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Supplementary Information for

Widespread hydroxylation of unstructured lysine-rich protein domains by JMJD6

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Supplementary Materials and Methods

Overview of data analysis

DDA or DIA MS data were first analysed by PEAKS Studio (Bioinformatics Solutions) or Spectronaut (Biognosys) software, respectively (details are described below). Subsequent analyses were performed using R (4.0.0)[1] with the following packages (data.table (1.12.8)[2], dplyr (1.0.0)[3], stringr (1.4.0)[4], magrittr (1.5)[5], and Biostrings (2.56.0)[6]); The computational analysis pipeline used for this study is available from (https://github.com/YoichiroSugimoto/20211110_JMJD6_K_hydroxylation). The data were visualised using either Microsoft Excel, Graphpad Prism (9.3), pheatmap (1.0.12)[7], ComplexHeatmap (2.4.3)[8] and ggplot2 (3.3.1)[9].

Initial analyses of BRD4 hydroxylation in publicly available data were performed on deep proteome datasets (PXD002395, PXD003977, PXD004452) downloaded from the PRIDE repository and processed with PEAKS Studio (v10). Processing parameters were as follows: Precursor ion tolerance was 10 ppm; Fragment ion tolerance was 0.5 Da for Ion Trap acquisitions and 0.02 Da for Orbitrap; trypsin cleavage rules were specific with a maximum of 2 missed cleavages; Carbamidomethylation (C) was selected as a fixed modification and variable modifications (up to 3 permitted) were deamidation (N,Q), acetylation of protein *N*-termini, oxidation (C, D, F, H, K, M, N, P, R, W, Y) and dioxidation (F, M, W, Y). Data were matched against the canonical human Uniprot database proteome (retrieved 24th September 2019).

Quantitation of fragment ions from PRM acquisitions were performed by manual extraction and area integration in Qualbrowser (Xcalibur v4.1; Thermo Scientific).

Database analyses of DDA data

Processing of "in-house" DDA data used PEAKS Studio (v10.5 and 10.6). The following parameters were applied to non-derivatised tryptic data acquired by Higher-energy C-trap dissociation (HCD): 15 ppm mass error tolerance for precursor ions and 0.02 Da tolerance for fragment ion masses; trypsin cleavage rules were specific with a maximum of 2 missed cleavages; carbamidomethylation (C) was selected as a fixed modification and variable modifications (up to 3 permitted) were: deamidation (N,Q), acetylation of protein *N*-termini, oxidation (M,W,K) and dioxidation (M,W). Data were matched against the appropriate species-specific (human/mouse) canonical Uniprot database (retrieved 8th February 2021) with a list of common contaminants appended (cRAP database; http://crapome.org). Peptide false discovery rate (FDR) was set to 1%

using a target-decoy method and PTM site determination was informed by a probability-based ambiguity score (Ascore; -10lgP). The number of variable modifications was increased to 5 for Asp-N digestion (cleavage before D, E) in order to monitor hydroxylation of lysine-rich sequences. To analyse data from propionylated samples, the DDA workflow was adapted for processing incompletely derivatised tryptic peptides. It was not possible to modify the *in-silico* specificity of trypsin toward propionylated lysine within the PEAKS DB search engine. Thus, a large number (n=5) number of missed cleavage occurrences was specified in order to detect derivatised lysine-rich polypeptides. A maximum number of 5 variable modifications were considered, specifically: deamidation (N,Q), acetylation of protein *N*-termini, oxidation (M,W,K), propionylation (K) and oxidised propionylation (K); note, carbamidomethylation (C) was considered a fixed modification only in preparations that were treated with iodoacetamide. To reduce prohibitively long search times, precursor mass error tolerance was reduced from 15 ppm to 7.5 ppm and, where appropriate, custom databases curated from DDA searches of non-derivatised experiments were specifically interrogated (e.g., JQ1 PD and FLAG-JMJD6 interactome PD). Peptides meeting the significance filter (-10lgP >15) and MS2 ion intensity filter (>1%) were exported as "protein-peptides.csv" files.

For the calculation of site-specific PTM stoichiometry, analyses were restricted to JQ1 and JMJD6 peptide pulldown datasets to enable direct comparison between wild-type and JMJD6-defective HeLa cells. PEAKS export files were filtered to remove peptides that were not uniquely assigned to a protein and peptides with an AUC (area under the curve, LC-MS/MS data) of 0. Peptides that were unlikely to be products of trypsinolysis were also filtered out. For this purpose, we assumed that trypsin cleaves *C*-terminal to lysine, hydroxylysine, arginine, and mono-methyl arginine, but not propionyl lysine and di-methyl arginine. Thus, peptides with a modified *C*-terminal amino acid incompatible with cleavage by trypsin were excluded. In addition, peptides that had more than one "genuine" tryptic cleavage site were filtered out; we did not consider lysine or arginine followed by a proline a tryptic cleavage site. We only considered PTMs that passed the PEAKS MS2 ion intensity filter (>1%). Based on the filtered data, the stoichiometry of a PTM at a specific residue of a protein was calculated using the following formula:

$$\frac{\sum_{\substack{\text{all the peptides with} \\ \text{the PTM at the residue}}} AUC}{\sum_{\substack{\text{all the peptides without} \\ \text{the PTM at the residue}}} AUC + \sum_{\substack{\text{all the peptides with} \\ \text{the PTM at the residue}}} AUC}$$

Note, these measurements are relative values, which are not corrected for any effect of propionylation and/or hydroxylation on ionisation efficiency. Filtered data comparing peptide identifications between wild-type and JMJD6-defective preparations were used to shortlist JMJD6-dependent hydroxylations that were verified by manual inspection of MSMS spectra.

De novo sequencing

De novo sequencing results, which assist the PEAKS DB search algorithm, were also analysed to identify hydroxylysines in peptides irrespective of protein assignment. The sequencing results were exported from PEAKS studio as a “de novo peptides”.csv file and pre-processed as follows: (1) tryptic peptides that did not have a *C*-terminus amino acid compatible with cleavage by trypsin, and peptides which had more than one “genuine” missed trypsin cleavage site were filtered out, as described above; (2) peptides with low sequence quality (average local confidence score < 50%) were filtered out. The local confidence score is reported by the PEAKS Studio software, and indicates the likelihood of the correct sequence assignment at a specific residue within a peptide. For heatmap visualization of hydroxylysine assignments (Fig. S11) peptides were aligned so that the hydroxylysine residues were clustered around the centre of the display (i.e. position 0). To this end, the sum of the local confidence scores for hydroxylysine residues within a 6-residue sliding window along the peptide was calculated. The position of the sliding window (4th residue from the start of the window) giving the highest aggregated score was defined as the position 0 of the peptide.

DIA data

DIA data corresponding to the FLAG-JMJD6 interactome were processed using Spectronaut (v14; Biognosys). DIA data were searched against a spectral library that was created by combining DIA plus DDA search results (DpD search) of FLAG-JMJD6 pulldowns obtained with the Spectronaut Pulsar search engine. DpD data were searched against the human proteome (Canonical Uniprot; downloaded August 2019) with the following modifications considered: fixed, carbamidomethyl (C); variable, oxidation (M), acetyl (N-terminal protein) and a maximum of 5 variable modifications and 2 missed cleavages permitted. A 1% FDR filter was applied at the peptide and protein level to yield a spectral library containing 14,996 precursors in 1517 protein groups determined by Spectronaut protein inference. DIA data were subsequently searched against the DpD library using default Spectronaut analysis settings, with the following modifications; (1) exclusion of protein identities based on less than 2 peptides; (2) quantitation: median peptide and precursor quantity, MS2 level area counts; (3) data filtering: Q-value percentile (fraction 0.16); (4) run-wise imputing strategy; (5) cross-run normalisation: no filter, local normalisation strategy and automatic selection. Protein level quantitation data were exported from Spectronaut as a pivot report for statistical analysis in R.

Data processing for heatmap visualisation

The display of proteins interacting with FLAG-tagged transgenes encoding: wild-type JMJD6, a catalytically-inactive form, or empty vector control, which are represented in Figure 3B, comprises all proteins manifesting: (i) differential interaction with wild-type JMJD6 versus empty vector or enzyme-dead JMJD6 or (ii) differential interaction with wild-type JMJD6 in the presence or absence of DMOG, as identified using an empirical Bayes moderated *t*-statistic on log2 transformed protein abundance data with the limma package (3.44.1)[10]. The heatmap illustrates the Z-score of log2 transformed abundance data for each protein relative to all replicates and experimental conditions. Proteins were ordered according to the results of hierarchical clustering using Spearman's rank correlation for the calculation of distance and applied Ward's algorithm for clustering.

Analysis of sequence and biophysical features of proteins

Protein disorder was predicted using IUPred2A software[11] with default parameters. The local charge in a protein was calculated using the idpr package (1.2.0)[12] by considering the sequence from -5 to +5 residues. K-score was calculated as the maximum number of lysine residues in a 10-residue sliding window along a protein sequence. Stoichiometry was only calculated for sites with more than two assigned peptide features (Figure 4E; bubble plot).

Supplemental References

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Supplementary Data Legends

Table S1: Summary of hydroxylation assignments on BRD4(520-537) from analysis of large-scale proteomic datasets. Counts relating to the oxidation site assignment of singly- (Δ mass: +15.99) and doubly-oxidised (Δ mass: +31.99) forms of the tryptic BRD4(520-537) peptide in publicly deposited proteome datasets using PEAKS software. The numbers of assigned peptide spectra (FDR 1%) were counted using stringency filters for PTM assignment confidence (AScore: >0) and fragment ion intensity (>5%), applied separately and in combination. Most of the singly-oxidised peptides failed to pass the combined stringency filter. In contrast, secure assignments were seen on doubly-oxidised peptides with all such assignments (i.e., passing both Ascore and Ion Intensity filters) supporting hydroxylation of the lysyl (K535 and K537) residues.

Table S2: Summary of all hydroxylation assignments from this study. List of all hydroxylation sites defined in this study; sites are presented in alphabetical order referenced to gene name, Uniprot accession, site of modification and representative MSMS assignment (Figure S14). † Denotes non-unique peptide shared between proteins that were expressed at similar levels.

Table S3: Summary of hydroxylation site sequence context. Reference table detailing the sequence context of all assigned hydroxylation sites. Sites are presented in alphabetical order referenced to gene name, Uniprot accession and site of modification. Site context is defined as residues -5 to +5 of the targeted lysine residue, which is indicated in bold font. † Denotes hydroxylation assignment from non-unique tryptic peptide shared between indicated proteins that were expressed at similar levels.

Figure S1: Triple Knockout Mouse Embryonic Fibroblasts are defective for HIF hydroxylase activity. Validation of PHD1,2,3 defective (TKO) MEFs used in Fig 1A. Wild type and TKO MEFs were treated with proteasomal inhibitor (MG132, 12.5 µM for 4 hours) in the presence or absence of the hydroxylase inhibitor DMOG (1 mM for 24 h). Hydroxylated HIF1α was detected by immunoblot (anti-Hyp564) in lysates derived from proteasomally-blocked wild type but not TKO MEFs.

Figure S2: MSMS fragmentation spectra and ion tables for BRD4 peptides depicted in Figure 1A. HCD fragmentation spectra were acquired in the orbitrap of: **(a)** unoxidised; **(b)** singly-oxidised; **(c)** doubly-oxidised forms of the tryptic BRD4(521-538) peptide. Figure header indicates: peptide sequence ([O] site of hydroxylation) and MS-related information including peptide significance score (-10 lgP value) and MSMS scan number with raw data file reference, provided in parentheses. Ion tables give the theoretical mass of each fragment ion; assigned fragment ions (within the defined mass tolerance of 0.02 Da) are displayed in colour; b-ions in blue, y-ions in red.

Figure S3: MSMS fragmentation spectra and ion tables for BRD4 peptides depicted in Figure 1B. HCD fragmentation spectra acquired in linear ion trap of: **(a)** unoxidised; **(b)** singly-oxidised; **(c)** doubly-oxidised forms of the tryptic BRD4(520-537) peptide; [O] site of hydroxylation. Additional peptide information is provided for each MSMS, including peptide significance score (-10 lgP value) and MSMS scan number with raw data file reference. Ion tables give the theoretical mass of each fragment ion; assigned fragment ions (within the defined mass tolerance of 0.5 Da) are displayed in colour; b-ions in blue, y-ions in red.

Figure S4: Assignment of K535 and K537 hydroxylation by parallel reaction monitoring (PRM). **(A)** DDA-derived XIC depicting precursor ion (MS1) intensities of m/z 663.0288, m/z 668.3605, and m/z 673.6921 corresponding to unoxidised (yellow-green), singly-oxidised (orange), and doubly-oxidised (red) forms of BRD4(520-537) derived from SH-SY5Y cells by LC-MSMS. **(B)** High resolution MS2 spectra were continually acquired from isolated BRD4(520-537) precursor ions (upper panels, i-iii for different hydroxylated forms) using the PRM methodology. Chromatograms of fragment ions, including ions of discriminatory mass for lysine and proline oxidation (see inset for schematic representation of fragment ions: dotted line, no mass adduct; dashed line, single oxidation; solid line, double oxidation) were extracted at 5 ppm mass tolerance and presented below the indicated precursor ion. The presence of m/z 163.1077 (dashed red line; K[O]) and absence of m/z 147.1128 (dotted red line; K) in the MS2 XIC for the singly-oxidised peptide (middle panel, ii), reliably assign K537ox and exclude P536ox, at least to the limit of detection. For the doubly oxidised peptide, the only diagnostic fragment ions detected were: m/z 163.1077 (dashed red line; K[O]); m/z 260.1605 (dashed yellow-green line; imputed from y1 as: PK[O]) and; m/z 404.2503 (solid green line; K[O]PK[O]).

Figure S5: Hydroxylation of BRD2 and BRD3 by JMJD6 (A) Extracted ion chromatograms (XIC) show peptide ion intensities corresponding to unoxidised (green-yellow) and singly-oxidised (turquoise) forms of the tryptic BRD2(529-546) ($[M+3H]^{3+}$) peptide isolated from HeLa cells. Hydroxylated BRD2(529-546) peptide ions are absent from JMJD6-defective HeLa cell preparations (right panel). **(B)** Extracted ion chromatograms (XIC) show peptide ion intensities corresponding to unoxidised (green-yellow) and singly-oxidised (pink) forms of the tryptic BRD3(472-489) ($[M+3H]^{3+}$) peptide isolated from HeLa cells. Hydroxylated BRD3(472-489) peptide ions are absent from JMJD6-defective HeLa cell preparations.

Figure S6: Fragmentation spectra and ion tables for assignment of BRD4(523-541) peptides depicted in Figure 1C. Exemplar orbitrap HCD fragmentation spectra corresponding to the different oxidation [O] states of the Asp-N proteolyzed BRD4(523-541) in SH-SY5Y cells: **(a)** unmodified; **(b)** 1[O]; **(c)** 2[O]; **(d)** 3[O]; **(e)** 4[O]; **(f)** 5[O]. Additional peptide information is provided for each MSMS, including peptide significance score (-10 lgP value) and scan number (in raw data file). Ion tables are provided for each MSMS spectra depicting the theoretical mass of each fragment ion. Assigned fragment ions (matching within the defined mass tolerance of 0.02 Da) are displayed in colour; *N*-terminal b-ions are blue, *C*-terminal y-ions are red.

Figure S7: JMJD6-catalysed hydroxylation of BRD4 peptide substrate. (A) A 40-residue synthetic peptide (20 µM) corresponding to residues 511-550 of BRD4 was incubated with recombinant

JMJD6 (2 µM) in the presence (i) or absence (ii) of an inhibitor, 2,4-pyridine-dicarboxylic acid (2,4-PDCA, 100 µM). LC-MS spectra showing efficient hydroxylation of BRD4 peptide; 3 successive +16 m/z shifts were observed following 60 min incubation with JMJD6 and co-factors (100 µM L-ascorbic acid, 10 µM ferrous ammonium sulphate, 200 µM 2-oxoglutarate). **(B)** MSMS assignment of K547ox in (Aii). A mass identical to a hydroxylysine-containing fragment ion is observed in the JMJD6-reacted peptide ($[M+9H]^{9+}$ = m/z 524.30) at the y4 position that assigns hydroxylation to Lysine-547.

Figure S8: Comparison of quantitative assessments of hydroxylysine modification by orthogonal proteomic methods. Site specific stoichiometry of hydroxylysine as assessed by (i) non-derivatised (Asp-N mediated proteolysis) and (ii) derivatised (propionic anhydride and trypsin) workflows was similar. BRD4 protein was immunopurified from HeLa cells.

Figure S9: Comparison of JMJD6-dependent hydroxylation of BRD4 across multiple cell lines. BRD4 was purified from HEK293, MCF-7 and HeLa cell lines, prior to derivatisation, trypsinolysis and LC-MSMS analysis. Site specific stoichiometry of hydroxylation was similar across these cells, but not detected in JMJD6-defective HeLa cell preparations (lower panel).

Figure S10: Assignment of BRD4 poly-lysyl hydroxylation in FLAG-JMJD6 pulldown. Fragmentation spectra of BRD4(547-553) obtained following FLAG-JMJD6 pulldown, derivatization with propionic anhydride and digestion with trypsin; * derivatised lysine, [O] site of hydroxylation. Additional peptide information is provided, including: peptide significance score (-10 lgP value) and scan number (in raw data file). An Ion table is provided showing the theoretical mass of each fragment ion; note, +72.02 Da corresponds to the mass of oxidised propionylated lysine. Assigned fragment ions (matching within the defined mass tolerance of 0.02 Da) are displayed in colour; *N*-terminal b-ions are blue, *C*-terminal y-ions are red.

Figure S11: *De-novo* MSMS sequencing indicate poly-lysine hydroxylation is a JMJD6-dependent property. Heatmap visualisation of lysine hydroxylation assigned by *de novo* sequencing of derivatised tryptic peptides from wild-type (left panel) and JMJD6-defective (right panel) HeLa cells. Each row represents a single peptide; purple tone indicates the confidence of hydroxylysine assignment at the indicated position in the peptide. All other amino acid assignments are represented as white tiles, with transition to grey indicating the limits of the sequenced peptide. Peptides are aligned (x-axis) by the position of a 6-mer window giving the highest hydroxylysine score across the sequenced peptide so that hydroxylysines are clustered around the centre of the plot (i.e. position 0), and sorted (y-axis) by that score. Separate heatmaps give the results for peptides binned according to the maximum K-score of a 6-residue sliding window across the peptide. A much higher level of hydroxylysine is observed in wild-type cells in the bin representing the highest K-score (top left). In this bin, high hydroxylysine scores are observed at multiple positions, indicating multiple hydroxylations of adjacent lysine residues. Within this bin of lysine rich sequences, many (top, purple) but not all peptides (bottom, white) are multiply hydroxylated. In contrast, hydroxylysine is only modestly increased in JMJD6 wild-type cells in bins representing a K-score of 4/6 and not evident below this score.

Figure S12: Analysis of sequence features surrounding sites of JMJD6-catalysed hydroxylation. Heatmap depicts enrichment or depletion of amino acids residues (y-axis) at positions (x-axis) adjacent to JMJD6-catalysed hydroxylated lysine residues. All hydroxylysine sites defined in this study were analysed. Data are expressed as an odds ratio relative to all lysine residues in the total proteome identified in these experiments.

Figure S13: Site-specific comparison of hydroxylysine and methylarginine PTM stoichiometry on derivatised tryptic peptides derived from wild-type and JMJD6-defective HeLa cells. Points represent the difference in (delta) stoichiometry (WT minus JMJD6-defective (KO) cells) x100 for each specific site of post-translational modification assigned as hydroxylysine (Hyl), mono-methylarginine (mme-R) or di-methylarginine (dme-R) in JQ1 and JMJD6(81-96) peptide pulldown experiments. To improve the accuracy of the PTM assignments, database search results were filtered by (i) minimal significance score (-10lgP) of peptide >15; (ii) modification-specific fragment ion intensity > 1%; (iii) minimum of 2 independent MSMS assignments per cell line in each experiment; (iv) exclusion of hydroxylysine assignments that were likely confounded by artefactual oxidation (i.e., within 2 residues of a methionine or tryptophan residue). Note, JMJD6-dependent modifications would manifest as positive delta values for hydroxylation and negative delta values for demethylation at methylarginine sites. A clear positive bias is observed for Hyl, whereas no such negative bias is observed for mme-R or dme-R; apparently randomly scattered positive and negative values likely represent noise, in part due to stochastic sampling of low abundance peptides in DDA mode.

Figure S14: MSMS assignment of JMJD6-dependent hydroxylations. Fragmentation spectra corresponding to sites of JMJD6-dependent lysyl hydroxylation defined in this study. Spectra are from protein pulldowns enriched by affinity to either: (i) JQ1; (ii) FLAG-JMJD6; or (iii) JMJD6(81-96) peptide, and subject to derivatization with propionic anhydride and digestion with trypsin. Sites are presented in alphabetical order referenced to gene name and target site (see Table S2 for summary). Figure header indicates: site assignment, peptide sequence (*derivatised lysine, [O] site of hydroxylation) and MS-related information including peptide significance score (-10 lgP value) and MSMS scan number with raw data file reference, provided in parentheses. An Ion table is provided showing the theoretical mass of each fragment ion; note, +56.03 Da and +72.02 Da corresponds to the mass of propionylated lysine and oxidised propionylated lysine, respectively. Assigned fragment ions (matching within the defined mass tolerance of 0.02 Da) are displayed in colour; *N*-terminal b-ions are blue, *C*-terminal y-ions are red.

Table S1

		# Spectra filtered by confidence of modification site			
Peptide delta mass	Oxidation sites	No filter	A score	Ion Intensity	A score & Ion Intensity
0	Unmodified	66	n/a	n/a	n/a
+15.99	K535	9	8	1	1
	P536	26	2	4	0
	K537	17	11	0	0
+31.99	K535 / P536	13	0	5	0
	K535 / K537	20	19	13	13

Table S2

Gene	Uniprot	# Hyl Sites	Target residue(s)	MSMS assignment
AP3D1	O14617	3	739; 749; 752	Figure S14: 1-2
ARGLU1	Q9NWB6	5	13; 16; 19; 22; 23	Figure S14: 3
ARL6IP4	Q66PJ3	3	290; 292; 294	Figure S14: 4-5
ATRX	P46100	2	1422; 1424	Figure S14: 6-7
BRD2	P25440	4	546; 586; 589; 755	Figure S14: 8-11
BRD3	Q15059	6	364; 487; 489; 651; 683; 684	Figure S14: 12-17
BRD4	O60885	19	286; 289; 291; 332; 535; 537; 538; 539; 541; 544; 547; 548; 550; 552; 561; 562; 572; 575; 727	Figure S14: 18-29
BRIX1	Q8TDN6	1	17	Figure S14: 30
CHD3	Q12873	1	55	Figure S14: 31
CHD4	Q14839	1	67	Figure S14: 32
CTR9	Q6PD62	1	993	Figure S14: 33
DHX15	O43143	1	18	Figure S14: 34
DKC1	O60832	1	475	Figure S14: 35
FAM133B	Q5BKY9	4	90; 208; 209; 210	Figure S14: 36-37
FIP1L1	Q6UN15	4	564; 566; 567; 569	Figure S14: 38
FRG1†	Q14331	3	27; 29; 30	Figure S14: 39
GNL3	Q9BVP2	3	20; 23; 221	Figure S14: 40-41
HSPA8	P11142	1	248	Figure S14: 42
JMJD6	Q6NYC1	2	219; 307	Figure S14: 43-44
LARP7	Q4G0J3	1	360	Figure S14: 45
LMNA	P02545	1	341	Figure S14: 46
LUC7L	Q9NQ29	2	323; 325	Figure S14: 47
LUC7L2	Q9Y383	4	266; 269; 365; 368	Figure S14: 48-49
LUC7L3	O95232	8	248; 249; 251; 359; 362; 375; 388; 392	Figure S14: 50-55
MRPL39	Q9NYK5	1	322	Figure S14: 56
NKAP	Q8N5F7	9	198; 199; 200; 203; 247; 248; 250; 251; 252	Figure S14: 57; 4A
NSD3	Q9BZ95	1	199	Figure S14: 58
PHF6	Q8IWS0	1	173	Figure S14: 59
PHRF1	Q9P1Y6	4	1068; 1069; 1071; 1073	Figure S14: 60
PPIL4	Q8WUA2	1	458	Figure S14: 61
RBM39	Q14498	2	103; 119	Figure S14: 62-63
RFC1	P35251	1	38	Figure S14: 64
RIOK1	Q9BRS2	4	535; 539; 552; 555	Figure S14: 65-66
RPL335A	P18077	1	45	Figure S14: 67
RPS7	P62081	1	113	Figure S14: 68
RPS25	P62851	1	14	Figure S14: 69
SF3B2	Q13435	5	320; 331; 332; 334; 335	Figure S14: 70-71
SREK1	Q8WXA9	6	269; 397; 400; 414; 415; 418	Figure S14: 72-74
SREK1IP1	Q8N9Q2	2	139; 140	Figure S14: 75
SRPK1	Q96SB4	3	16; 18; 19	Figure S14: 76
SRRM2†	Q9UQ35	3	241; 243; 244	Figure S14: 39
SRSF11	Q05519	3	242; 314; 411	Figure S14: 77-79
SSRP1	Q08945	2	521; 524	Figure S14: 80-81
SUPT16H	Q9Y5B9	2	1043; 1044	Figure 4C
TCOF1	Q13428	7	1348; 1389; 1440; 1442; 1443; 1444; 1447	Figure S14: 82-84
TOP1	P11387	5	25; 36; 39; 40; 159	Figure S14: 85-88
TSR1	Q2NL82	1	42	Figure S14: 89
U2AF2	P26368	2	15; 70	Figure S14: 90-91
U2SURP	O15042	4	962; 972; 980; 981	Figure S14: 92-94

