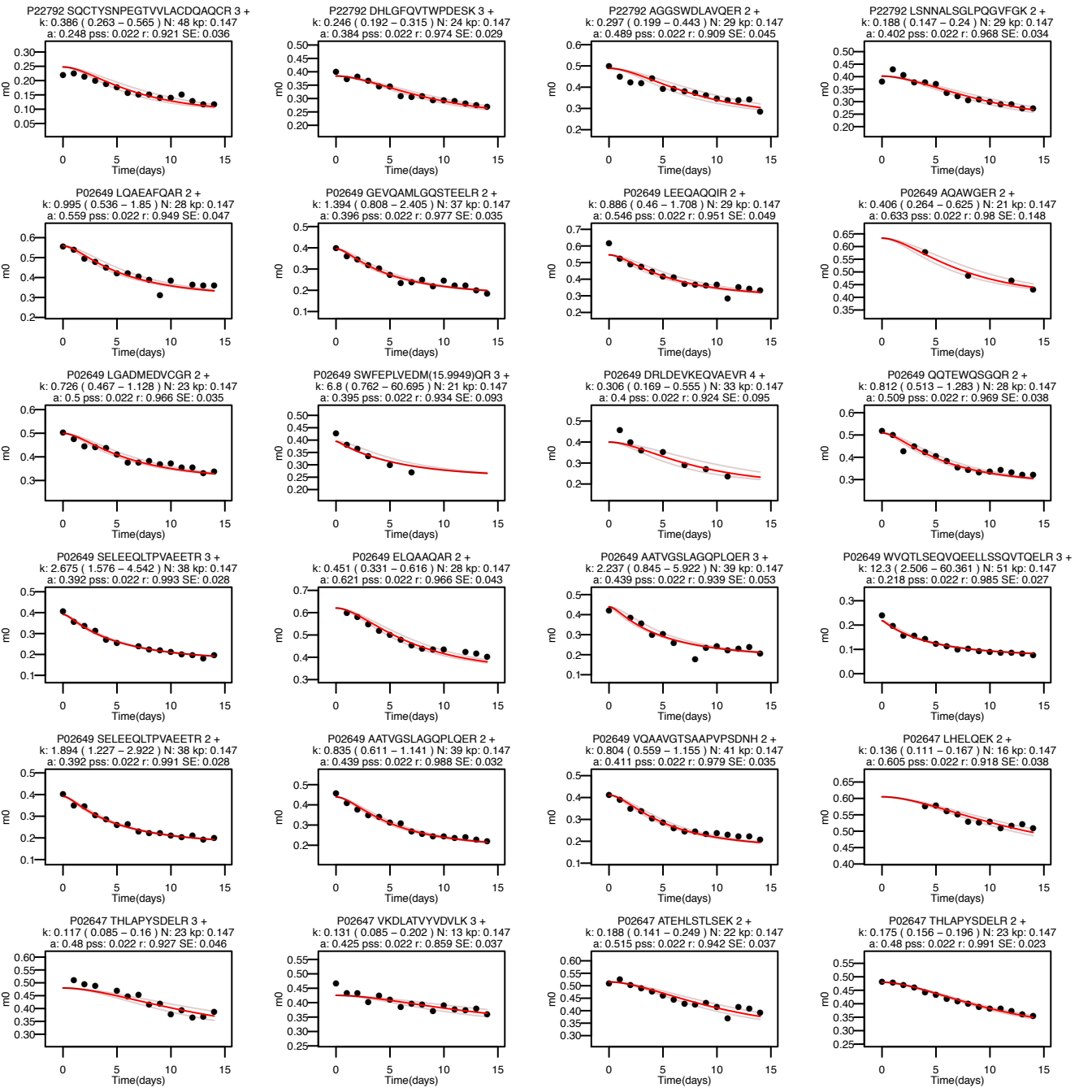


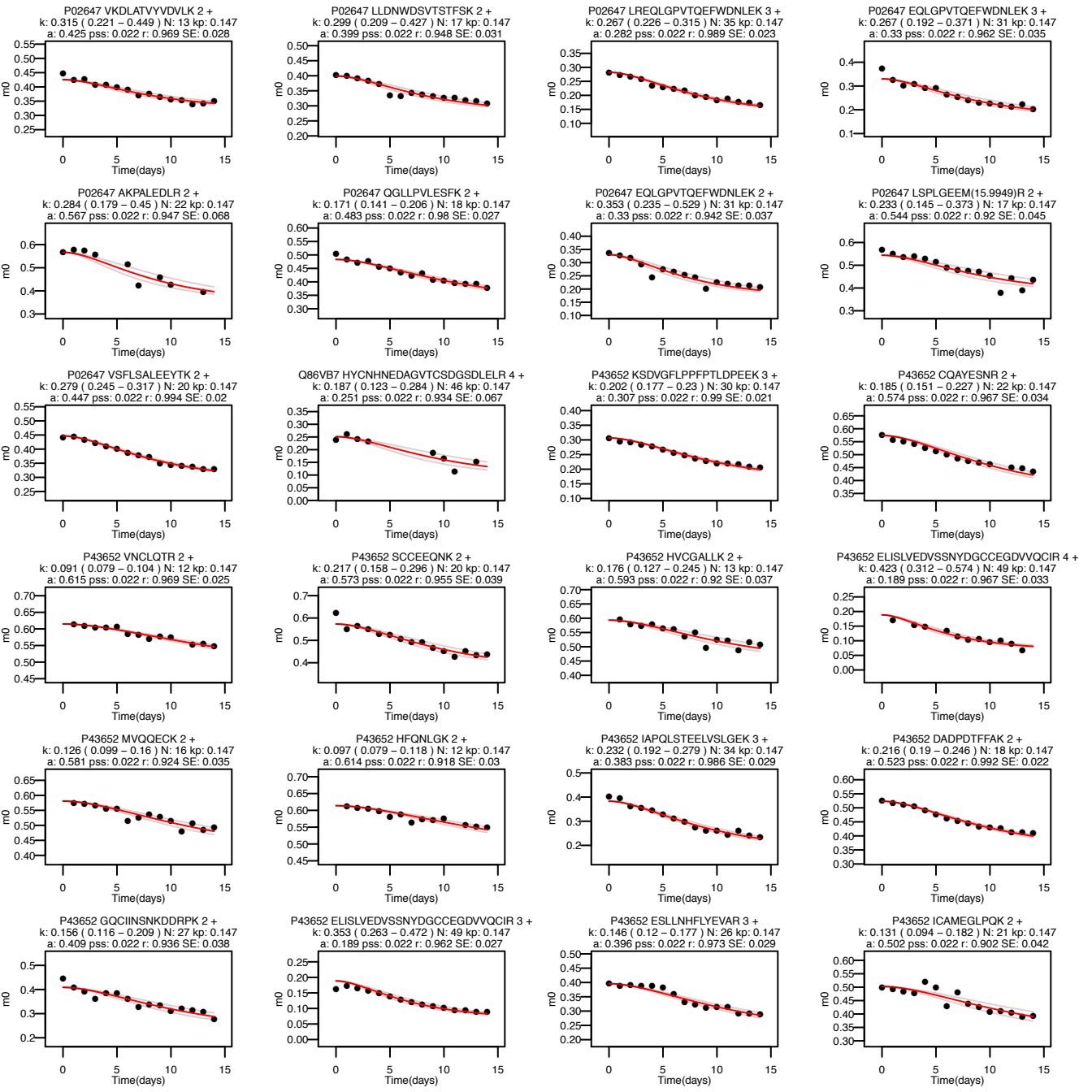

Q14624 ETLFSVMPGLK 2 +
k: 0.162 (0.107 – 0.247) N: 15 kp: 0.258
a: 0.471 pss: 0.018 r: 0.916 SE: 0.039
Q14624 EYPSNAVEEVTQNNF 2 +
k: 0.294 (0.254 – 0.341) N: 33 kp: 0.258
a: 0.38 pss: 0.018 r: 0.991 SE: 0.027
Q14624 LLDSSNQEER 2 +
k: 0.415 (0.247 – 0.698) N: 25 kp: 0.258
a: 0.535 pss: 0.018 r: 0.914 SE: 0.056
Q14624 ANTVQEATFQMELPK 3 +
k: 0.427 (0.264 – 0.691) N: 32 kp: 0.258
a: 0.368 pss: 0.018 r: 0.946 SE: 0.044
Q14624 DQFNLIVFSTEATQWR 2 +
k: 0.146 (0.109 – 0.195) N: 29 kp: 0.258
a: 0.322 pss: 0.018 r: 0.923 SE: 0.036
Q14624 PSLVPASAENVNK 2 +
k: 0.195 (0.161 – 0.236) N: 28 kp: 0.258
a: 0.479 pss: 0.018 r: 0.982 SE: 0.032
Q14624 ANTVQEATFQMELPK 2 +
k: 0.548 (0.326 – 0.921) N: 32 kp: 0.258
a: 0.368 pss: 0.018 r: 0.922 SE: 0.044
Q14624 EYPSNAVEEVTQNNFR 3 +
k: 0.375 (0.28 – 0.503) N: 36 kp: 0.258
a: 0.349 pss: 0.018 r: 0.978 SE: 0.038
Q14624 AILPLPGQSVER 2 +
k: 0.28 (0.235 – 0.334) N: 28 kp: 0.258
a: 0.482 pss: 0.018 r: 0.987 SE: 0.057
Q14624 NPLVWVHASPEHVVVTR 3 +
k: 0.115 (0.093 – 0.143) N: 30 kp: 0.258
a: 0.322 pss: 0.018 r: 0.958 SE: 0.03
Q14624 FKPTLSQQQK 2 +
k: 0.698 (0.359 – 1.358) N: 19 kp: 0.258
a: 0.501 pss: 0.018 r: 0.912 SE: 0.048
Q14624 RLDYQEGPPGVEISCWSVEL 3 +
k: 0.321 (0.261 – 0.396) N: 41 kp: 0.258
a: 0.262 pss: 0.018 r: 0.984 SE: 0.029
Q14624 QLGLPGPPDVPDHAAYHPF 3 +
k: 0.15 (0.1 – 0.225) N: 41 kp: 0.258
a: 0.301 pss: 0.018 r: 0.855 SE: 0.046
Q14624 LTIQQLLEQTVSASDADQQALR 3 +
k: 0.398 (0.315 – 0.502) N: 52 kp: 0.258
a: 0.265 pss: 0.018 r: 0.983 SE: 0.033
Q14624 VGGTLGQFYQEVLWGSPAASDDGR 3 +
k: 0.282 (0.2 – 0.4) N: 49 kp: 0.258
a: 0.24 pss: 0.018 r: 0.957 SE: 0.045
Q14624 LVPASAENVNK 2 +
k: 0.141 (0.116 – 0.171) N: 23 kp: 0.258
a: 0.531 pss: 0.018 r: 0.973 SE: 0.033
Q14624 DQFNLIVFSTEATQWRPSLVPASAENVNK 4 +
k: 0.322 (0.227 – 0.458) N: 57 kp: 0.258
a: 0.155 pss: 0.018 r: 0.95 SE: 0.038
Q14624 TGLLLLSDPDK 2 +
k: 0.312 (0.252 – 0.386) N: 14 kp: 0.258
a: 0.516 pss: 0.018 r: 0.987 SE: 0.024
Q14624 KPEASFSPR 2 +
k: 0.25 (0.206 – 0.302) N: 23 kp: 0.258
a: 0.561 pss: 0.018 r: 0.984 SE: 0.053
Q14624 SPEQQETVLDGNLIIR 3 +
k: 0.315 (0.247 – 0.401) N: 34 kp: 0.258
a: 0.368 pss: 0.018 r: 0.978 SE: 0.032
Q14624 NTVQEATFQMELPK 3 +
k: 0.241 (0.162 – 0.359) N: 28 kp: 0.258
a: 0.383 pss: 0.018 r: 0.921 SE: 0.044
Q14624 NPLVWVHASPEHVVVT 3 +
k: 0.162 (0.14 – 0.187) N: 27 kp: 0.258
a: 0.35 pss: 0.018 r: 0.984 SE: 0.024
Q14624 QLGLPGPPDVPDHAAYHPFR 4 +
k: 0.187 (0.148 – 0.237) N: 44 kp: 0.258
a: 0.277 pss: 0.018 r: 0.962 SE: 0.037
Q14624 GIDIYSLTVDSR 2 +
k: 0.648 (0.351 – 1.196) N: 18 kp: 0.258
a: 0.474 pss: 0.018 r: 0.928 SE: 0.046
m0
Time(days)

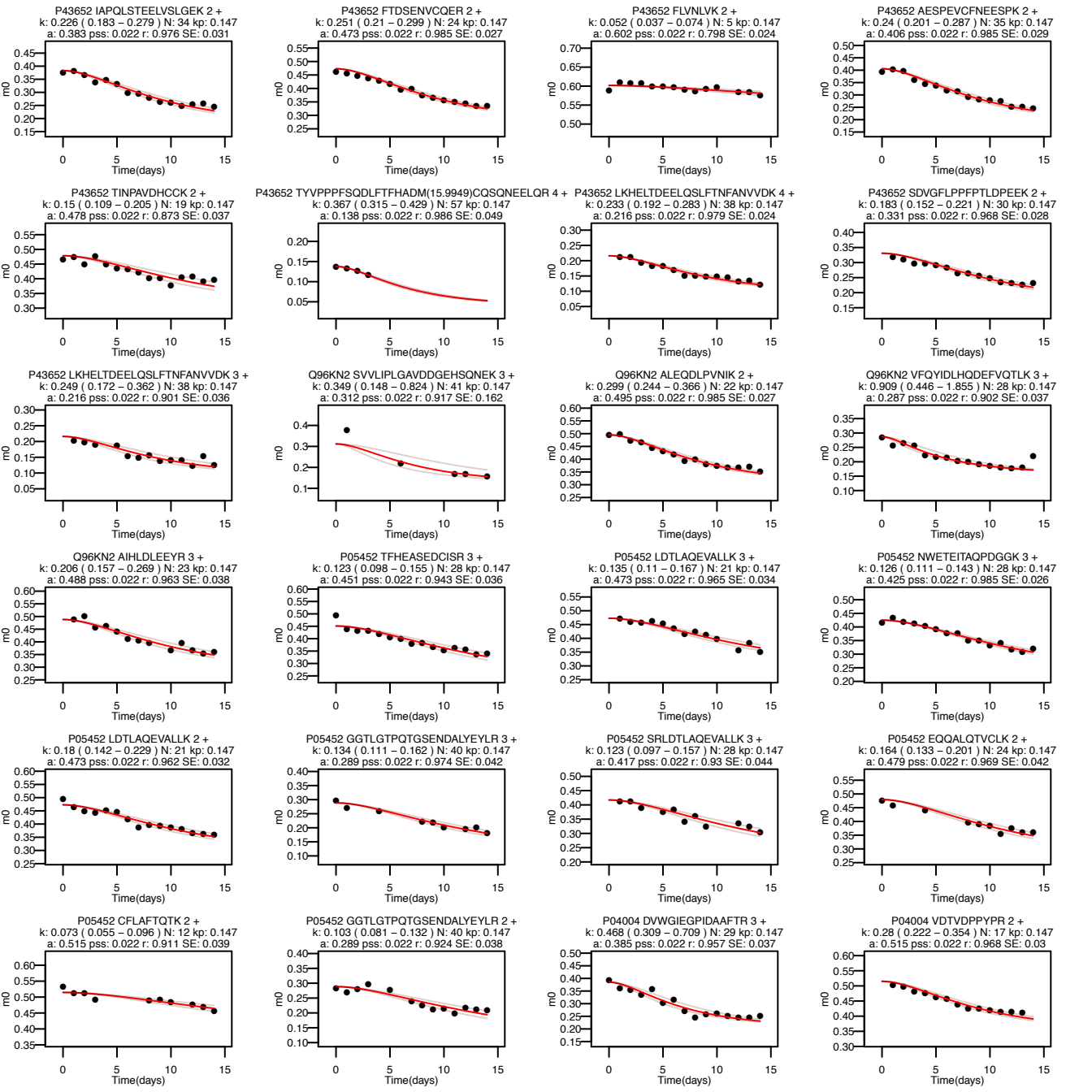

Q14624 PTLSQQQK 2 +
k: 0.138 (0.094 – 0.204) N: 18 kp: 0.258
a: 0.601 pss: 0.018 r: 0.877 SE: 0.048
Q14624 SPEQQETVLDGNLIIR 2 +
k: 0.262 (0.169 – 0.407) N: 34 kp: 0.258
a: 0.368 pss: 0.018 r: 0.893 SE: 0.047
Q14624 NVVFVIDK 2 +
k: 0.199 (0.092 – 0.43) N: 7 kp: 0.258
a: 0.576 pss: 0.018 r: 0.782 SE: 0.044
Q14624 QLGLPGPPDVPDHAAYHPFR 3 +
k: 0.194 (0.139 – 0.27) N: 44 kp: 0.258
a: 0.277 pss: 0.018 r: 0.931 SE: 0.041
Q14624 HLQMDIH 2 +
k: 0.052 (0.034 – 0.079) N: 14 kp: 0.258
a: 0.582 pss: 0.018 r: 0.823 SE: 0.045
Q14624 GPDVLTATVSGK 2 +
k: 0.235 (0.199 – 0.278) N: 18 kp: 0.258
a: 0.531 pss: 0.018 r: 0.988 SE: 0.025
Q14624 NPLVWVH 2 +
k: 0.044 (0.031 – 0.063) N: 9 kp: 0.258
a: 0.591 pss: 0.018 r: 0.836 SE: 0.031
Q14624 KPTLSQQQK 2 +
k: 0.331 (0.272 – 0.403) N: 19 kp: 0.258
a: 0.557 pss: 0.018 r: 0.989 SE: 0.027
Q14624 STEATQWRPSLVPASAENVNK 3 +
k: 0.243 (0.205 – 0.288) N: 47 kp: 0.258
a: 0.28 pss: 0.018 r: 0.988 SE: 0.027
Q14624 VVTKPDDQEQSQVAEKPMEGESR 4 +
k: 0.245 (0.18 – 0.335) N: 55 kp: 0.258
a: 0.238 pss: 0.018 r: 0.966 SE: 0.04
Q14624 ITFELVYEELLK 2 +
k: 0.337 (0.22 – 0.517) N: 17 kp: 0.258
a: 0.409 pss: 0.018 r: 0.953 SE: 0.035
Q14624 PEHVVVTR 2 +
k: 0.074 (0.05 – 0.109) N: 15 kp: 0.258
a: 0.589 pss: 0.018 r: 0.812 SE: 0.047
Q14624 LPEGSVSLIILLTDGDPTVGETNPR 3 +
k: 0.279 (0.209 – 0.371) N: 42 kp: 0.258
a: 0.234 pss: 0.018 r: 0.958 SE: 0.041
Q14624 HTVVTSR 2 +
k: 0.085 (0.069 – 0.104) N: 10 kp: 0.258
a: 0.647 pss: 0.018 r: 0.919 SE: 0.027
P22352 FLVGPDGIPIM(15.9949)R 2 +
k: 0.127 (0.094 – 0.171) N: 19 kp: 0.258
a: 0.441 pss: 0.018 r: 0.94 SE: 0.036
P22352 QEPGENSEILPTLK 2 +
k: 0.074 (0.065 – 0.084) N: 30 kp: 0.258
a: 0.422 pss: 0.018 r: 0.978 SE: 0.033
Q6EMK4 LAGLGLQQLDEGLFS 2 +
k: 0.139 (0.082 – 0.237) N: 30 kp: 0.258
a: 0.41 pss: 0.018 r: 0.901 SE: 0.196
Q6EMK4 NLHDLDVSDNQLER 3 +
k: 0.117 (0.08 – 0.171) N: 29 kp: 0.258
a: 0.408 pss: 0.018 r: 0.901 SE: 0.053
P22692 DEAIHCPPCSEEK 3 +
k: 1023.3 (2.989 – 350345.071) N: 33 kp: 0.258
a: 0.42 pss: 0.018 r: 0.953 SE: 0.04
P05452 TFHEASEDCISR 3 +
k: 0.087 (0.074 – 0.102) N: 28 kp: 0.258
a: 0.451 pss: 0.018 r: 0.971 SE: 0.03
P05452 TFHEASEDCISR 2 +
k: 0.08 (0.067 – 0.096) N: 28 kp: 0.258
a: 0.451 pss: 0.018 r: 0.959 SE: 0.031
P05452 LDTLAQEVALL 2 +
k: 0.118 (0.097 – 0.144) N: 21 kp: 0.258
a: 0.51 pss: 0.018 r: 0.957 SE: 0.036
P05452 LDTLAQEVALLK 2 +
k: 0.12 (0.094 – 0.154) N: 21 kp: 0.258
a: 0.473 pss: 0.018 r: 0.957 SE: 0.034
P05452 TENCAVLSGAANGK 2 +
k: 0.088 (0.077 – 0.101) N: 30 kp: 0.258
a: 0.473 pss: 0.018 r: 0.976 SE: 0.028
m0
Time(days)