Table S3

Gene	Uniprot	Site	Site Context
AP3D1	O14617	739	RQKLEKDKRRK
		749	KKRKEKEKKGK
		752	KEKEKKGKRRH
ARGLU1	Q9NWB6	13	SSSRSKHTKSS
		16	RSKHTKSSKHN
		19	HTKSSKHNKKR
		22	SSKHNKKRSRS
		23	SKHNKKRSRSR
ARL6IP4	Q66PJ3	290	RKKRGKYKDKR
		292	KRGKYKDKRRK
		294	GKYKDKRRKKK
ATRX	P46100	1422	RSYKQKKKRRR
		1424	YKQKKKRRRIK
BRD2	P25440	546	PISKPKRKREK
		586	PPQPKKSKKAS
		589	PKKSKKASGSG
		755	TKKPPKKANEK
BRD3	Q15059	364	STVKRKMDGRE
		487	QAPVNKPKKKK
		489	PVNKPKKKKEK
		651	SASGKKQAAKS
		683	QLSSSKKPARK
		684	LSSSKKPARKE
BRD4	O60885	286	PVKTKKGVKRK
		289	TKKGVKRKADT
		291	KGVKRKADTTT
		332	PVKPPKKDVPD
		535	QPQQNKPKKKE
		537	QQNKPKKKEKD
		538	QNKPKKKEKDK
		539	NKPKKKEKDKK
		541	PKKKEKDKKEK
		544	KEKDKKEKKKE
		547	DKKEKKKEKHK
		548	KKEKKKEKHKR
		550	EKKKEKHKRKE
		552	KKEKHKRKEEV
		561	EVEENKKSKAK
		562	VEENKKSKAKE
		572	EPPPKKTKKNN
		575	PKKTKKNNSSN
		727	APKSKKKGHPG
BRIX1	Q8TDN6	17	FAVQAKKPKRN
CHD3	Q12873	55	RKRGPKKQKEN
CHD4	Q14839	67	DPKIPKSKRQK
CTR9	Q6PD62	993	KAEKKKAPKPE
DHX15	O43143	18	YPSGKKRAGTD
DKC1	O60832	475	KKKSKKDKKAK
FAM133B	Q5BKY9	90	ESSSKKRQRKK
		208	EVRAKKKKSSE
		209	VRAKKKKSSEE
		210	RAKKKKSSEER

Gene	Uniprot	Site	Site Context
FIP1L1	Q6UN15	564	SHRRHKHKKSK
		566	RRHKHKKSKRS
		567	RHKHKKSKRSK
		569	KHKKSKRSKEG
FRG1†	Q14331	27	KKKKSKDKKRK
		29	KKSKDKKRKRE
		30	KSKDKKRKREE
GNL3	Q9BVP2	20	CHKRYKIQKKV
		23	RYKIQKKVREH
		221	ITKRVKAKKNA
HSPA8	P11142	248	AEFKRKHKKDI
JMJD6	Q6NYC1	219	PRELIKVTRDE
		307	VRGRPKLSRKW
LARP7	Q4G0J3	360	TKRKHKKKHKE
LMNA	P02545	341	RLLAEKEREMA
LUC7L	Q9NQ29	323	RDRSAKYKFSR
		325	RSAKYKFSRER
LUC7L2	Q9Y383	266	SRSHSKNPKRS
		269	HSKNPKRSRSR
		365	RDRDRKDKKRS
		368	DRKDKKRSYES
LUC7L3	O95232	248	RDERLKKEKQE
		249	DERLKKEKQER
		251	RLKKEKQEREE
		359	KSRDRKSYKHR
		362	DRKSYKHRSKS
		375	REQDRKSKEKE
		388	GSDDKKSSVKS
		392	KKSSVKSGSRE
MRPL39	Q9NYK5	322	LERSRKMVTED
NKAP	Q8N5F7	198	SKKRRKKKSSK
		199	KKRRKKKSSKR
		200	KRRKKKSSKRK
		203	KKKSSKRKHKK
		247	KKHRSKKYKKK
		248	KHRSKKYKKKR
		250	RSKKYKKKRSK
		251	SKKYKKKRSKK
		252	KKYKKKRSKKS
NSD3	Q9BZ95	199	KEKRKKSNKHD
PHF6	Q8IWS0	173	RKTNFKGLSED
PHRF1	Q9P1Y6	1068	ERAKRKKAKDK
		1069	RAKRKKAKDKS
		1071	KRKKAKDKSRE
		1073	KKAKDKSREHR
PPIL4	Q8WUA2	458	YSNSHKSKYQT
RBM39	Q14498	103	PYSGPKFNSAI
		119	LPHSIKLSRRR
RFC1	P35251	38	TLKAKKGIKEI

Gene	Uniprot	Site	Site Context
RIOK1	Q9BRS2	535	DKKERKKMVKE
		539	RKKMVKEAQRE
		552	KNKIPKHVKKR
		555	IPKHVKKRKEK
RPL335A	P18077	45	EFYLGKRCAYV
RPS7	P62081	113	SRTKNKQKRPR
RPS25	P62851	14	KKDAGKSAKKD
SF3B2	Q13435	320	TVSVSKKEKNR
		331	KRRNRKKKKKP
		332	RRNRKKKKKPQ
		334	NRKKKKKPQRV
		335	RKKKKKPQRVR
SREK1	Q8WXA9	269	TREKIKEKERV
		397	SPRTSKTIKRK
		400	TSKTIKRKSSR
		414	PRSRNKKDKKR
		415	RSRNKKDKKRE
		418	NKKDKKREKER
SREK1IP1	Q8N9Q2	139	EKKKRKKEKHS
		140	KKKRKKEKHSS
SRPK1	Q96SB4	16	RKKRTKAKKDK
		18	KRTKAKKDKAQ
		19	RTKAKKDKAQR
SRRM2†	Q9UQ35	241	SKRKSKDKKRK
		243	RKSKDKKRKRS
		244	KSKDKKRKRSR
SRSF11	Q05519	242	IEPDKKEEKRR
		314	KTRDKKKEDKE
		411	KDRERKSESDK
SSRP1	Q08945	521	KRKQLKKAKMA
		524	QLKKAKMAKDR
SUPT16H	Q9Y5B9	1043	SSAPPKKKRK-
		1044	SAPPKKKRK--
TCOF1	Q13428	1348	ESRKRKLSGDQ
		1389	TTSKGKAKRDK
		1440	NPKSKKEKKKS
		1442	KSKKEKKKSDK
		1443	SKKEKKKSDKR
		1444	KKEKKKSDKRK
		1447	KKKSDKRKKDK
TOP1	P11387	25	DSHKHKDKHKD
		36	REHRHKEHKKE
		39	RHKEHKKEKDR
		40	HKEHKKEKDRE
		159	TEDTKKEKKRK
TSR1	Q2NL82	42	LKTLSKKVRKE
U2AF2	P26368	15	QLNENKQERDK
		70	LTRGAKEEHGG
U2SURP	O15042	962	SERSHKESSRS
		972	SRSSHKDSPRD
		980	PRDVSKKAKRS
		981	RDVSKKAKRSP

Figure S1

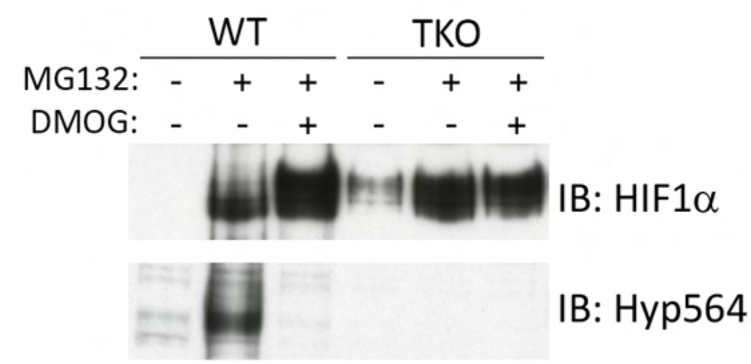
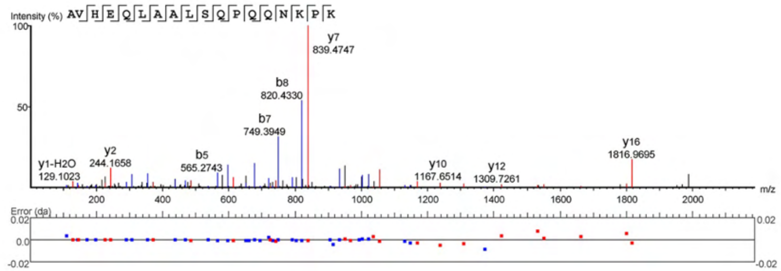


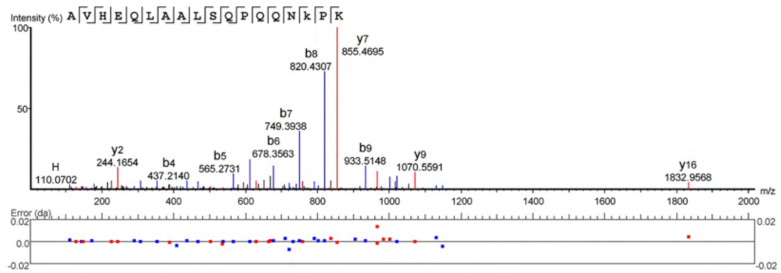
Figure S2

(A) BRD4(521-538): AVHEQLAALSQPQQNKPK; -10lgP=60.84; Scan 7844 (MC91)



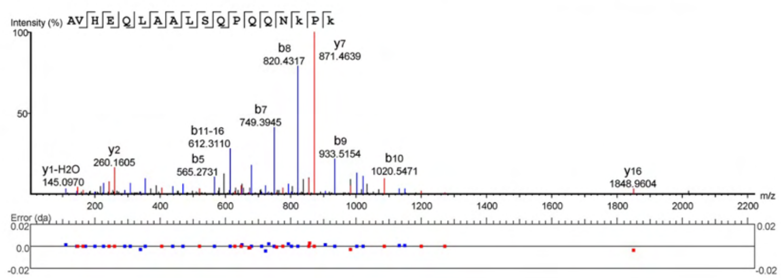
#	Immonium	b	b-H2O	a	b (2+)	Seq	y	y-H2O	y (2+)	#
1	44.0499	72.0449	54.0344	44.0499	36.5225	A				18
2	72.0812	171.1129	153.1028	143.1177	86.0567	V	1916.0348	1898.0243	958.5174	17
3	110.0676	308.1721	290.1613	280.1772	154.5861	H	1816.9695	1798.9496	908.9832	16
4	102.0554	437.2152	419.2043	409.2198	219.1074	E	1679.9075	1661.8938	840.4537	15
5	101.0714	565.2743	547.2629	537.2789	283.1367	Q	1550.8632	1532.8458	775.9324	14
6	86.0969	678.3580	660.3478	650.3636	339.6787	L	1422.8022	1404.7958	711.9031	13
7	44.0499	749.3949	731.3848	721.3969	375.1973	A	1309.7261	1291.7117	655.3611	12
8	44.0499	820.4330	802.4223	792.4372	410.7159	A	1238.6902	1220.6746	619.8425	11
9	86.0969	933.5153	915.5098	905.5204	467.2579	L	1167.6514	1149.6375	584.3240	10
10	60.0449	1020.5464	1002.5360	992.5529	510.7739	S	1054.5660	1036.5502	527.7820	9
11	101.0714	1148.6095	1130.5979	1120.6113	574.8032	Q	967.5331	949.5206	484.2660	8
12	70.0656	1245.6592	1227.6487	1217.6642	623.3296	P	839.4747	821.4628	420.2367	7
13	101.0714	1373.7263	1355.7072	1345.7227	687.3588	Q	742.4227	724.4098	371.7103	6
14	101.0714	1501.7762	1483.7657	1473.7812	751.3881	Q	614.3633	596.3514	307.6810	5
15	87.0558	1615.8192	1597.8087	1587.8242	808.4096	N	486.3044	468.2928	243.6517	4
16	101.1078	1743.9142	1725.9037	1715.9192	872.4571	K	372.2612	354.2499	186.6302	3
17	70.0656	1840.9669	1822.9564	1812.9719	920.9835	P	244.1658	226.1552	122.5828	2
18	101.1078					K	147.1127	129.1023	74.0564	1

(B) BRD4(521-538)AVHEQLAALSQPQQNK[O]PK; -10lgP=59.64; Scan 7620 (MC91)



#	Immonium	b	b-H2O	a	b (2+)	Seq	y	y-H2O	y (2+)	#
1	44.0499	72.0449	54.0344	44.0499	36.5225	A				18
2	72.0812	171.1125	153.1028	143.1177	86.0567	V	1932.0297	1914.0192	966.5009	17
3	110.0702	308.1717	290.1609	280.1772	154.5861	H	1832.9568	1814.9508	916.9807	16
4	102.0554	437.2140	419.2043	409.2241	219.1074	E	1695.9023	1677.8918	848.4512	15
5	101.0714	565.2731	547.2629	537.2784	283.1367	Q	1566.8597	1548.8492	783.9299	14
6	86.0969	678.3563	660.3469	650.3625	339.6787	L	1438.8011	1420.7906	719.9006	13
7	44.0499	749.3938	731.3837	721.4071	375.1973	A	1325.7172	1307.7067	663.3591	12
8	44.0499	820.4307	802.4204	792.4333	410.7159	A	1254.6801	1236.6696	627.8400	11
9	86.0969	933.5148	915.5052	905.5182	467.2579	L	1183.6429	1165.6324	592.3215	10
10	60.0449	1020.5482	1002.5347	992.5528	510.7739	S	1070.5591	1052.5483	535.7822	9
11	101.0714	1148.6107	1130.5918	1120.6113	574.8032	Q	983.5244	965.5179	492.2634	8
12	70.0656	1245.6592	1227.6487	1217.6642	623.3296	P	855.4695	837.4547	428.2341	7
13	101.0714	1373.7177	1355.7072	1345.7227	687.3588	Q	758.4158	740.4050	379.7078	6
14	101.0714	1501.7762	1483.7657	1473.7812	751.3881	Q	630.3575	612.3464	315.6785	5
15	87.0558	1615.8192	1597.8087	1587.8242	808.4096	N	502.2989	484.2878	251.6492	4
16	117.1027	1759.9091	1741.8986	1731.9141	880.4545	K(+15.99)	388.2566	370.2448	194.6277	3
17	70.0656	1856.9618	1838.9513	1828.9668	928.9809	P	244.1654	226.1551	122.5828	2
18	101.1078					K	147.1126	129.1018	74.0564	1

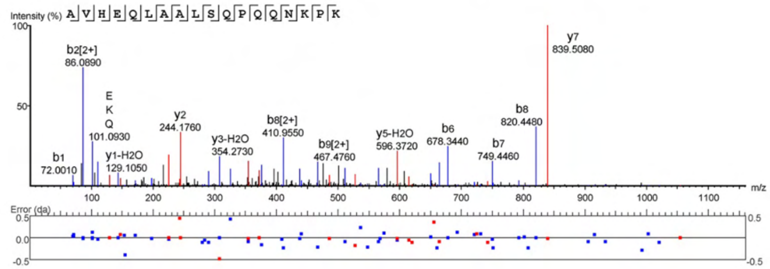
(C) BRD4(521-538)AVHEQLAALSQPQQNK[O]PK[O]; -10lgP=58.47; Scan 7381 (MC91)



#	Immonium	b	b-H2O	a	b (2+)	Seq	y	y-H2O	y (2+)	#
1	44.0499	72.0449	54.0344	44.0499	36.5225	A				18
2	72.0812	171.1129	153.1028	143.1177	86.0567	V	1948.0247	1930.0142	974.5123	17
3	110.0699	308.1717	290.1613	280.1772	154.5861	H	1848.9604	1830.9457	924.9781	16
4	102.0554	437.2146	419.2043	409.2198	219.1074	E	1711.8973	1693.8868	856.4456	15
5	101.0714	565.2731	547.2629	537.2784	283.1367	Q	1582.8547	1564.8442	791.9274	14
6	86.0969	678.3568	660.3469	650.3606	339.6821	L	1454.7961	1436.7856	727.8981	13
7	44.0499	749.3945	731.3812	721.4043	375.1973	A	1341.7120	1323.7015	671.3579	12
8	44.0499	820.4317	802.4205	792.4340	410.7159	A	1270.6748	1252.6644	635.8375	11
9	86.0969	933.5154	915.5052	905.5186	467.2579	L	1199.6379	1181.6273	600.3189	10
10	60.0449	1020.5471	1002.5377	992.5528	510.7739	S	1086.5542	1068.5433	543.7769	9
11	101.0714	1148.6052	1130.5945	1120.6113	574.8032	Q	999.5217	981.5145	500.2609	8
12	70.0656	1245.6592	1227.6487	1217.6642	623.3296	P	871.4639	853.4525	436.2316	7
13	101.0714	1373.7177	1355.7072	1345.7227	687.3588	Q	774.4100	756.4008	387.7052	6
14	101.0714	1501.7762	1483.7657	1473.7812	751.3881	Q	646.3522	628.3416	323.6759	5
15	87.0558	1615.8192	1597.8087	1587.8242	808.4096	N	518.2935	500.2827	259.6466	4
16	117.1027	1759.9091	1741.8986	1731.9141	880.4545	K(+15.99)	404.2503	386.2398	202.6252	3
17	70.0656	1856.9618	1838.9513	1828.9668	928.9809	P	260.1605	242.1499	130.5802	2
18	117.1027					K(+15.99)	163.1077	145.0970	82.0539	1

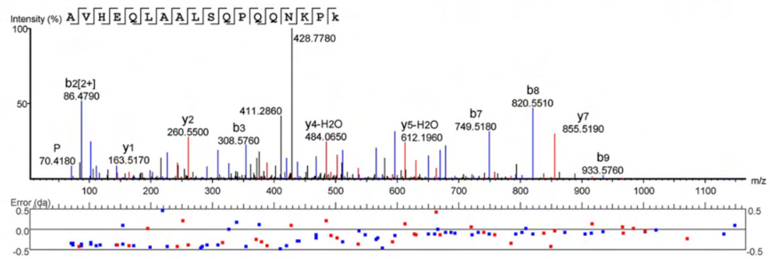
Figure S3

(A) BRD4(520-537)AVHEQLAALSQPQQNKPK; -10lgP=72.53; Scan 4653 (MC15)



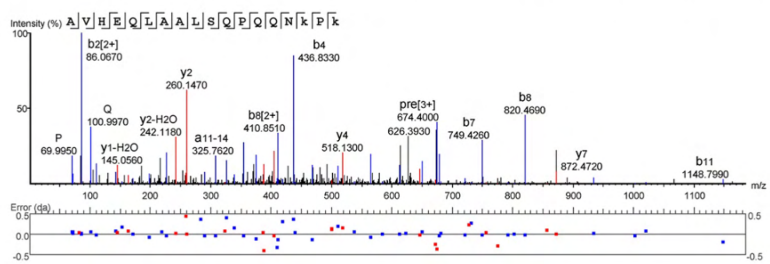
#	Immonium	b	b-H2O	a	b (2+)	Seq	y	y-H2O	y (2+)	#
1	44.0499	72.0010	54.0344	44.0499	36.5225	A				18
2	72.0010	171.0460	153.0430	143.1320	86.0890	V	1916.0348	1898.0243	958.5174	17
3	110.1100	308.1680	290.2800	280.2970	154.9950	H	1816.9663	1798.9558	908.9832	16
4	101.9190	437.2480	419.2043	409.2580	219.1074	E	1679.9075	1661.8970	840.4537	15
5	101.0930	565.3670	547.4870	537.0430	283.2030	Q	1550.8649	1532.8544	775.9324	14
6	86.0890	678.3440	660.5960	650.3300	339.6787	L	1422.8063	1404.7958	711.9031	13
7	44.0499	749.4460	731.2830	721.3250	375.3620	A	1309.7222	1291.7117	655.0030	12
8	44.0499	820.4480	802.3880	792.4440	410.9550	A	1238.6851	1220.6746	619.9520	11
9	86.0969	933.6070	915.4190	905.6110	467.4760	L	1167.6479	1149.6375	584.3240	10
10	60.0449	1020.6660	1002.4430	992.8500	510.8680	S	1054.5601	1036.5535	527.9780	9
11	101.0714	1148.6063	1130.5958	1120.6113	574.6890	Q	967.5319	949.5214	484.2660	8
12	70.0160	1245.6592	1227.6487	1217.6642	623.3296	P	839.5080	821.4628	420.2367	7
13	101.0714	1373.7177	1355.7072	1345.7227	687.3588	Q	742.5350	724.3090	371.7103	6
14	101.0714	1501.7762	1483.7657	1473.7812	751.6310	Q	614.4230	596.3720	308.1680	5
15	87.0558	1615.8192	1597.8087	1587.8242	808.6460	N	486.3300	468.2928	243.2000	4
16	101.0930	1743.9142	1725.9037	1715.9192	872.4571	K	372.2480	354.2730	186.6302	3
17	70.0656	1840.9669	1822.9564	1812.9719	920.9835	P	244.1760	226.1670	122.5828	2
18	101.1078					K	147.0250	129.1050	74.0564	1

(B) BRD4(520-537)AVHEQLAALSQPQQNKPK[O]; -10lgP=62.03; Scan 4581 (MC15)



#	Immonium	b	b-H2O	a	b (2+)	Seq	y	y-H2O	y (2+)	#
1	44.0499	72.4430	54.0344	44.0499	36.5225	A				18
2	72.4430	171.5200	153.4850	143.5170	86.4790	V	1932.0297	1914.0192	966.6290	17
3	110.4890	308.5760	290.5510	280.6430	154.4760	H	1832.9613	1814.9508	916.8350	16
4	102.0554	437.5110	419.6160	409.7040	218.6440	E	1695.9023	1677.8918	848.8810	15
5	101.4420	565.5360	547.4040	537.3280	283.5730	Q	1566.8597	1548.8492	784.2820	14
6	86.4790	678.4490	660.4770	650.4880	339.4990	L	1438.8011	1420.7906	719.8280	13
7	44.0499	749.5180	731.4690	721.5360	375.0740	A	1325.7172	1307.7067	662.9320	12
8	44.0499	820.5510	802.5020	792.5550	410.7159	A	1254.6801	1236.6696	627.9730	11
9	86.0969	933.5760	915.6070	905.6410	467.4760	L	1183.6429	1165.6324	592.6450	10
10	60.0449	1020.5710	1002.5950	992.5528	511.0830	S	1070.7980	1052.5483	536.1490	9
11	101.0714	1148.4969	1130.7200	1120.6113	575.2750	Q	983.5040	965.4450	492.4240	8
12	70.4180	1245.6592	1227.6487	1217.6642	623.3296	P	855.5190	837.5600	428.1330	7
13	101.0714	1373.7177	1355.7072	1345.7227	687.4470	Q	758.5540	740.4870	380.0200	6
14	101.0714	1501.7762	1483.7657	1473.7812	751.3881	Q	630.5060	612.1960	316.0060	5
15	87.0558	1615.8192	1597.8087	1587.8242	808.3820	N	502.5250	484.0650	251.4230	4
16	101.4420	1743.9142	1725.9037	1715.9192	872.5410	K	388.6740	370.4990	194.5900	3
17	70.0656	1840.9669	1822.9564	1812.9719	920.9835	P	260.5500	242.5790	130.5802	2
18	117.5040					K(+15.99)	163.5170	145.4960	82.4900	1

(C) BRD4(520-537)AVHEQLAALSQPQQNK[O]PK[O]; -10lgP=57.70; Scan 4745 (MC15)



#	Immonium	b	b-H2O	a	b (2+)	Seq	y	y-H2O	y (2+)	#
1	44.0499	72.0090	54.0344	44.0499	36.5225	A				18
2	72.0090	171.1240	152.9240	143.0250	86.0670	V	1948.0247	1930.0142	974.5123	17
3	110.0920	308.2180	290.2190	280.1772	154.5861	H	1848.9562	1830.9457	924.9781	16
4	102.0554	436.8330	418.8850	409.5470	219.0320	E	1711.8973	1693.8868	856.3380	15
5	100.9970	565.3550	547.2629	537.2180	282.7570	Q	1582.8547	1564.8442	791.9274	14
6	86.0670	678.4140	660.3469	650.3020	339.5070	L	1454.7961	1436.7856	727.6640	13
7	44.0499	749.4260	731.1060	721.4300	375.3130	A	1341.7120	1323.7015	671.6200	12
8	44.0499	820.4690	802.4330	792.4650	410.8510	A	1270.6749	1252.6644	635.8375	11
9	86.0969	933.4840	915.5052	905.5208	467.3970	L	1199.6378	1181.6273	600.3189	10
10	60.0449	1020.4660	1002.5860	992.5528	510.5700	S	1086.5538	1068.5433	543.7769	9
11	101.0714	1148.7990	1130.5958	1120.6113	574.8032	Q	999.5217	981.5112	500.1390	8
12	69.9950	1245.6592	1227.6487	1217.6642	623.3090	P	871.4680	853.4526	436.2316	7
13	101.0714	1373.7177	1355.7072	1345.7227	687.3588	Q	774.7100	756.3480	388.1160	6
14	101.0714	1501.7762	1483.7657	1473.7812	751.3881	Q	646.3900	628.3412	323.5900	5
15	87.0558	1615.8192	1597.8087	1587.8242	808.4096	N	518.1300	500.1390	259.1960	4
16	117.1027	1759.9091	1741.8986	1731.9141	880.4545	K(+15.99)	404.2900	386.1840	202.6252	3
17	70.0656	1856.9618	1838.9513	1828.9668	928.9809	P	260.1470	242.1180	130.5802	2
18	117.1027					K(+15.99)	163.0180	145.0560	82.0000	1

Figure S4

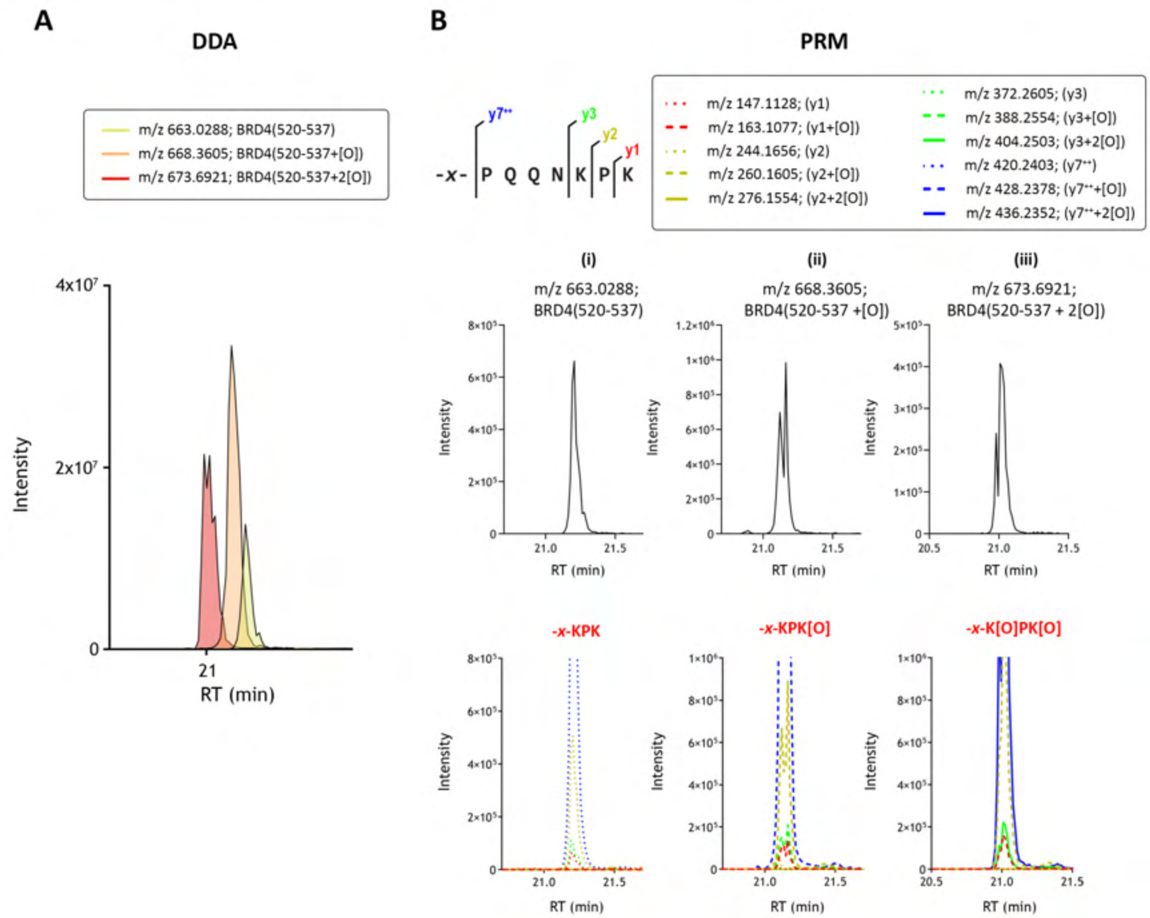

A
DDA
m/z 663.0288; BRD4(520-537)
m/z 668.3605; BRD4(520-537+[O])
m/z 673.6921; BRD4(520-537+2[O])
Intensity
RT (min)
B
PRM
-x- P Q Q N K P K
y7⁺⁺
y3
y2
y1
m/z 147.1128; (y1)
m/z 163.1077; (y1+[O])
m/z 244.1656; (y2)
m/z 260.1605; (y2+[O])
m/z 276.1554; (y2+2[O])
m/z 372.2605; (y3)
m/z 388.2554; (y3+[O])
m/z 404.2503; (y3+2[O])
m/z 420.2403; (y7⁺⁺)
m/z 428.2378; (y7⁺⁺+[O])
m/z 436.2352; (y7⁺⁺+2[O])
(i)
m/z 663.0288;
BRD4(520-537)
(ii)
m/z 668.3605;
BRD4(520-537 +[O])
(iii)
m/z 673.6921;
BRD4(520-537 + 2[O])
-x-KPK
-x-KPK[O]
-x-K[O]PK[O]
Intensity
RT (min)

Figure S5

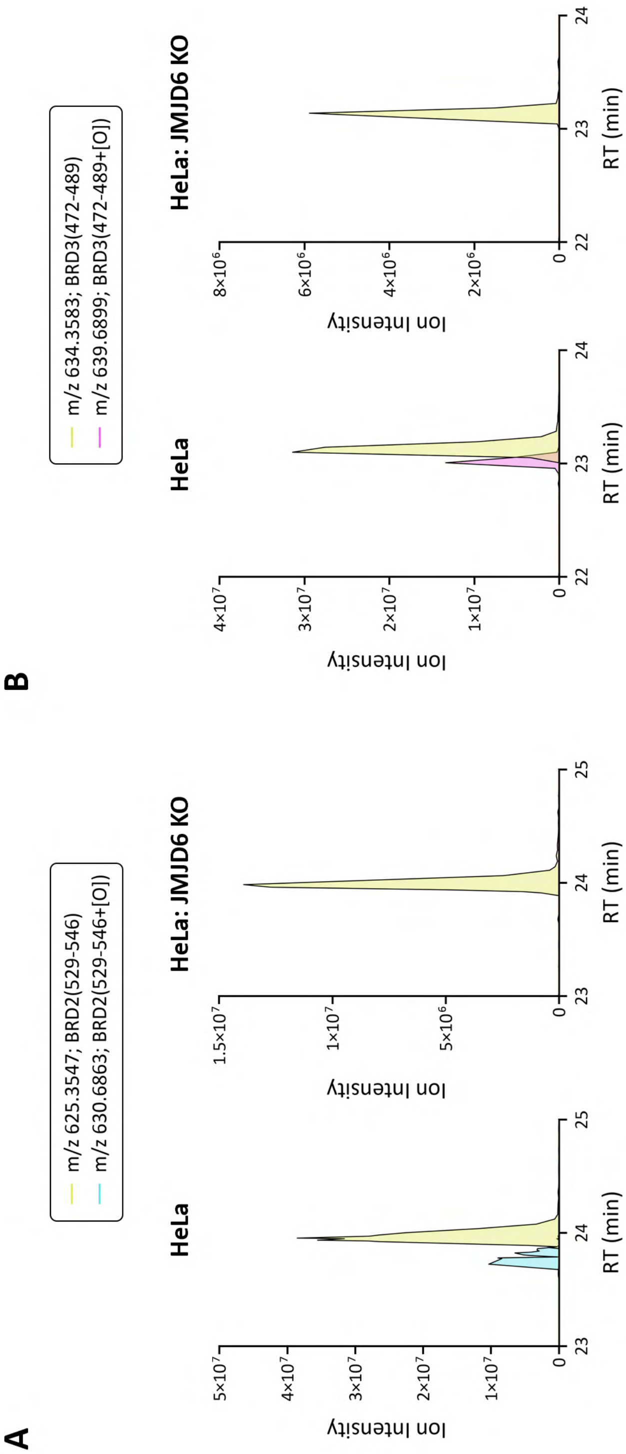
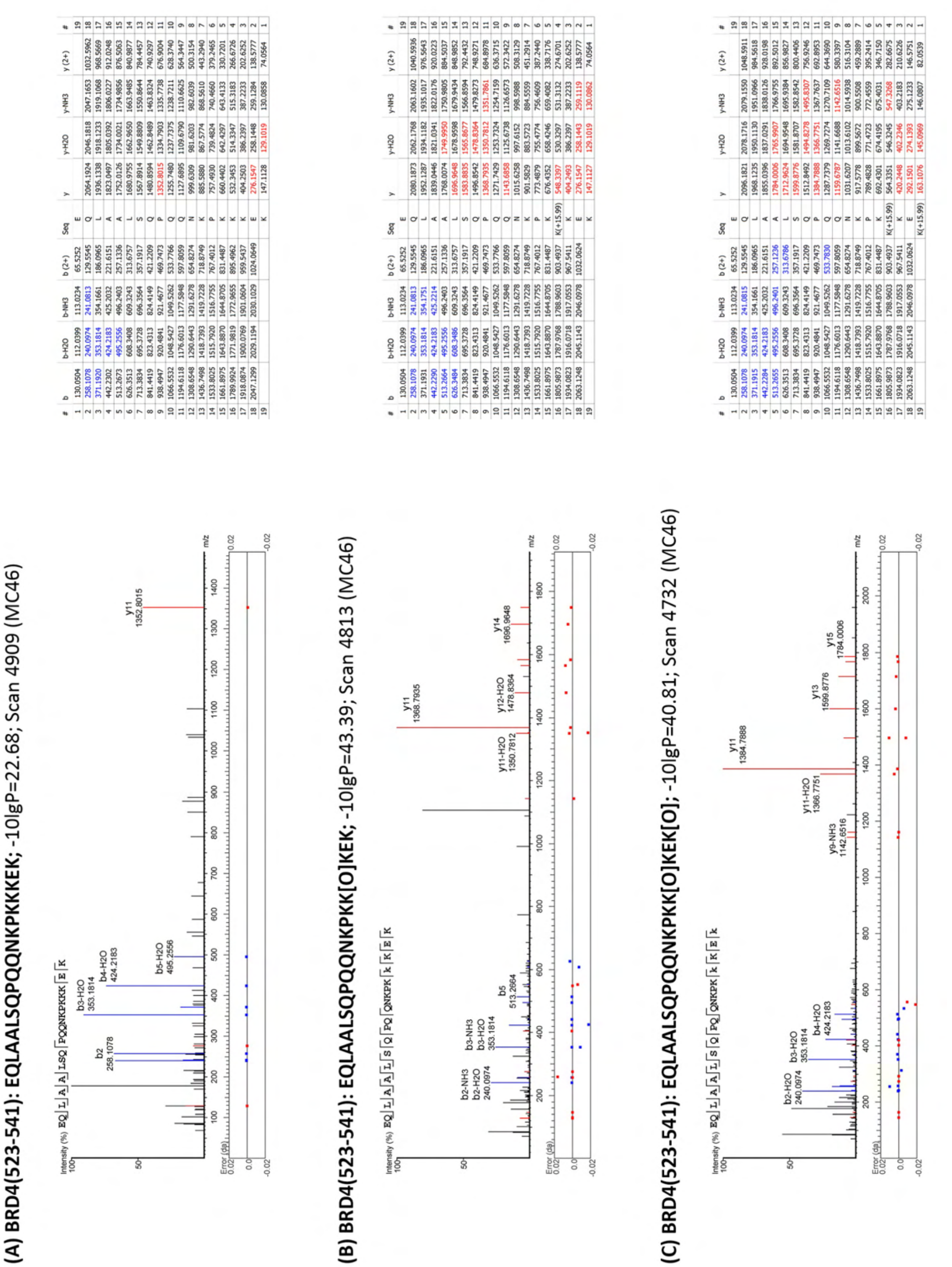

A
B
HeLa
HeLa: JMJD6 KO
m/z 625.3547; BRD2(529-546)
m/z 630.6863; BRD2(529-546+[O])
m/z 634.3583; BRD3(472-489)
m/z 639.6899; BRD3(472-489+[O])
Ion Intensity
RT (min)

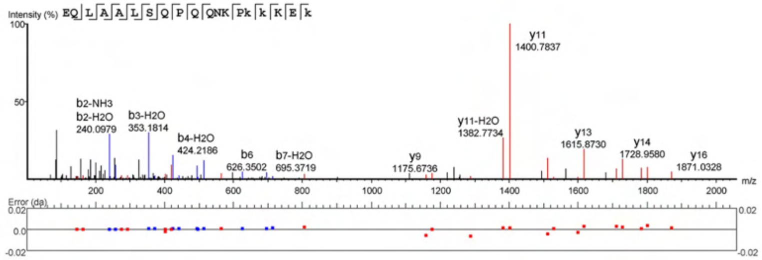
Figure S6(A-C)



(A) BRD4(523-541): EQLAALSQPQQNKPKKKEK; -10lgP=22.68; Scan 4909 (MC46)
(B) BRD4(523-541): EQLAALSQPQQNKPK[O]KEK; -10lgP=43.39; Scan 4813 (MC46)
(C) BRD4(523-541): EQLAALSQPQQNKPKK[O]KEK[O]; -10lgP=40.81; Scan 4732 (MC46)

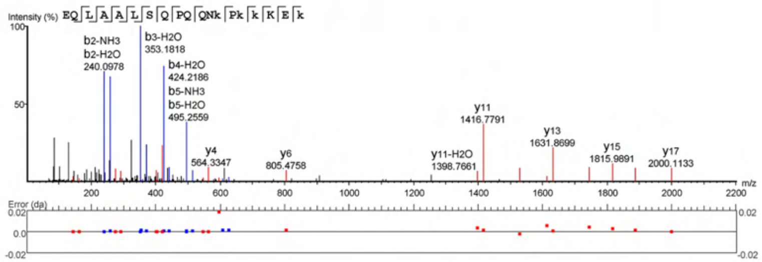
Figure S6(D-F)

(D) BRD4(523-541): EQLAALSQPQQNKPK[O]K[O]KEK[O]; -10lgP=44.69; Scan 4694 (MC46)



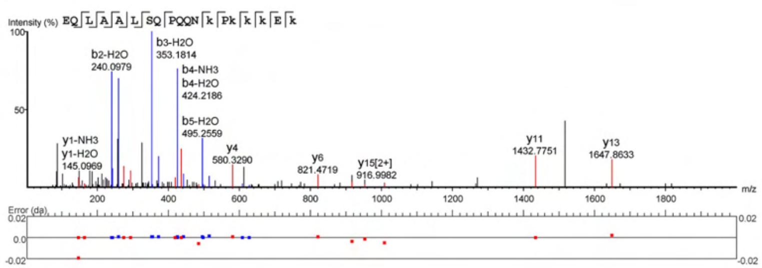
#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	130.0504	112.0399	113.0234	65.5252	E					19
2	258.1084	240.0979	241.0817	129.5545	Q	2112.1770	2094.1665	2095.1499	1056.5885	18
3	371.1920	353.1814	354.1661	186.0965	L	1984.1185	1966.1080	1967.0916	992.5593	17
4	442.2293	424.2186	425.2032	221.6151	A	1871.0328	1853.0239	1854.0074	936.0172	16
5	513.2660	495.2559	496.2397	257.1336	A	1799.9930	1781.9858	1782.9703	900.4987	15
6	626.3502	608.3408	609.3243	313.6757	L	1728.9580	1710.9463	1711.9332	864.9801	14
7	713.3815	695.3719	696.3564	357.1917	S	1615.8730	1597.8656	1598.8524	808.4380	13
8	841.4419	823.4313	824.4149	421.2209	Q	1528.8433	1510.8336	1511.8220	764.9221	12
9	938.4947	920.4841	921.4677	469.7473	P	1400.7837	1382.7734	1383.7585	700.8928	11
10	1066.5532	1048.5427	1049.5262	533.7766	Q	1303.7328	1285.7223	1286.7126	652.3664	10
11	1194.6118	1176.6013	1177.5848	597.8059	Q	1175.6736	1157.6637	1158.6533	588.3371	9
12	1308.6548	1290.6443	1291.6278	654.8274	N	1047.6156	1029.6051	1030.5886	524.3078	8
13	1436.7498	1418.7393	1419.7228	718.8749	K	933.5727	915.5621	916.5457	467.2863	7
14	1533.8025	1515.7920	1516.7755	767.4012	P	805.4750	787.4672	788.4507	403.2412	6
15	1677.8923	1659.8818	1660.8654	839.4462	K(+15.99)	708.4250	690.4144	691.3980	354.7125	5
16	1821.9822	1803.9717	1804.9552	911.4911	K(+15.99)	564.3342	546.3245	547.3081	282.6675	4
17	1950.0771	1932.0667	1933.0502	975.5386	K	420.2448	402.2343	403.2183	210.6226	3
18	2079.1199	2061.1094	2062.0928	1040.0599	E	292.1501	274.1393	275.1233	146.5751	2
19					K(+15.99)	163.1076	145.0969	146.0807	82.0539	1

(E) BRD4(523-541): EQLAALSQPQQNK[O]PK[O]K[O]KEK[O]; -10lgP=36.26; Scan 4572 (MC46)



#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	130.0504	112.0399	113.0234	65.5252	E					19
2	258.1081	240.0978	241.0817	129.5545	Q	2128.1719	2110.1614	2111.1448	1064.5859	18
3	371.1920	353.1818	354.1644	186.0965	L	2000.1133	1982.1029	1983.0864	1000.5567	17
4	442.2290	424.2186	425.2032	221.6151	A	1887.0276	1869.0188	1870.0023	944.0146	16
5	513.2660	495.2559	496.2409	257.1336	A	1815.9891	1797.9817	1798.9652	908.4961	15
6	626.3497	608.3391	609.3243	313.6757	L	1744.9502	1726.9446	1727.9281	872.9775	14
7	713.3834	695.3728	696.3564	357.1917	S	1631.8699	1613.8545	1614.8441	816.4355	13
8	841.4419	823.4313	824.4149	421.2209	Q	1544.8390	1526.8285	1527.8145	772.9195	12
9	938.4947	920.4841	921.4677	469.7473	P	1416.7791	1398.7661	1399.7535	708.8903	11
10	1066.5532	1048.5427	1049.5262	533.7766	Q	1319.7277	1301.7172	1302.7007	660.3638	10
11	1194.6118	1176.6013	1177.5848	597.8059	Q	1191.6692	1173.6587	1174.6422	596.3154	9
12	1308.6548	1290.6443	1291.6278	654.8274	N	1063.6106	1045.6001	1046.5836	532.3053	8
13	1452.7446	1434.7341	1435.7177	726.8723	K(+15.99)	949.5676	931.5571	932.5406	475.2838	7
14	1549.7974	1531.7869	1532.7704	775.3987	P	805.4758	787.4672	788.4507	403.2387	6
15	1693.8873	1675.8768	1676.8604	847.4437	K(+15.99)	708.4250	690.4144	691.3980	354.7125	5
16	1837.9772	1819.9667	1820.9502	919.4886	K(+15.99)	564.3347	546.3239	547.3081	282.6675	4
17	1966.0721	1948.0616	1949.0452	983.5361	K	420.2448	402.2346	403.2183	210.6226	3
18	2095.1147	2077.1042	2078.0876	1048.0574	E	292.1501	274.1393	275.1233	146.5751	2
19					K(+15.99)	163.1076	145.0969	146.0807	82.0539	1

(F) BRD4(523-541): EQLAALSQPQQNK[O]PK[O]K[O]K[O]EK[O]; -10lgP=28.72; Scan 4500 (MC46)



#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	130.0504	112.0399	113.0234	65.5252	E					19
2	258.1081	240.0979	241.0817	129.5545	Q	2144.1670	2126.1565	2127.1399	1072.5835	18
3	371.1920	353.1814	354.1649	186.0965	L	2016.1083	1998.0978	1999.0813	1008.5593	17
4	442.2290	424.2186	425.2038	221.6151	A	1903.0243	1885.0138	1885.9973	952.0142	16
5	513.2655	495.2559	496.2397	257.1336	A	1831.9872	1813.9767	1814.9602	916.4973	15
6	626.3507	608.3414	609.3243	313.6757	L	1760.9501	1742.9396	1743.9231	880.9750	14
7	713.3834	695.3728	696.3564	357.1917	S	1647.8633	1629.8555	1630.8390	824.4330	13
8	841.4419	823.4313	824.4149	421.2209	Q	1560.8340	1542.8235	1543.8070	780.9170	12
9	938.4947	920.4841	921.4677	469.7473	P	1432.7751	1414.7649	1415.7484	716.8877	11
10	1066.5532	1048.5427	1049.5262	533.7766	Q	1335.7227	1317.7122	1318.6957	668.3613	10
11	1194.6118	1176.6013	1177.5848	597.8059	Q	1207.6641	1189.6536	1190.6371	604.3320	9
12	1308.6548	1290.6443	1291.6278	654.8274	N	1079.6055	1061.5950	1062.5785	540.3027	8
13	1452.7446	1434.7341	1435.7177	726.8723	K(+15.99)	965.5626	947.5520	948.5356	483.2875	7
14	1549.7974	1531.7869	1532.7704	775.3987	P	821.4719	803.4621	804.4457	411.2363	6
15	1693.8873	1675.8768	1676.8604	847.4437	K(+15.99)	724.4199	706.4094	707.3929	362.7100	5
16	1837.9772	1819.9667	1820.9502	919.4886	K(+15.99)	580.3290	562.3195	563.3030	290.6650	4
17	1982.0670	1964.0565	1965.0400	991.5335	K(+15.99)	436.2396	418.2297	419.2132	218.6201	3
18	2111.1096	2093.0991	2094.0825	1056.0548	E	292.1501	274.1396	275.1233	146.5751	2
19					K(+15.99)	163.1076	145.0969	146.1002	82.0539	1

Figure S7

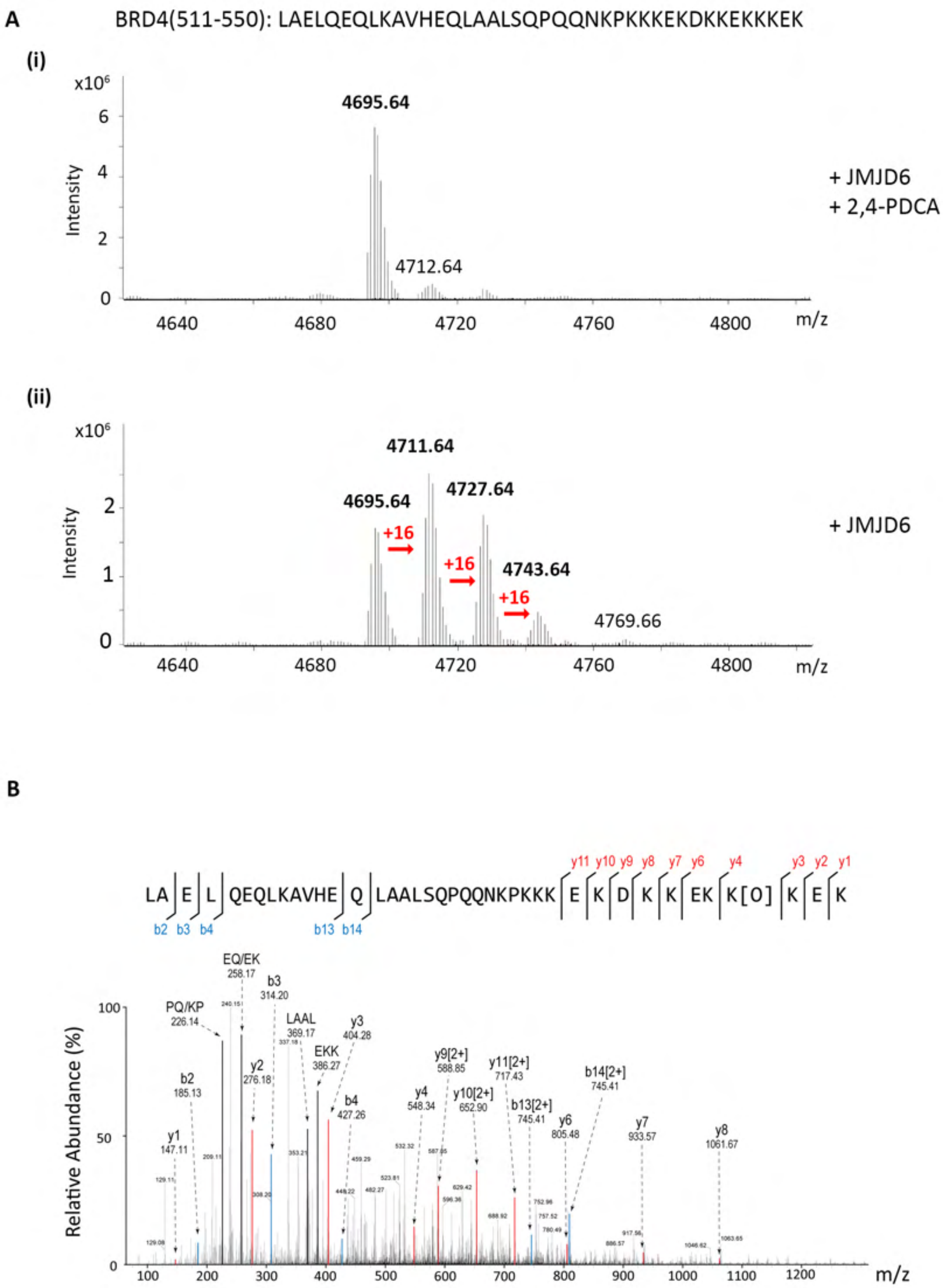

A
BRD4(511-550): LAELQEQLKAVHEQLAALSQPQQNKPKKKEKDKKEKKKEK
(i)
x10⁶
Intensity
4695.64
4712.64
+ JMJD6
+ 2,4-PDCA
m/z
(ii)
x10⁶
Intensity
4711.64
4695.64
4727.64
4743.64
4769.66
+16
+16
+16
+ JMJD6
m/z
B
LA E L QEQLKAVHE Q LAALSQPQQNKPKKK E K D K K EK K[O] K E K
y11 y10 y9 y8 y7 y6 y4 y3 y2 y1
b2 b3 b4 b13 b14
Relative Abundance (%)
m/z

Figure S8

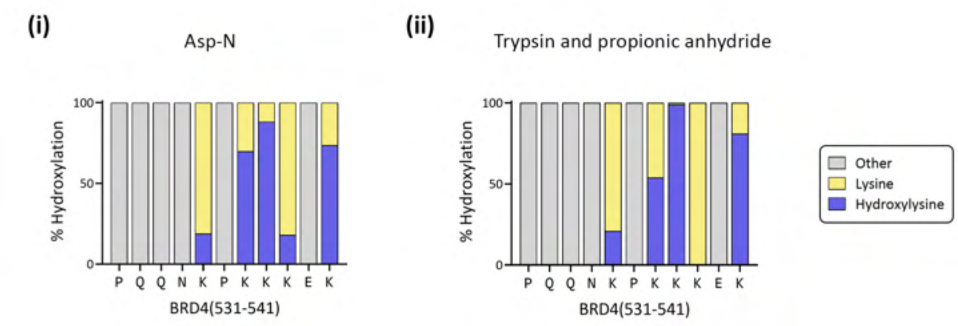

(i)
Asp-N
(ii)
Trypsin and propionic anhydride
% Hydroxylation
100
50
0
P Q Q N K P K K K E K
BRD4(531-541)
Other
Lysine
Hydroxylysine