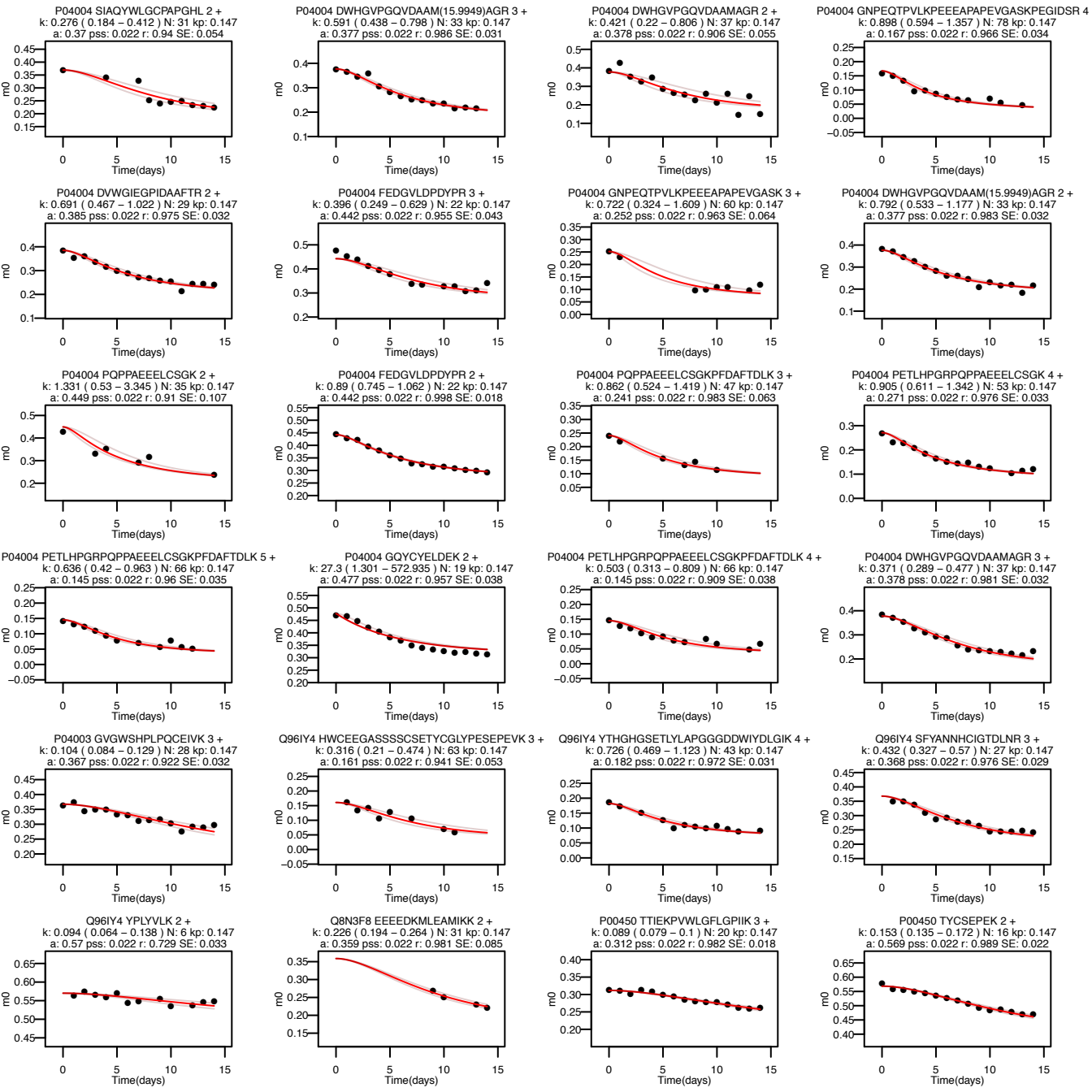

P05452 EQQALQTVCLK 2 +
k: 0.13 (0.121 – 0.139) N: 24 kp: 0.258
a: 0.479 pss: 0.018 r: 0.999 SE: 0.036
P05452 DQLPYICQFGIV 2 +
k: 0.122 (0.096 – 0.154) N: 20 kp: 0.258
a: 0.421 pss: 0.018 r: 0.963 SE: 0.033
P05452 DTLAQEVALLK 2 +
k: 0.107 (0.091 – 0.126) N: 21 kp: 0.258
a: 0.508 pss: 0.018 r: 0.978 SE: 0.028
P05452 NWETEITAQPDGGK 3 +
k: 0.093 (0.079 – 0.11) N: 28 kp: 0.258
a: 0.425 pss: 0.018 r: 0.973 SE: 0.031
P05452 NWETEITAQPDGGK 2 +
k: 0.105 (0.099 – 0.113) N: 28 kp: 0.258
a: 0.425 pss: 0.018 r: 0.995 SE: 0.019
P04004 YCYELDEK 2 +
k: 1.488 (0.664 – 3.333) N: 13 kp: 0.258
a: 0.525 pss: 0.018 r: 0.944 SE: 0.038
P04004 RVDTVDPPYPR 2 +
k: 0.12 (0.097 – 0.149) N: 20 kp: 0.258
a: 0.474 pss: 0.018 r: 0.969 SE: 0.061
P04004 GNPEQTPVLKPEEEAPAPEVGASK 3 +
k: 0.463 (0.361 – 0.594) N: 60 kp: 0.258
a: 0.252 pss: 0.018 r: 0.982 SE: 0.031
P04004 GNPEQTPVLKPEEEAPAPEVGA 3 +
k: 0.306 (0.203 – 0.461) N: 57 kp: 0.258
a: 0.283 pss: 0.018 r: 0.917 SE: 0.06
P04004 PQPPAEEELCSGK 2 +
k: 0.425 (0.341 – 0.529) N: 35 kp: 0.258
a: 0.449 pss: 0.018 r: 0.989 SE: 0.037
P04004 FEDGVLDPDYPR 2 +
k: 0.412 (0.331 – 0.513) N: 22 kp: 0.258
a: 0.442 pss: 0.018 r: 0.989 SE: 0.026
P04004 CTDYTAECKPQVTR 3 +
k: 0.589 (0.369 – 0.94) N: 25 kp: 0.258
a: 0.383 pss: 0.018 r: 0.931 SE: 0.039
P04004 PQPPAEEELCSGKPFDAFTDLK 3 +
k: 0.433 (0.323 – 0.58) N: 47 kp: 0.258
a: 0.241 pss: 0.018 r: 0.972 SE: 0.052
P04004 EDGVLDPDYPR 2 +
k: 0.367 (0.283 – 0.476) N: 22 kp: 0.258
a: 0.492 pss: 0.018 r: 0.981 SE: 0.031
P04004 PETLHPGRPQPPAEEELCSGK 4 +
k: 0.348 (0.285 – 0.425) N: 53 kp: 0.258
a: 0.271 pss: 0.018 r: 0.988 SE: 0.036
P04004 NISDGFDGIPDNVDAALALPAHSYSGR 3 +
k: 0.495 (0.307 – 0.799) N: 57 kp: 0.258
a: 0.212 pss: 0.018 r: 0.931 SE: 0.047
P04004 DAFTDLK 2 +
k: 0.238 (0.184 – 0.309) N: 9 kp: 0.258
a: 0.632 pss: 0.018 r: 0.976 SE: 0.033
P04004 DWHGVPGQVDAAMAG 2 +
k: 0.313 (0.251 – 0.39) N: 34 kp: 0.258
a: 0.411 pss: 0.018 r: 0.98 SE: 0.033
P04004 DWHGVPGQVDAA 2 +
k: 0.266 (0.208 – 0.342) N: 27 kp: 0.258
a: 0.492 pss: 0.018 r: 0.974 SE: 0.038
P04004 GQYCYELDEK 2 +
k: 1.011 (0.599 – 1.707) N: 19 kp: 0.258
a: 0.477 pss: 0.018 r: 0.969 SE: 0.034
P04004 QSCCTDYTAECKPQVTR 3 +
k: 7.175 (1.74 – 29.59) N: 33 kp: 0.258
a: 0.314 pss: 0.018 r: 0.964 SE: 0.125
P04004 PETLHPGRPQPPAEEELCSGKPFDAFTDLK 4 +
k: 0.33 (0.219 – 0.497) N: 66 kp: 0.258
a: 0.145 pss: 0.018 r: 0.935 SE: 0.068
P04004 DWHGVPGQVDAAMAGR 3 +
k: 0.275 (0.208 – 0.363) N: 37 kp: 0.258
a: 0.378 pss: 0.018 r: 0.967 SE: 0.037
P04004 DVWGIEGPIDAAFTR 3 +
k: 0.302 (0.228 – 0.4) N: 29 kp: 0.258
a: 0.385 pss: 0.018 r: 0.971 SE: 0.033
m0
Time(days)

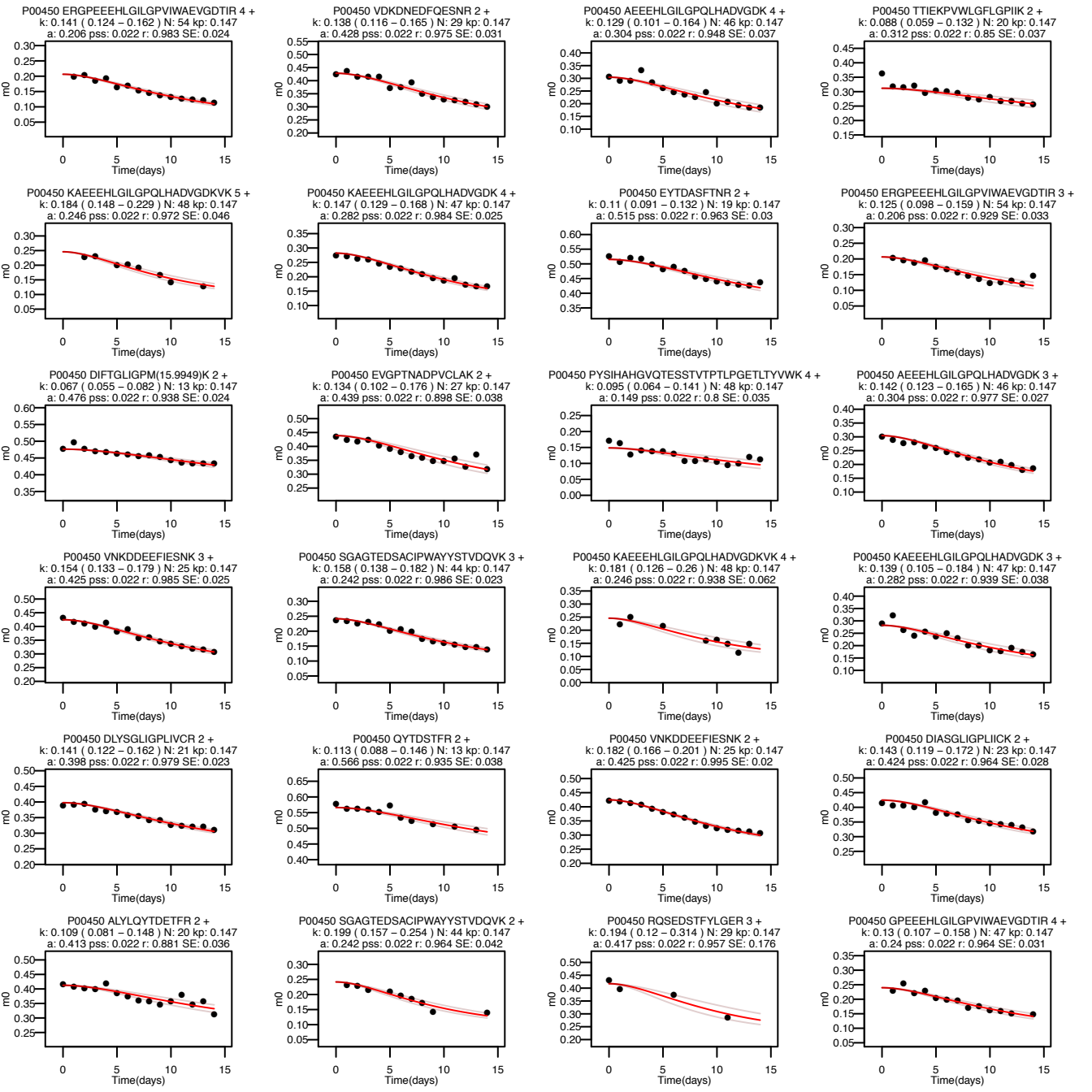

P04004 SIAQYWLGCPAPGHL 2 +
k: 0.383 (0.305 – 0.481) N: 31 kp: 0.258
a: 0.37 pss: 0.018 r: 0.979 SE: 0.03
P04004 YISGMAPR 2 +
k: 0.119 (0.091 – 0.155) N: 17 kp: 0.258
a: 0.578 pss: 0.018 r: 0.912 SE: 0.037
P04004 GNPEQTPVLKPEEEAPAPEVGASKPEGIDSR 4 +
k: 0.372 (0.292 – 0.475) N: 78 kp: 0.258
a: 0.167 pss: 0.018 r: 0.981 SE: 0.043
P04004 CTEGFNVDKK 2 +
k: 0.286 (0.16 – 0.511) N: 14 kp: 0.258
a: 0.512 pss: 0.018 r: 0.875 SE: 0.048
P04004 DVWGIEGPIDAAFTR 2 +
k: 0.363 (0.298 – 0.443) N: 29 kp: 0.258
a: 0.385 pss: 0.018 r: 0.988 SE: 0.027
P04004 M(15.9949)DWLVPATCEPIQSVFFFSGDK 3 +
k: 0.498 (0.411 – 0.605) N: 35 kp: 0.258
a: 0.208 pss: 0.018 r: 0.991 SE: 0.024
P04004 DVWGIEGPIDAA 2 +
k: 0.445 (0.315 – 0.628) N: 25 kp: 0.258
a: 0.49 pss: 0.018 r: 0.936 SE: 0.053
P04004 CTEGFNVDK 2 +
k: 0.238 (0.157 – 0.362) N: 13 kp: 0.258
a: 0.552 pss: 0.018 r: 0.931 SE: 0.037
P04004 ISDGFDGIPDNVDAALALPAHSYSGR 3 +
k: 0.546 (0.279 – 1.068) N: 55 kp: 0.258
a: 0.224 pss: 0.018 r: 0.9 SE: 0.071
P04004 EQVGGPSLTSDLQAQSK 2 +
k: 0.268 (0.181 – 0.398) N: 39 kp: 0.258
a: 0.39 pss: 0.018 r: 0.932 SE: 0.049
P04004 SIAQYWLGCPAPGH 2 +
k: 0.119 (0.086 – 0.164) N: 30 kp: 0.258
a: 0.397 pss: 0.018 r: 0.878 SE: 0.043
P04004 CTDYTAECK 2 +
k: 0.714 (0.308 – 1.654) N: 14 kp: 0.258
a: 0.531 pss: 0.018 r: 0.962 SE: 0.166
P04004 QYCYELDEK 2 +
k: 1.011 (0.568 – 1.798) N: 17 kp: 0.258
a: 0.491 pss: 0.018 r: 0.964 SE: 0.035
P04004 PFDAFTDLK 2 +
k: 0.333 (0.225 – 0.493) N: 12 kp: 0.258
a: 0.535 pss: 0.018 r: 0.956 SE: 0.032
P04004 PEQTPVLKPEEEAPAPEVGASKPEGIDSR 4 +
k: 0.458 (0.281 – 0.746) N: 74 kp: 0.258
a: 0.182 pss: 0.018 r: 0.921 SE: 0.059
P12259 EKPQSTISGLLGPTLYAEVGDIIK 3 +
k: 0.48 (0.26 – 0.884) N: 42 kp: 0.258
a: 0.235 pss: 0.018 r: 0.91 SE: 0.047
P12259 DKPLSIHPQGIR 3 +
k: 0.207 (0.143 – 0.299) N: 25 kp: 0.258
a: 0.461 pss: 0.018 r: 0.882 SE: 0.049
P12259 SQHLDNFSNQIGK 3 +
k: 0.445 (0.296 – 0.668) N: 26 kp: 0.258
a: 0.439 pss: 0.018 r: 0.962 SE: 0.046
P12259 TYEDDSPEWFK 2 +
k: 0.597 (0.285 – 1.251) N: 18 kp: 0.258
a: 0.44 pss: 0.018 r: 0.897 SE: 0.049
P12259 DGTDYIEIIPK 2 +
k: 0.278 (0.213 – 0.362) N: 17 kp: 0.258
a: 0.486 pss: 0.018 r: 0.968 SE: 0.031
P12259 ETDIEDSDDIPEDTTYKK 3 +
k: 1.202 (0.433 – 3.336) N: 31 kp: 0.258
a: 0.319 pss: 0.018 r: 0.96 SE: 0.181
P12259 AADIEQQAVFAVFDENK 3 +
k: 0.495 (0.263 – 0.931) N: 41 kp: 0.258
a: 0.341 pss: 0.018 r: 0.915 SE: 0.054
P12259 AADIEQQAVFAVFDENK 2 +
k: 0.722 (0.523 – 0.996) N: 41 kp: 0.258
a: 0.341 pss: 0.018 r: 0.983 SE: 0.033
P12259 FCENPDEVKR 3 +
k: 1.054 (0.643 – 1.728) N: 21 kp: 0.258
a: 0.485 pss: 0.018 r: 0.957 SE: 0.045
m0
Time(days)