Figure S9

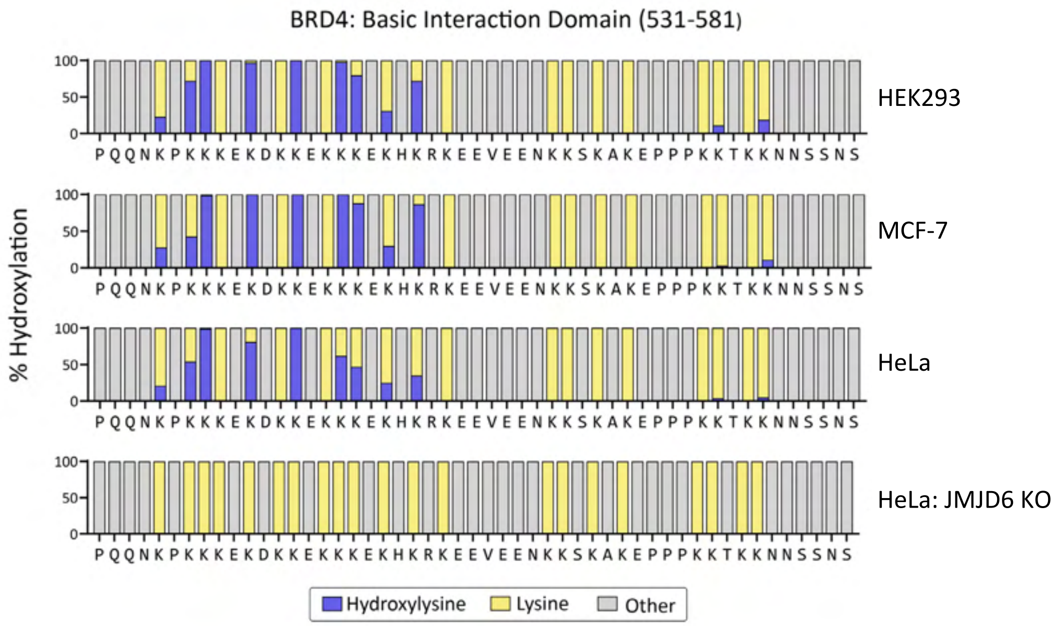
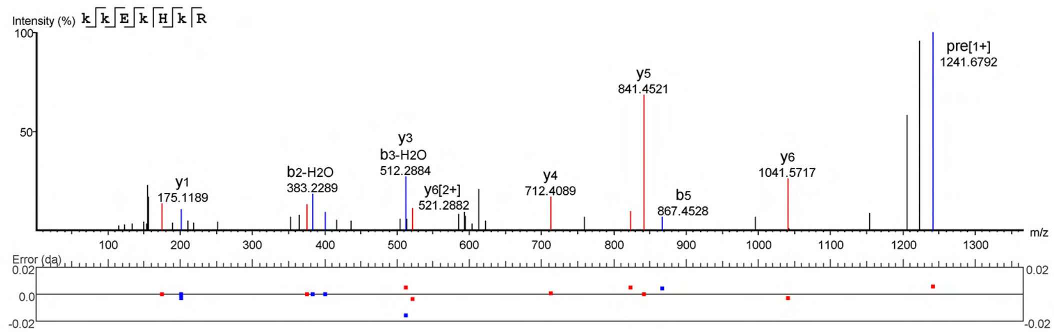

BRD4: Basic Interaction Domain (531-581)
% Hydroxylation
100
50
0
P Q Q N K P K K K E K D K K E K K K E K H K R K E E V E E N K K S K A K E P P P K K T K K N N S S N S
HEK293
MCF-7
HeLa
HeLa: JMJD6 KO
Hydroxylysine
Lysine
Other

Figure S10

BRD4(547-553): K*[O]K*[O]EK*[O]HK*[O]R; -10lgP=15.11; Scan 5469 (MC304)



#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	201.1232	183.1134	184.0969	101.0620	K(+72.02)					7
2	401.2399	383.2289	384.2130	201.1232	K(+72.02)	1041.5717	1023.5581	1024.5417	521.2882	6
3	530.2826	512.2884	513.2556	265.6413	E	841.4521	823.4368	824.4257	421.2263	5
4	730.3987	712.3881	713.3717	365.6993	K(+72.02)	712.4089	694.3995	695.3831	356.7050	4
5	867.4528	849.4470	850.4306	434.2288	H	512.2884	494.2834	495.2670	256.6470	3
6	1067.5737	1049.5632	1050.5468	534.2869	K(+72.02)	375.2346	357.2245	358.2080	188.1175	2
7					R	175.1189	157.1084	158.0919	88.0595	1

Figure S11

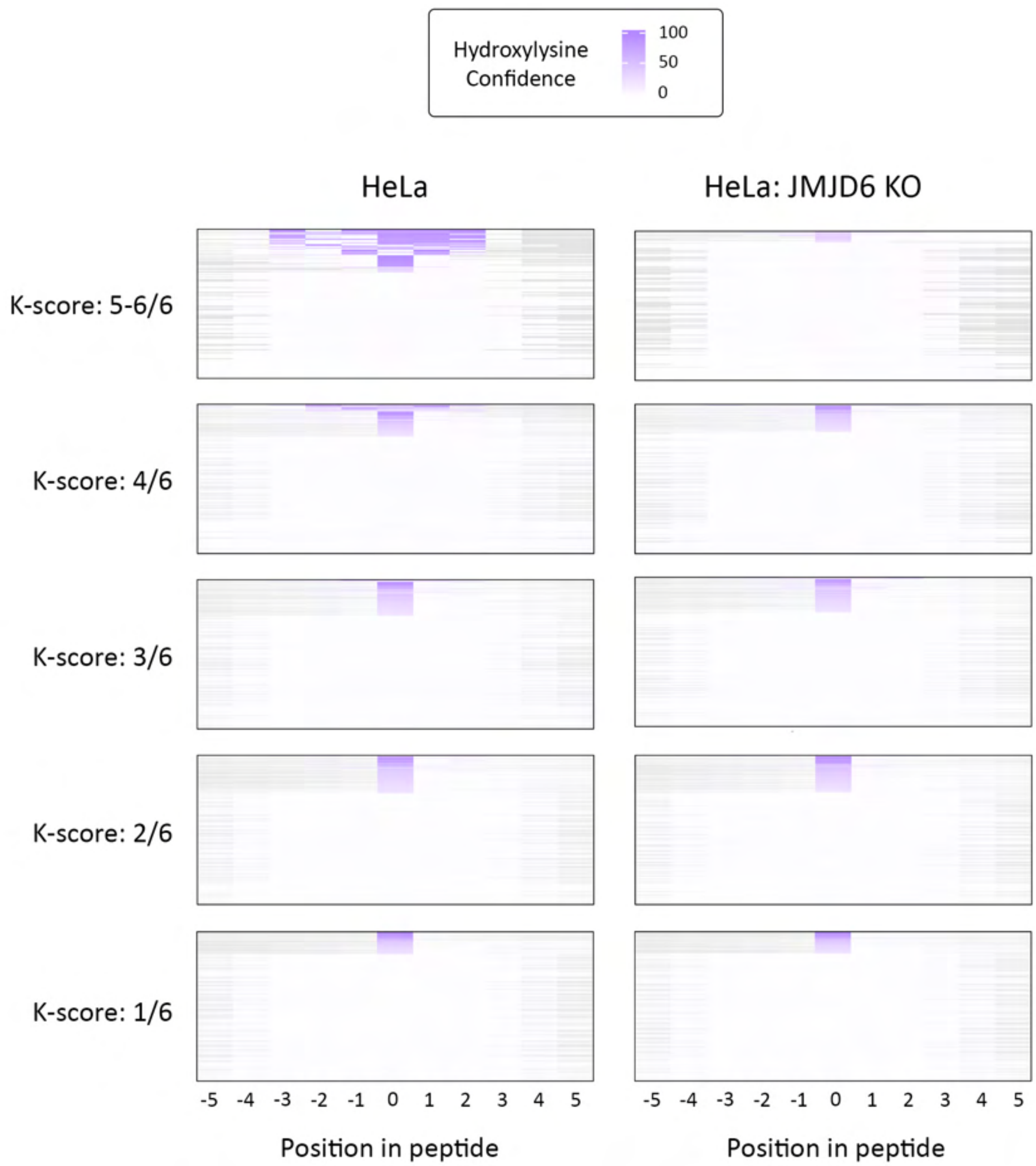

Hydroxylysine Confidence
100
50
0
HeLa
HeLa: JMJD6 KO
K-score: 5-6/6
K-score: 4/6
K-score: 3/6
K-score: 2/6
K-score: 1/6
-5 -4 -3 -2 -1 0 1 2 3 4 5
Position in peptide
-5 -4 -3 -2 -1 0 1 2 3 4 5
Position in peptide

Figure S12

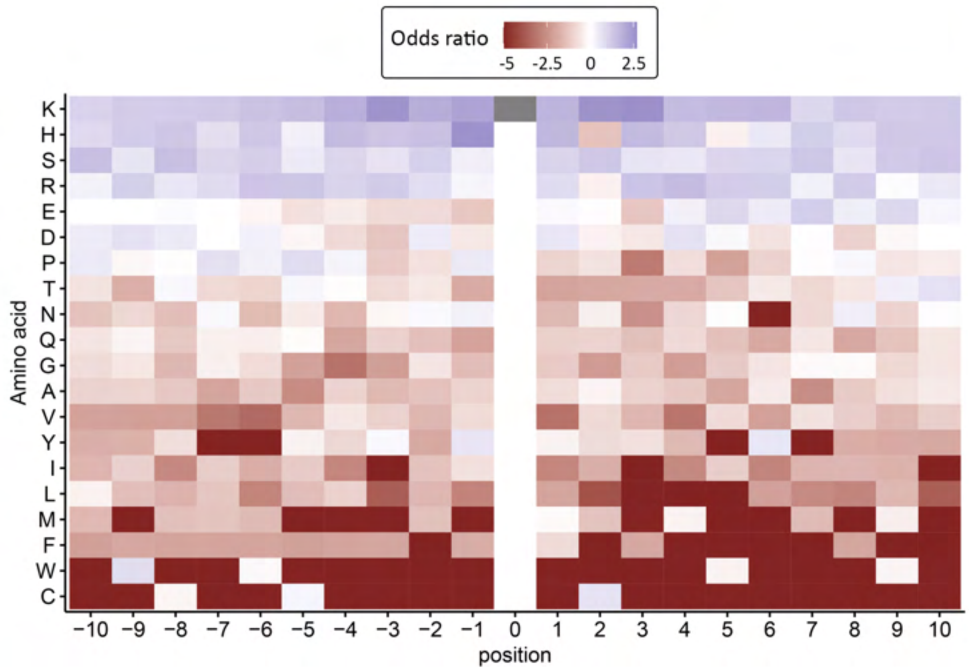

Odds ratio
-5
-2.5
0
2.5
Amino acid
K
H
S
R
E
D
P
T
N
Q
G
A
V
Y
I
L
M
F
W
C
−10 −9 −8 −7 −6 −5 −4 −3 −2 −1 0 1 2 3 4 5 6 7 8 9 10
position

Figure S13

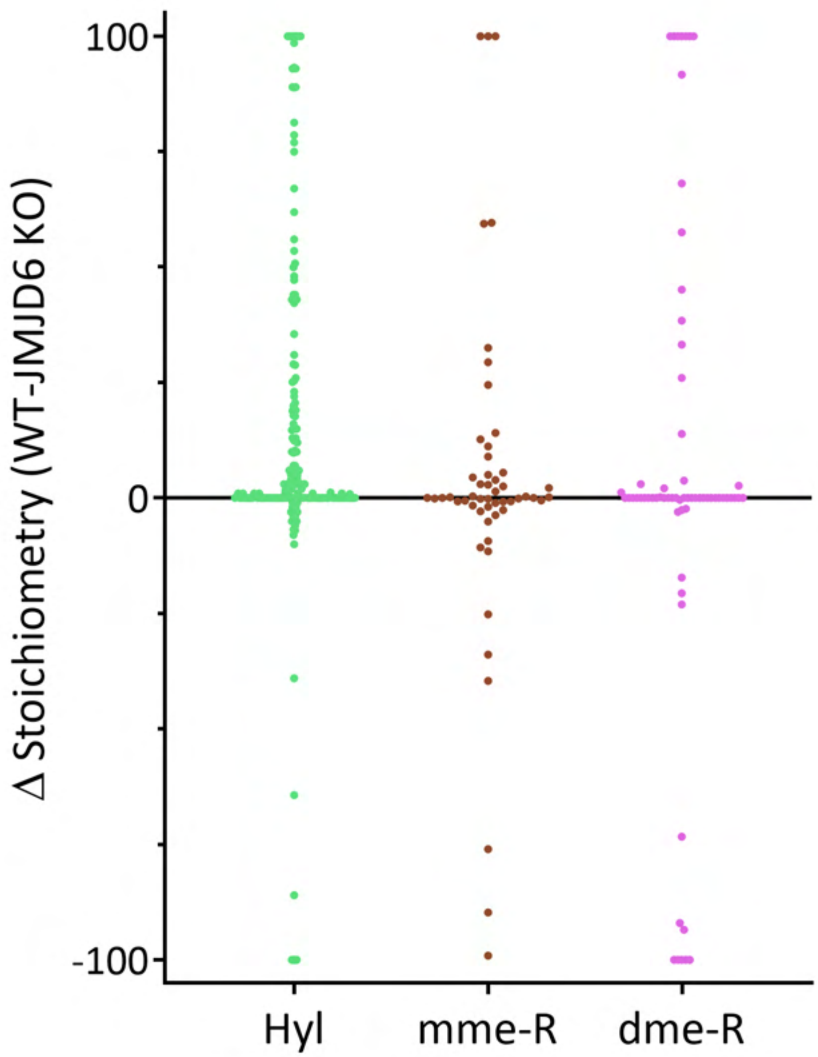
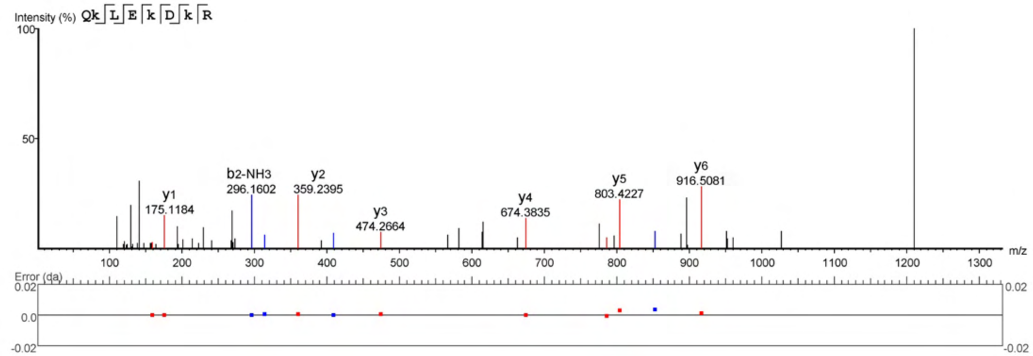


Figure S14_1

MSMS assignment of K739ox in AP-3 complex subunit delta-1

AP3D1(735-742): QK*LEK*[O]DK*R; -10lgP 26.50; Scan 10727 (MC303)

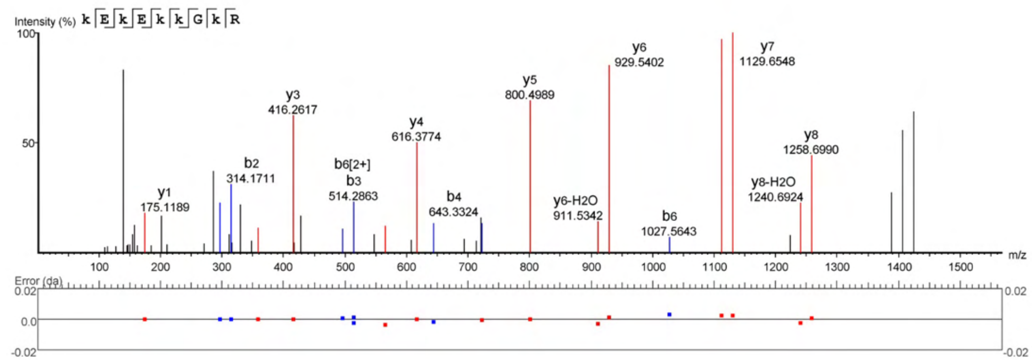


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	129.0664	111.0558	112.0394	65.0332	Q					8
2	313.1865	295.1770	296.1602	157.0938	K(+56.03)	1100.6310	1082.6205	1083.6040	550.8155	7
3	426.2716	408.2610	409.2445	213.6358	L	916.5081	898.4992	899.4828	458.7549	6
4	555.3142	537.3036	538.2872	278.1571	E	803.4227	785.4158	786.3987	402.2129	5
5	755.4303	737.4197	738.4033	378.2151	K(+72.02)	674.3835	656.3726	657.3561	337.6916	4
6	870.4572	852.4429	853.4302	435.7286	D	474.2664	456.2565	457.2401	237.6335	3
7	1054.5784	1036.5679	1037.5514	527.7892	K(+56.03)	359.2395	341.2296	342.2131	180.1201	2
8					R	175.1184	157.1084	158.0924	88.0595	1

Figure S14_2

MSMS assignment of K749ox, K752ox in AP-3 complex subunit delta-1

AP3D1(747-755): K*EK*[O]EK*K[O]GK*R; -10lgP 20.67; Scan 10022 (MC303)

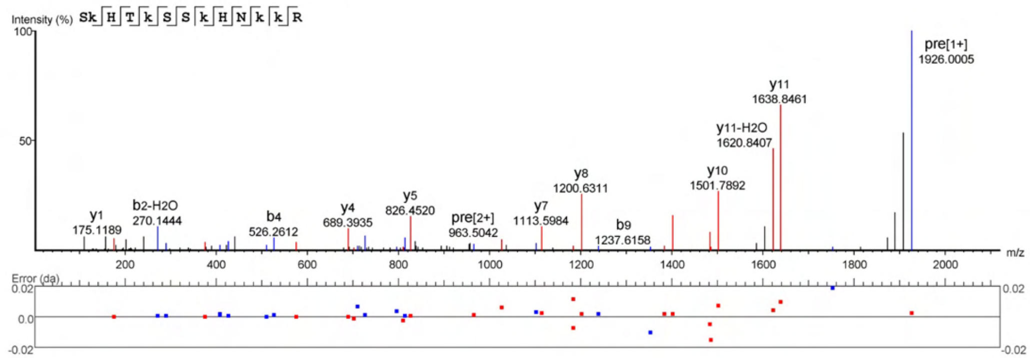


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	185.1290	167.1184	168.1020	93.0645	K(+56.03)					9
2	314.1711	296.1609	297.1446	157.5858	E	1258.6990	1240.6924	1241.6731	629.8500	8
3	514.2863	496.2761	497.2607	257.6438	K(+72.02)	1129.6548	1111.6444	1112.6305	565.3329	7
4	643.3324	625.3197	626.3033	322.1651	E	929.5402	911.5342	912.5144	465.2707	6
5	827.4514	809.4409	810.4244	414.2257	K(+56.03)	800.4989	782.4883	783.4719	400.7494	5
6	1027.5643	1009.5569	1010.5405	514.2863	K(+72.02)	616.3774	598.3671	599.3506	308.6888	4
7	1084.5890	1066.5785	1067.5620	542.7945	G	416.2617	398.2510	399.2346	208.6308	3
8	1268.7101	1250.6996	1251.6831	634.8550	K(+56.03)	359.2404	341.2296	342.2131	180.1201	2
9					R	175.1189	157.1084	158.0919	88.0595	1

Figure S14_3

MSMS assignment of K13ox, K16ox, K19ox, K22ox, K23ox in Arginine and glutamate-rich protein 1

ARGLU1(12-24): SK*[O]HTK*[O]SSK*[O]HNK*[O]K*[O]R; -10lgP 56.55; Scan 4848 (MC309)

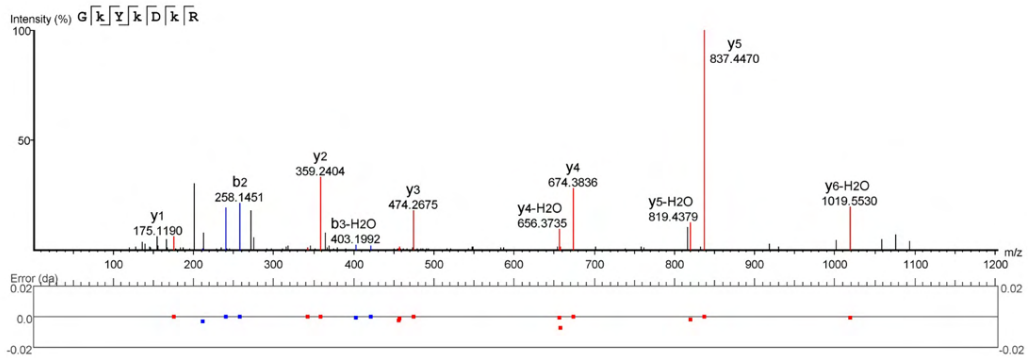


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	88.0399	70.0293	71.0129	44.5199	S					13
2	288.1550	270.1444	271.1290	144.5780	K(+72.02)	1838.9719	1820.9614	1821.9449	919.9860	12
3	425.2141	407.2029	408.1879	213.1074	H	1638.8461	1620.8407	1621.8289	819.9279	11
4	526.2612	508.2516	509.2355	263.6313	T	1501.7892	1483.7913	1484.7852	751.3984	10
5	726.3773	708.3613	709.3516	363.6893	K(+72.02)	1400.7468	1382.7368	1383.7222	700.8763	9
6	813.4095	795.3960	796.3837	407.2029	S	1200.6311	1182.6106	1183.6136	600.8165	8
7	900.4427	882.4321	883.4157	450.7213	S	1113.5984	1095.5906	1096.5741	557.3005	7
8	1100.5554	1082.5482	1083.5317	550.7794	K(+72.02)	1026.5625	1008.5585	1009.5421	513.7845	6
9	1237.6158	1219.6072	1220.5907	619.3088	H	826.4520	808.4424	809.4285	413.7265	5
10	1351.6713	1333.6501	1334.6337	676.3303	N	689.3935	671.3835	672.3671	345.1970	4
11	1551.7767	1533.7662	1534.7498	776.3884	K(+72.02)	575.3508	557.3405	558.3241	288.1755	3
12	1751.8737	1733.8823	1734.8658	876.4464	K(+72.02)	375.2349	357.2245	358.2080	188.1175	2
13					R	175.1189	157.1084	158.0919	88.0595	1

Figure S14_4

MSMS assignment of K290ox and K292ox in ADP-ribosylation factor-like protein 6-interacting protein 4

ARL6IP4(289-295): GK*[O]YK*[O]DK*R; 10lgP 27.45; Scan 6783 (MC319)

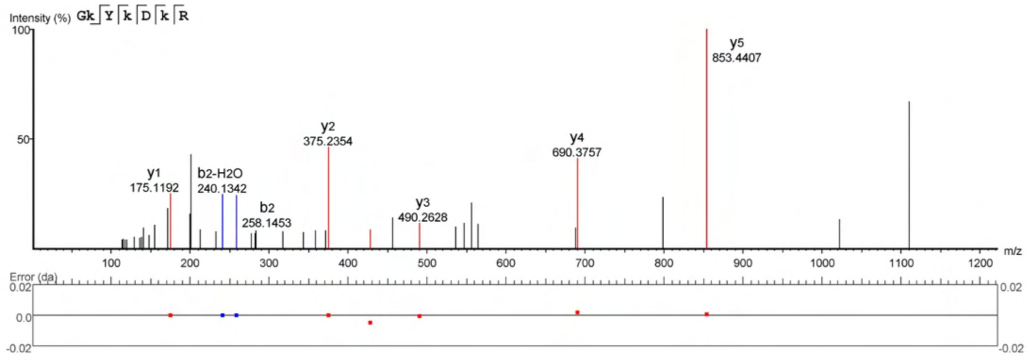


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	58.0293	40.0187	41.0023	29.5146	G					7
2	258.1451	240.1346	241.1184	129.5727	K(+72.02)	1037.5626	1019.5530	1020.5356	519.2813	6
3	421.2086	403.1992	404.1817	211.1075	Y	837.4470	819.4379	820.4195	419.2232	5
4	621.3248	603.3142	604.2978	311.1624	K(+72.02)	674.3836	656.3735	657.3640	337.6916	4
5	736.3517	718.3411	719.3247	368.6758	D	474.2675	456.2593	457.2413	237.6335	3
6	920.4729	902.4623	903.4459	460.7365	K(+56.03)	359.2404	341.2296	342.2131	180.1201	2
7					R	175.1190	157.1084	158.0919	88.0595	1

Figure S14_5

MSMS assignment of K294ox in ADP-ribosylation factor-like protein 6-interacting protein 4

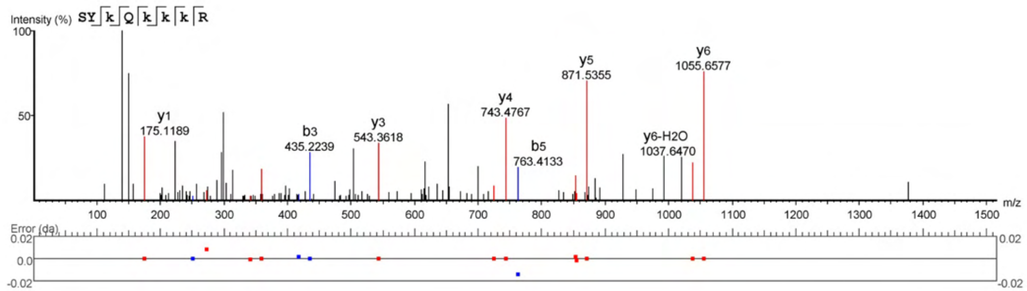
ARL6IP4(289-295): GK*[O]YK*[O]DK*[O]R; -10lgP 17.62; Scan 6784 (MC312)



#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	58.0293	40.0187	41.0023	29.5146	G					7
2	258.1453	240.1342	241.1184	129.5727	K(+72.02)	1053.5575	1035.5470	1036.5305	527.2787	6
3	421.2087	403.1981	404.1817	211.1043	Y	853.4407	835.4308	836.4144	427.2255	5
4	621.3248	603.3142	604.2978	311.1624	K(+72.02)	690.3757	672.3675	673.3511	345.6890	4
5	736.3517	718.3411	719.3247	368.6758	D	490.2628	472.2514	473.2350	245.6310	3
6	936.4678	918.4572	919.4408	468.7339	K(+72.02)	375.2354	357.2245	358.2080	188.1175	2
7					R	175.1192	157.1084	158.0919	88.0595	1

Figure S14_6

MSMS assignment of K1422ox in Transcriptional regulator ATRX
ATRX(1418-1425): SYK*QK*[O]K*K*R; -10lgP 20.23; Scan 17325 (MC356)

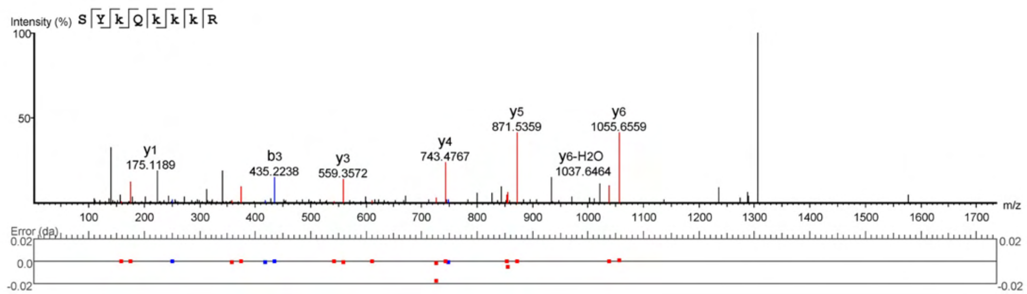


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	88.0399	70.0293	71.0129	44.5199	S					8
2	251.1031	233.0926	234.0762	126.0516	Y	1218.7205	1200.7100	1201.6935	609.8602	7
3	435.2239	417.2120	418.1974	218.1122	K(+56.03)	1055.6577	1037.6470	1038.6301	528.3286	6
4	563.2829	545.2723	546.2559	282.1414	Q	871.5355	853.5229	854.5114	436.2680	5
5	763.4133	745.3884	746.3720	382.1995	K(+72.02)	743.4767	725.4666	726.4504	372.2387	4
6	947.5201	929.5096	930.4932	474.2601	K(+56.03)	543.3618	525.3507	526.3343	272.1721	3
7	1131.6414	1113.6309	1114.6144	566.3207	K(+56.03)	359.2404	341.2296	342.2140	180.1201	2
8					R	175.1189	157.1084	158.0919	88.0595	1

Figure S14_7

MSMS assignment of K1424ox in Transcriptional regulator ATRX

ATRX(1418-1425): SYK*QK*K*K*[O]R; -10lgP 21.81; Scan 16964 (MC355)

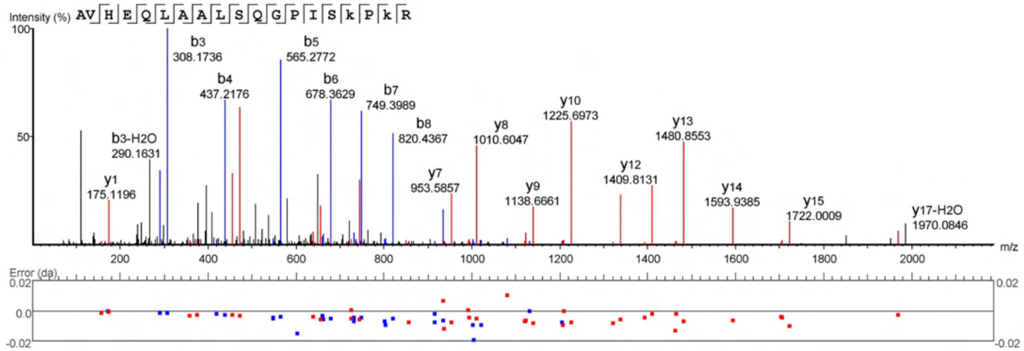


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	88.0399	70.0293	71.0129	44.5199	S					8
2	251.1025	233.0926	234.0762	126.0516	Y	1218.7205	1200.7100	1201.6935	609.8606	7
3	435.2238	417.2152	418.1974	218.1122	K(+56.03)	1055.6559	1037.6464	1038.6301	528.3286	6
4	563.2829	545.2723	546.2559	282.1414	Q	871.5359	853.5251	854.5140	436.2680	5
5	747.4056	729.3935	730.3771	374.2020	K(+56.03)	743.4767	725.4690	726.4680	372.2387	4
6	931.5253	913.5147	914.4983	466.2626	K(+56.03)	559.3572	541.3456	542.3292	280.1781	3
7	1131.6414	1113.6309	1114.6144	566.3207	K(+72.02)	375.2352	357.2257	358.2080	188.1175	2
8					R	175.1189	157.1084	158.0927	88.0595	1

Figure S14_8

MSMS assignment of K546ox in Bromodomain-containing protein 2

BRD2(529-547): AVHEQLAALSQGPISK*PK*[O]R; -10lgP 84.85; Scan 24877 (MC275)

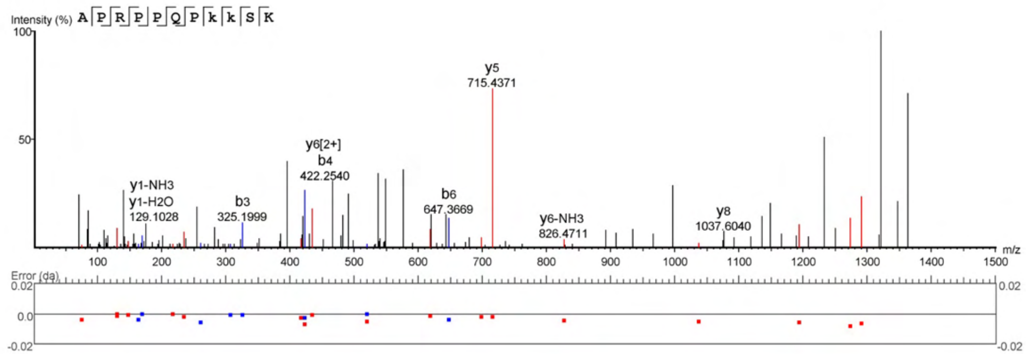


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	72.0449	54.0344	55.0179	36.5225	A					19
2	171.1134	153.1028	154.0863	86.0567	V	2087.1606	2069.1501	2070.1335	1044.0803	18
3	308.1736	290.1631	291.1453	154.5861	H	1988.0923	1970.0846	1971.0653	994.5461	17
4	437.2176	419.2066	420.1879	219.1074	E	1851.0333	1833.0228	1834.0063	926.0167	16
5	565.2772	547.2675	548.2519	283.1367	Q	1722.0009	1703.9841	1704.9686	861.4954	15
6	678.3629	660.3503	661.3364	339.6787	L	1593.9385	1575.9218	1576.9053	797.4661	14
7	749.3989	731.3885	732.3748	375.1973	A	1480.8553	1462.8506	1463.8235	740.9241	13
8	820.4367	802.4283	803.4141	410.7159	A	1409.8131	1391.8005	1392.7886	705.4055	12
9	933.5220	915.5074	916.4963	467.2579	L	1338.7798	1320.7634	1321.7551	669.8870	11
10	1020.5575	1002.5466	1003.5403	510.7739	S	1225.6973	1207.6890	1208.6630	613.3449	10
11	1148.6063	1130.5953	1131.5793	574.8032	Q	1138.6661	1120.6547	1121.6375	569.8289	9
12	1205.6356	1187.6173	1188.6008	603.3288	G	1010.6047	992.5878	993.5769	505.7996	8
13	1302.6805	1284.6700	1285.6536	651.8403	P	953.5857	935.5600	936.5630	477.2889	7
14	1415.7646	1397.7542	1398.7377	708.3823	I	856.5325	838.5145	839.4980	428.7625	6
15	1502.7966	1484.7861	1485.7697	751.8983	S	743.4465	725.4292	726.4191	372.2205	5
16	1686.9178	1668.9073	1669.8909	843.9589	K(+56.03)	656.4146	638.3984	639.3858	328.7045	4
17	1783.9706	1765.9601	1766.9436	892.4853	P	472.2911	454.2772	455.2638	236.6439	3
18	1984.0867	1966.0762	1967.0597	992.5433	K(+72.02)	375.2378	357.2245	358.2117	188.1175	2
19					R	175.1196	157.1084	158.0932	88.0595	1

Figure S14_9

MSMS assignment of K586ox in Bromodomain-containing protein 2

BRD2(578-588): APRPPQPK*K*[O]SK; -10lgP 53.56; Scan 3410 (MC277)

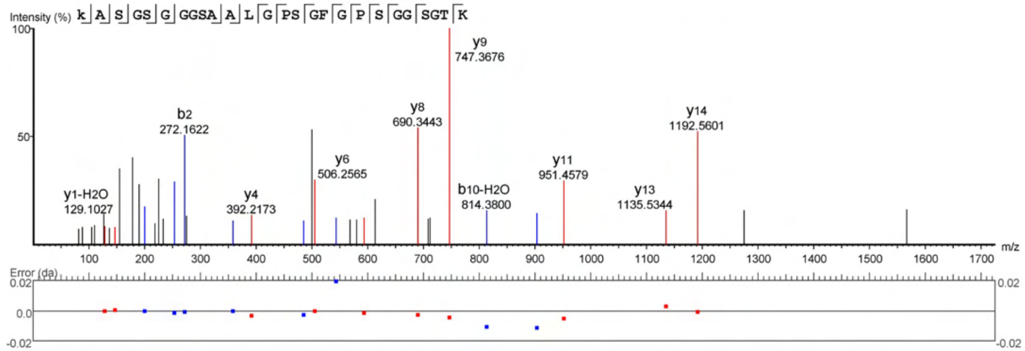


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	72.0449	54.0344	55.0179	36.5225	A					11
2	169.0978	151.0871	152.0707	85.0489	P	1290.7594	1272.7423	1273.7344	645.8764	10
3	325.1999	307.1892	308.1718	163.1037	R	1193.7058	1175.6896	1176.6731	597.3500	9
4	422.2540	404.2410	405.2245	211.6258	P	1037.6040	1019.5884	1020.5720	519.3046	8
5	519.3046	501.2938	502.2773	260.1579	P	940.5461	922.5356	923.5192	470.7731	7
6	647.3669	629.3523	630.3359	324.1814	Q	843.4934	825.4828	826.4711	422.2540	6
7	744.4156	726.4051	727.3887	372.7078	P	715.4371	697.4265	698.4078	358.2174	5
8	928.5368	910.5262	911.5098	464.7684	K(+56.03)	618.3834	600.3715	601.3551	309.6910	4
9	1128.6528	1110.6423	1111.6259	564.8264	K(+72.02)	434.2621	416.2531	417.2339	217.6304	3
10	1215.6849	1197.6744	1198.6580	608.3425	S	234.1470	216.1347	217.1178	117.5724	2
11					K	147.1137	129.1028	130.0871	74.0602	1

Figure S14_10

MSMS assignment of K589ox in Bromodomain-containing protein 2

BRD2(589-614): K*[O]ASGSGGGSAALGPSGFGPSGGSGTK; -10lgP 57.22; Scan 14997 (MC271)

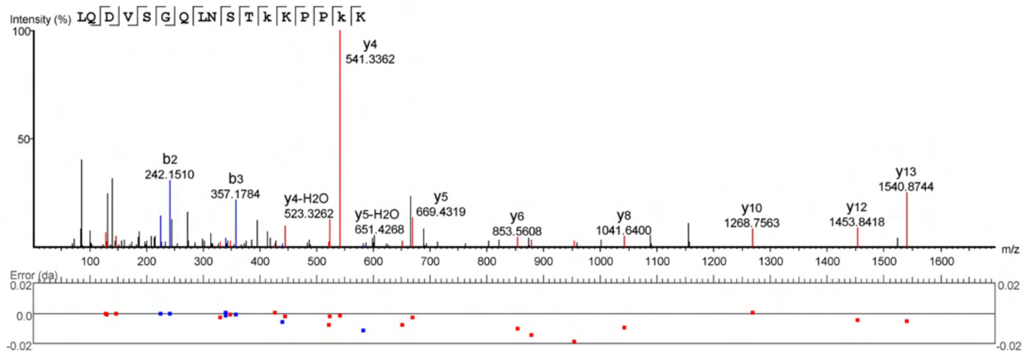


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	201.1243	183.1134	184.0969	101.0620	K(+72.02)					26
2	272.1622	254.1519	255.1340	136.5805	A	2007.9365	1989.9260	1990.9095	1004.4683	25
3	359.1927	341.1825	342.1661	180.0965	S	1936.8994	1918.8889	1919.8724	968.9497	24
4	416.2145	398.2039	399.1875	208.6073	G	1849.8674	1831.8569	1832.8405	925.4337	23
5	503.2465	485.2386	486.2195	252.1233	S	1792.8459	1774.8354	1775.8190	896.9230	22
6	560.2680	542.2574	543.2211	280.6340	G	1705.8140	1687.8035	1688.7870	853.4070	21
7	617.2894	599.2789	600.2625	309.1447	G	1648.7925	1630.7820	1631.7655	824.8962	20
8	674.3109	656.3004	657.2839	337.6555	G	1591.7710	1573.7605	1574.7440	796.3855	19
9	761.3430	743.3324	744.3160	381.1715	S	1534.7495	1516.7390	1517.7225	767.8748	18
10	832.3801	814.3800	815.3531	416.6900	A	1447.7175	1429.7070	1430.6906	724.3588	17
11	903.4285	885.4066	886.3902	452.2086	A	1376.6804	1358.6699	1359.6534	688.8402	16
12	1016.5012	998.4907	999.4742	508.7506	L	1305.6433	1287.6328	1288.6163	653.3217	15
13	1073.5227	1055.5122	1056.4957	537.2614	G	1192.5601	1174.5487	1175.5322	596.7796	14
14	1170.5754	1152.5649	1153.5485	585.7877	P	1135.5344	1117.5272	1118.5107	568.2689	13
15	1257.6074	1239.5969	1240.5804	629.3037	S	1038.4850	1020.4744	1021.4580	519.7425	12
16	1314.6289	1296.6184	1297.6019	657.8145	G	951.4579	933.4424	934.4260	476.2265	11
17	1461.6974	1443.6869	1444.6704	731.3487	F	894.4315	876.4210	877.4045	447.7158	10
18	1518.7188	1500.7083	1501.6918	759.8594	G	747.3676	729.3525	730.3361	374.1815	9
19	1615.7716	1597.7611	1598.7446	808.3858	P	690.3443	672.3311	673.3147	345.6708	8
20	1702.8036	1684.7931	1685.7766	851.9018	S	593.2904	575.2783	576.2619	297.1444	7
21	1759.8251	1741.8146	1742.7981	880.4125	G	506.2565	488.2463	489.2299	253.6284	6
22	1816.8466	1798.8361	1799.8196	908.9233	G	449.2354	431.2249	432.2084	225.1177	5
23	1903.8785	1885.8680	1886.8516	952.4393	S	392.2173	374.2034	375.1870	196.6070	4
24	1960.9000	1942.8895	1943.8730	980.9500	G	305.1819	287.1714	288.1549	153.0910	3
25	2061.9478	2043.9373	2044.9208	1031.4739	T	248.1605	230.1499	231.1335	124.5802	2
26					K	147.1121	129.1027	130.0858	74.0564	1

Figure S14_11

MSMS assignment of K755ox in Bromodomain-containing protein 2

BRD2(740-756): LQDVSGQLNSTK*KPPK*[O]K; -10lgP 52.01; Scan 12987 (MC271)

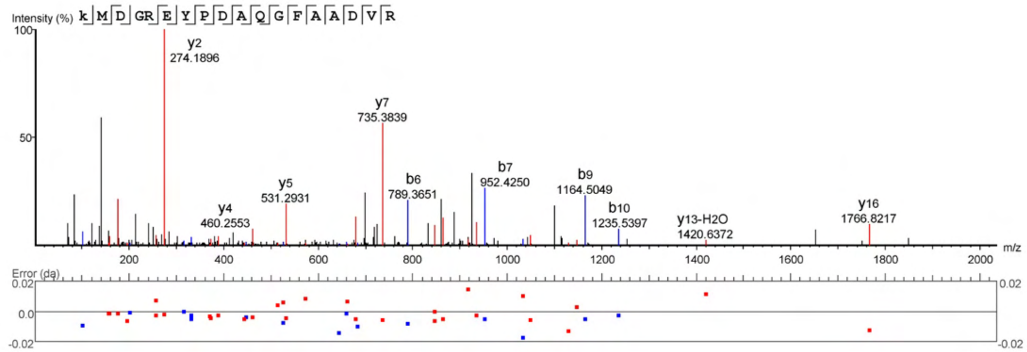


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	114.0919	96.0813	97.0649	57.5459	L					17
2	242.1510	224.1399	225.1240	121.5752	Q	1883.0232	1865.0127	1865.9962	942.0116	16
3	357.1784	339.1660	340.1518	179.0887	D	1754.9646	1736.9541	1737.9376	877.9968	15
4	456.2458	438.2352	439.2244	228.6229	V	1639.9377	1621.9272	1622.9108	820.4689	14
5	543.2778	525.2673	526.2509	272.1389	S	1540.8744	1522.8588	1523.8423	770.9346	13
6	600.2993	582.3002	583.2723	300.6497	G	1453.8418	1435.8268	1436.8103	727.4186	12
7	728.3578	710.3473	711.3309	364.6789	Q	1396.8158	1378.8053	1379.7888	698.9079	11
8	841.4420	823.4314	824.4150	421.2210	L	1268.7563	1250.7467	1251.7302	634.8786	10
9	955.4849	937.4743	938.4579	478.2424	N	1155.6731	1137.6626	1138.6461	578.3365	9
10	1042.5168	1024.5063	1025.4899	521.7584	S	1041.6400	1023.6196	1024.6033	521.3225	8
11	1143.5646	1125.5541	1126.5376	572.2823	T	954.6168	936.5876	937.5712	477.7991	7
12	1327.6858	1309.6753	1310.6588	664.3429	K(+56.03)	853.5608	835.5400	836.5236	427.2753	6
13	1455.7808	1437.7703	1438.7538	728.3904	K	669.4319	651.4268	652.4023	335.2147	5
14	1552.8335	1534.8230	1535.8065	776.9167	P	541.3362	523.3262	524.3074	271.1672	4
15	1649.8862	1631.8757	1632.8593	825.4431	P	444.2838	426.2702	427.2546	222.6408	3
16	1850.0023	1831.9918	1832.9753	925.5012	K(+72.02)	347.2300	329.2211	330.2019	174.1144	2
17					K	147.1131	129.1023	130.0866	74.0564	1

Figure S14_12

MSMS assignment of K364ox in Bromodomain-containing protein 3

BRD3(364-381): K*[O]MDGREYPDAQGFAADVR; -10lgP 67.92; Scan 18664 (MC277)

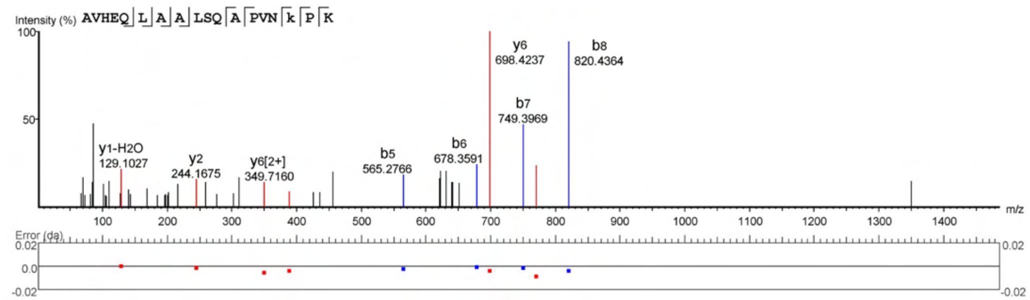


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	201.1251	183.1134	184.0969	101.0713	K(+72.02)					18
2	332.1671	314.1538	315.1379	166.5822	M	1897.8496	1879.8391	1880.8226	949.4248	17
3	447.1956	429.1808	430.1644	224.0957	D	1766.8217	1748.7987	1749.7822	883.9046	16
4	504.2128	486.2022	487.1858	252.6064	G	1651.7822	1633.7717	1634.7552	826.3911	15
5	660.3157	642.3033	643.3013	330.6621	R	1594.7607	1576.7502	1577.7338	797.8804	14
6	789.3651	771.3459	772.3295	395.1783	E	1438.6597	1420.6372	1421.6327	719.8298	13
7	952.4250	934.4092	935.3928	476.7099	Y	1309.6171	1291.6066	1292.5901	655.3085	12
8	1049.4725	1031.4620	1032.4630	525.2439	P	1146.5500	1128.5432	1129.5397	573.7678	11
9	1164.5049	1146.4890	1147.4725	582.7498	D	1049.5067	1031.4905	1032.4630	525.2439	10
10	1235.5397	1217.5261	1218.5096	618.2683	A	934.4766	916.4635	917.4320	467.7370	9
11	1363.5952	1345.5847	1346.5682	682.3079	Q	863.4421	845.4261	846.4167	432.2185	8
12	1420.6167	1402.6062	1403.5897	710.8083	G	735.3839	717.3678	718.3514	368.1892	7
13	1567.6851	1549.6746	1550.6581	784.3425	F	678.3624	660.3464	661.3229	339.6785	6
14	1638.7222	1620.7117	1621.6952	819.8611	A	531.2931	513.2780	514.2572	266.1443	5
15	1709.7593	1691.7488	1692.7323	855.3796	A	460.2553	442.2408	443.2299	230.6257	4
16	1824.7863	1806.7758	1807.7593	912.8931	D	389.2171	371.2073	372.1920	195.1134	3
17	1923.8546	1905.8441	1906.8276	962.4273	V	274.1896	256.1693	257.1630	137.5937	2
18					R	175.1203	157.1099	158.0934	88.0595	1

Figure S14_13

MSMS assignment of K487ox in Bromodomain-containing protein 3

BRD3(472-489): AVHEQLAALSQAPVNK[O]PK; -10lgP 47.68; Scan 12743 (MC271)

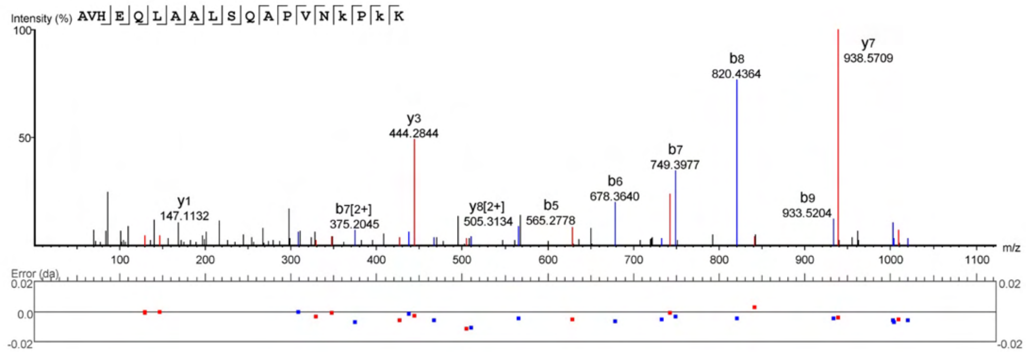


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	72.0449	54.0344	55.0179	36.5225	A					18
2	171.1134	153.1028	154.0863	86.0567	V	1846.0181	1828.0076	1828.9911	923.5090	17
3	308.1722	290.1617	291.1453	154.5861	H	1746.9496	1728.9391	1729.9226	873.9748	16
4	437.2148	419.2043	420.1879	219.1074	E	1609.8907	1591.8802	1592.8638	805.4454	15
5	565.2766	547.2629	548.2465	283.1367	Q	1480.8481	1462.8376	1463.8212	740.9241	14
6	678.3591	660.3469	661.3305	339.6787	L	1352.7896	1334.7791	1335.7626	676.8948	13
7	749.3969	731.3840	732.3676	375.1973	A	1239.7054	1221.6949	1222.6785	620.3527	12
8	820.4364	802.4211	803.4047	410.7159	A	1168.6683	1150.6578	1151.6414	584.8342	11
9	933.5157	915.5052	916.4888	467.2579	L	1097.6312	1079.6207	1080.6042	549.3156	10
10	1020.5478	1002.5372	1003.5208	510.7739	S	984.5472	966.5367	967.5203	492.7736	9
11	1148.6063	1130.5958	1131.5793	574.8032	Q	897.5152	879.5046	880.4882	449.2576	8
12	1219.6434	1201.6329	1202.6165	610.3217	A	769.4656	751.4460	752.4296	385.2283	7
13	1316.6963	1298.6858	1299.6693	658.8481	P	698.4237	680.4089	681.3925	349.7160	6
14	1415.7646	1397.7542	1398.7377	708.3823	V	601.3668	583.3562	584.3398	301.1834	5
15	1529.8076	1511.7971	1512.7806	765.4038	N	502.2983	484.2878	485.2714	251.6492	4
16	1673.8975	1655.8870	1656.8705	837.4487	K(+15.99)	388.2600	370.2448	371.2284	194.6277	3
17	1770.9502	1752.9397	1753.9232	885.9751	P	244.1675	226.1550	227.1385	122.5828	2
18					K	147.1128	129.1027	130.0858	74.0564	1

Figure S14_14

MSMS assignment of K489ox in Bromodomain-containing protein 3

BRD3(472-490): AVHEQLAALSQAPVNK*PK*[O]K; -10lgP 53.80; Scan 19269 (MC271)

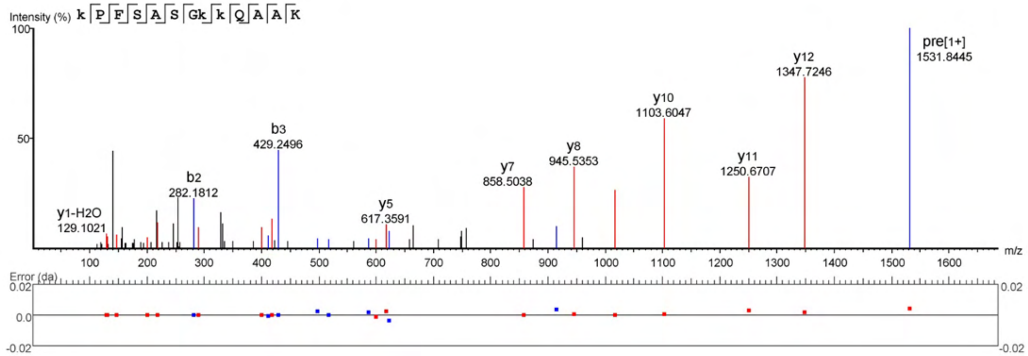


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	72.0449	54.0344	55.0179	36.5225	A					19
2	171.1134	153.1028	154.0863	86.0567	V	2086.1655	2068.1550	2069.1384	1043.5828	18
3	308.1729	290.1617	291.1453	154.5861	H	1987.0970	1969.0865	1970.0701	994.0485	17
4	437.2166	419.2043	420.1879	219.1074	E	1850.0381	1832.0276	1833.0111	925.5190	16
5	565.2778	547.2629	548.2465	283.1367	Q	1720.9955	1702.9850	1703.9685	860.9977	15
6	678.3640	660.3469	661.3305	339.6787	L	1592.9370	1574.9265	1575.9100	796.9685	14
7	749.3977	731.3840	732.3727	375.2045	A	1479.8529	1461.8424	1462.8259	740.4265	13
8	820.4364	802.4211	803.4047	410.7159	A	1408.8158	1390.8053	1391.7888	704.9079	12
9	933.5204	915.5052	916.4888	467.2638	L	1337.7787	1319.7682	1320.7517	669.3893	11
10	1020.5537	1002.5432	1003.5280	510.7845	S	1224.6946	1206.6841	1207.6676	612.8473	10
11	1148.6063	1130.5958	1131.5793	574.8032	Q	1137.6626	1119.6521	1120.6356	569.3313	9
12	1219.6434	1201.6329	1202.6165	610.3217	A	1009.6091	991.5934	992.5770	505.3134	8
13	1316.6963	1298.6858	1299.6693	658.8481	P	938.5709	920.5563	921.5399	469.7834	7
14	1415.7646	1397.7542	1398.7377	708.3823	V	841.5107	823.5036	824.4872	421.2571	6
15	1529.8076	1511.7971	1512.7806	765.4038	N	742.4467	724.4352	725.4188	371.7229	5
16	1713.9287	1695.9182	1696.9017	857.4644	K(+56.03)	628.4083	610.3922	611.3758	314.7014	4
17	1810.9814	1792.9709	1793.9545	905.9907	P	444.2844	426.2767	427.2546	222.6408	3
18	2011.0975	1993.0870	1994.0706	1006.0488	K(+72.02)	347.2301	329.2216	330.2019	174.1144	2
19					K	147.1132	129.1027	130.0869	74.0564	1