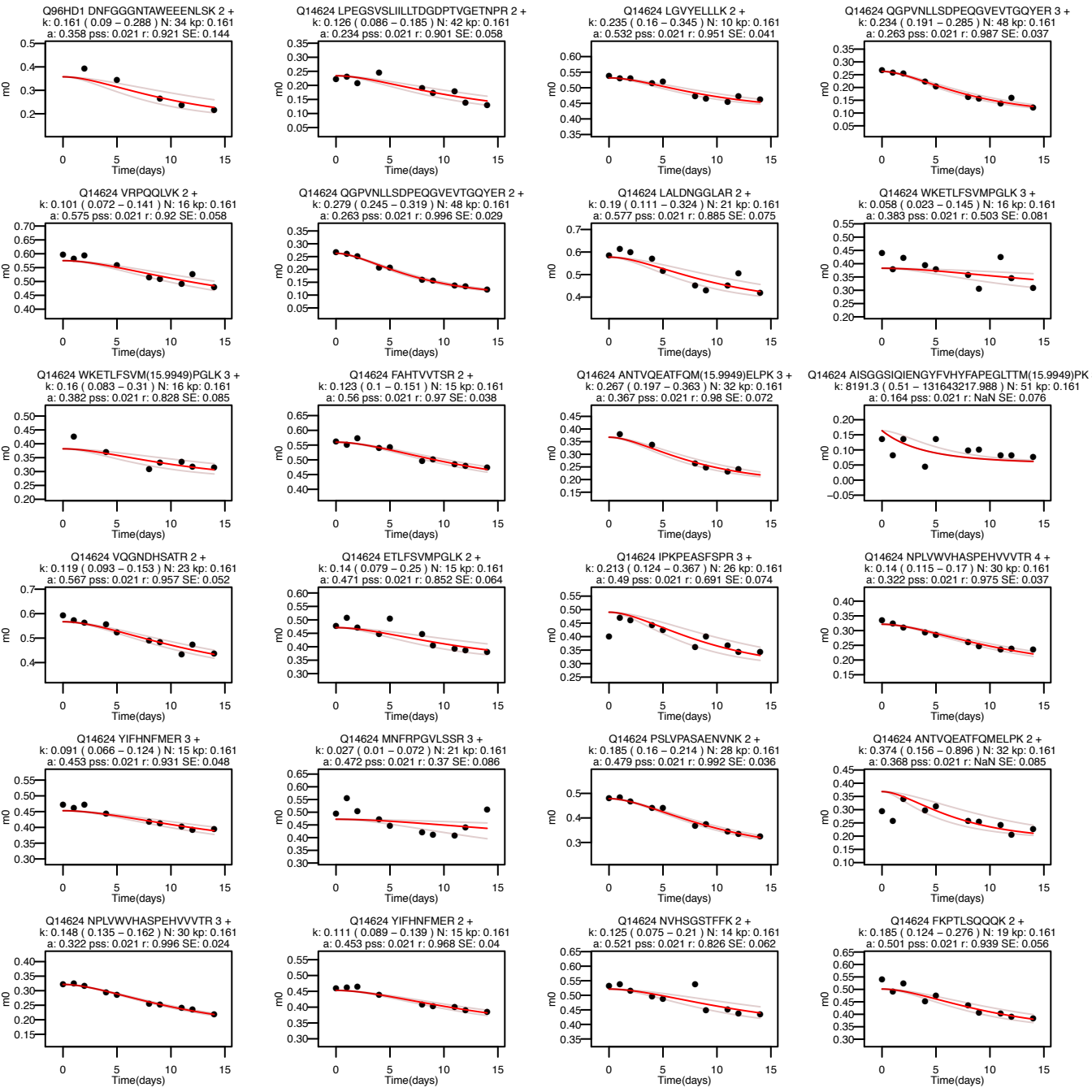

P22792 SQCTYSNPEGTVVLACDQAQCR 3 +
k: 0.386 (0.263 – 0.565) N: 48 kp: 0.147
a: 0.248 pss: 0.022 r: 0.921 SE: 0.036
P22792 DHLGFQVTWPDESK 3 +
k: 0.246 (0.192 – 0.315) N: 24 kp: 0.147
a: 0.384 pss: 0.022 r: 0.974 SE: 0.029
P22792 AGGSWDLAVQER 2 +
k: 0.297 (0.199 – 0.443) N: 29 kp: 0.147
a: 0.489 pss: 0.022 r: 0.909 SE: 0.045
P22792 LSNNALSGLPQGVFGK 2 +
k: 0.188 (0.147 – 0.24) N: 29 kp: 0.147
a: 0.402 pss: 0.022 r: 0.968 SE: 0.034
P02649 LQAEAFQAR 2 +
k: 0.995 (0.536 – 1.85) N: 28 kp: 0.147
a: 0.559 pss: 0.022 r: 0.949 SE: 0.047
P02649 GEVQAMLGQSTEELR 2 +
k: 1.394 (0.808 – 2.405) N: 37 kp: 0.147
a: 0.396 pss: 0.022 r: 0.977 SE: 0.035
P02649 LEEQAQQIR 2 +
k: 0.886 (0.46 – 1.708) N: 29 kp: 0.147
a: 0.546 pss: 0.022 r: 0.951 SE: 0.049
P02649 AQAWGER 2 +
k: 0.406 (0.264 – 0.625) N: 21 kp: 0.147
a: 0.633 pss: 0.022 r: 0.98 SE: 0.148
P02649 LGADMEDVCGR 2 +
k: 0.726 (0.467 – 1.128) N: 23 kp: 0.147
a: 0.5 pss: 0.022 r: 0.966 SE: 0.035
P02649 SWFEPLVEDM(15.9949)QR 3 +
k: 6.8 (0.762 – 60.695) N: 21 kp: 0.147
a: 0.395 pss: 0.022 r: 0.934 SE: 0.093
P02649 DRLDEVKEQVAEVR 4 +
k: 0.306 (0.169 – 0.555) N: 33 kp: 0.147
a: 0.4 pss: 0.022 r: 0.924 SE: 0.095
P02649 QQTEWQSGQR 2 +
k: 0.812 (0.513 – 1.283) N: 28 kp: 0.147
a: 0.509 pss: 0.022 r: 0.969 SE: 0.038
P02649 SELEEQLTPVAEETR 3 +
k: 2.675 (1.576 – 4.542) N: 38 kp: 0.147
a: 0.392 pss: 0.022 r: 0.993 SE: 0.028
P02649 ELQAAQAR 2 +
k: 0.451 (0.331 – 0.616) N: 28 kp: 0.147
a: 0.621 pss: 0.022 r: 0.966 SE: 0.043
P02649 AATVGSLAGQPLQER 3 +
k: 2.237 (0.845 – 5.922) N: 39 kp: 0.147
a: 0.439 pss: 0.022 r: 0.939 SE: 0.053
P02649 WVQTLSEQVQEELLSSQVTQELR 3 +
k: 12.3 (2.506 – 60.361) N: 51 kp: 0.147
a: 0.218 pss: 0.022 r: 0.985 SE: 0.027
P02649 SELEEQLTPVAEETR 2 +
k: 1.894 (1.227 – 2.922) N: 38 kp: 0.147
a: 0.392 pss: 0.022 r: 0.991 SE: 0.028
P02649 AATVGSLAGQPLQER 2 +
k: 0.835 (0.611 – 1.141) N: 39 kp: 0.147
a: 0.439 pss: 0.022 r: 0.988 SE: 0.032
P02649 VQAAVGTSAAPVPSDNH 2 +
k: 0.804 (0.559 – 1.155) N: 41 kp: 0.147
a: 0.411 pss: 0.022 r: 0.979 SE: 0.035
P02647 LHELQEK 2 +
k: 0.136 (0.111 – 0.167) N: 16 kp: 0.147
a: 0.605 pss: 0.022 r: 0.918 SE: 0.038
P02647 THLAPYSDELR 3 +
k: 0.117 (0.085 – 0.16) N: 23 kp: 0.147
a: 0.48 pss: 0.022 r: 0.927 SE: 0.046
P02647 VKDLATVYVDVLK 3 +
k: 0.131 (0.085 – 0.202) N: 13 kp: 0.147
a: 0.425 pss: 0.022 r: 0.859 SE: 0.037
P02647 ATEHLSTLSEK 2 +
k: 0.188 (0.141 – 0.249) N: 22 kp: 0.147
a: 0.515 pss: 0.022 r: 0.942 SE: 0.037
P02647 THLAPYSDELR 2 +
k: 0.175 (0.156 – 0.196) N: 23 kp: 0.147
a: 0.48 pss: 0.022 r: 0.991 SE: 0.023
m0
Time(days)

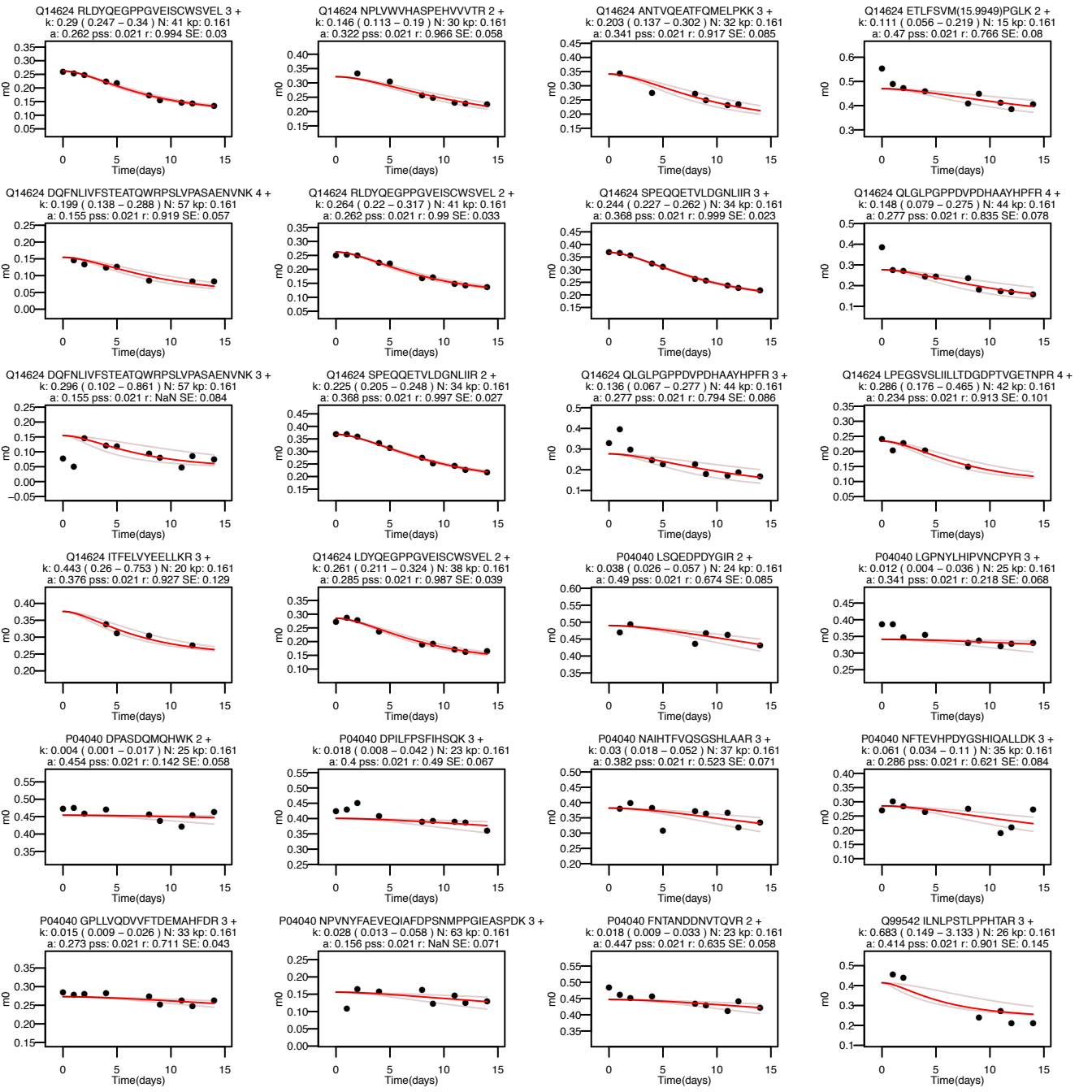

P02647 VKDLATVYVDVLK 2 +
k: 0.315 (0.221 – 0.449) N: 13 kp: 0.147
a: 0.425 pss: 0.022 r: 0.969 SE: 0.028
P02647 LLDNWDSVTSTFSK 2 +
k: 0.299 (0.209 – 0.427) N: 17 kp: 0.147
a: 0.399 pss: 0.022 r: 0.948 SE: 0.031
P02647 LREQLGPVTQEFWDNLEK 3 +
k: 0.267 (0.226 – 0.315) N: 35 kp: 0.147
a: 0.282 pss: 0.022 r: 0.989 SE: 0.023
P02647 EQLGPVTQEFWDNLEK 3 +
k: 0.267 (0.192 – 0.371) N: 31 kp: 0.147
a: 0.33 pss: 0.022 r: 0.962 SE: 0.035
P02647 AKPALEDLR 2 +
k: 0.284 (0.179 – 0.45) N: 22 kp: 0.147
a: 0.567 pss: 0.022 r: 0.947 SE: 0.068
P02647 QGLLPVLESFK 2 +
k: 0.171 (0.141 – 0.206) N: 18 kp: 0.147
a: 0.483 pss: 0.022 r: 0.98 SE: 0.027
P02647 EQLGPVTQEFWDNLEK 2 +
k: 0.353 (0.235 – 0.529) N: 31 kp: 0.147
a: 0.33 pss: 0.022 r: 0.942 SE: 0.037
P02647 LSPLGEEM(15.9949)R 2 +
k: 0.233 (0.145 – 0.373) N: 17 kp: 0.147
a: 0.544 pss: 0.022 r: 0.92 SE: 0.045
P02647 VSFLSALEEYTK 2 +
k: 0.279 (0.245 – 0.317) N: 20 kp: 0.147
a: 0.447 pss: 0.022 r: 0.994 SE: 0.02
Q86VB7 HYCNHNEDAGVTCSDGSDLELR 4 +
k: 0.187 (0.123 – 0.284) N: 46 kp: 0.147
a: 0.251 pss: 0.022 r: 0.934 SE: 0.067
P43652 KSDVGFLPPFPTLDPEEK 3 +
k: 0.202 (0.177 – 0.23) N: 30 kp: 0.147
a: 0.307 pss: 0.022 r: 0.99 SE: 0.021
P43652 CQAYESNR 2 +
k: 0.185 (0.151 – 0.227) N: 22 kp: 0.147
a: 0.574 pss: 0.022 r: 0.967 SE: 0.034
P43652 VNCLQTR 2 +
k: 0.091 (0.079 – 0.104) N: 12 kp: 0.147
a: 0.615 pss: 0.022 r: 0.969 SE: 0.025
P43652 SCCEEQNK 2 +
k: 0.217 (0.158 – 0.296) N: 20 kp: 0.147
a: 0.573 pss: 0.022 r: 0.955 SE: 0.039
P43652 HVCGALLK 2 +
k: 0.176 (0.127 – 0.245) N: 13 kp: 0.147
a: 0.593 pss: 0.022 r: 0.92 SE: 0.037
P43652 ELISLVEDVSSNYDGCCEGDVVQCIR 4 +
k: 0.423 (0.312 – 0.574) N: 49 kp: 0.147
a: 0.189 pss: 0.022 r: 0.967 SE: 0.033
P43652 MVQQECK 2 +
k: 0.126 (0.099 – 0.16) N: 16 kp: 0.147
a: 0.581 pss: 0.022 r: 0.924 SE: 0.035
P43652 HFQNLGK 2 +
k: 0.097 (0.079 – 0.118) N: 12 kp: 0.147
a: 0.614 pss: 0.022 r: 0.918 SE: 0.03
P43652 IAPQLSTEELVSLGEK 3 +
k: 0.232 (0.192 – 0.279) N: 34 kp: 0.147
a: 0.383 pss: 0.022 r: 0.986 SE: 0.029
P43652 DADPDTFFAK 2 +
k: 0.216 (0.19 – 0.246) N: 18 kp: 0.147
a: 0.523 pss: 0.022 r: 0.992 SE: 0.022
P43652 GQCIINSNKDDRPK 2 +
k: 0.156 (0.116 – 0.209) N: 27 kp: 0.147
a: 0.409 pss: 0.022 r: 0.936 SE: 0.038
P43652 ELISLVEDVSSNYDGCCEGDVVQCIR 3 +
k: 0.353 (0.263 – 0.472) N: 49 kp: 0.147
a: 0.189 pss: 0.022 r: 0.962 SE: 0.027
P43652 ESLLNHFLYEVAR 3 +
k: 0.146 (0.12 – 0.177) N: 26 kp: 0.147
a: 0.396 pss: 0.022 r: 0.973 SE: 0.029
P43652 ICAMEGLPQK 2 +
k: 0.131 (0.094 – 0.182) N: 21 kp: 0.147
a: 0.502 pss: 0.022 r: 0.902 SE: 0.042
m0
Time(days)