Figure S14_15

MSMS assignment of K651ox in Bromodomain-containing protein 3

BRD3(643-655): K*PFSASGK*K*[O]QAAK; -10lgP 55.45; Scan 12620 (MC303)

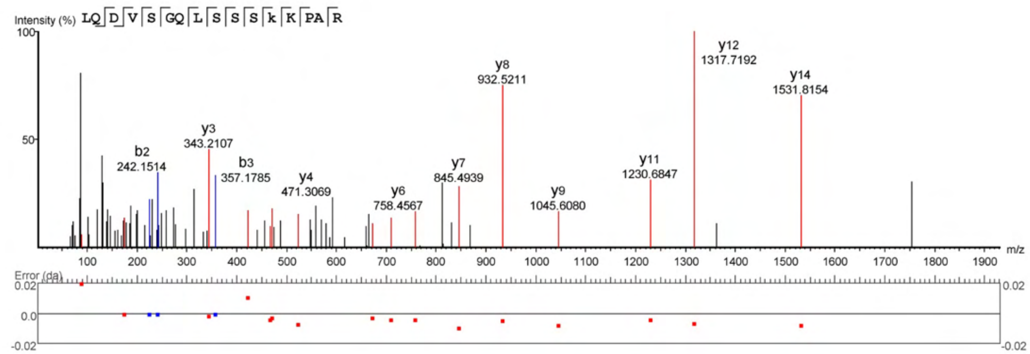


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	185.1290	167.1184	168.1020	93.0645	K(+56.03)					13
2	282.1812	264.1712	265.1548	141.5909	P	1347.7246	1329.7161	1330.6996	674.3633	12
3	429.2496	411.2403	412.2232	215.1251	F	1250.6707	1232.6633	1233.6469	625.8369	11
4	516.2827	498.2689	499.2552	258.6411	S	1103.6047	1085.5950	1086.5785	552.3027	10
5	587.3170	569.3087	570.2923	294.1596	A	1016.5729	998.5629	999.5464	508.7867	9
6	674.3513	656.3408	657.3243	337.6757	S	945.5353	927.5258	928.5093	473.2682	8
7	731.3728	713.3622	714.3458	366.1864	G	858.5038	840.4937	841.4773	429.7521	7
8	915.4902	897.4834	898.4670	458.2470	K(+56.03)	801.4828	783.4723	784.4559	401.2414	6
9	1115.6100	1097.5995	1098.5830	558.3050	K(+72.02)	617.3591	599.3511	600.3362	309.1808	5
10	1243.6686	1225.6581	1226.6416	622.3385	Q	417.2452	399.2350	400.2191	209.1228	4
11	1314.7057	1296.6952	1297.6787	657.8528	A	289.1874	271.1765	272.1600	145.0935	3
12	1385.7428	1367.7323	1368.7158	693.3714	A	218.1498	200.1393	201.1233	109.5750	2
13					K	147.1128	129.1021	130.0863	74.0564	1

Figure S14_16

MSMS assignment of K683ox in Bromodomain-containing protein 3

BRD3(672-687): LQDVSGQLSSSK*[O]KPAR; -10lgP 44.60; Scan 10327 (MC271)

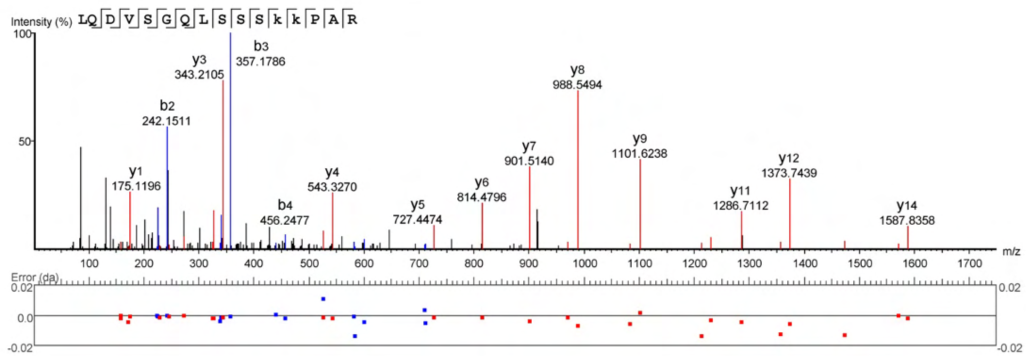


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	114.0919	96.0813	97.0649	57.5459	L					16
2	242.1514	224.1399	225.1243	121.5752	Q	1659.8660	1641.8555	1642.8390	830.4330	15
3	357.1785	339.1668	340.1504	179.0887	D	1531.8154	1513.7969	1514.7804	766.4037	14
4	456.2458	438.2352	439.2188	228.6229	V	1416.7805	1398.7700	1399.7535	708.8950	13
5	543.2778	525.2673	526.2509	272.1389	S	1317.7192	1299.7015	1300.6851	659.3560	12
6	600.2993	582.2888	583.2723	300.6497	G	1230.6847	1212.6696	1213.6531	615.8400	11
7	728.3578	710.3473	711.3309	364.6789	Q	1173.6586	1155.6481	1156.6316	587.3293	10
8	841.4420	823.4314	824.4150	421.2210	L	1045.6080	1027.5895	1028.5730	523.3078	9
9	928.4739	910.4634	911.4470	464.7370	S	932.5211	914.5054	915.4890	466.7626	8
10	1015.5060	997.4954	998.4790	508.2530	S	845.4939	827.4733	828.4569	423.2310	7
11	1102.5380	1084.5275	1085.5110	551.7690	S	758.4567	740.4413	741.4249	379.7259	6
12	1302.6541	1284.6436	1285.6271	651.8270	K(+72.02)	671.4230	653.4093	654.3929	336.2099	5
13	1430.7490	1412.7385	1413.7220	715.8745	K	471.3069	453.2932	454.2768	236.1519	4
14	1527.8018	1509.7913	1510.7748	764.4009	P	343.2107	325.1982	326.1818	172.1044	3
15	1598.8389	1580.8284	1581.8119	799.9194	A	246.1561	228.1455	229.1290	123.5780	2
16					R	175.1200	157.1084	158.0919	88.0397	1

Figure S14_17

MSMS assignment of K684ox in Bromodomain-containing protein 3

BRD3(672-687): LQDVSGQLSSSK*K*[O]PAR; -10lgP 63.47; Scan 14671 (MC277)

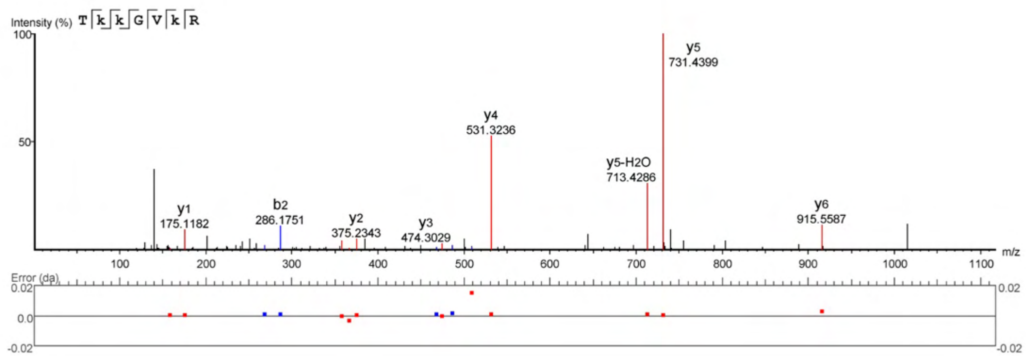


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	114.0919	96.0813	97.0649	57.5459	L					16
2	242.1511	224.1402	225.1245	121.5752	Q	1715.8922	1697.8817	1698.8652	858.4461	15
3	357.1786	339.1705	340.1520	179.0887	D	1587.8358	1569.8231	1570.8066	794.4168	14
4	456.2477	438.2352	439.2176	228.6229	V	1472.8197	1454.7961	1455.7797	736.9033	13
5	543.2778	525.2557	526.2509	272.1389	S	1373.7439	1355.7278	1356.7241	687.3691	12
6	600.3038	582.2896	583.2861	300.6497	G	1286.7112	1268.6958	1269.6793	643.8531	11
7	728.3578	710.3431	711.3362	364.6789	Q	1229.6882	1211.6743	1212.6714	615.3424	10
8	841.4420	823.4314	824.4150	421.2210	L	1101.6238	1083.6218	1084.5992	551.3131	9
9	928.4739	910.4634	911.4470	464.7370	S	988.5494	970.5330	971.5151	494.7711	8
10	1015.5060	997.4954	998.4790	508.2530	S	901.5140	883.4996	884.4832	451.2551	7
11	1102.5380	1084.5275	1085.5110	551.7690	S	814.4796	796.4675	797.4511	407.7390	6
12	1286.6592	1268.6487	1269.6322	643.8296	K(+56.03)	727.4474	709.4355	710.4191	364.2230	5
13	1486.7753	1468.7648	1469.7483	743.8876	K(+72.02)	543.3270	525.3143	526.2993	272.1624	4
14	1583.8280	1565.8175	1566.8010	792.4140	P	343.2105	325.2004	326.1840	172.1088	3
15	1654.8651	1636.8546	1637.8381	827.9326	A	246.1571	228.1455	229.1308	123.5780	2
16					R	175.1196	157.1102	158.0924	88.0595	1

Figure S14_18

MSMS assignment of K286ox, K289ox in Bromodomain-containing protein 4

BRD4(284-290): TK*K*[O]GVK*[O]R; -10lgP 27.87; Scan 4997 (MC264)

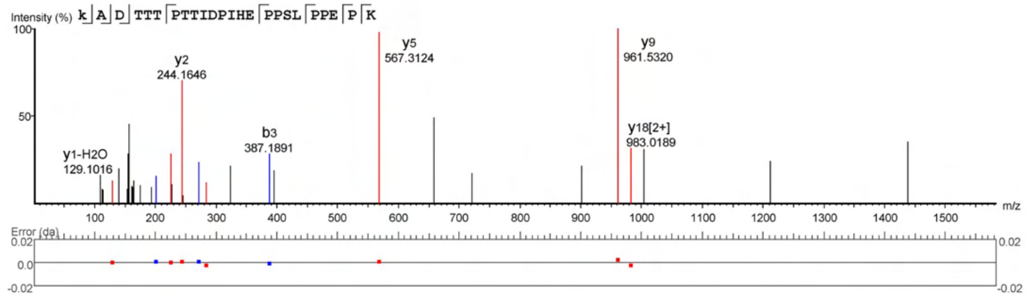


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	102.0555	84.0450	85.0285	51.5278	T					7
2	286.1751	268.1649	269.1497	143.5883	K(+56.03)	915.5587	897.5516	898.5352	458.2811	6
3	486.2903	468.2805	469.2658	243.6464	K(+72.02)	731.4399	713.4286	714.4140	366.2236	5
4	543.3142	525.3036	526.2872	272.1571	G	531.3236	513.3143	514.2979	266.1624	4
5	642.3826	624.3721	625.3557	321.6913	V	474.3029	456.2929	457.2765	237.6517	3
6	842.4987	824.4882	825.4717	421.7494	K(+72.02)	375.2343	357.2245	358.2078	188.1175	2
7					R	175.1182	157.1084	158.0913	88.0595	1

Figure S14_19

MSMS assignment of K291ox in Bromodomain-containing protein 4

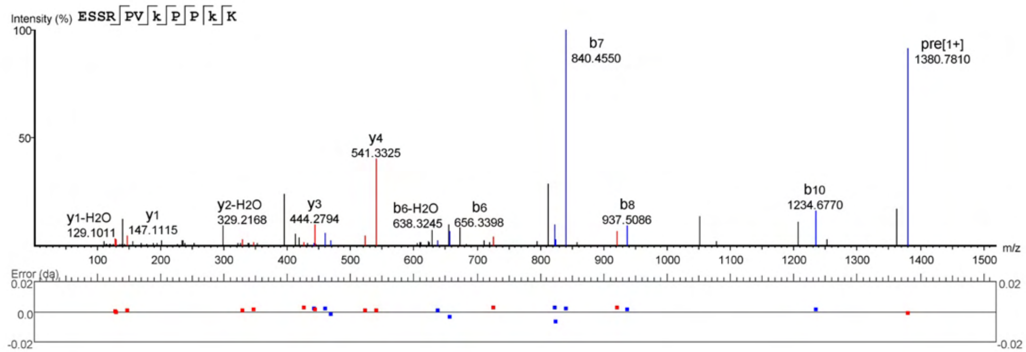
BRD4(291-314): K*[O]ADTTTPTTIDPIHEPPSLPPEPK; -10lgP 40.91; Scan 12172 (MC264)



#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	201.1227	183.1134	184.0969	101.0620	K(+72.02)					24
2	272.1597	254.1505	255.1340	136.5805	A	2454.2397	2436.2292	2437.2126	1227.6199	23
3	387.1891	369.1774	370.1610	194.0940	D	2383.2026	2365.1921	2366.1755	1192.1013	22
4	488.2356	470.2251	471.2086	244.6178	T	2268.1758	2250.1653	2251.1487	1134.5879	21
5	589.2833	571.2728	572.2563	295.1417	T	2167.1282	2149.1177	2150.1011	1084.0641	20
6	690.3310	672.3204	673.3040	345.6655	T	2066.0803	2048.0698	2049.0532	1033.5402	19
7	787.3838	769.3732	770.3568	394.1919	P	1965.0327	1947.0222	1948.0057	983.0189	18
8	888.4315	870.4209	871.4045	444.7157	T	1867.9800	1849.9695	1850.9530	934.4900	17
9	989.4791	971.4686	972.4521	495.2396	T	1766.9323	1748.9218	1749.9053	883.9661	16
10	1102.5632	1084.5527	1085.5363	551.7816	I	1665.8845	1647.8740	1648.8575	833.4423	15
11	1217.5901	1199.5796	1200.5631	609.2950	D	1552.8005	1534.7900	1535.7736	776.9003	14
12	1314.6428	1296.6323	1297.6158	657.8214	P	1437.7736	1419.7631	1420.7466	719.3868	13
13	1427.7269	1409.7164	1410.7000	714.3635	I	1340.7208	1322.7103	1323.6938	670.8604	12
14	1564.7859	1546.7754	1547.7589	782.8929	H	1227.6367	1209.6262	1210.6097	614.3184	11
15	1693.8285	1675.8180	1676.8015	847.4142	E	1090.5779	1072.5674	1073.5509	545.7889	10
16	1790.8812	1772.8707	1773.8542	895.9406	P	961.5320	943.5247	944.5082	481.2676	9
17	1887.9340	1869.9235	1870.9070	944.4670	P	864.4825	846.4719	847.4555	432.7412	8
18	1974.9659	1956.9554	1957.9390	987.9830	S	767.4297	749.4192	750.4028	384.2149	7
19	2088.0500	2070.0396	2071.0229	1044.5250	L	680.3977	662.3871	663.3707	340.6989	6
20	2185.1028	2167.0923	2168.0757	1093.0514	P	567.3124	549.3031	550.2867	284.1596	5
21	2282.1555	2264.1450	2265.1284	1141.5778	P	470.2609	452.2503	453.2339	235.6304	4
22	2411.1982	2393.1877	2394.1711	1206.0991	E	373.2081	355.1976	356.1812	187.1041	3
23	2508.2510	2490.2405	2491.2239	1254.6255	P	244.1646	226.1545	227.1385	122.5828	2
24					K	147.1128	129.1016	130.0858	74.0564	1

Figure S14_20

MSMS assignment of K332ox in Bromodomain-containing protein 4
BRD4(323-333): ESSRPVK*PPK*[O]K; -10lgP 42.3; Scan 4602 (MC264)

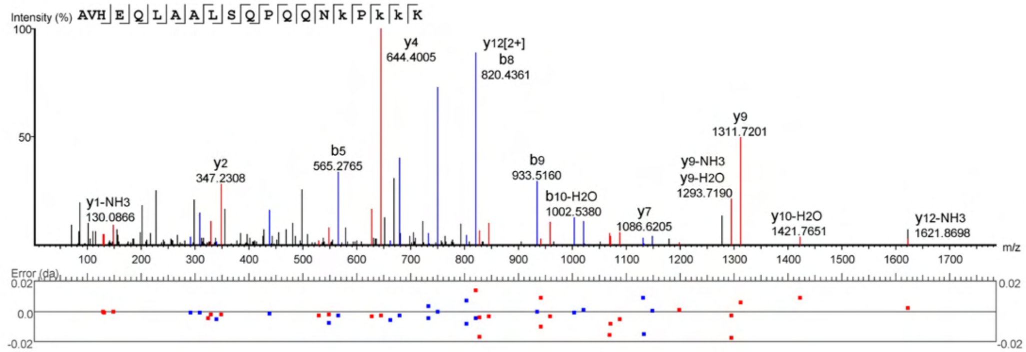


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	130.0504	112.0399	113.0234	65.5252	E					11
2	217.0824	199.0719	200.0554	109.0412	S	1251.7419	1233.7314	1234.7150	626.3710	10
3	304.1144	286.1039	287.0875	152.5572	S	1164.7098	1146.6993	1147.6829	582.8549	9
4	460.2129	442.2024	443.1886	230.6078	R	1077.6779	1059.6674	1060.6509	539.3389	8
5	557.2683	539.2578	540.2413	279.1342	P	921.5731	903.5662	904.5497	461.2884	7
6	656.3398	638.3245	639.3098	328.6684	V	824.5240	806.5134	807.4970	412.7620	6
7	840.4550	822.4440	823.4376	420.7289	K(+56.03)	725.4521	707.4450	708.4286	363.2278	5
8	937.5086	919.5001	920.4837	469.2566	P	541.3325	523.3224	524.3074	271.1672	4
9	1034.5635	1016.5529	1017.5365	517.7817	P	444.2794	426.2679	427.2546	222.6408	3
10	1234.6770	1216.6689	1217.6525	617.8397	K(+72.02)	347.2268	329.2168	330.2019	174.1144	2
11					K	147.1115	129.1011	130.0854	74.0564	1

Figure S14_21

MSMS assignment of K535ox, K537ox, K538ox in Bromodomain-containing protein 4

BRD4(520-539): AVHEQLAALSQPQQNK*[O]PK*[O]K*[O]K; -10lgP 68.97; Scan 16259 (MC273)

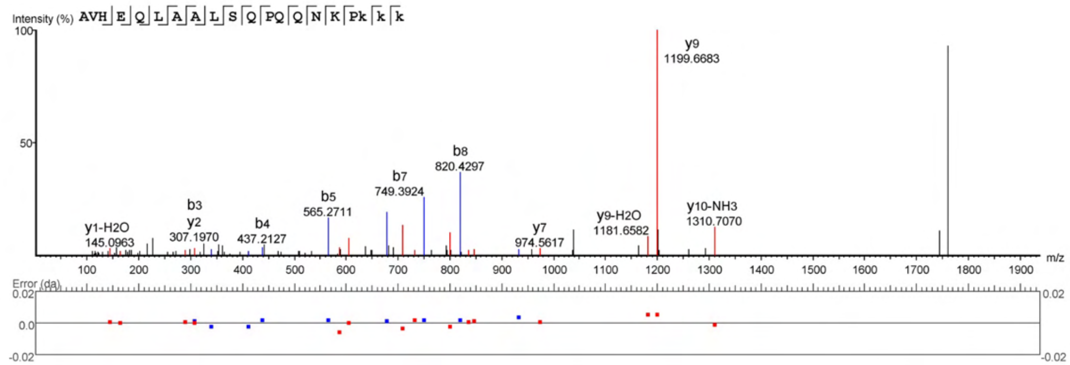


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	72.0449	54.0344	55.0179	36.5225	A					20
2	171.1134	153.1028	154.0863	86.0567	V	2388.2881	2370.2776	2371.2610	1194.6440	19
3	308.1733	290.1629	291.1453	154.5861	H	2289.2197	2271.2092	2272.1926	1145.1099	18
4	437.2165	419.2043	420.1879	219.1074	E	2152.1606	2134.1501	2135.1335	1076.5803	17
5	565.2765	547.2703	548.2465	283.1367	Q	2023.1182	2005.1077	2006.0912	1012.0591	16
6	678.3603	660.3469	661.3363	339.6843	L	1895.0596	1877.0491	1878.0326	948.0298	15
7	749.3951	731.3802	732.3719	375.1973	A	1781.9756	1763.9651	1764.9486	891.4878	14
8	820.4361	802.4137	803.4129	410.7159	A	1710.9385	1692.9280	1693.9115	855.9692	13
9	933.5160	915.5052	916.4888	467.2579	L	1639.9014	1621.8909	1622.8717	820.4361	12
10	1020.5461	1002.5380	1003.5208	510.7739	S	1526.8173	1508.8068	1509.7903	763.9086	11
11	1148.6055	1130.5862	1131.5945	574.8032	Q	1439.7853	1421.7651	1422.7583	720.3926	10
12	1245.6592	1227.6487	1228.6322	623.3296	P	1311.7201	1293.7190	1294.7170	656.3633	9
13	1373.7177	1355.7072	1356.6907	687.3588	Q	1214.6738	1196.6633	1197.6453	607.8369	8
14	1501.7762	1483.7657	1484.7493	751.3881	Q	1086.6205	1068.6204	1069.5966	543.8077	7
15	1615.8192	1597.8087	1598.7922	808.4096	N	958.5603	940.5367	941.5397	479.7784	6
16	1815.9353	1797.9248	1798.9083	908.4677	K(+72.02)	844.5172	826.5071	827.5037	422.7569	5
17	1912.9880	1894.9775	1895.9611	956.9940	P	644.4005	626.3903	627.3707	322.7035	4
18	2113.1042	2095.0938	2096.0771	1057.0521	K(+72.02)	547.3474	529.3374	530.3180	274.1725	3
19	2313.2202	2295.2097	2296.1931	1157.1101	K(+72.02)	347.2308	329.2203	330.2019	174.1144	2
20					K	147.1132	129.1027	130.0866	74.0564	1

Figure S14_22

MSMS assignment of K539ox in Bromodomain-containing protein 4

BRD4(520-539): AVHEQLAALSQPQQNKPK*[O]K[O]K[O]; -10lgP 50.12; Scan 7539 (MC264)

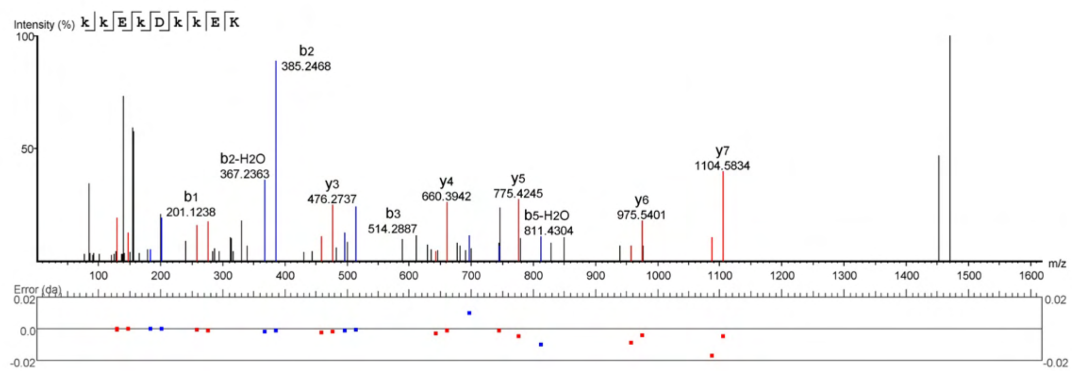


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	72.0449	54.0344	55.0179	36.5225	A					20
2	171.1134	153.1028	154.0863	86.0567	V	2276.2356	2258.2251	2259.2085	1138.6178	19
3	308.1708	290.1617	291.1453	154.5861	H	2177.1672	2159.1567	2160.1401	1089.0836	18
4	437.2127	419.2043	420.1879	219.1074	E	2040.1083	2022.0978	2023.0813	1020.5541	17
5	565.2711	547.2629	548.2465	283.1367	Q	1911.0658	1893.0553	1894.0388	956.0329	16
6	678.3560	660.3469	661.3305	339.6815	L	1783.0072	1764.9967	1765.9802	892.0036	15
7	749.3924	731.3840	732.3676	375.1973	A	1669.9231	1651.9126	1652.8961	835.4606	14
8	820.4297	802.4211	803.4047	410.7183	A	1598.8860	1580.8755	1581.8590	799.9457	13
9	933.5121	915.5052	916.4888	467.2579	L	1527.8489	1509.8384	1510.8219	764.4244	12
10	1020.5478	1002.5372	1003.5208	510.7739	S	1414.7648	1396.7543	1397.7378	707.8861	11
11	1148.6063	1130.5958	1131.5793	574.8032	Q	1327.7328	1309.7223	1310.7070	664.3664	10
12	1245.6592	1227.6487	1228.6322	623.3296	P	1199.6683	1181.6582	1182.6472	600.3371	9
13	1373.7177	1355.7072	1356.6907	687.3588	Q	1102.6215	1084.6110	1085.5945	551.8107	8
14	1501.7762	1483.7657	1484.7493	751.3881	Q	974.5617	956.5523	957.5359	487.7814	7
15	1615.8192	1597.8087	1598.7922	808.4096	N	846.5031	828.4937	829.4773	423.7521	6
16	1743.9142	1725.9037	1726.8872	872.4571	K	732.4590	714.4508	715.4344	366.7307	5
17	1840.9669	1822.9564	1823.9399	920.9835	P	604.3669	586.3558	587.3459	302.6832	4
18	2041.0830	2023.0725	2024.0560	1021.0415	K(+72.02)	507.3137	489.3031	490.2867	254.1568	3
19	2185.1729	2167.1624	2168.1458	1093.0864	K(+15.99)	307.1970	289.1860	290.1706	154.0988	2
20					K(+15.99)	163.1072	145.0963	146.0807	82.0539	1

Figure S14_23

MSMS assignment of K541ox, K544ox in Bromodomain-containing protein 4

BRD4(538-546): K*[O]K*EK*[O]DK*K*[O]EK; -10lgP 16.75; Scan 9090 (MC273)

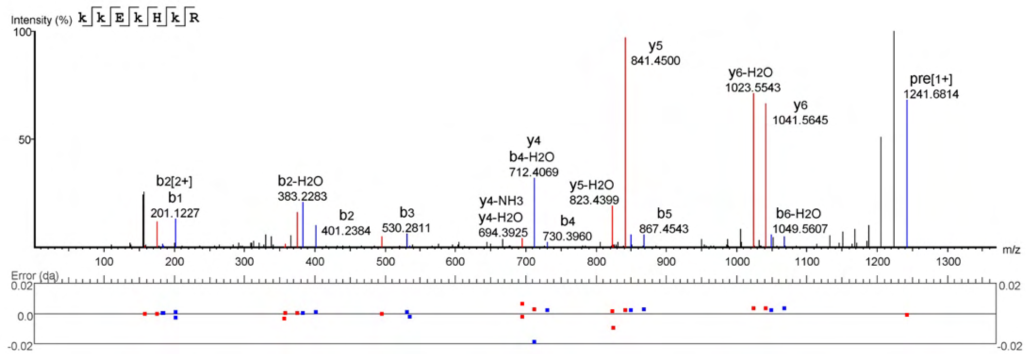


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	201.1238	183.1132	184.0969	101.0620	K(+72.02)					9
2	385.2468	367.2363	368.2181	193.1225	K(+56.03)	1288.6995	1270.6890	1271.6725	644.8497	8
3	514.2887	496.2787	497.2607	257.6438	E	1104.5834	1086.5850	1087.5513	552.7891	7
4	714.4037	696.3829	697.3768	357.7019	K(+72.02)	975.5401	957.5343	958.5087	488.2678	6
5	829.4307	811.4304	812.4037	415.2153	D	775.4245	757.4090	758.3926	388.2098	5
6	1013.5519	995.5413	996.5249	507.2759	K(+56.03)	660.3942	642.3855	643.3657	330.6963	4
7	1213.6680	1195.6575	1196.6410	607.3340	K(+72.02)	476.2737	458.2635	459.2445	238.6357	3
8	1342.7106	1324.7001	1325.6836	671.8553	E	276.1567	258.1460	259.1284	138.5777	2
9					K	147.1132	129.1024	130.0866	74.0564	1

Figure S14_24

MSMS assignment of K547ox, K548ox, K550ox, K552ox in Bromodomain-containing protein 4

BRD4(547-553): K*[O]K*[O]EK*[O]HK*[O]R; -10lgP 19.78; Scan 3905 (MC264)

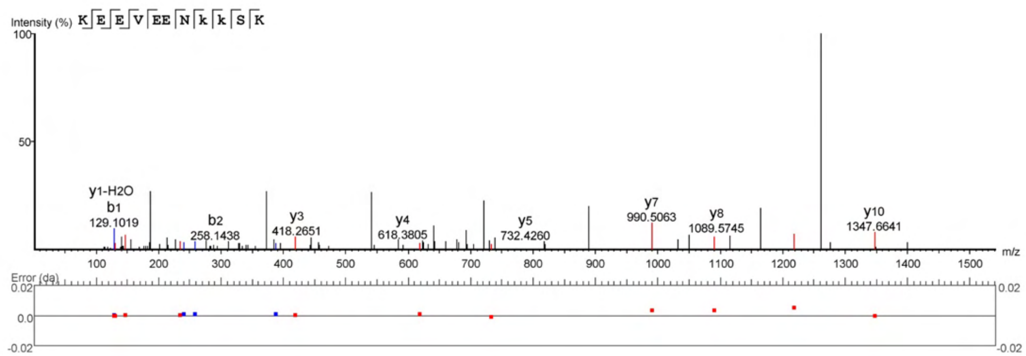


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	201.1227	183.1123	184.0961	101.0620	K(+72.02)					7
2	401.2384	383.2283	384.2130	201.1227	K(+72.02)	1041.5645	1023.5543	1024.5417	521.2844	6
3	530.2811	512.2720	513.2556	265.6413	E	841.4500	823.4399	824.4351	421.2263	5
4	730.3960	712.4069	713.3717	365.6993	K(+72.02)	712.4069	694.3925	695.3849	356.7081	4
5	867.4543	849.4443	850.4306	434.2288	H	512.2939	494.2834	495.2664	256.6470	3
6	1067.5698	1049.5607	1050.5468	534.2888	K(+72.02)	375.2344	357.2235	358.2072	188.1175	2
7					R	175.1185	157.1084	158.0918	88.0595	1

Figure S14_25

MSMS assignment of K561ox in Bromodomain-containing protein 4

BRD4(554-564): KEEVEENK*[O]K*SK; -10lgP 34.63; Scan 4151 (MC264)

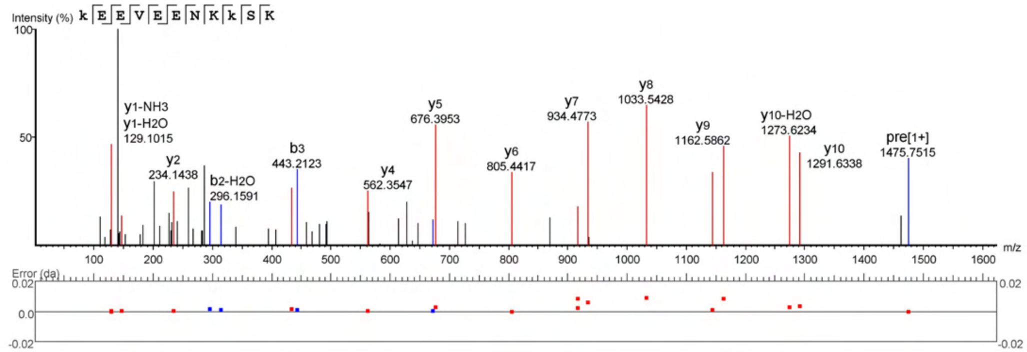


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	129.1019	111.0922	112.0758	65.0514	K					11
2	258.1438	240.1333	241.1184	129.5727	E	1347.6641	1329.6533	1330.6368	674.3319	10
3	387.1861	369.1774	370.1609	194.0940	E	1218.6151	1200.6107	1201.5942	609.8106	9
4	486.2563	468.2458	469.2294	243.6282	V	1089.5745	1071.5681	1072.5516	545.2893	8
5	615.2990	597.2884	598.2720	308.1495	E	990.5063	972.4996	973.4832	495.7551	7
6	744.3416	726.3310	727.3146	372.6708	E	861.4676	843.4570	844.4406	431.2338	6
7	858.3845	840.3739	841.3575	429.6922	N	732.4260	714.4144	715.3980	366.7125	5
8	1058.5005	1040.4900	1041.4735	529.7502	K(+72.02)	618.3805	600.3715	601.3551	309.6910	4
9	1242.6217	1224.6112	1225.5947	621.8109	K(+56.03)	418.2651	400.2554	401.2390	209.6330	3
10	1329.6538	1311.6433	1312.6268	665.3269	S	234.1438	216.1343	217.1178	117.5724	2
11					K	147.1122	129.1019	130.0854	74.0564	1

Figure S14_26

MSMS assignment of K562ox in Bromodomain-containing protein 4

BRD4(554-564): KEEVEENK*K*[O]SK; -10lgP 44.51; Scan 4019 (MC264)

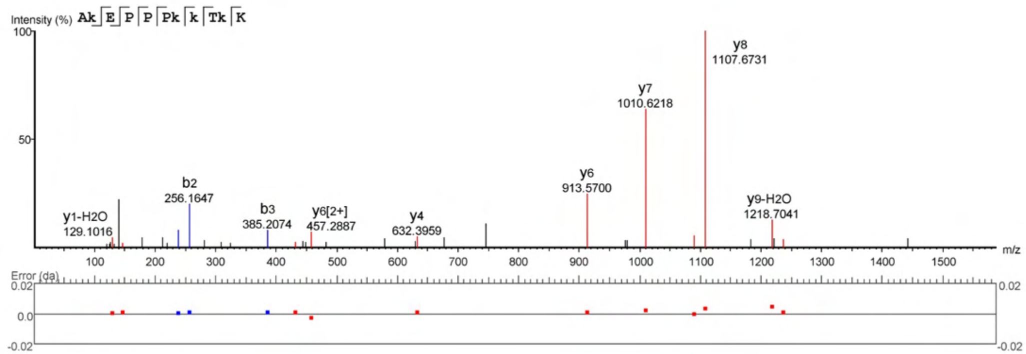


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	185.1290	167.1184	168.1020	93.0645	K(+56.03)					11
2	314.1702	296.1591	297.1446	157.5858	E	1291.6338	1273.6234	1274.6106	646.3188	10
3	443.2123	425.2036	426.1872	222.1071	E	1162.5862	1144.5828	1145.5680	581.7975	9
4	542.2826	524.2720	525.2556	271.6413	V	1033.5428	1015.5418	1016.5254	517.2762	8
5	671.3242	653.3146	654.2982	336.1626	E	934.4773	916.4644	917.4540	467.7420	7
6	800.3677	782.3572	783.3408	400.6839	E	805.4417	787.4308	788.4144	403.2207	6
7	914.4106	896.4001	897.3837	457.7053	N	676.3953	658.3882	659.3718	338.6994	5
8	1042.5056	1024.4951	1025.4786	521.7528	K	562.3547	544.3453	545.3289	281.6779	4
9	1242.6217	1224.6112	1225.5947	621.8109	K(+72.02)	434.2587	416.2503	417.2339	217.6304	3
10	1329.6538	1311.6433	1312.6268	665.3269	S	234.1438	216.1343	217.1178	117.5724	2
11					K	147.1120	129.1015	130.0858	74.0564	1

Figure S14_27

MSMS assignment of K572ox in Bromodomain-containing protein 4

BRD4(565-575): AK*EPPPK*K*[O]TK*K; -10lgP 39.21; Scan 7630 (MC264)

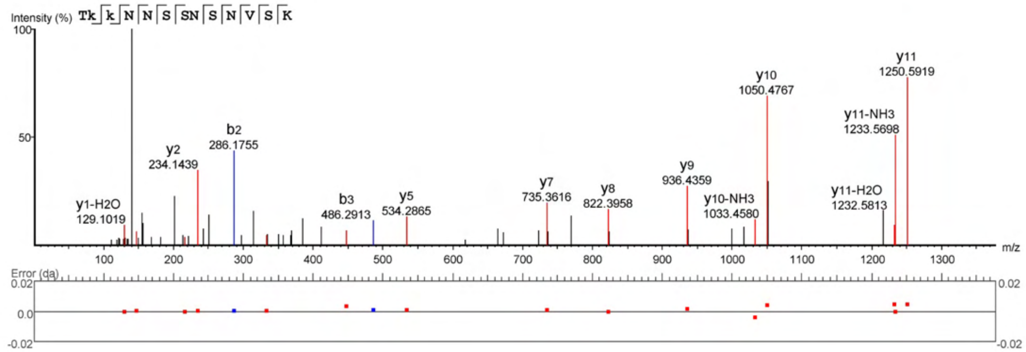


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	72.0449	54.0344	55.0179	36.5225	A					11
2	256.1647	238.1555	239.1382	128.5831	K(+56.03)	1420.8409	1402.8304	1403.8140	710.9205	10
3	385.2074	367.1981	368.1817	193.1043	E	1236.7179	1218.7041	1219.6927	618.8599	9
4	482.2614	464.2509	465.2345	241.6307	P	1107.6731	1089.6672	1090.6501	554.3386	8
5	579.3142	561.3036	562.2872	290.1571	P	1010.6218	992.6138	993.5974	505.8122	7
6	676.3669	658.3564	659.3400	338.6835	P	913.5700	895.5611	896.5447	457.2887	6
7	860.4881	842.4775	843.4611	430.7440	K(+56.03)	816.5189	798.5084	799.4919	408.7595	5
8	1060.6042	1042.5938	1043.5773	530.8021	K(+72.02)	632.3959	614.3871	615.3707	316.6989	4
9	1161.6519	1143.6414	1144.6249	581.3259	T	432.2802	414.2711	415.2546	216.6408	3
10	1345.7731	1327.7626	1328.7461	673.3865	K(+56.03)	331.2339	313.2234	314.2070	166.1170	2
11					K	147.1115	129.1016	130.0858	74.0564	1

Figure S14_28

MSMS assignment of K575ox in Bromodomain-containing protein 4

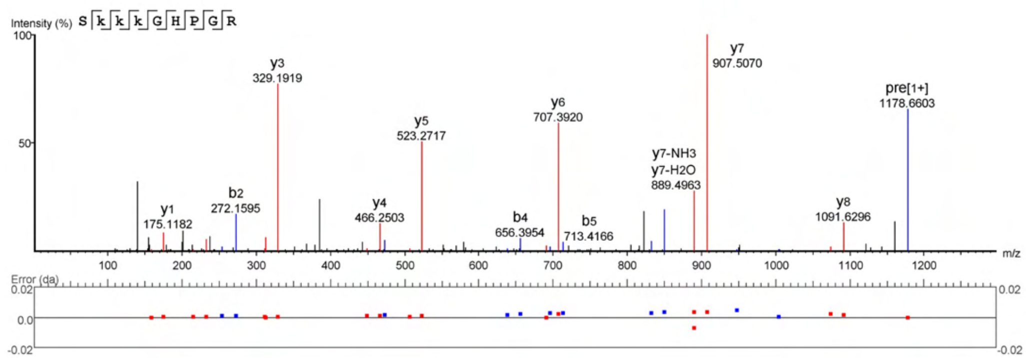
BRD4(573-585): TK*K*[O]NNSSNSNVSK; -10lgP 51.76; Scan 3741 (MC264)



#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	102.0555	84.0450	85.0285	51.5278	T					13
2	286.1755	268.1661	269.1497	143.5883	K(+56.03)	1434.7183	1416.7078	1417.6913	717.8591	12
3	486.2913	468.2822	469.2658	243.6464	K(+72.02)	1250.5919	1232.5813	1233.5698	625.7986	11
4	600.3357	582.3251	583.3087	300.6678	N	1050.4767	1032.4706	1033.4580	525.7405	10
5	714.3786	696.3680	697.3516	357.6893	N	936.4359	918.4276	919.4111	468.7191	9
6	801.4106	783.4001	784.3837	401.2053	S	822.3958	804.3846	805.3682	411.6976	8
7	888.4427	870.4321	871.4157	444.7213	S	735.3616	717.3526	718.3362	368.1816	7
8	1002.4856	984.4750	985.4586	501.7428	N	648.3311	630.3206	631.3041	324.6656	6
9	1089.5176	1071.5071	1072.4906	545.2588	S	534.2865	516.2776	517.2612	267.6441	5
10	1203.5605	1185.5500	1186.5336	602.2803	N	447.2523	429.2456	430.2292	224.1281	4
11	1302.6290	1284.6185	1285.6021	651.8145	V	333.2122	315.2027	316.1862	167.1066	3
12	1389.6610	1371.6505	1372.6340	695.3305	S	234.1439	216.1340	217.1178	117.5724	2
13					K	147.1121	129.1019	130.0858	74.0564	1

Figure S14_29

MSMS assignment of K727ox in Bromodomain-containing protein 4
BRD4(725-733): SK*K*[O]K*GHPGR; -10lgP 39.08; Scan 4485 (MC264)

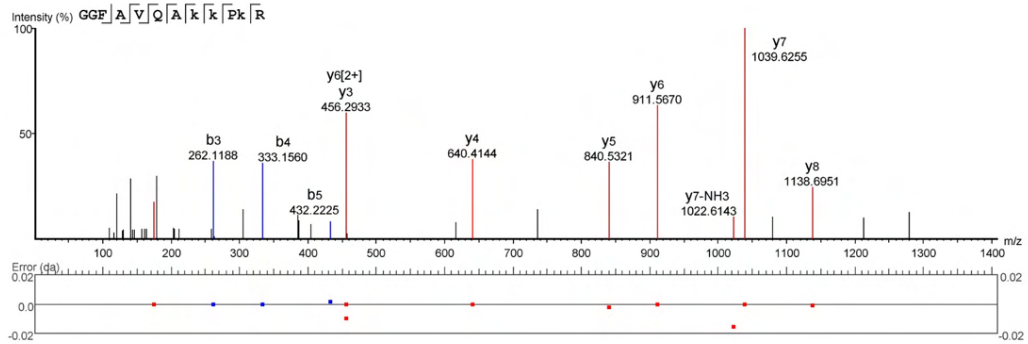


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	88.0399	70.0293	71.0129	44.5199	S					9
2	272.1595	254.1490	255.1340	136.5805	K(+56.03)	1091.6296	1073.6184	1074.6050	546.3160	8
3	472.2748	454.2665	455.2501	236.6385	K(+72.02)	907.5070	889.4963	890.4911	454.2554	7
4	656.3954	638.3853	639.3713	328.6991	K(+56.03)	707.3920	689.3842	690.3677	354.1974	6
5	713.4166	695.4056	696.3928	357.2099	G	523.2717	505.2630	506.2457	262.1368	5
6	850.4747	832.4647	833.4517	425.7393	H	466.2503	448.2415	449.2238	233.6260	4
7	947.5264	929.5208	930.5044	474.2657	P	329.1919	311.1814	312.1659	165.0966	3
8	1004.5521	986.5423	987.5259	502.7764	G	232.1394	214.1298	215.1127	116.5702	2
9					R	175.1182	157.1084	158.0921	88.0595	1

Figure S14_30

MSMS assignment of K17ox in Ribosome biogenesis protein BRX1 homolog

BRIX1(10-21): GGFAVQAK*[O]K*PK*R; -10lgP 32.83; Scan 25446 (MC336)

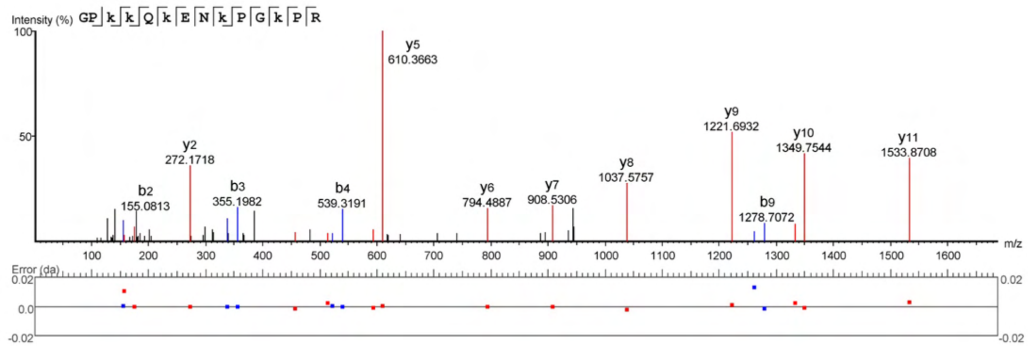


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	58.0293	40.0187	41.0023	29.5146	G					12
2	115.0508	97.0402	98.0238	58.0254	G	1413.8212	1395.8107	1396.7942	707.4106	11
3	262.1188	244.1086	245.0921	131.5596	F	1356.7997	1338.7892	1339.7727	678.8998	10
4	333.1560	315.1457	316.1293	167.0781	A	1209.7313	1191.7208	1192.7043	605.3657	9
5	432.2225	414.2141	415.1977	216.6123	V	1138.6951	1120.6837	1121.6672	569.8471	8
6	560.2833	542.2727	543.2563	280.6416	Q	1039.6255	1021.6152	1022.6143	520.3129	7
7	631.3204	613.3098	614.2934	316.1602	A	911.5670	893.5566	894.5402	456.2933	6
8	831.4365	813.4259	814.4095	416.2182	K(+72.02)	840.5321	822.5195	823.5031	420.7650	5
9	1015.5576	997.5471	998.5306	508.2788	K(+56.03)	640.4144	622.4034	623.3870	320.7070	4
10	1112.6104	1094.5999	1095.5834	556.8052	P	456.2933	438.2823	439.2659	228.6464	3
11	1296.7316	1278.7211	1279.7046	648.8658	K(+56.03)	359.2401	341.2296	342.2131	180.1201	2
12					R	175.1191	157.1084	158.0919	88.0595	1

Figure S14_31

MSMS assignment of K55ox in Chromodomain-helicase-DNA-binding protein 3

CHD3(53-66): GPK*[O]K*QK*ENK*PGK*PR; -10lgP 44.75; Scan 27652 (MC356)

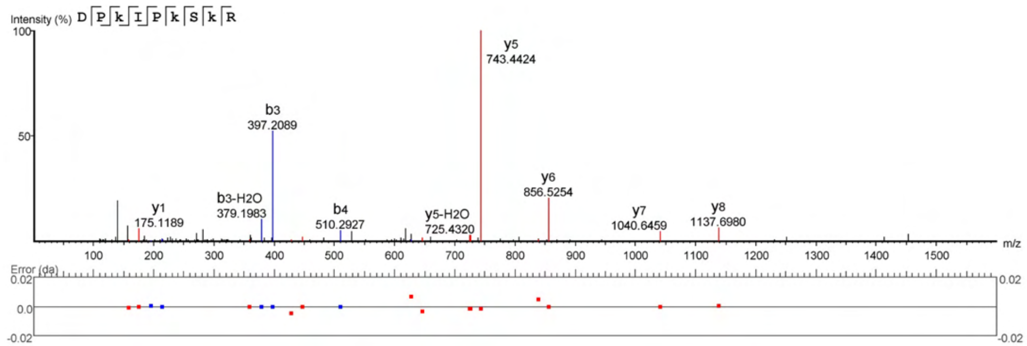


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	58.0293	40.0187	41.0023	29.5146	G					14
2	155.0813	137.0715	138.0550	78.0410	P	1831.0436	1813.0331	1814.0166	916.0218	13
3	355.1982	337.1872	338.1711	178.0991	K(+72.02)	1733.9907	1715.9802	1716.9637	867.4954	12
4	539.3191	521.3075	522.2923	270.1596	K(+56.03)	1533.8708	1515.8641	1516.8477	767.4373	11
5	667.3779	649.3673	650.3509	334.1889	Q	1349.7544	1331.7430	1332.7234	675.3768	10
6	851.4990	833.4885	834.4720	426.2495	K(+56.03)	1221.6932	1203.6844	1204.6680	611.3475	9
7	980.5416	962.5311	963.5146	490.7708	E	1037.5757	1019.5632	1020.5468	519.2869	8
8	1094.5846	1076.5741	1077.5576	547.7923	N	908.5306	890.5206	891.5042	454.7656	7
9	1278.7072	1260.6813	1261.6787	639.8528	K(+56.03)	794.4887	776.4777	777.4612	397.7441	6
10	1375.7585	1357.7480	1358.7316	688.3793	P	610.3663	592.3565	593.3411	305.6835	5
11	1432.7799	1414.7694	1415.7529	716.8900	G	513.3114	495.3038	496.2874	257.1572	4
12	1616.9011	1598.8906	1599.8741	808.9506	K(+56.03)	456.2947	438.2823	439.2659	228.6464	3
13	1713.9539	1695.9434	1696.9269	857.4769	P	272.1718	254.1611	255.1447	136.5858	2
14					R	175.1188	157.0974	158.0919	88.0595	1

Figure S14_32

MSMS assignment of K67ox in Chromodomain-helicase-DNA-binding protein 4

CHD4(62-70): DPK*IPK*[O]SK*R; -10lgP 32.94; Scan 23506 (MC355)

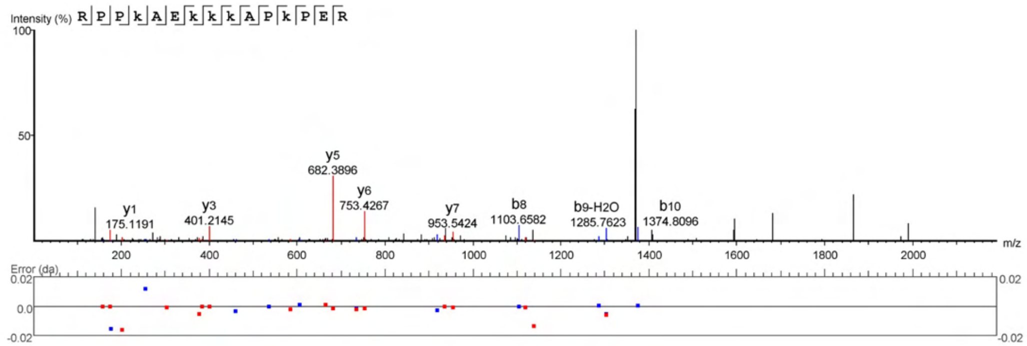


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	116.0348	98.0242	99.0078	58.5174	D					9
2	213.0872	195.0763	196.0605	107.0438	P	1137.6980	1119.6885	1120.6720	569.3495	8
3	397.2089	379.1983	380.1817	199.1043	K(+56.03)	1040.6459	1022.6356	1023.6191	520.8231	7
4	510.2927	492.2822	493.2657	255.6464	I	856.5254	838.5092	839.4980	428.7670	6
5	607.3455	589.3350	590.3185	304.1728	P	743.4424	725.4320	726.4156	372.2205	5
6	807.4616	789.4510	790.4346	404.2308	K(+72.02)	646.3915	628.3776	629.3612	323.6941	4
7	894.4936	876.4830	877.4666	447.7468	S	446.2727	428.2616	429.2451	223.6361	3
8	1078.6147	1060.6042	1061.5878	539.8074	K(+56.03)	359.2398	341.2296	342.2131	180.1201	2
9					R	175.1189	157.1084	158.0927	88.0595	1