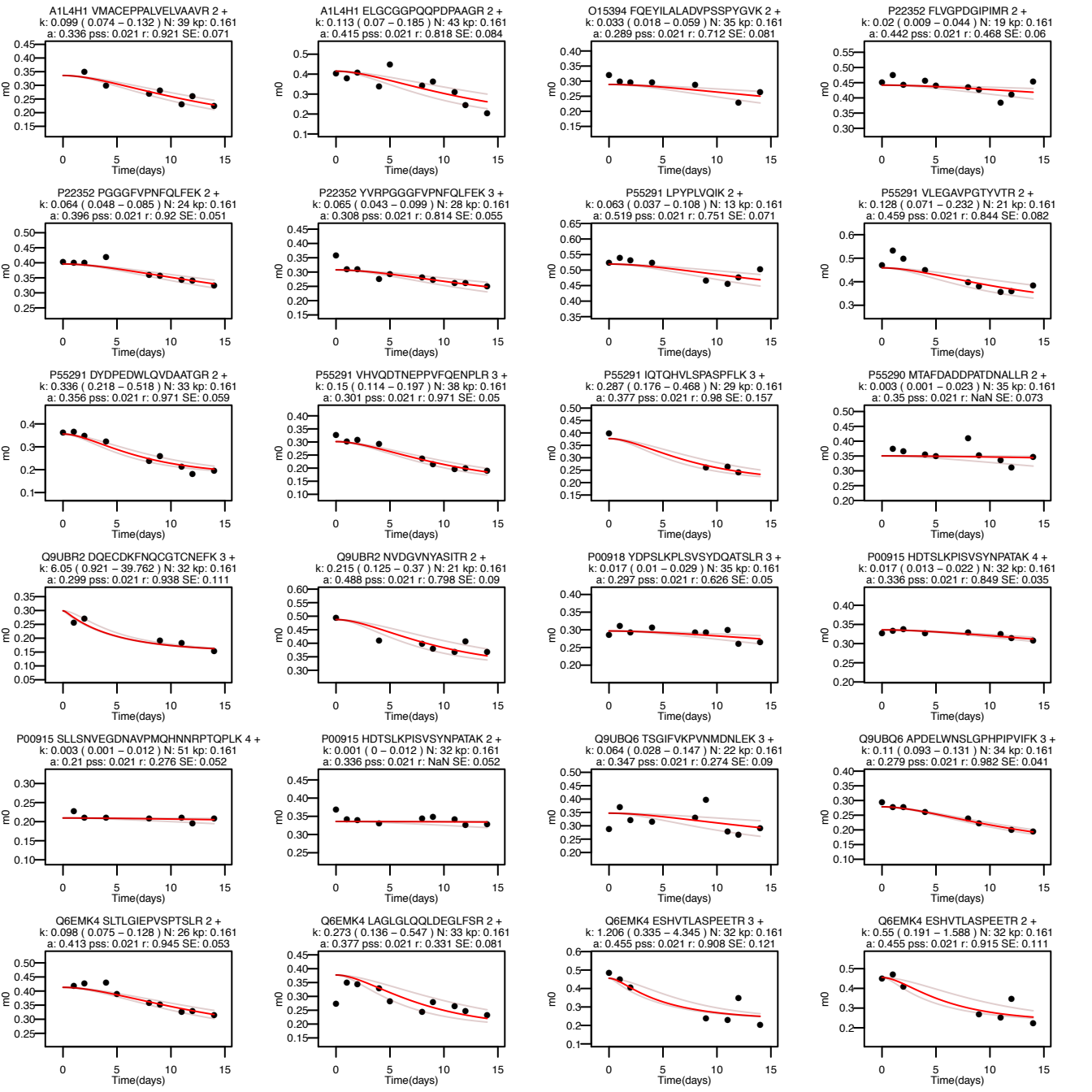

P43652 IAPQLSTEELVSLGEK 2 +
k: 0.226 (0.183 – 0.279) N: 34 kp: 0.147
a: 0.383 pss: 0.022 r: 0.976 SE: 0.031
P43652 FTDSENVCQER 2 +
k: 0.251 (0.21 – 0.299) N: 24 kp: 0.147
a: 0.473 pss: 0.022 r: 0.985 SE: 0.027
P43652 FLVNLVK 2 +
k: 0.052 (0.037 – 0.074) N: 5 kp: 0.147
a: 0.602 pss: 0.022 r: 0.798 SE: 0.024
P43652 AESPEVCFNEESPK 2 +
k: 0.24 (0.201 – 0.287) N: 35 kp: 0.147
a: 0.406 pss: 0.022 r: 0.985 SE: 0.029
P43652 TINPAVDHCCK 2 +
k: 0.15 (0.109 – 0.205) N: 19 kp: 0.147
a: 0.478 pss: 0.022 r: 0.873 SE: 0.037
P43652 TYVPPPFSQDLFTFHADM(15.9949)CQSQNEELQR 4 +
k: 0.367 (0.315 – 0.429) N: 57 kp: 0.147
a: 0.138 pss: 0.022 r: 0.986 SE: 0.049
P43652 LKHELTDEELQSLFTNFANVVDK 4 +
k: 0.233 (0.192 – 0.283) N: 38 kp: 0.147
a: 0.216 pss: 0.022 r: 0.979 SE: 0.024
P43652 SDVGFLPPFPTLDPEEK 2 +
k: 0.183 (0.152 – 0.221) N: 30 kp: 0.147
a: 0.331 pss: 0.022 r: 0.968 SE: 0.028
P43652 LKHELTDEELQSLFTNFANVVDK 3 +
k: 0.249 (0.172 – 0.362) N: 38 kp: 0.147
a: 0.216 pss: 0.022 r: 0.901 SE: 0.036
Q96KN2 SVVLIPLGAVDDGEHSQNEK 3 +
k: 0.349 (0.148 – 0.824) N: 41 kp: 0.147
a: 0.312 pss: 0.022 r: 0.917 SE: 0.162
Q96KN2 ALEQDLPVNIK 2 +
k: 0.299 (0.244 – 0.366) N: 22 kp: 0.147
a: 0.495 pss: 0.022 r: 0.985 SE: 0.027
Q96KN2 VFQYIDLHQDEFVQTLK 3 +
k: 0.909 (0.446 – 1.855) N: 28 kp: 0.147
a: 0.287 pss: 0.022 r: 0.902 SE: 0.037
Q96KN2 AIHLDLEEYR 3 +
k: 0.206 (0.157 – 0.269) N: 23 kp: 0.147
a: 0.488 pss: 0.022 r: 0.963 SE: 0.038
P05452 TFHEASEDCISR 3 +
k: 0.123 (0.098 – 0.155) N: 28 kp: 0.147
a: 0.451 pss: 0.022 r: 0.943 SE: 0.036
P05452 LDTLAQEVALLK 3 +
k: 0.135 (0.11 – 0.167) N: 21 kp: 0.147
a: 0.473 pss: 0.022 r: 0.965 SE: 0.034
P05452 NWETEITAQPDGGK 3 +
k: 0.126 (0.111 – 0.143) N: 28 kp: 0.147
a: 0.425 pss: 0.022 r: 0.985 SE: 0.026
P05452 LDTLAQEVALLK 2 +
k: 0.18 (0.142 – 0.229) N: 21 kp: 0.147
a: 0.473 pss: 0.022 r: 0.962 SE: 0.032
P05452 GGTGLGTPQTGSENDALYEYLR 3 +
k: 0.134 (0.111 – 0.162) N: 40 kp: 0.147
a: 0.289 pss: 0.022 r: 0.974 SE: 0.042
P05452 SRLDTLAQEVALLK 3 +
k: 0.123 (0.097 – 0.157) N: 28 kp: 0.147
a: 0.417 pss: 0.022 r: 0.93 SE: 0.044
P05452 EQQALQTVCLK 2 +
k: 0.164 (0.133 – 0.201) N: 24 kp: 0.147
a: 0.479 pss: 0.022 r: 0.969 SE: 0.042
P05452 CFLAFTQTK 2 +
k: 0.073 (0.055 – 0.096) N: 12 kp: 0.147
a: 0.515 pss: 0.022 r: 0.911 SE: 0.039
P05452 GGTGLGTPQTGSENDALYEYLR 2 +
k: 0.103 (0.081 – 0.132) N: 40 kp: 0.147
a: 0.289 pss: 0.022 r: 0.924 SE: 0.038
P04004 DVWGIEGPIDAAFTR 3 +
k: 0.468 (0.309 – 0.709) N: 29 kp: 0.147
a: 0.385 pss: 0.022 r: 0.957 SE: 0.037
P04004 VDTVDPPYPR 2 +
k: 0.28 (0.222 – 0.354) N: 17 kp: 0.147
a: 0.515 pss: 0.022 r: 0.968 SE: 0.03
m0
Time(days)


P04004 SIAQYWLGCPAPGHL 2 +
k: 0.276 (0.184 – 0.412) N: 31 kp: 0.147
a: 0.37 pss: 0.022 r: 0.94 SE: 0.054
P04004 DWHGVPGQVDAAM(15.9949)AGR 3 +
k: 0.591 (0.438 – 0.798) N: 33 kp: 0.147
a: 0.377 pss: 0.022 r: 0.986 SE: 0.031
P04004 DWHGVPGQVDAAMAGR 2 +
k: 0.421 (0.22 – 0.806) N: 37 kp: 0.147
a: 0.378 pss: 0.022 r: 0.906 SE: 0.055
P04004 GNPEQTPVLKPEEEAPAPEVGASKPEGIDSR 4 +
k: 0.898 (0.594 – 1.357) N: 78 kp: 0.147
a: 0.167 pss: 0.022 r: 0.966 SE: 0.034
P04004 DVWGIEGPIDAAFTR 2 +
k: 0.691 (0.467 – 1.022) N: 29 kp: 0.147
a: 0.385 pss: 0.022 r: 0.975 SE: 0.032
P04004 FEDGVLDPDYPR 3 +
k: 0.396 (0.249 – 0.629) N: 22 kp: 0.147
a: 0.442 pss: 0.022 r: 0.955 SE: 0.043
P04004 GNPEQTPVLKPEEEAPAPEVGASK 3 +
k: 0.722 (0.324 – 1.609) N: 60 kp: 0.147
a: 0.252 pss: 0.022 r: 0.963 SE: 0.064
P04004 DWHGVPGQVDAAM(15.9949)AGR 2 +
k: 0.792 (0.533 – 1.177) N: 33 kp: 0.147
a: 0.377 pss: 0.022 r: 0.983 SE: 0.032
P04004 PQPPAEEELCSGK 2 +
k: 1.331 (0.53 – 3.345) N: 35 kp: 0.147
a: 0.449 pss: 0.022 r: 0.91 SE: 0.107
P04004 FEDGVLDPDYPR 2 +
k: 0.89 (0.745 – 1.062) N: 22 kp: 0.147
a: 0.442 pss: 0.022 r: 0.998 SE: 0.018
P04004 PQPPAEEELCSGKPFDAFTDLK 3 +
k: 0.862 (0.524 – 1.419) N: 47 kp: 0.147
a: 0.241 pss: 0.022 r: 0.983 SE: 0.063
P04004 PETLHPGRPQPPAEEELCSGK 4 +
k: 0.905 (0.611 – 1.342) N: 53 kp: 0.147
a: 0.271 pss: 0.022 r: 0.976 SE: 0.033
P04004 PETLHPGRPQPPAEEELCSGKPFDAFTDLK 5 +
k: 0.636 (0.42 – 0.963) N: 66 kp: 0.147
a: 0.145 pss: 0.022 r: 0.96 SE: 0.035
P04004 GQYCYELDEK 2 +
k: 27.3 (1.301 – 572.935) N: 19 kp: 0.147
a: 0.477 pss: 0.022 r: 0.957 SE: 0.038
P04004 PETLHPGRPQPPAEEELCSGKPFDAFTDLK 4 +
k: 0.503 (0.313 – 0.809) N: 66 kp: 0.147
a: 0.145 pss: 0.022 r: 0.909 SE: 0.038
P04004 DWHGVPGQVDAAMAGR 3 +
k: 0.371 (0.289 – 0.477) N: 37 kp: 0.147
a: 0.378 pss: 0.022 r: 0.981 SE: 0.032
P04003 GVGWSHPLPQCEIVK 3 +
k: 0.104 (0.084 – 0.129) N: 28 kp: 0.147
a: 0.367 pss: 0.022 r: 0.922 SE: 0.032
Q96IY4 HWCEEGASSSSCSETYCGLYPESEPEVK 3 +
k: 0.316 (0.21 – 0.474) N: 63 kp: 0.147
a: 0.161 pss: 0.022 r: 0.941 SE: 0.053
Q96IY4 YTHGHGSETLYLAPGGGDDWIYDLGIK 4 +
k: 0.726 (0.469 – 1.123) N: 43 kp: 0.147
a: 0.182 pss: 0.022 r: 0.972 SE: 0.031
Q96IY4 SFYANNHCIGTDLNR 3 +
k: 0.432 (0.327 – 0.57) N: 27 kp: 0.147
a: 0.368 pss: 0.022 r: 0.976 SE: 0.029
Q96IY4 YPLYVLK 2 +
k: 0.094 (0.064 – 0.138) N: 6 kp: 0.147
a: 0.57 pss: 0.022 r: 0.729 SE: 0.033
Q8N3F8 EEEEDKMLEAMIKK 2 +
k: 0.226 (0.194 – 0.264) N: 31 kp: 0.147
a: 0.359 pss: 0.022 r: 0.981 SE: 0.085
P00450 TTIEKPVWLGFLGPIIK 3 +
k: 0.089 (0.079 – 0.1) N: 20 kp: 0.147
a: 0.312 pss: 0.022 r: 0.982 SE: 0.018
P00450 TYCSEPEK 2 +
k: 0.153 (0.135 – 0.172) N: 16 kp: 0.147
a: 0.569 pss: 0.022 r: 0.989 SE: 0.022
m0
Time(days)

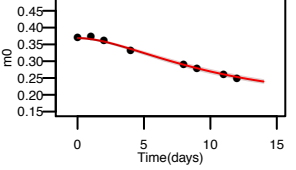

P00450 ERGPEEEHLGILGPVIWAEVGDTIR 4 +
k: 0.141 (0.124 – 0.162) N: 54 kp: 0.147
a: 0.206 pss: 0.022 r: 0.983 SE: 0.024
P00450 VDKDNEDFQESNR 2 +
k: 0.138 (0.116 – 0.165) N: 29 kp: 0.147
a: 0.428 pss: 0.022 r: 0.975 SE: 0.031
P00450 AEEEHLGILGPQLHADVGDK 4 +
k: 0.129 (0.101 – 0.164) N: 46 kp: 0.147
a: 0.304 pss: 0.022 r: 0.948 SE: 0.037
P00450 TTIEKPVWLGFLGPIIK 2 +
k: 0.088 (0.059 – 0.132) N: 20 kp: 0.147
a: 0.312 pss: 0.022 r: 0.85 SE: 0.037
P00450 KAEEEHLGILGPQLHADVGDKVK 5 +
k: 0.184 (0.148 – 0.229) N: 48 kp: 0.147
a: 0.246 pss: 0.022 r: 0.972 SE: 0.046
P00450 KAEEEHLGILGPQLHADVGDK 4 +
k: 0.147 (0.129 – 0.168) N: 47 kp: 0.147
a: 0.282 pss: 0.022 r: 0.984 SE: 0.025
P00450 EYTDASFTNR 2 +
k: 0.11 (0.091 – 0.132) N: 19 kp: 0.147
a: 0.515 pss: 0.022 r: 0.963 SE: 0.03
P00450 ERGPEEEHLGILGPVIWAEVGDTIR 3 +
k: 0.125 (0.098 – 0.159) N: 54 kp: 0.147
a: 0.206 pss: 0.022 r: 0.929 SE: 0.033
P00450 DIFTGLIGPM(15.9949)K 2 +
k: 0.067 (0.055 – 0.082) N: 13 kp: 0.147
a: 0.476 pss: 0.022 r: 0.938 SE: 0.024
P00450 EVGPTNADPVCLAK 2 +
k: 0.134 (0.102 – 0.176) N: 27 kp: 0.147
a: 0.439 pss: 0.022 r: 0.898 SE: 0.038
P00450 PYSIHAHGVQTESSTVTPTLPGETLTYVWK 4 +
k: 0.095 (0.064 – 0.141) N: 48 kp: 0.147
a: 0.149 pss: 0.022 r: 0.8 SE: 0.035
P00450 AEEEHLGILGPQLHADVGDK 3 +
k: 0.142 (0.123 – 0.165) N: 46 kp: 0.147
a: 0.304 pss: 0.022 r: 0.977 SE: 0.027
P00450 VNKDDEEFIESNK 3 +
k: 0.154 (0.133 – 0.179) N: 25 kp: 0.147
a: 0.425 pss: 0.022 r: 0.985 SE: 0.025
P00450 SGAGTEDSACIPWAYYSTVDQVK 3 +
k: 0.158 (0.138 – 0.182) N: 44 kp: 0.147
a: 0.242 pss: 0.022 r: 0.986 SE: 0.023
P00450 KAEEEHLGILGPQLHADVGDKVK 4 +
k: 0.181 (0.126 – 0.26) N: 48 kp: 0.147
a: 0.246 pss: 0.022 r: 0.938 SE: 0.062
P00450 KAEEEHLGILGPQLHADVGDK 3 +
k: 0.139 (0.105 – 0.184) N: 47 kp: 0.147
a: 0.282 pss: 0.022 r: 0.939 SE: 0.038
P00450 DLYSGLIGPLIVCR 2 +
k: 0.141 (0.122 – 0.162) N: 21 kp: 0.147
a: 0.398 pss: 0.022 r: 0.979 SE: 0.023
P00450 QYTDSTFR 2 +
k: 0.113 (0.088 – 0.146) N: 13 kp: 0.147
a: 0.566 pss: 0.022 r: 0.935 SE: 0.038
P00450 VNKDDEEFIESNK 2 +
k: 0.182 (0.166 – 0.201) N: 25 kp: 0.147
a: 0.425 pss: 0.022 r: 0.995 SE: 0.02
P00450 DIASGLIGPLIICK 2 +
k: 0.143 (0.119 – 0.172) N: 23 kp: 0.147
a: 0.424 pss: 0.022 r: 0.964 SE: 0.028
P00450 ALYLQYTDETFR 2 +
k: 0.109 (0.081 – 0.148) N: 20 kp: 0.147
a: 0.413 pss: 0.022 r: 0.881 SE: 0.036
P00450 SGAGTEDSACIPWAYYSTVDQVK 2 +
k: 0.199 (0.157 – 0.254) N: 44 kp: 0.147
a: 0.242 pss: 0.022 r: 0.964 SE: 0.042
P00450 RQSEDSTFYLGER 3 +
k: 0.194 (0.12 – 0.314) N: 29 kp: 0.147
a: 0.417 pss: 0.022 r: 0.957 SE: 0.176
P00450 GPEEEHLGILGPVIWAEVGDTIR 4 +
k: 0.13 (0.107 – 0.158) N: 47 kp: 0.147
a: 0.24 pss: 0.022 r: 0.964 SE: 0.031
m0
Time(days)


Q96HD1 DNFGGGNTAWEEENLSK 2 +
k: 0.161 (0.09 – 0.288) N: 34 kp: 0.161
a: 0.358 pss: 0.021 r: 0.921 SE: 0.144
Q14624 LPEGSVSLIILLTDGDPTVGETNPR 2 +
k: 0.126 (0.086 – 0.185) N: 42 kp: 0.161
a: 0.234 pss: 0.021 r: 0.901 SE: 0.058
Q14624 LGVYELLLK 2 +
k: 0.235 (0.16 – 0.345) N: 10 kp: 0.161
a: 0.532 pss: 0.021 r: 0.951 SE: 0.041
Q14624 QGPVNLLSDPEQGVEVTGQYER 3 +
k: 0.234 (0.191 – 0.285) N: 48 kp: 0.161
a: 0.263 pss: 0.021 r: 0.987 SE: 0.037
Q14624 VRPQQLVK 2 +
k: 0.101 (0.072 – 0.141) N: 16 kp: 0.161
a: 0.575 pss: 0.021 r: 0.92 SE: 0.058
Q14624 QGPVNLLSDPEQGVEVTGQYER 2 +
k: 0.279 (0.245 – 0.319) N: 48 kp: 0.161
a: 0.263 pss: 0.021 r: 0.996 SE: 0.029
Q14624 LALDNGGLAR 2 +
k: 0.19 (0.111 – 0.324) N: 21 kp: 0.161
a: 0.577 pss: 0.021 r: 0.885 SE: 0.075
Q14624 WKETLFSVMPGLK 3 +
k: 0.058 (0.023 – 0.145) N: 16 kp: 0.161
a: 0.383 pss: 0.021 r: 0.503 SE: 0.081
Q14624 WKETLFSVM(15.9949)PGLK 3 +
k: 0.16 (0.083 – 0.31) N: 16 kp: 0.161
a: 0.382 pss: 0.021 r: 0.828 SE: 0.085
Q14624 FAHTVVTSR 2 +
k: 0.123 (0.1 – 0.151) N: 15 kp: 0.161
a: 0.56 pss: 0.021 r: 0.97 SE: 0.038
Q14624 ANTVQEATFQM(15.9949)ELPK 3 +
k: 0.267 (0.197 – 0.363) N: 32 kp: 0.161
a: 0.367 pss: 0.021 r: 0.98 SE: 0.072
Q14624 AISGGSIQIENGYFVHYFAPEGLTTM(15.9949)PK
k: 8191.3 (0.51 – 131643217.988) N: 51 kp: 0.161
a: 0.164 pss: 0.021 r: NaN SE: 0.076
Q14624 VQGNDHSATR 2 +
k: 0.119 (0.093 – 0.153) N: 23 kp: 0.161
a: 0.567 pss: 0.021 r: 0.957 SE: 0.052
Q14624 ETLFSVMPGLK 2 +
k: 0.14 (0.079 – 0.25) N: 15 kp: 0.161
a: 0.471 pss: 0.021 r: 0.852 SE: 0.064
Q14624 IPKPEASFSPR 3 +
k: 0.213 (0.124 – 0.367) N: 26 kp: 0.161
a: 0.49 pss: 0.021 r: 0.691 SE: 0.074
Q14624 NPLVWVHASPEHVVVTR 4 +
k: 0.14 (0.115 – 0.17) N: 30 kp: 0.161
a: 0.322 pss: 0.021 r: 0.975 SE: 0.037
Q14624 YIFHNFMER 3 +
k: 0.091 (0.066 – 0.124) N: 15 kp: 0.161
a: 0.453 pss: 0.021 r: 0.931 SE: 0.048
Q14624 MNFRPGVLSSR 3 +
k: 0.027 (0.01 – 0.072) N: 21 kp: 0.161
a: 0.472 pss: 0.021 r: 0.37 SE: 0.086
Q14624 PSLVPASAENVNK 2 +
k: 0.185 (0.16 – 0.214) N: 28 kp: 0.161
a: 0.479 pss: 0.021 r: 0.992 SE: 0.036
Q14624 ANTVQEATFQMELPK 2 +
k: 0.374 (0.156 – 0.896) N: 32 kp: 0.161
a: 0.368 pss: 0.021 r: NaN SE: 0.085
Q14624 NPLVWVHASPEHVVVTR 3 +
k: 0.148 (0.135 – 0.162) N: 30 kp: 0.161
a: 0.322 pss: 0.021 r: 0.996 SE: 0.024
Q14624 YIFHNFMER 2 +
k: 0.111 (0.089 – 0.139) N: 15 kp: 0.161
a: 0.453 pss: 0.021 r: 0.968 SE: 0.04
Q14624 NVHSGSTFFK 2 +
k: 0.125 (0.075 – 0.21) N: 14 kp: 0.161
a: 0.521 pss: 0.021 r: 0.826 SE: 0.062
Q14624 FKPTLSQQQK 2 +
k: 0.185 (0.124 – 0.276) N: 19 kp: 0.161
a: 0.501 pss: 0.021 r: 0.939 SE: 0.056
m0
Time(days)

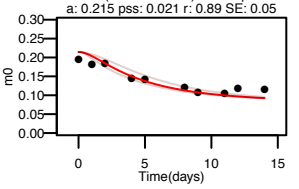

Q14624 RLDYQEGPPGVEISCWSVEL 3 +
k: 0.29 (0.247 – 0.34) N: 41 kp: 0.161
a: 0.262 pss: 0.021 r: 0.994 SE: 0.03
Q14624 NPLVWVHASPEHVVVTR 2 +
k: 0.146 (0.113 – 0.19) N: 30 kp: 0.161
a: 0.322 pss: 0.021 r: 0.966 SE: 0.058
Q14624 ANTVQEATFQMELPKK 3 +
k: 0.203 (0.137 – 0.302) N: 32 kp: 0.161
a: 0.341 pss: 0.021 r: 0.917 SE: 0.085
Q14624 ETLFSVM(15.9949)PGLK 2 +
k: 0.111 (0.056 – 0.219) N: 15 kp: 0.161
a: 0.47 pss: 0.021 r: 0.766 SE: 0.08
Q14624 DQFNLIVFSTEATQWRPSLVPASAENVNK 4 +
k: 0.199 (0.138 – 0.288) N: 57 kp: 0.161
a: 0.155 pss: 0.021 r: 0.919 SE: 0.057
Q14624 RLDYQEGPPGVEISCWSVEL 2 +
k: 0.264 (0.22 – 0.317) N: 41 kp: 0.161
a: 0.262 pss: 0.021 r: 0.99 SE: 0.033
Q14624 SPEQQETVLDGNLIIR 3 +
k: 0.244 (0.227 – 0.262) N: 34 kp: 0.161
a: 0.368 pss: 0.021 r: 0.999 SE: 0.023
Q14624 QLGLPGPPDVPDHAAYHPFR 4 +
k: 0.148 (0.079 – 0.275) N: 44 kp: 0.161
a: 0.277 pss: 0.021 r: 0.835 SE: 0.078
Q14624 DQFNLIVFSTEATQWRPSLVPASAENVNK 3 +
k: 0.296 (0.102 – 0.861) N: 57 kp: 0.161
a: 0.155 pss: 0.021 r: NaN SE: 0.084
Q14624 SPEQQETVLDGNLIIR 2 +
k: 0.225 (0.205 – 0.248) N: 34 kp: 0.161
a: 0.368 pss: 0.021 r: 0.997 SE: 0.027
Q14624 QLGLPGPPDVPDHAAYHPFR 3 +
k: 0.136 (0.067 – 0.277) N: 44 kp: 0.161
a: 0.277 pss: 0.021 r: 0.794 SE: 0.086
Q14624 LPEGSVSLIILLTDGDPTVGETNPR 4 +
k: 0.286 (0.176 – 0.465) N: 42 kp: 0.161
a: 0.234 pss: 0.021 r: 0.913 SE: 0.101
Q14624 ITFELVYEELLKR 3 +
k: 0.443 (0.26 – 0.753) N: 20 kp: 0.161
a: 0.376 pss: 0.021 r: 0.927 SE: 0.129
Q14624 LDYQEGPPGVEISCWSVEL 2 +
k: 0.261 (0.211 – 0.324) N: 38 kp: 0.161
a: 0.285 pss: 0.021 r: 0.987 SE: 0.039
P04040 LSQEDPDYGIR 2 +
k: 0.038 (0.026 – 0.057) N: 24 kp: 0.161
a: 0.49 pss: 0.021 r: 0.674 SE: 0.085
P04040 LGPNYLHIPVNCPYR 3 +
k: 0.012 (0.004 – 0.036) N: 25 kp: 0.161
a: 0.341 pss: 0.021 r: 0.218 SE: 0.068
P04040 DPASDQMQHWK 2 +
k: 0.004 (0.001 – 0.017) N: 25 kp: 0.161
a: 0.454 pss: 0.021 r: 0.142 SE: 0.058
P04040 DPILFPSFIHSQK 3 +
k: 0.018 (0.008 – 0.042) N: 23 kp: 0.161
a: 0.4 pss: 0.021 r: 0.49 SE: 0.067
P04040 NAIHTFVQSGSHLAAR 3 +
k: 0.03 (0.018 – 0.052) N: 37 kp: 0.161
a: 0.382 pss: 0.021 r: 0.523 SE: 0.071
P04040 NFTEVHPDYGSHIQALLDK 3 +
k: 0.061 (0.034 – 0.11) N: 35 kp: 0.161
a: 0.286 pss: 0.021 r: 0.621 SE: 0.084
P04040 GPLLVQDVVFTDEMAHFDR 3 +
k: 0.015 (0.009 – 0.026) N: 33 kp: 0.161
a: 0.273 pss: 0.021 r: 0.711 SE: 0.043
P04040 NPVNYFAEVEQIAFDPSNMPPGIEASPDK 3 +
k: 0.028 (0.013 – 0.058) N: 63 kp: 0.161
a: 0.156 pss: 0.021 r: NaN SE: 0.071
P04040 FNTANDDNVTQVR 2 +
k: 0.018 (0.009 – 0.033) N: 23 kp: 0.161
a: 0.447 pss: 0.021 r: 0.635 SE: 0.058
Q99542 ILNLPSTLPPHTAR 3 +
k: 0.683 (0.149 – 3.133) N: 26 kp: 0.161
a: 0.414 pss: 0.021 r: 0.901 SE: 0.145
m0
Time(days)


A1L4H1 VMACEPPALVELVAAVR 2 +
k: 0.099 (0.074 – 0.132) N: 39 kp: 0.161
a: 0.336 pss: 0.021 r: 0.921 SE: 0.071
A1L4H1 ELGCGGPQQPDPAAGR 2 +
k: 0.113 (0.07 – 0.185) N: 43 kp: 0.161
a: 0.415 pss: 0.021 r: 0.818 SE: 0.084
O15394 FQEYILALADVPSSPYGVK 2 +
k: 0.033 (0.018 – 0.059) N: 35 kp: 0.161
a: 0.289 pss: 0.021 r: 0.712 SE: 0.081
P22352 FLVGPDGIPIMR 2 +
k: 0.02 (0.009 – 0.044) N: 19 kp: 0.161
a: 0.442 pss: 0.021 r: 0.468 SE: 0.06
P22352 PGGGFVPNFQLFEK 2 +
k: 0.064 (0.048 – 0.085) N: 24 kp: 0.161
a: 0.396 pss: 0.021 r: 0.92 SE: 0.051
P22352 YVRPGGGFVPNFQLFEK 3 +
k: 0.065 (0.043 – 0.099) N: 28 kp: 0.161
a: 0.308 pss: 0.021 r: 0.814 SE: 0.055
P55291 LPYPLVQIK 2 +
k: 0.063 (0.037 – 0.108) N: 13 kp: 0.161
a: 0.519 pss: 0.021 r: 0.751 SE: 0.071
P55291 VLEGAVPGTYVTR 2 +
k: 0.128 (0.071 – 0.232) N: 21 kp: 0.161
a: 0.459 pss: 0.021 r: 0.844 SE: 0.082
P55291 DYDPEDWLQVDAATGR 2 +
k: 0.336 (0.218 – 0.518) N: 33 kp: 0.161
a: 0.356 pss: 0.021 r: 0.971 SE: 0.059
P55291 VHVQDTNEPPVFQENPLR 3 +
k: 0.15 (0.114 – 0.197) N: 38 kp: 0.161
a: 0.301 pss: 0.021 r: 0.971 SE: 0.05
P55291 IQTQHVLSPASPFLK 3 +
k: 0.287 (0.176 – 0.468) N: 29 kp: 0.161
a: 0.377 pss: 0.021 r: 0.98 SE: 0.157
P55290 MTAFDADDPATDNALLR 2 +
k: 0.003 (0.001 – 0.023) N: 35 kp: 0.161
a: 0.35 pss: 0.021 r: NaN SE: 0.073
Q9UBR2 DQECDKFNQCGTCNEFK 3 +
k: 6.05 (0.921 – 39.762) N: 32 kp: 0.161
a: 0.299 pss: 0.021 r: 0.938 SE: 0.111
Q9UBR2 NVDGVNYASITR 2 +
k: 0.215 (0.125 – 0.37) N: 21 kp: 0.161
a: 0.488 pss: 0.021 r: 0.798 SE: 0.09
P00918 YDPSLKPLSVSYDQATSLR 3 +
k: 0.017 (0.01 – 0.029) N: 35 kp: 0.161
a: 0.297 pss: 0.021 r: 0.626 SE: 0.05
P00915 HDTSLKPISVSYNPATAK 4 +
k: 0.017 (0.013 – 0.022) N: 32 kp: 0.161
a: 0.336 pss: 0.021 r: 0.849 SE: 0.035
P00915 SLLSNVEGDNAVPMQHNNRPTQPLK 4 +
k: 0.003 (0.001 – 0.012) N: 51 kp: 0.161
a: 0.21 pss: 0.021 r: 0.276 SE: 0.052
P00915 HDTSLKPISVSYNPATAK 2 +
k: 0.001 (0 – 0.012) N: 32 kp: 0.161
a: 0.336 pss: 0.021 r: NaN SE: 0.052
Q9UBQ6 TSGIFVKPVNMDNLEK 3 +
k: 0.064 (0.028 – 0.147) N: 22 kp: 0.161
a: 0.347 pss: 0.021 r: 0.274 SE: 0.09
Q9UBQ6 APDELWNSLGPHPIPVIFK 3 +
k: 0.11 (0.093 – 0.131) N: 34 kp: 0.161
a: 0.279 pss: 0.021 r: 0.982 SE: 0.041
Q6EMK4 SLTLGIEPVSPTSLR 2 +
k: 0.098 (0.075 – 0.128) N: 26 kp: 0.161
a: 0.413 pss: 0.021 r: 0.945 SE: 0.053
Q6EMK4 LAGLGLQQLDEGLFSR 2 +
k: 0.273 (0.136 – 0.547) N: 33 kp: 0.161
a: 0.377 pss: 0.021 r: 0.331 SE: 0.081
Q6EMK4 ESHVTLASPEETR 3 +
k: 1.206 (0.335 – 4.345) N: 32 kp: 0.161
a: 0.455 pss: 0.021 r: 0.908 SE: 0.121
Q6EMK4 ESHVTLASPEETR 2 +
k: 0.55 (0.191 – 1.588) N: 32 kp: 0.161
a: 0.455 pss: 0.021 r: 0.915 SE: 0.111
m0
Time(days)

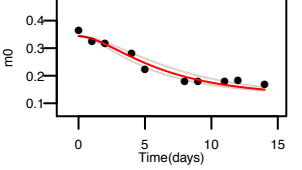
Q9UEW3 VGAGTGQIWLDNVQCR 2 +
k: 0.187 (0.17 – 0.206) N: 30 kp: 0.161
a: 0.369 pss: 0.021 r: 0.997 SE: 0.031



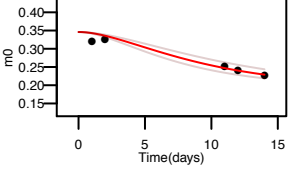
P22692 EPGCGCCATCALGLGMPCGVYTPR 3 +
k: 1.003 (0.48 – 2.095) N: 45 kp: 0.161
a: 0.215 pss: 0.021 r: 0.89 SE: 0.05



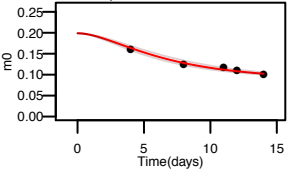
P22692 EDARPVPQGSCQSELHR 3 +
k: 0.419 (0.292 – 0.601) N: 47 kp: 0.161
a: 0.344 pss: 0.021 r: 0.973 SE: 0.053



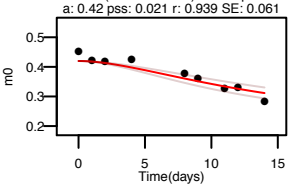
P22692 THEDLYIIPIPNCDR 3 +
k: 0.217 (0.148 – 0.319) N: 27 kp: 0.161
a: 0.346 pss: 0.021 r: 0.963 SE: 0.094



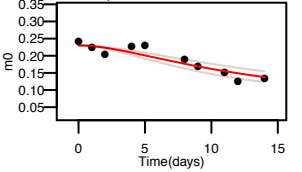
P07998 CKPVNTFVHEPLVDVQNVCFQEK 4 +
k: 0.388 (0.303 – 0.496) N: 38 kp: 0.161
a: 0.199 pss: 0.021 r: 0.983 SE: 0.055



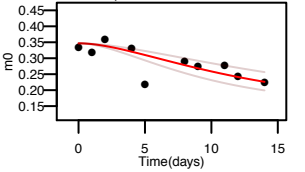
P07996 IEDANLIPPVPDDK 2 +
k: 0.111 (0.08 – 0.154) N: 27 kp: 0.161
a: 0.42 pss: 0.021 r: 0.939 SE: 0.061



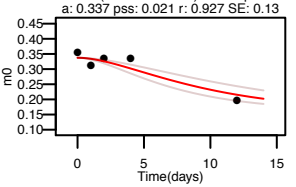
P07996 IEDANLIPPVPDDKFQDLVDAVR 3 +
k: 0.13 (0.089 – 0.188) N: 44 kp: 0.161
a: 0.23 pss: 0.021 r: 0.918 SE: 0.052



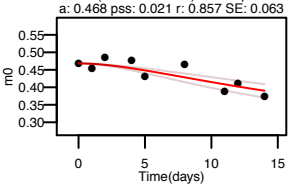
P07996 FTGSQPFGQGVEHATANK 3 +
k: 0.12 (0.072 – 0.198) N: 38 kp: 0.161
a: 0.347 pss: 0.021 r: 0.71 SE: 0.075



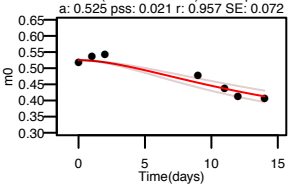
P07996 QHVVSVEEALLATGQWK 3 +
k: 0.198 (0.114 – 0.345) N: 35 kp: 0.161
a: 0.337 pss: 0.021 r: 0.927 SE: 0.13



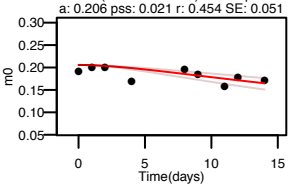
P07996 LCNNPTPQFGGK 2 +
k: 0.08 (0.054 – 0.119) N: 20 kp: 0.161
a: 0.468 pss: 0.021 r: 0.857 SE: 0.063



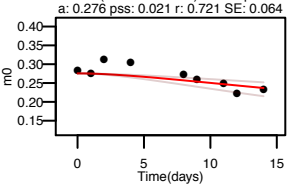
P32754 ENIDALEELK 2 +
k: 0.106 (0.079 – 0.143) N: 22 kp: 0.161
a: 0.525 pss: 0.021 r: 0.957 SE: 0.072



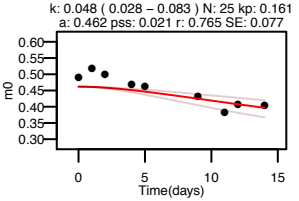
Q13508 TENCIENLEYFQPIYVYNPGEK 3 +
k: 0.047 (0.031 – 0.071) N: 40 kp: 0.161
a: 0.206 pss: 0.021 r: 0.454 SE: 0.051



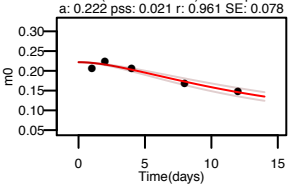
Q13867 AQHVFQHAVPQEGKPITNQK 4 +
k: 0.027 (0.016 – 0.047) N: 46 kp: 0.161
a: 0.276 pss: 0.021 r: 0.721 SE: 0.064



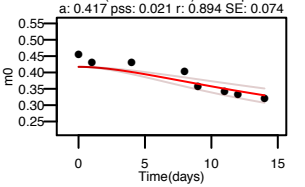
P55268 IQNVVTSFAPQR 2 +
k: 0.048 (0.028 – 0.083) N: 25 kp: 0.161
a: 0.462 pss: 0.021 r: 0.765 SE: 0.077



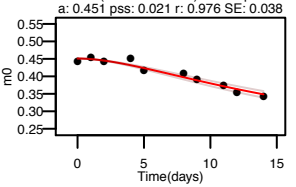
P55268 TGGSAQPETPYSGPGLLIDSLVLLPR 3 +
k: 0.107 (0.084 – 0.136) N: 49 kp: 0.161
a: 0.222 pss: 0.021 r: 0.961 SE: 0.078



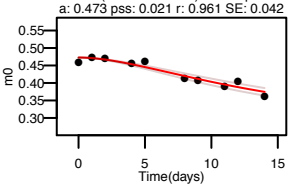
P05452 SRLDTLAQEVALLK 2 +
k: 0.074 (0.05 – 0.109) N: 28 kp: 0.161
a: 0.417 pss: 0.021 r: 0.894 SE: 0.074



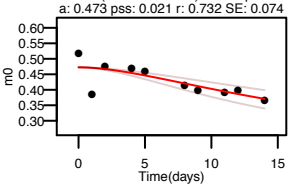
P05452 TFHEASEDCISR 3 +
k: 0.084 (0.073 – 0.098) N: 28 kp: 0.161
a: 0.451 pss: 0.021 r: 0.976 SE: 0.038



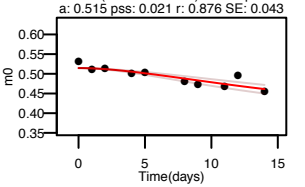
P05452 LDTLAQEVALLK 2 +
k: 0.109 (0.088 – 0.134) N: 21 kp: 0.161
a: 0.473 pss: 0.021 r: 0.961 SE: 0.042



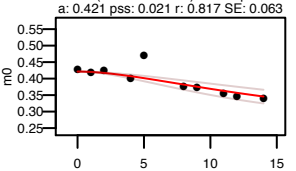
P05452 TENCAVLSGAANGK 2 +
k: 0.071 (0.045 – 0.112) N: 30 kp: 0.161
a: 0.473 pss: 0.021 r: 0.732 SE: 0.074



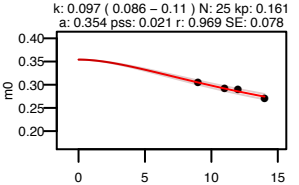
P05452 CFLAFTQTK 2 +
k: 0.077 (0.056 – 0.106) N: 12 kp: 0.161
a: 0.515 pss: 0.021 r: 0.876 SE: 0.043



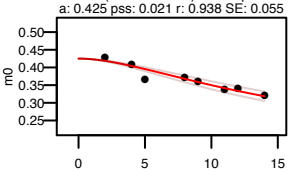
P05452 DQLPYICQFGIV 2 +
k: 0.09 (0.056 – 0.145) N: 20 kp: 0.161
a: 0.421 pss: 0.021 r: 0.817 SE: 0.063



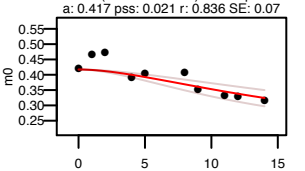
P05452 CRDQLPYICQFGIV 2 +
k: 0.097 (0.086 – 0.11) N: 25 kp: 0.161
a: 0.354 pss: 0.021 r: 0.969 SE: 0.078

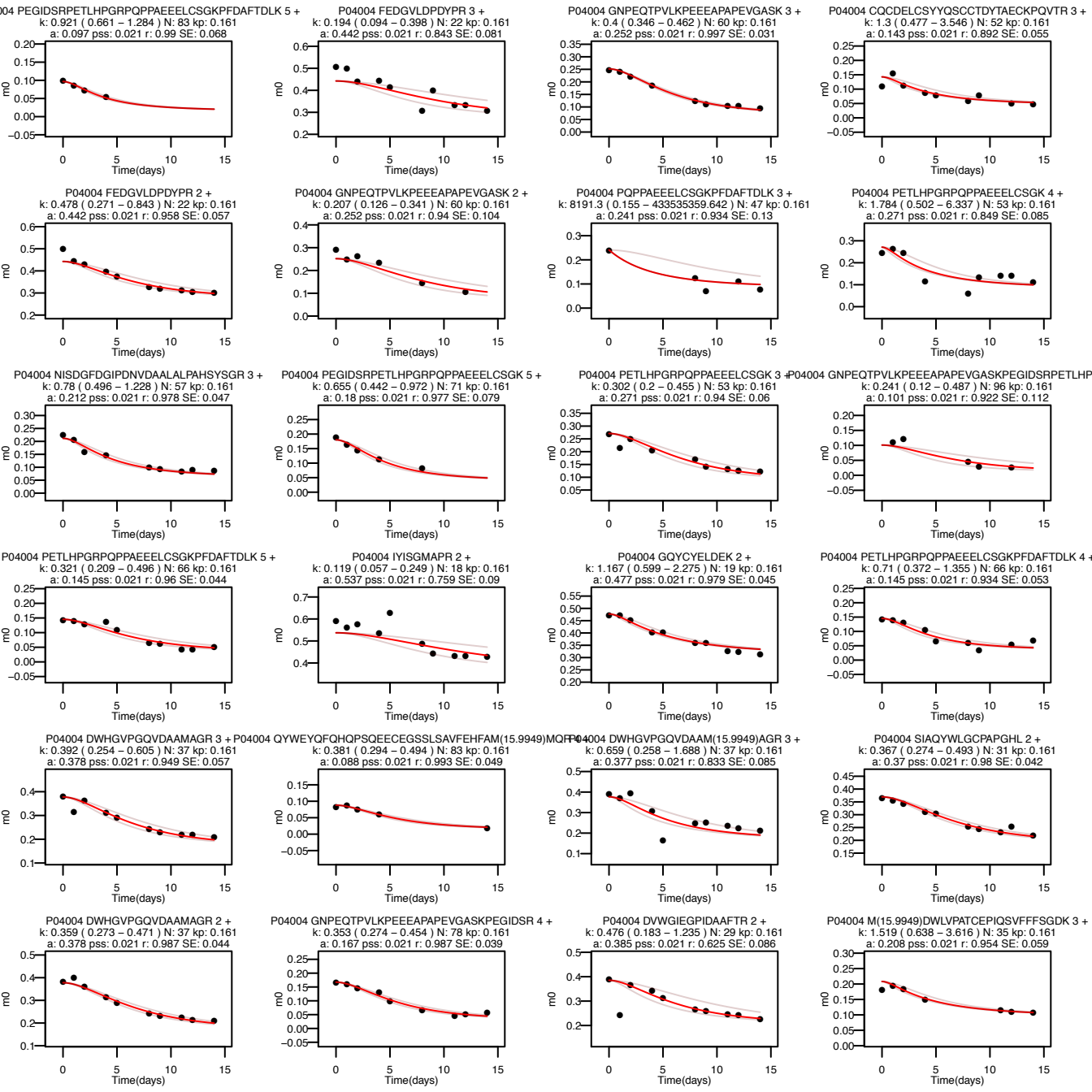


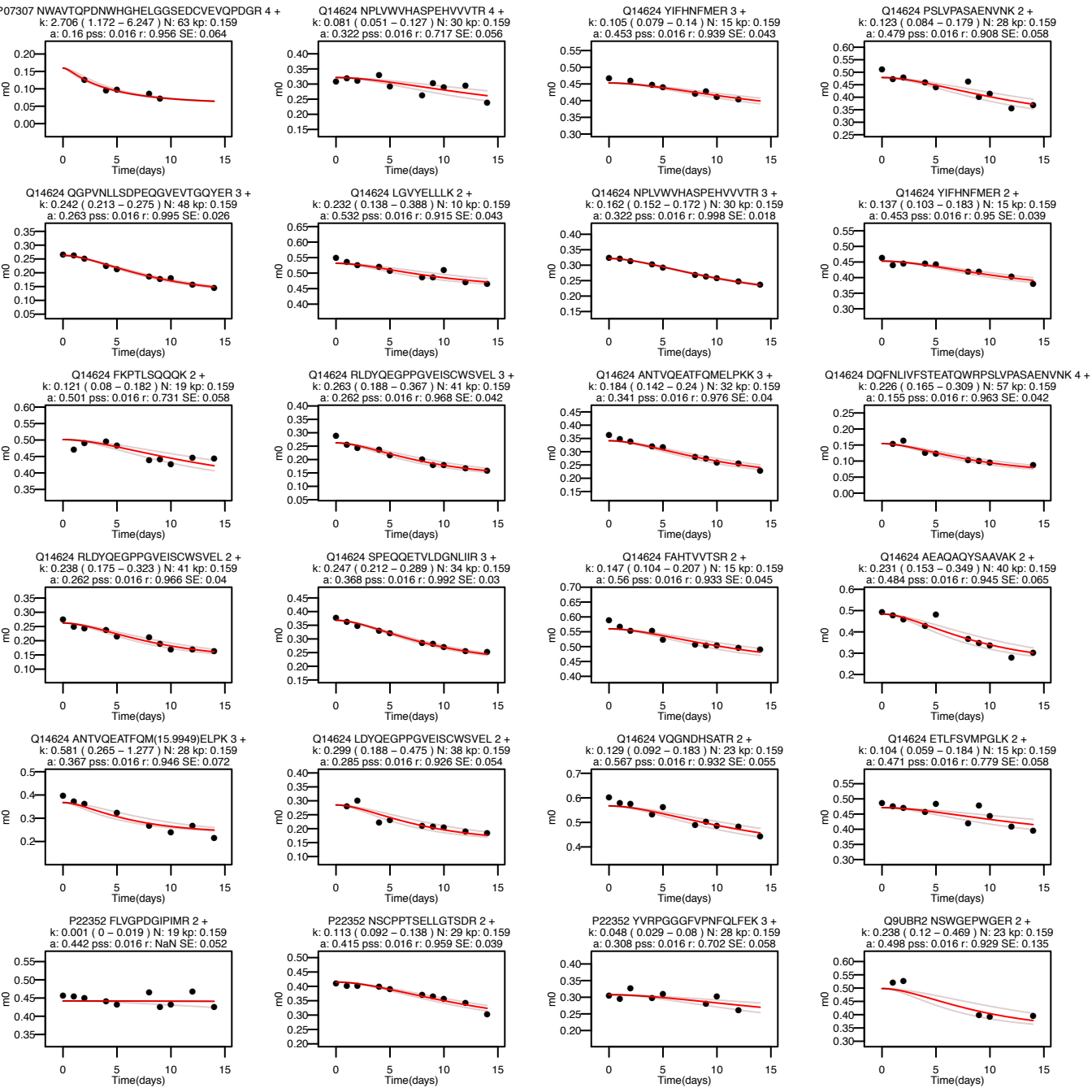
P05452 NWETEITAQPDGGK 3 +
k: 0.099 (0.08 – 0.124) N: 28 kp: 0.161
a: 0.425 pss: 0.021 r: 0.938 SE: 0.055

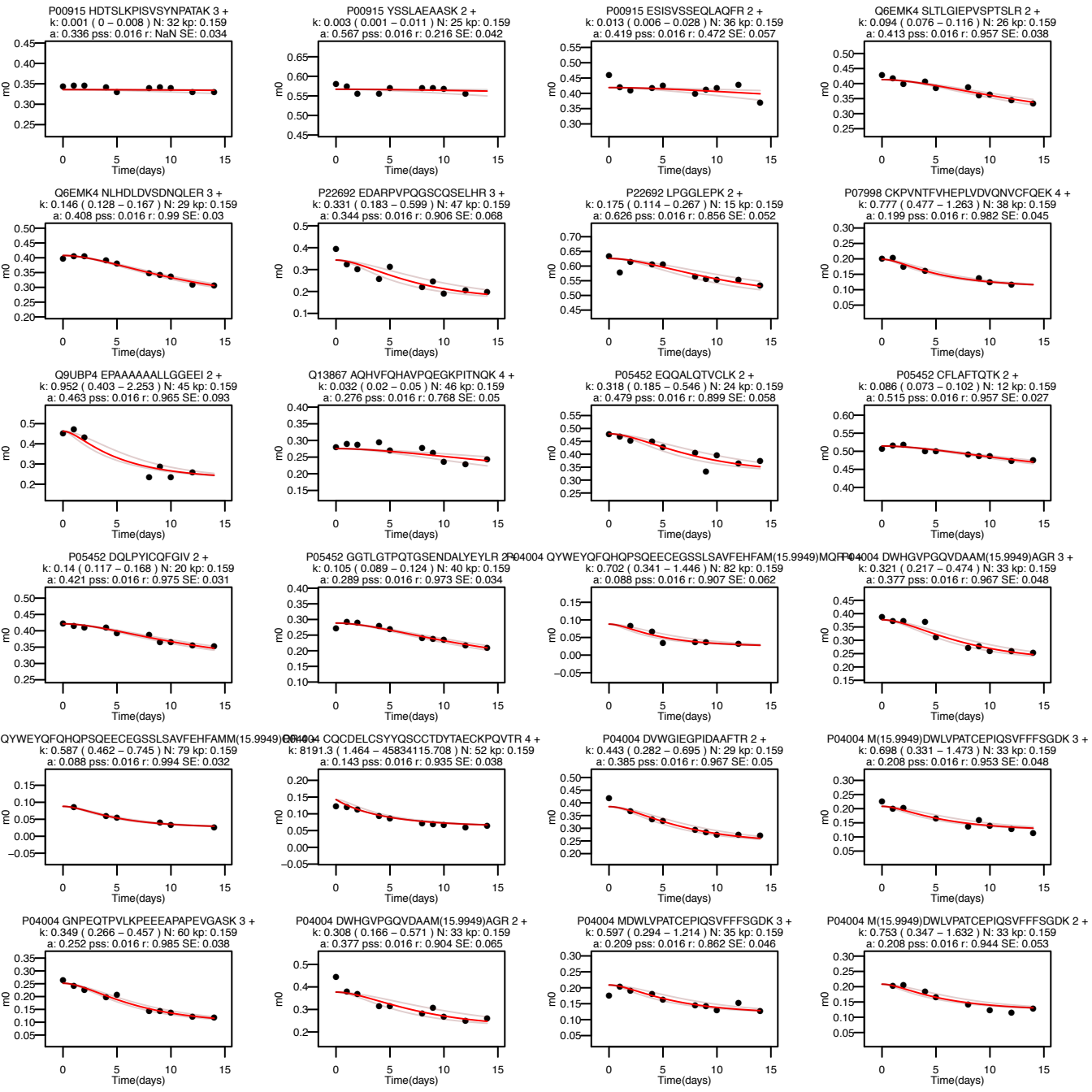


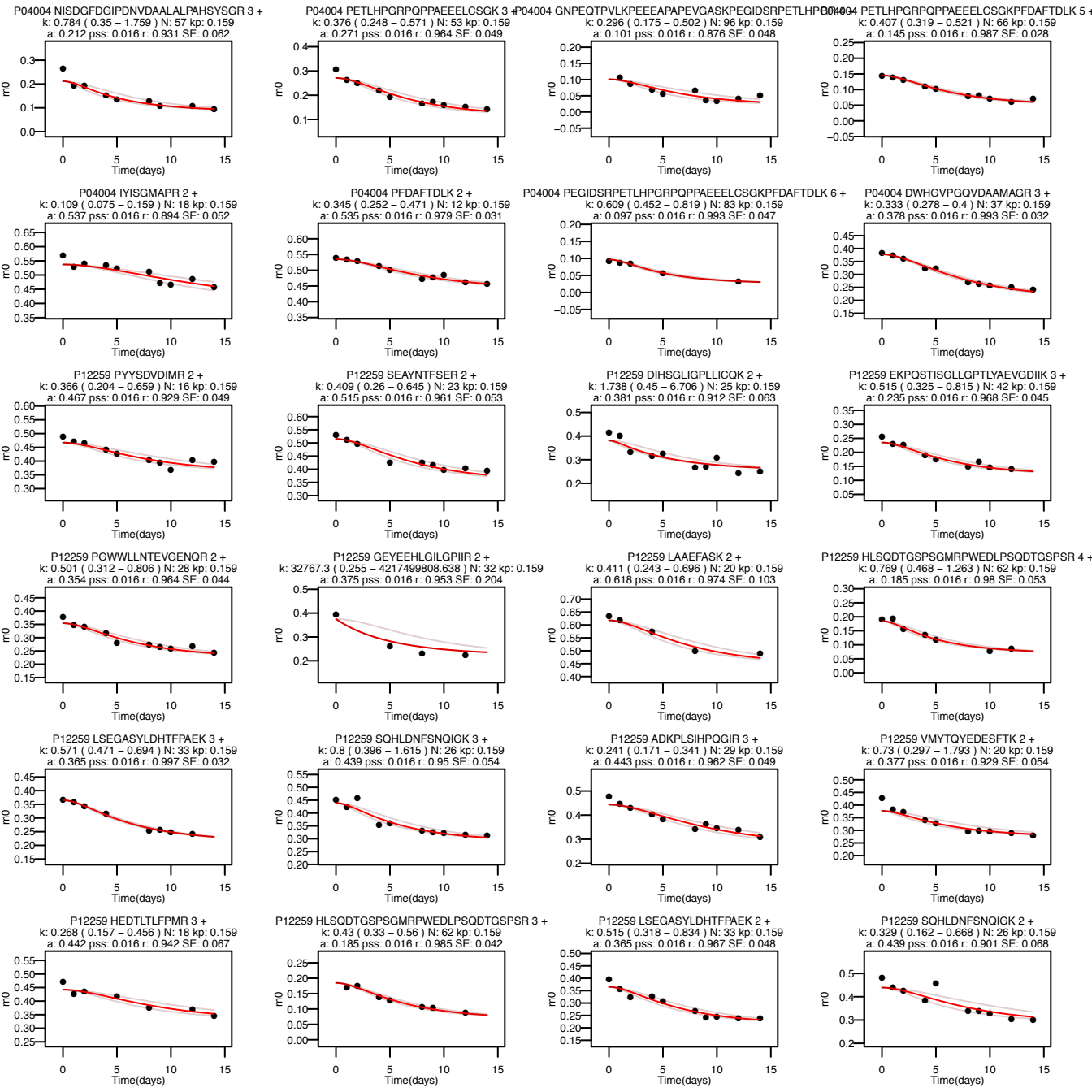
P05452 SRLDTLAQEVALLK 3 +
k: 0.082 (0.051 – 0.131) N: 28 kp: 0.161
a: 0.417 pss: 0.021 r: 0.836 SE: 0.07

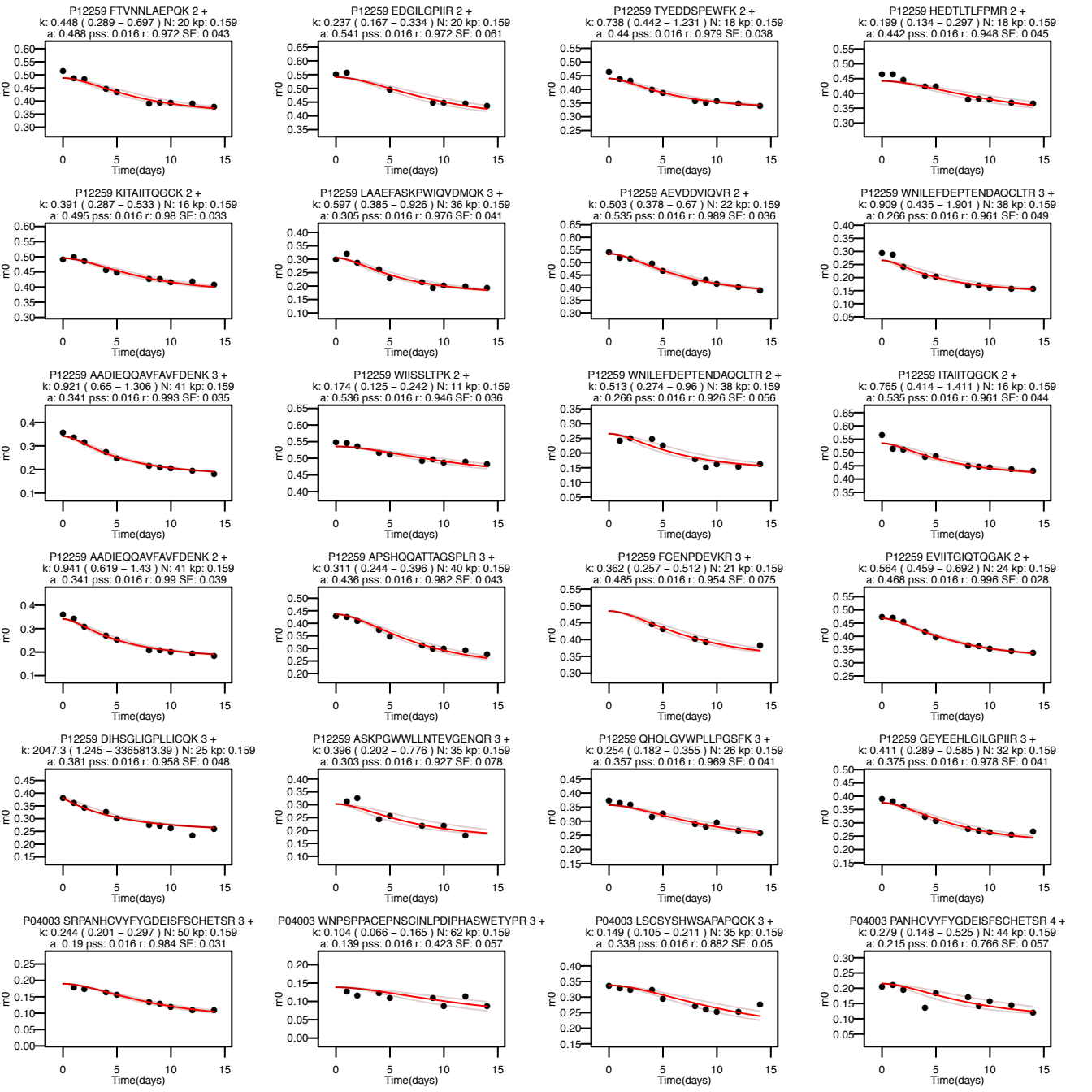


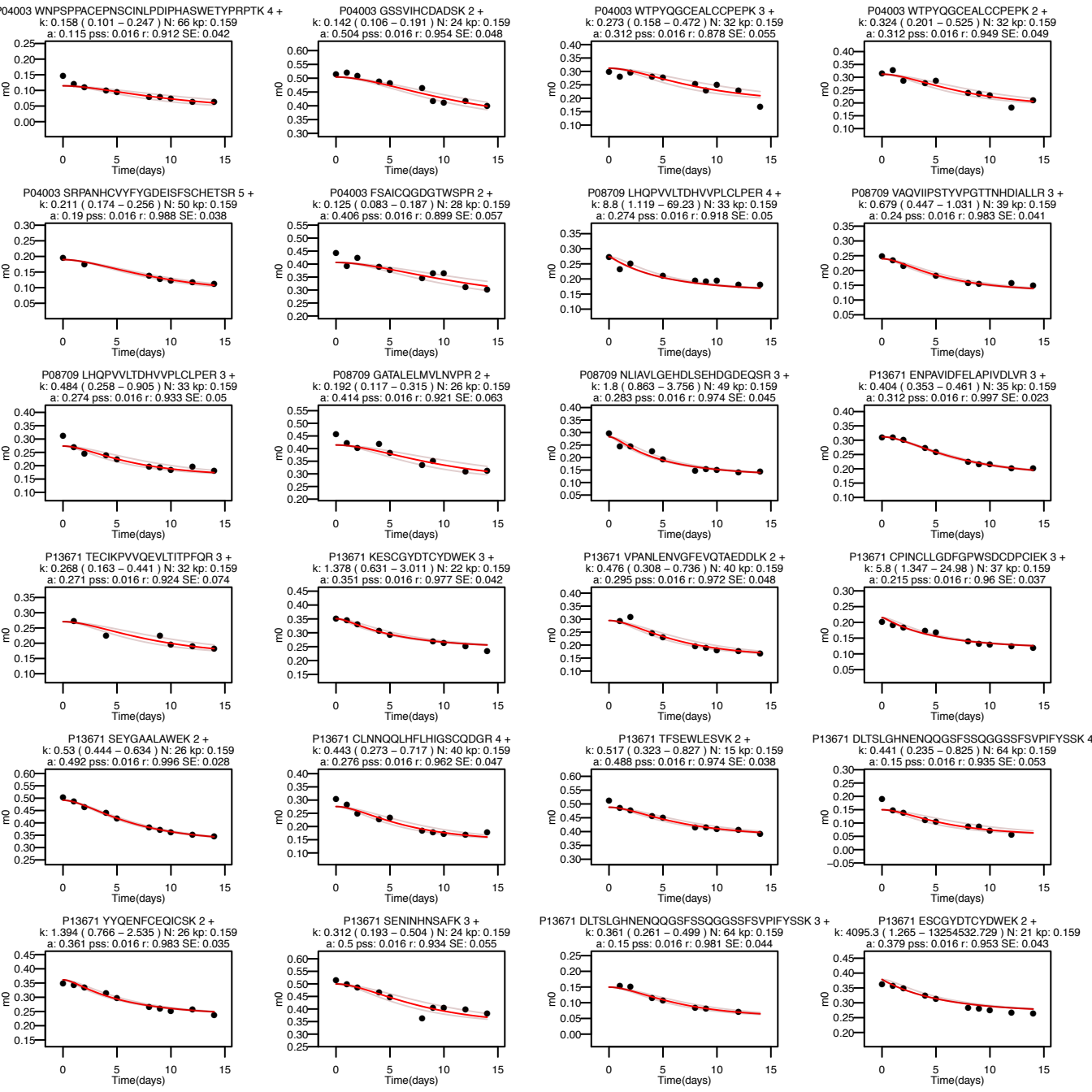

004 PEGIDSRPETLHPGRPQPPAEEELCSGKPFDAFTDLK 5 +
k: 0.921 (0.661 – 1.284) N: 83 kp: 0.161
a: 0.097 pss: 0.021 r: 0.99 SE: 0.068
P04004 FEDGVLDPDYPR 3 +
k: 0.194 (0.094 – 0.398) N: 22 kp: 0.161
a: 0.442 pss: 0.021 r: 0.843 SE: 0.081
P04004 GNPEQTPVLKPEEEAPAPEVGASK 3 +
k: 0.4 (0.346 – 0.462) N: 60 kp: 0.161
a: 0.252 pss: 0.021 r: 0.997 SE: 0.031
P04004 CQCDELCSYYQSCCTDYTAECKPQVTR 3 +
k: 1.3 (0.477 – 3.546) N: 52 kp: 0.161
a: 0.143 pss: 0.021 r: 0.892 SE: 0.055
P04004 FEDGVLDPDYPR 2 +
k: 0.478 (0.271 – 0.843) N: 22 kp: 0.161
a: 0.442 pss: 0.021 r: 0.958 SE: 0.057
P04004 GNPEQTPVLKPEEEAPAPEVGASK 2 +
k: 0.207 (0.126 – 0.341) N: 60 kp: 0.161
a: 0.252 pss: 0.021 r: 0.94 SE: 0.104
P04004 PQPPAEEELCSGKPFDAFTDLK 3 +
k: 8191.3 (0.155 – 433535359.642) N: 47 kp: 0.161
a: 0.241 pss: 0.021 r: 0.934 SE: 0.13
P04004 PETLHPGRPQPPAEEELCSGK 4 +
k: 1.784 (0.502 – 6.337) N: 53 kp: 0.161
a: 0.271 pss: 0.021 r: 0.849 SE: 0.085
P04004 NISDGFDGIPDNVDAALALPAHSYSGR 3 +
k: 0.78 (0.496 – 1.228) N: 57 kp: 0.161
a: 0.212 pss: 0.021 r: 0.978 SE: 0.047
P04004 PEGIDSRPETLHPGRPQPPAEEELCSGK 5 +
k: 0.655 (0.442 – 0.972) N: 71 kp: 0.161
a: 0.18 pss: 0.021 r: 0.977 SE: 0.079
P04004 PETLHPGRPQPPAEEELCSGK 3 +
k: 0.302 (0.2 – 0.455) N: 53 kp: 0.161
a: 0.271 pss: 0.021 r: 0.94 SE: 0.06
P04004 GNPEQTPVLKPEEEAPAPEVGASKPEGIDSRPETLHP
k: 0.241 (0.12 – 0.487) N: 96 kp: 0.161
a: 0.101 pss: 0.021 r: 0.922 SE: 0.112
P04004 PETLHPGRPQPPAEEELCSGKPFDAFTDLK 5 +
k: 0.321 (0.209 – 0.496) N: 66 kp: 0.161
a: 0.145 pss: 0.021 r: 0.96 SE: 0.044
P04004 IYISGMAPR 2 +
k: 0.119 (0.057 – 0.249) N: 18 kp: 0.161
a: 0.537 pss: 0.021 r: 0.759 SE: 0.09
P04004 GQYCYELDEK 2 +
k: 1.167 (0.599 – 2.275) N: 19 kp: 0.161
a: 0.477 pss: 0.021 r: 0.979 SE: 0.045
P04004 PETLHPGRPQPPAEEELCSGKPFDAFTDLK 4 +
k: 0.71 (0.372 – 1.355) N: 66 kp: 0.161
a: 0.145 pss: 0.021 r: 0.934 SE: 0.053
P04004 DWHGVPGQVDAAMAGR 3 +
k: 0.392 (0.254 – 0.605) N: 37 kp: 0.161
a: 0.378 pss: 0.021 r: 0.949 SE: 0.057
P04004 QYWEYQFQHQPSQEECEGSSLSAVFEHFAM(15.9949)MQFP
k: 0.381 (0.294 – 0.494) N: 83 kp: 0.161
a: 0.088 pss: 0.021 r: 0.993 SE: 0.049
P04004 DWHGVPGQVDAAM(15.9949)AGR 3 +
k: 0.659 (0.258 – 1.688) N: 37 kp: 0.161
a: 0.377 pss: 0.021 r: 0.833 SE: 0.085
P04004 SIAQYWLGCPAPGHL 2 +
k: 0.367 (0.274 – 0.493) N: 31 kp: 0.161
a: 0.37 pss: 0.021 r: 0.98 SE: 0.042
P04004 DWHGVPGQVDAAMAGR 2 +
k: 0.359 (0.273 – 0.471) N: 37 kp: 0.161
a: 0.378 pss: 0.021 r: 0.987 SE: 0.044
P04004 GNPEQTPVLKPEEEAPAPEVGASKPEGIDSR 4 +
k: 0.353 (0.274 – 0.454) N: 78 kp: 0.161
a: 0.167 pss: 0.021 r: 0.987 SE: 0.039
P04004 DVWGIEGPIDAAFTR 2 +
k: 0.476 (0.183 – 1.235) N: 29 kp: 0.161
a: 0.385 pss: 0.021 r: 0.625 SE: 0.086
P04004 M(15.9949)DWLVPATCEPIQSVFFFSGDK 3 +
k: 1.519 (0.638 – 3.616) N: 35 kp: 0.161
a: 0.208 pss: 0.021 r: 0.954 SE: 0.059
m0
Time(days)


P07307 NWAVTQPDNWHGHELGGSEDCVEVQPDGR 4 +
k: 2.706 (1.172 – 6.247) N: 63 kp: 0.159
a: 0.16 pss: 0.016 r: 0.956 SE: 0.064
Q14624 NPLVWVHASPEHVVVTR 4 +
k: 0.081 (0.051 – 0.127) N: 30 kp: 0.159
a: 0.322 pss: 0.016 r: 0.717 SE: 0.056
Q14624 YIFHNFMER 3 +
k: 0.105 (0.079 – 0.14) N: 15 kp: 0.159
a: 0.453 pss: 0.016 r: 0.939 SE: 0.043
Q14624 PSLVPASAENVNK 2 +
k: 0.123 (0.084 – 0.179) N: 28 kp: 0.159
a: 0.479 pss: 0.016 r: 0.908 SE: 0.058
Q14624 QGPVNLLSDPEQGVEVTGQYER 3 +
k: 0.242 (0.213 – 0.275) N: 48 kp: 0.159
a: 0.263 pss: 0.016 r: 0.995 SE: 0.026
Q14624 LGVYELLLK 2 +
k: 0.232 (0.138 – 0.388) N: 10 kp: 0.159
a: 0.532 pss: 0.016 r: 0.915 SE: 0.043
Q14624 NPLVWVHASPEHVVVTR 3 +
k: 0.162 (0.152 – 0.172) N: 30 kp: 0.159
a: 0.322 pss: 0.016 r: 0.998 SE: 0.018
Q14624 YIFHNFMER 2 +
k: 0.137 (0.103 – 0.183) N: 15 kp: 0.159
a: 0.453 pss: 0.016 r: 0.95 SE: 0.039
Q14624 FKPTLSQQQK 2 +
k: 0.121 (0.08 – 0.182) N: 19 kp: 0.159
a: 0.501 pss: 0.016 r: 0.731 SE: 0.058
Q14624 RLDYQEGPPGVEISCWSVEL 3 +
k: 0.263 (0.188 – 0.367) N: 41 kp: 0.159
a: 0.262 pss: 0.016 r: 0.968 SE: 0.042
Q14624 ANTVQEATFQMELPKK 3 +
k: 0.184 (0.142 – 0.24) N: 32 kp: 0.159
a: 0.341 pss: 0.016 r: 0.976 SE: 0.04
Q14624 DQFNLIVFSTEATQWRPSLVPASAENVNK 4 +
k: 0.226 (0.165 – 0.309) N: 57 kp: 0.159
a: 0.155 pss: 0.016 r: 0.963 SE: 0.042
Q14624 RLDYQEGPPGVEISCWSVEL 2 +
k: 0.238 (0.175 – 0.323) N: 41 kp: 0.159
a: 0.262 pss: 0.016 r: 0.966 SE: 0.04
Q14624 SPEQQETVLDGNLIIR 3 +
k: 0.247 (0.212 – 0.289) N: 34 kp: 0.159
a: 0.368 pss: 0.016 r: 0.992 SE: 0.03
Q14624 FAHTVVTSR 2 +
k: 0.147 (0.104 – 0.207) N: 15 kp: 0.159
a: 0.56 pss: 0.016 r: 0.933 SE: 0.045
Q14624 AEAQAQYSAAVAK 2 +
k: 0.231 (0.153 – 0.349) N: 40 kp: 0.159
a: 0.484 pss: 0.016 r: 0.945 SE: 0.065
Q14624 ANTVQEATFQM(15.9949)ELPK 3 +
k: 0.581 (0.265 – 1.277) N: 28 kp: 0.159
a: 0.367 pss: 0.016 r: 0.946 SE: 0.072
Q14624 LDYQEGPPGVEISCWSVEL 2 +
k: 0.299 (0.188 – 0.475) N: 38 kp: 0.159
a: 0.285 pss: 0.016 r: 0.926 SE: 0.054
Q14624 VQGNDHSATR 2 +
k: 0.129 (0.092 – 0.183) N: 23 kp: 0.159
a: 0.567 pss: 0.016 r: 0.932 SE: 0.055
Q14624 ETLFSVMPGLK 2 +
k: 0.104 (0.059 – 0.184) N: 15 kp: 0.159
a: 0.471 pss: 0.016 r: 0.779 SE: 0.058
P22352 FLVGPDGIPIMR 2 +
k: 0.001 (0 – 0.019) N: 19 kp: 0.159
a: 0.442 pss: 0.016 r: NaN SE: 0.052
P22352 NSCPPTSELLGTSDR 2 +
k: 0.113 (0.092 – 0.138) N: 29 kp: 0.159
a: 0.415 pss: 0.016 r: 0.959 SE: 0.039
P22352 YVRPGGGFVPNFQLFEK 3 +
k: 0.048 (0.029 – 0.08) N: 28 kp: 0.159
a: 0.308 pss: 0.016 r: 0.702 SE: 0.058
Q9UBR2 NSWGEPWGER 2 +
k: 0.238 (0.12 – 0.469) N: 23 kp: 0.159
a: 0.498 pss: 0.016 r: 0.929 SE: 0.135
m0
Time(days)


P00915 HDTSLKPISVSYNPATAK 3 +
k: 0.001 (0 – 0.008) N: 32 kp: 0.159
a: 0.336 pss: 0.016 r: NaN SE: 0.034
P00915 YSSLAEAASK 2 +
k: 0.003 (0.001 – 0.011) N: 25 kp: 0.159
a: 0.567 pss: 0.016 r: 0.216 SE: 0.042
P00915 ESISVSSEQLAQFR 2 +
k: 0.013 (0.006 – 0.028) N: 36 kp: 0.159
a: 0.419 pss: 0.016 r: 0.472 SE: 0.057
Q6EMK4 SLTLGIEPVSPTSLR 2 +
k: 0.094 (0.076 – 0.116) N: 26 kp: 0.159
a: 0.413 pss: 0.016 r: 0.957 SE: 0.038
Q6EMK4 NLHDLDVSDNQLER 3 +
k: 0.146 (0.128 – 0.167) N: 29 kp: 0.159
a: 0.408 pss: 0.016 r: 0.99 SE: 0.03
P22692 EDARPVPQGSCQSELHR 3 +
k: 0.331 (0.183 – 0.599) N: 47 kp: 0.159
a: 0.344 pss: 0.016 r: 0.906 SE: 0.068
P22692 LPGGLEPK 2 +
k: 0.175 (0.114 – 0.267) N: 15 kp: 0.159
a: 0.626 pss: 0.016 r: 0.856 SE: 0.052
P07998 CKPVNTFVHEPLVDVQNVCFQEK 4 +
k: 0.777 (0.477 – 1.263) N: 38 kp: 0.159
a: 0.199 pss: 0.016 r: 0.982 SE: 0.045
Q9UBP4 EPAAAAAALLGGEEI 2 +
k: 0.952 (0.403 – 2.253) N: 45 kp: 0.159
a: 0.463 pss: 0.016 r: 0.965 SE: 0.093
Q13867 AQHVFQHAVPQEGKPITNQK 4 +
k: 0.032 (0.02 – 0.05) N: 46 kp: 0.159
a: 0.276 pss: 0.016 r: 0.768 SE: 0.05
P05452 EQQALQTVCLK 2 +
k: 0.318 (0.185 – 0.546) N: 24 kp: 0.159
a: 0.479 pss: 0.016 r: 0.899 SE: 0.058
P05452 CFLAFTQTK 2 +
k: 0.086 (0.073 – 0.102) N: 12 kp: 0.159
a: 0.515 pss: 0.016 r: 0.957 SE: 0.027
P05452 DQLPYICQFGIV 2 +
k: 0.14 (0.117 – 0.168) N: 20 kp: 0.159
a: 0.421 pss: 0.016 r: 0.975 SE: 0.031
P05452 GGTLGTPQTGSENDALYEYLR 2 +
k: 0.105 (0.089 – 0.124) N: 40 kp: 0.159
a: 0.289 pss: 0.016 r: 0.973 SE: 0.034
P04004 QYWEYQFQHQPSQEECEGSSLSAVFEHFAM(15.9949)MQPP 4 +
k: 0.702 (0.341 – 1.446) N: 82 kp: 0.159
a: 0.088 pss: 0.016 r: 0.907 SE: 0.062
P04004 DWHGVPGQVDAAM(15.9949)AGR 3 +
k: 0.321 (0.217 – 0.474) N: 33 kp: 0.159
a: 0.377 pss: 0.016 r: 0.967 SE: 0.048
QYWEYQFQHQPSQEECEGSSLSAVFEHFAMM(15.9949)QPP 4 +
k: 0.587 (0.462 – 0.745) N: 79 kp: 0.159
a: 0.088 pss: 0.016 r: 0.994 SE: 0.032
P04004 CQCDELCSYYQSCCTDYTAECKPQVTR 4 +
k: 8191.3 (1.464 – 45834115.708) N: 52 kp: 0.159
a: 0.143 pss: 0.016 r: 0.935 SE: 0.038
P04004 DVWGIEGPIDAAFTR 2 +
k: 0.443 (0.282 – 0.695) N: 29 kp: 0.159
a: 0.385 pss: 0.016 r: 0.967 SE: 0.05
P04004 M(15.9949)DWLVPATCEPIQSVFFFSGDK 3 +
k: 0.698 (0.331 – 1.473) N: 33 kp: 0.159
a: 0.208 pss: 0.016 r: 0.953 SE: 0.048
P04004 GNPEQTPVLKPEEEAPAPEVGASK 3 +
k: 0.349 (0.266 – 0.457) N: 60 kp: 0.159
a: 0.252 pss: 0.016 r: 0.985 SE: 0.038
P04004 DWHGVPGQVDAAM(15.9949)AGR 2 +
k: 0.308 (0.166 – 0.571) N: 33 kp: 0.159
a: 0.377 pss: 0.016 r: 0.904 SE: 0.065
P04004 MDWLVPATCEPIQSVFFFSGDK 3 +
k: 0.597 (0.294 – 1.214) N: 35 kp: 0.159
a: 0.209 pss: 0.016 r: 0.862 SE: 0.046
P04004 M(15.9949)DWLVPATCEPIQSVFFFSGDK 2 +
k: 0.753 (0.347 – 1.632) N: 33 kp: 0.159
a: 0.208 pss: 0.016 r: 0.944 SE: 0.053
m0
Time(days)


P04004 NISDGFDGIPDNVDAALALPAHSYSGGR 3 +
k: 0.784 (0.35 – 1.759) N: 57 kp: 0.159
a: 0.212 pss: 0.016 r: 0.931 SE: 0.062
P04004 PETLHPGRPQPPAEEELCSGK 3 +
k: 0.376 (0.248 – 0.571) N: 53 kp: 0.159
a: 0.271 pss: 0.016 r: 0.964 SE: 0.049
P04004 GNPEQTPVLKPEEEAPAPEVGASKPEGIDSRPETLHPGRPQP
k: 0.296 (0.175 – 0.502) N: 96 kp: 0.159
a: 0.101 pss: 0.016 r: 0.876 SE: 0.048
P04004 PETLHPGRPQPPAEEELCSGKPFDAFTDLK 5 +
k: 0.407 (0.319 – 0.521) N: 66 kp: 0.159
a: 0.145 pss: 0.016 r: 0.987 SE: 0.028
P04004 IYISGMAPR 2 +
k: 0.109 (0.075 – 0.159) N: 18 kp: 0.159
a: 0.537 pss: 0.016 r: 0.894 SE: 0.052
P04004 PFDAFTDLK 2 +
k: 0.345 (0.252 – 0.471) N: 12 kp: 0.159
a: 0.535 pss: 0.016 r: 0.979 SE: 0.031
P04004 PEGIDSRPETLHPGRPQPPAEEELCSGKPFDAFTDLK 6 +
k: 0.609 (0.452 – 0.819) N: 83 kp: 0.159
a: 0.097 pss: 0.016 r: 0.993 SE: 0.047
P04004 DWHGVPGQVDAAMAGR 3 +
k: 0.333 (0.278 – 0.4) N: 37 kp: 0.159
a: 0.378 pss: 0.016 r: 0.993 SE: 0.032
P12259 PYYSDVDIMR 2 +
k: 0.366 (0.204 – 0.659) N: 16 kp: 0.159
a: 0.467 pss: 0.016 r: 0.929 SE: 0.049
P12259 SEAYNTFSER 2 +
k: 0.409 (0.26 – 0.645) N: 23 kp: 0.159
a: 0.515 pss: 0.016 r: 0.961 SE: 0.053
P12259 DIHSGLIGPLLICQK 2 +
k: 1.738 (0.45 – 6.706) N: 25 kp: 0.159
a: 0.381 pss: 0.016 r: 0.912 SE: 0.063
P12259 EKPQSTISGLLGPTLYAEVGDIIK 3 +
k: 0.515 (0.325 – 0.815) N: 42 kp: 0.159
a: 0.235 pss: 0.016 r: 0.968 SE: 0.045
P12259 PGWWLLNTEVGENQR 2 +
k: 0.501 (0.312 – 0.806) N: 28 kp: 0.159
a: 0.354 pss: 0.016 r: 0.964 SE: 0.044
P12259 GEYEEHLGILGPIIR 2 +
k: 32767.3 (0.255 – 4217499808.638) N: 32 kp: 0.159
a: 0.375 pss: 0.016 r: 0.953 SE: 0.204
P12259 LAAEFASK 2 +
k: 0.411 (0.243 – 0.696) N: 20 kp: 0.159
a: 0.618 pss: 0.016 r: 0.974 SE: 0.103
P12259 HLSQDTGSPSGMRPWEDLPSQDTGSPSR 4 +
k: 0.769 (0.468 – 1.263) N: 62 kp: 0.159
a: 0.185 pss: 0.016 r: 0.98 SE: 0.053
P12259 LSEGASYLDHTFPAEK 3 +
k: 0.571 (0.471 – 0.694) N: 33 kp: 0.159
a: 0.365 pss: 0.016 r: 0.997 SE: 0.032
P12259 SQHLDNFSNQIGK 3 +
k: 0.8 (0.396 – 1.615) N: 26 kp: 0.159
a: 0.439 pss: 0.016 r: 0.95 SE: 0.054
P12259 ADKPLSIHPQGIR 3 +
k: 0.241 (0.171 – 0.341) N: 29 kp: 0.159
a: 0.443 pss: 0.016 r: 0.962 SE: 0.049
P12259 VMYTQYEDESFTK 2 +
k: 0.73 (0.297 – 1.793) N: 20 kp: 0.159
a: 0.377 pss: 0.016 r: 0.929 SE: 0.054
P12259 HEDTLTLFPMR 3 +
k: 0.268 (0.157 – 0.456) N: 18 kp: 0.159
a: 0.442 pss: 0.016 r: 0.942 SE: 0.067
P12259 HLSQDTGSPSGMRPWEDLPSQDTGSPSR 3 +
k: 0.43 (0.33 – 0.56) N: 62 kp: 0.159
a: 0.185 pss: 0.016 r: 0.985 SE: 0.042
P12259 LSEGASYLDHTFPAEK 2 +
k: 0.515 (0.318 – 0.834) N: 33 kp: 0.159
a: 0.365 pss: 0.016 r: 0.967 SE: 0.048
P12259 SQHLDNFSNQIGK 2 +
k: 0.329 (0.162 – 0.668) N: 26 kp: 0.159
a: 0.439 pss: 0.016 r: 0.901 SE: 0.068
m0
Time(days)


P12259 FTVNNLAEPQK 2 +
k: 0.448 (0.289 – 0.697) N: 20 kp: 0.159
a: 0.488 pss: 0.016 r: 0.972 SE: 0.043
P12259 EDGILGPIIR 2 +
k: 0.237 (0.167 – 0.334) N: 20 kp: 0.159
a: 0.541 pss: 0.016 r: 0.972 SE: 0.061
P12259 TYEDDSPEWFK 2 +
k: 0.738 (0.442 – 1.231) N: 18 kp: 0.159
a: 0.44 pss: 0.016 r: 0.979 SE: 0.038
P12259 HEDTLTLFPMR 2 +
k: 0.199 (0.134 – 0.297) N: 18 kp: 0.159
a: 0.442 pss: 0.016 r: 0.948 SE: 0.045
P12259 KITAIITQGCK 2 +
k: 0.391 (0.287 – 0.533) N: 16 kp: 0.159
a: 0.495 pss: 0.016 r: 0.98 SE: 0.033
P12259 LAAEFASKPWIQVDMQK 3 +
k: 0.597 (0.385 – 0.926) N: 36 kp: 0.159
a: 0.305 pss: 0.016 r: 0.976 SE: 0.041
P12259 AEVDDVIQVR 2 +
k: 0.503 (0.378 – 0.67) N: 22 kp: 0.159
a: 0.535 pss: 0.016 r: 0.989 SE: 0.036
P12259 WNILEFDEPTENDAQCLTR 3 +
k: 0.909 (0.435 – 1.901) N: 38 kp: 0.159
a: 0.266 pss: 0.016 r: 0.961 SE: 0.049
P12259 AADIEQQAVFAVFDENK 3 +
k: 0.921 (0.65 – 1.306) N: 41 kp: 0.159
a: 0.341 pss: 0.016 r: 0.993 SE: 0.035
P12259 WIISSLTPK 2 +
k: 0.174 (0.125 – 0.242) N: 11 kp: 0.159
a: 0.536 pss: 0.016 r: 0.946 SE: 0.036
P12259 WNILEFDEPTENDAQCLTR 2 +
k: 0.513 (0.274 – 0.96) N: 38 kp: 0.159
a: 0.266 pss: 0.016 r: 0.926 SE: 0.056
P12259 ITAIITQGCK 2 +
k: 0.765 (0.414 – 1.411) N: 16 kp: 0.159
a: 0.535 pss: 0.016 r: 0.961 SE: 0.044
P12259 AADIEQQAVFAVFDENK 2 +
k: 0.941 (0.619 – 1.43) N: 41 kp: 0.159
a: 0.341 pss: 0.016 r: 0.99 SE: 0.039
P12259 APSHQQATTAGSPLR 3 +
k: 0.311 (0.244 – 0.396) N: 40 kp: 0.159
a: 0.436 pss: 0.016 r: 0.982 SE: 0.043
P12259 FCENPDEVKR 3 +
k: 0.362 (0.257 – 0.512) N: 21 kp: 0.159
a: 0.485 pss: 0.016 r: 0.954 SE: 0.075
P12259 EVIITGIQTQGAK 2 +
k: 0.564 (0.459 – 0.692) N: 24 kp: 0.159
a: 0.468 pss: 0.016 r: 0.996 SE: 0.028
P12259 DIHSGLIGPLLICQK 3 +
k: 2047.3 (1.245 – 3365813.39) N: 25 kp: 0.159
a: 0.381 pss: 0.016 r: 0.958 SE: 0.048
P12259 ASKPGWWLLNTEVGENQR 3 +
k: 0.396 (0.202 – 0.776) N: 35 kp: 0.159
a: 0.303 pss: 0.016 r: 0.927 SE: 0.078
P12259 QHQLGVWPLLPGSFK 3 +
k: 0.254 (0.182 – 0.355) N: 26 kp: 0.159
a: 0.357 pss: 0.016 r: 0.969 SE: 0.041
P12259 GEYEEHLGILGPIIR 3 +
k: 0.411 (0.289 – 0.585) N: 32 kp: 0.159
a: 0.375 pss: 0.016 r: 0.978 SE: 0.041
P04003 SRPANHCVYFYGDEISFSCHETSR 3 +
k: 0.244 (0.201 – 0.297) N: 50 kp: 0.159
a: 0.19 pss: 0.016 r: 0.984 SE: 0.031
P04003 WNPSPPACEPNSCINLPDIPHASWETYPR 3 +
k: 0.104 (0.066 – 0.165) N: 62 kp: 0.159
a: 0.139 pss: 0.016 r: 0.423 SE: 0.057
P04003 LSCSYSHWSAPAPQCK 3 +
k: 0.149 (0.105 – 0.211) N: 35 kp: 0.159
a: 0.338 pss: 0.016 r: 0.882 SE: 0.05
P04003 PANHCVYFYGDEISFSCHETSR 4 +
k: 0.279 (0.148 – 0.525) N: 44 kp: 0.159
a: 0.215 pss: 0.016 r: 0.766 SE: 0.057
m0
Time(days)


P04003 WNPSPPACEPNSCINLPDIPHASWETYPRPTK 4 +
k: 0.158 (0.101 – 0.247) N: 66 kp: 0.159
a: 0.115 pss: 0.016 r: 0.912 SE: 0.042
P04003 GSSVIHCDADSK 2 +
k: 0.142 (0.106 – 0.191) N: 24 kp: 0.159
a: 0.504 pss: 0.016 r: 0.954 SE: 0.048
P04003 WTPYQGCEALCCPEPK 3 +
k: 0.273 (0.158 – 0.472) N: 32 kp: 0.159
a: 0.312 pss: 0.016 r: 0.878 SE: 0.055
P04003 WTPYQGCEALCCPEPK 2 +
k: 0.324 (0.201 – 0.525) N: 32 kp: 0.159
a: 0.312 pss: 0.016 r: 0.949 SE: 0.049
P04003 SRPANHCVYFYGDEISFSCHETSR 5 +
k: 0.211 (0.174 – 0.256) N: 50 kp: 0.159
a: 0.19 pss: 0.016 r: 0.988 SE: 0.038
P04003 FSAICQGDGTWSPR 2 +
k: 0.125 (0.083 – 0.187) N: 28 kp: 0.159
a: 0.406 pss: 0.016 r: 0.899 SE: 0.057
P08709 LHQPVVLTDHVVPLCLPER 4 +
k: 8.8 (1.119 – 69.23) N: 33 kp: 0.159
a: 0.274 pss: 0.016 r: 0.918 SE: 0.05
P08709 VAQVIIPSTYVPGTTNHDIALLR 3 +
k: 0.679 (0.447 – 1.031) N: 39 kp: 0.159
a: 0.24 pss: 0.016 r: 0.983 SE: 0.041
P08709 LHQPVVLTDHVVPLCLPER 3 +
k: 0.484 (0.258 – 0.905) N: 33 kp: 0.159
a: 0.274 pss: 0.016 r: 0.933 SE: 0.05
P08709 GATALELMVLNVPR 2 +
k: 0.192 (0.117 – 0.315) N: 26 kp: 0.159
a: 0.414 pss: 0.016 r: 0.921 SE: 0.063
P08709 NLIAVLGEHDLSEHDGDEQSR 3 +
k: 1.8 (0.863 – 3.756) N: 49 kp: 0.159
a: 0.283 pss: 0.016 r: 0.974 SE: 0.045
P13671 ENPAVIDFELAPIVDLVR 3 +
k: 0.404 (0.353 – 0.461) N: 35 kp: 0.159
a: 0.312 pss: 0.016 r: 0.997 SE: 0.023
P13671 TECIKPVVQEVLTITPFQR 3 +
k: 0.268 (0.163 – 0.441) N: 32 kp: 0.159
a: 0.271 pss: 0.016 r: 0.924 SE: 0.074
P13671 KESCGYDTCYDWEK 3 +
k: 1.378 (0.631 – 3.011) N: 22 kp: 0.159
a: 0.351 pss: 0.016 r: 0.977 SE: 0.042
P13671 VPANLENVGFEVQTAEDDLK 2 +
k: 0.476 (0.308 – 0.736) N: 40 kp: 0.159
a: 0.295 pss: 0.016 r: 0.972 SE: 0.048
P13671 CPINCLLGDFGPWSDCDPCIEK 3 +
k: 5.8 (1.347 – 24.98) N: 37 kp: 0.159
a: 0.215 pss: 0.016 r: 0.96 SE: 0.037
P13671 SEYGAALAWEK 2 +
k: 0.53 (0.444 – 0.634) N: 26 kp: 0.159
a: 0.492 pss: 0.016 r: 0.996 SE: 0.028
P13671 CLNNQQLHFLHIGSCQDGR 4 +
k: 0.443 (0.273 – 0.717) N: 40 kp: 0.159
a: 0.276 pss: 0.016 r: 0.962 SE: 0.047
P13671 TFSEWLESVK 2 +
k: 0.517 (0.323 – 0.827) N: 15 kp: 0.159
a: 0.488 pss: 0.016 r: 0.974 SE: 0.038
P13671 DLTSLGHNENQQGSFSSQGGSSFSVPIFYSSK 4 +
k: 0.441 (0.235 – 0.825) N: 64 kp: 0.159
a: 0.15 pss: 0.016 r: 0.935 SE: 0.053
P13671 YYQENFCEQICSK 2 +
k: 1.394 (0.766 – 2.535) N: 26 kp: 0.159
a: 0.361 pss: 0.016 r: 0.983 SE: 0.035
P13671 SENINHNSAFK 3 +
k: 0.312 (0.193 – 0.504) N: 24 kp: 0.159
a: 0.5 pss: 0.016 r: 0.934 SE: 0.055
P13671 DLTSLGHNENQQGSFSSQGGSSFSVPIFYSSK 3 +
k: 0.361 (0.261 – 0.499) N: 64 kp: 0.159
a: 0.15 pss: 0.016 r: 0.981 SE: 0.044
P13671 ESCGYDTCYDWEK 2 +
k: 4095.3 (1.265 – 13254532.729) N: 21 kp: 0.159
a: 0.379 pss: 0.016 r: 0.953 SE: 0.043
m0
Time(days)