Figure S14_33

MSMS assignment of K993ox in RNA polymerase-associated protein CTR9 homolog

CTR9(985-999): RPPK*AEK*K*K*[O]APK*PER; -10lgP 42.79; Scan 23004 (MC355)

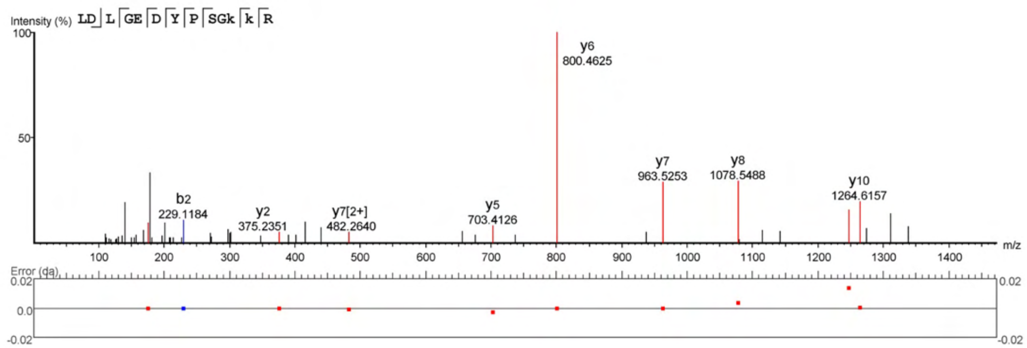


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	157.1085	139.0984	140.0819	79.0545	R					15
2	254.1493	236.1511	237.1347	127.5808	P	1900.0901	1882.0796	1883.0631	950.5450	14
3	351.2144	333.2039	334.1874	176.1226	P	1803.0374	1785.0269	1786.0104	902.0187	13
4	535.3361	517.3250	518.3086	268.1678	K(+56.03)	1705.9846	1687.9741	1688.9576	853.4923	12
5	606.3709	588.3621	589.3457	303.6863	A	1521.8634	1503.8529	1504.8364	761.4317	11
6	735.4172	717.4047	718.3883	368.2076	E	1450.8263	1432.8158	1433.7993	725.9131	10
7	919.5397	901.5259	902.5095	460.2715	K(+56.03)	1321.7837	1303.7793	1304.7567	661.3918	9
8	1103.6582	1085.6471	1086.6306	552.3288	K(+56.03)	1137.6763	1119.6531	1120.6356	569.3313	8
9	1303.7793	1285.7623	1286.7467	652.3868	K(+72.02)	953.5424	935.5312	936.5144	477.2707	7
10	1374.8096	1356.8003	1357.7838	687.9054	A	753.4267	735.4172	736.3983	377.2178	6
11	1471.8636	1453.8531	1454.8367	736.4318	P	682.3896	664.3776	665.3595	341.6941	5
12	1655.9847	1637.9742	1638.9578	828.4924	K(+56.03)	585.3375	567.3249	568.3085	293.1677	4
13	1753.0375	1735.0270	1736.0105	877.0187	P	401.2145	383.2037	384.1877	201.1234	3
14	1882.0801	1864.0696	1865.0531	941.5400	E	304.1621	286.1509	287.1345	152.5807	2
15					R	175.1191	157.1085	158.0919	88.0595	1

Figure S14_34

MSMS assignment of K18ox in Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15

DHX15(7-19): LDLGEDYPSGK*K*[O]R; -10lgP 34.92; Scan 33966 (MC362)

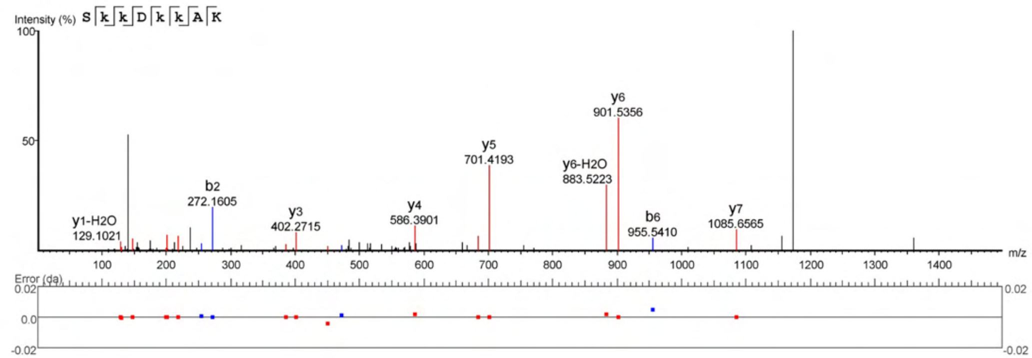


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	114.0919	96.0813	97.0649	57.5459	L					13
2	229.1184	211.1083	212.0918	115.0594	D	1492.7278	1474.7173	1475.7008	746.8639	12
3	342.2029	324.1923	325.1759	171.6014	L	1377.7008	1359.6903	1360.6738	689.3504	11
4	399.2243	381.2138	382.1974	200.1122	G	1264.6157	1246.5920	1247.5897	632.8083	10
5	528.2669	510.2563	511.2399	264.6335	E	1207.5953	1189.5848	1190.5684	604.2977	9
6	643.2939	625.2833	626.2669	322.1469	D	1078.5488	1060.5422	1061.5258	539.7764	8
7	806.3572	788.3466	789.3302	403.6786	Y	963.5253	945.5152	946.4988	482.2640	7
8	903.4099	885.3994	886.3829	452.2050	P	800.4625	782.4518	783.4354	400.7312	6
9	990.4420	972.4314	973.4150	495.7210	S	703.4126	685.3991	686.3827	352.2048	5
10	1047.4634	1029.4529	1030.4364	524.2317	G	616.3776	598.3671	599.3506	308.6888	4
11	1231.5846	1213.5741	1214.5576	616.2923	K(+56.03)	559.3562	541.3456	542.3292	280.1781	3
12	1431.7007	1413.6902	1414.6737	716.3503	K(+72.02)	375.2351	357.2245	358.2080	188.1175	2
13					R	175.1190	157.1084	158.0919	88.0595	1

Figure S14_35

MSMS assignment of K475ox in H/ACA ribonucleoprotein complex subunit DKC1

DKC(473-480): SK*K*[O]DK*K*AK; -10lgP 27.46; Scan 8697 (MC309)

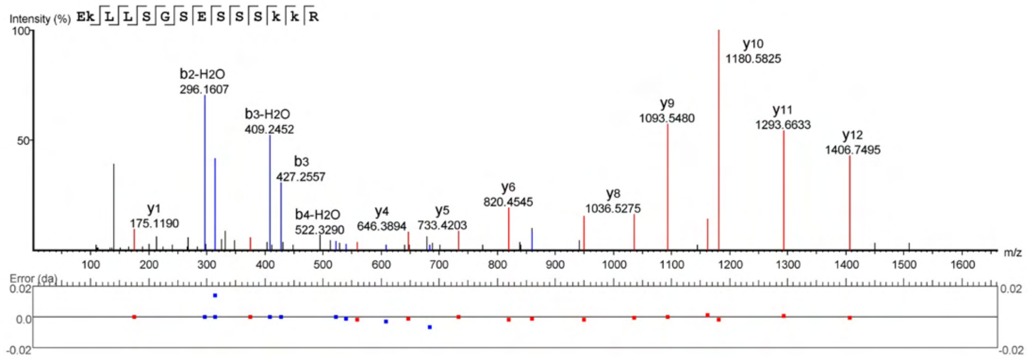


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	88.0399	70.0293	71.0129	44.5199	S					8
2	272.1605	254.1498	255.1340	136.5805	K(+56.03)	1085.6565	1067.6459	1068.6294	543.3282	7
3	472.2758	454.2665	455.2501	236.6385	K(+72.02)	901.5356	883.5223	884.5083	451.2719	6
4	587.3040	569.2935	570.2770	294.1520	D	701.4193	683.4086	684.3928	351.2096	5
5	771.4252	753.4147	754.3983	386.2126	K(+56.03)	586.3901	568.3817	569.3652	293.6961	4
6	955.5410	937.5358	938.5194	478.2732	K(+56.03)	402.2715	384.2605	385.2439	201.6355	3
7	1026.5835	1008.5729	1009.5565	513.7917	A	218.1502	200.1391	201.1233	109.5750	2
8					K	147.1124	129.1021	130.0864	74.0564	1

Figure S14_36

MSMS assignment of K90ox in Protein FAM133B

FAM133B(78-91): EK*LLSGSESSSK*K*[O]R; -10lgP 51.19; Scan 13718 (MC315)

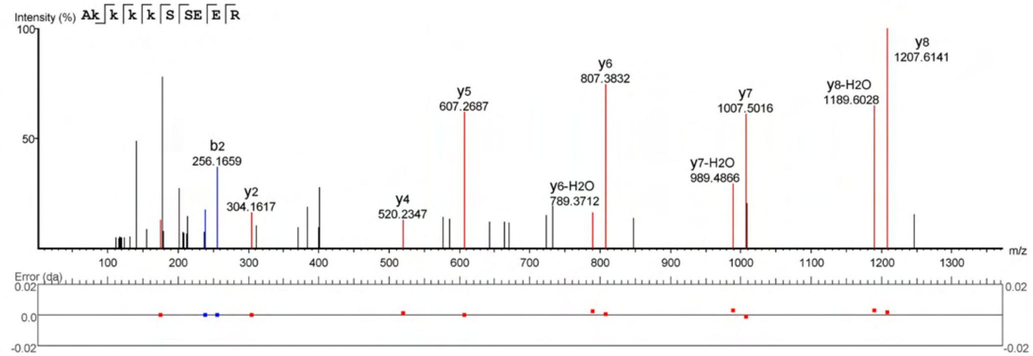


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	130.0504	112.0399	113.0234	65.5252	E					14
2	314.1714	296.1607	297.1446	157.5858	K(+56.03)	1590.8696	1572.8591	1573.8427	795.9348	13
3	427.2557	409.2452	410.2286	214.1278	L	1406.7495	1388.7380	1389.7216	703.8743	12
4	540.3412	522.3290	523.3127	270.6699	L	1293.6633	1275.6539	1276.6375	647.3322	11
5	627.3717	609.3643	610.3447	314.1714	S	1180.5825	1162.5684	1163.5533	590.7902	10
6	684.4003	666.3826	667.3662	342.6966	G	1093.5480	1075.5378	1076.5214	547.2742	9
7	771.4252	753.4147	754.3983	386.2126	S	1036.5275	1018.5163	1019.4999	518.7634	8
8	900.4678	882.4572	883.4408	450.7339	E	949.4969	931.4843	932.4679	475.2474	7
9	987.4998	969.4893	970.4728	494.2499	S	820.4545	802.4417	803.4253	410.7261	6
10	1074.5319	1056.5214	1057.5049	537.7659	S	733.4203	715.4097	716.3932	367.2101	5
11	1161.5638	1143.5533	1144.5369	581.2819	S	646.3894	628.3776	629.3612	323.6941	4
12	1345.6851	1327.6746	1328.6581	673.3425	K(+56.03)	559.3580	541.3456	542.3292	280.1781	3
13	1545.8011	1527.7906	1528.7742	773.4006	K(+72.02)	375.2356	357.2245	358.2080	188.1175	2
14					R	175.1190	157.1084	158.0919	88.0595	1

Figure S14_37

MSMS assignment of K208ox, K209ox, K210ox in Protein FAM133B

FAM133B(206-215): **AK*K*[O]K*[O]K*[O]SSEER**; -10lgP 34.34; Scan 6424 (MC309)

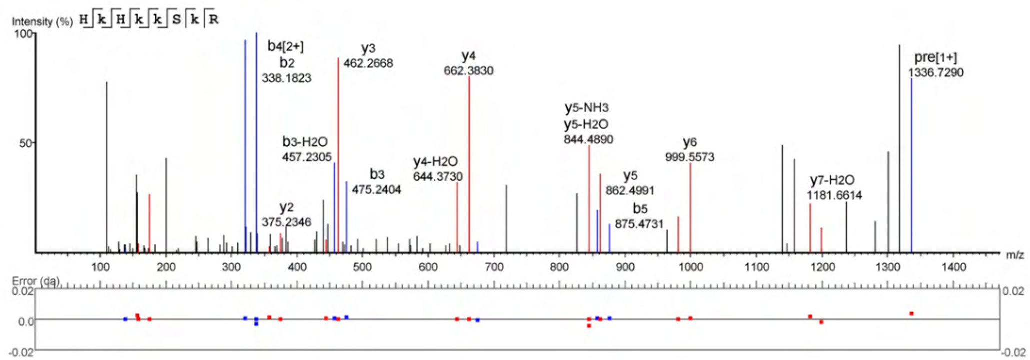


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	72.0449	54.0344	55.0179	36.5225	A					10
2	256.1659	238.1555	239.1389	128.5831	K(+56.03)	1391.7375	1373.7271	1374.7106	696.3688	9
3	456.2822	438.2716	439.2552	228.6411	K(+72.02)	1207.6141	1189.6028	1190.5895	604.3082	8
4	656.3983	638.3877	639.3713	328.6991	K(+72.02)	1007.5016	989.4866	990.4734	504.2502	7
5	856.5143	838.5038	839.4874	428.7572	K(+72.02)	807.3832	789.3712	790.3573	404.1921	6
6	943.5464	925.5358	926.5194	472.2732	S	607.2687	589.2576	590.2412	304.1341	5
7	1030.5784	1012.5678	1013.5514	515.7892	S	520.2347	502.2256	503.2092	260.6181	4
8	1159.6210	1141.6105	1142.5940	580.3105	E	433.2041	415.1935	416.1771	217.1021	3
9	1288.6636	1270.6531	1271.6366	644.8318	E	304.1617	286.1509	287.1345	152.5807	2
10					R	175.1192	157.1084	158.0919	88.0595	1

Figure S14_38

MSMS assignment of K564ox, K566ox, K567ox, K569ox in Pre-mRNA 3'-end-processing factor FIP1

FIP1L1(563-570): HK*[O]HK*[O]K*[O]SK*[O]R; -10lgP 37.45; Scan 4737 (MC308)



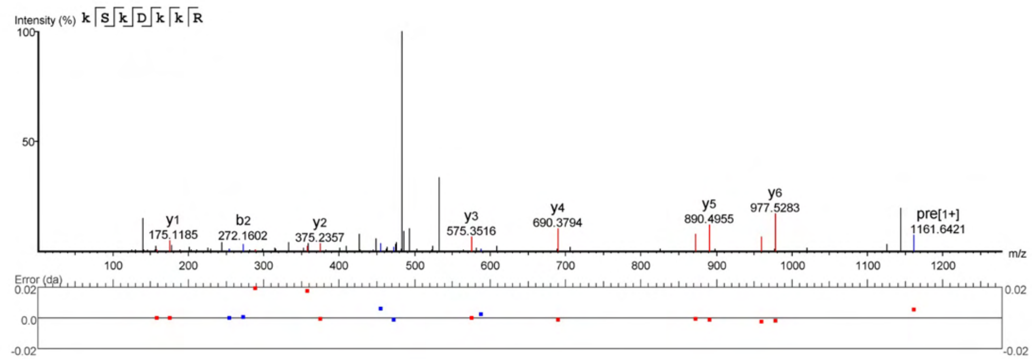
#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	138.0664	120.0562	121.0397	69.5334	H					8
2	338.1823	320.1715	321.1558	169.5914	K(+72.02)	1199.6763	1181.6614	1182.6472	600.3371	7
3	475.2404	457.2305	458.2148	238.1209	H	999.5573	981.5475	982.5311	500.2791	6
4	675.3588	657.3472	658.3308	338.1823	K(+72.02)	862.4991	844.4890	845.4769	431.7496	5
5	875.4731	857.4622	858.4469	438.2369	K(+72.02)	662.3830	644.3730	645.3561	331.6916	4
6	962.5059	944.4954	945.4789	481.7530	S	462.2668	444.2559	445.2401	231.6335	3
7	1162.6221	1144.6116	1145.5951	581.8110	K(+72.02)	375.2346	357.2245	358.2063	188.1175	2
8					R	175.1188	157.1055	158.0919	88.0595	1

Figure S14_39

Non-unique MSMS assignment: K*SK*[O]DK*[O]K*[O]R; -10lgP 15.85; Scan 6660 (MC305)

1. K27ox, K29ox, K30ox in Protein FRG1; FRG1(25-31)

2. K241ox, K242ox, K244ox in Serine/arginine repetitive matrix protein 2; SRRM2(239-245)

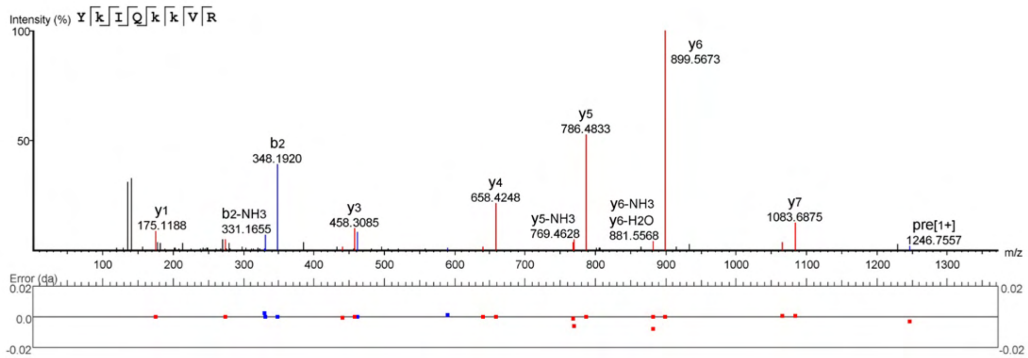


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	185.1290	167.1184	168.1020	93.0645	K(+56.03)					7
2	272.1602	254.1501	255.1340	136.5805	S	977.5283	959.5181	960.4992	489.2631	6
3	472.2786	454.2600	455.2501	236.6385	K(+72.02)	890.4955	872.4845	873.4672	445.7471	5
4	587.3014	569.2935	570.2770	294.1520	D	690.3794	672.3675	673.3511	345.6890	4
5	787.4201	769.4095	770.3931	394.2101	K(+72.02)	575.3516	557.3405	558.3241	288.1558	3
6	987.5362	969.5256	970.5092	494.2681	K(+72.02)	375.2357	357.2064	358.2080	188.1175	2
7					R	175.1185	157.1084	158.0919	88.0595	1

Figure S14_40

MSMS assignment of K20ox, K23ox in Guanine nucleotide-binding protein-like 3

GNL3(19-26): YK*[O]IQK*[O]K*VR; -10lgP 26.57; Scan 12215 (MC309)

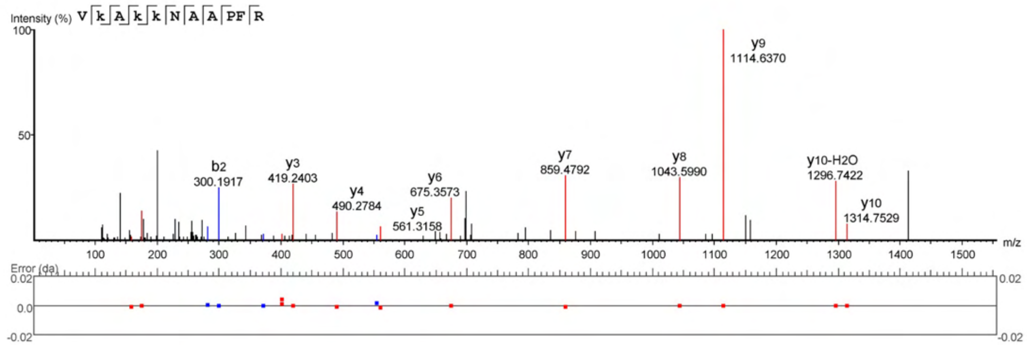


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	164.0712	146.0606	147.0441	82.5356	Y					8
2	348.1920	330.1790	331.1655	174.5962	K(+56.03)	1083.6875	1065.6770	1066.6614	542.3442	7
3	461.2763	443.2658	444.2494	231.1382	I	899.5673	881.5568	882.5487	450.2836	6
4	589.3336	571.3244	572.3080	295.1675	Q	786.4833	768.4741	769.4628	393.7416	5
5	789.4510	771.4405	772.4241	395.2255	K(+72.02)	658.4248	640.4139	641.3976	329.7123	4
6	973.5722	955.5616	956.5452	487.2861	K(+56.03)	458.3085	440.2979	441.2827	229.6543	3
7	1072.6406	1054.6301	1055.6136	536.8203	V	274.1875	256.1768	257.1604	137.5937	2
8					R	175.1188	157.1084	158.0919	88.0595	1

Figure S14_41

MSMS assignment of K221ox in Guanine nucleotide-binding protein-like 3

GNL3(220-230): VK*[O]AK*K*NAAPFR; -10lgP 25.05 Scan 27049 (MC361)

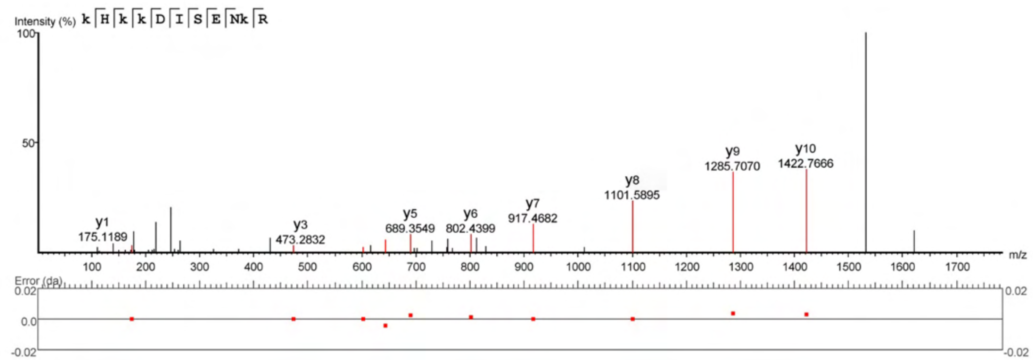


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	100.0762	82.0657	83.0492	50.5381	V					11
2	300.1917	282.1811	283.1653	150.5962	K(+72.02)	1314.7529	1296.7422	1297.7258	657.8764	10
3	371.2299	353.2189	354.2025	186.1147	A	1114.6370	1096.6262	1097.6097	557.8184	9
4	555.3486	537.3400	538.3236	278.1753	K(+56.03)	1043.5990	1025.5891	1026.5726	522.2998	8
5	739.4717	721.4612	722.4448	370.2359	K(+56.03)	859.4792	841.4678	842.4514	430.2392	7
6	853.5147	835.5042	836.4877	427.2574	N	675.3573	657.3467	658.3303	338.1786	6
7	924.5518	906.5413	907.5248	462.7759	A	561.3158	543.3038	544.2874	281.1572	5
8	995.5889	977.5784	978.5620	498.2945	A	490.2784	472.2666	473.2502	245.6386	4
9	1092.6417	1074.6312	1075.6147	546.8209	P	419.2403	401.2247	402.2115	210.1200	3
10	1239.7101	1221.6996	1222.6831	620.3550	F	322.1873	304.1768	305.1603	161.5937	2
11					R	175.1188	157.1084	158.0931	88.0595	1

Figure S14_42

MSMS assignment of K248ox in Heat shock cognate 71 kDa protein

HSPA8(248-258): K*[O]HK*K*DISENK*R; -10lgP 36.09; Scan 9710 (MC309)

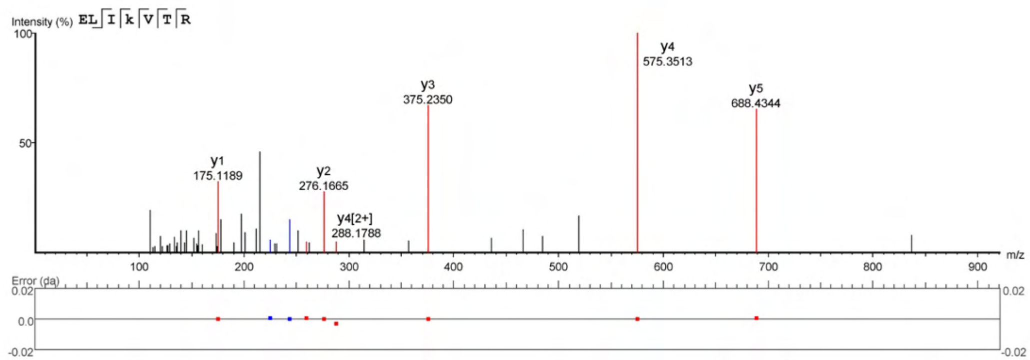


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	201.1239	183.1134	184.0969	101.0620	K(+72.02)					11
2	338.1828	320.1722	321.1558	169.5914	H	1422.7666	1404.7594	1405.7429	711.8849	10
3	522.3040	504.2934	505.2770	261.6520	K(+56.03)	1285.7070	1267.7004	1268.6840	643.3599	9
4	706.4252	688.4146	689.3982	353.7126	K(+56.03)	1101.5895	1083.5793	1084.5629	551.2949	8
5	821.4521	803.4415	804.4251	411.2260	D	917.4682	899.4581	900.4417	459.2343	7
6	934.5361	916.5256	917.5092	467.7681	I	802.4399	784.4312	785.4147	401.7209	6
7	1021.5682	1003.5576	1004.5412	511.2841	S	689.3549	671.3471	672.3307	345.1788	5
8	1150.6107	1132.6002	1133.5837	575.8054	E	602.3257	584.3151	585.2986	301.6628	4
9	1264.6537	1246.6432	1247.6267	632.8268	N	473.2832	455.2725	456.2560	237.1415	3
10	1448.7749	1430.7644	1431.7479	724.8875	K(+56.03)	359.2401	341.2296	342.2131	180.1201	2
11					R	175.1189	157.1084	158.0919	88.0595	1

Figure S14_43

MSMS assignment for K219ox in Bifunctional arginine demethylase and lysyl-hydroxylase JMJD6

JMJD6(216-222): ELIK*[O]VTR; -10lgP 29.89; Scan 11429 (MC317)

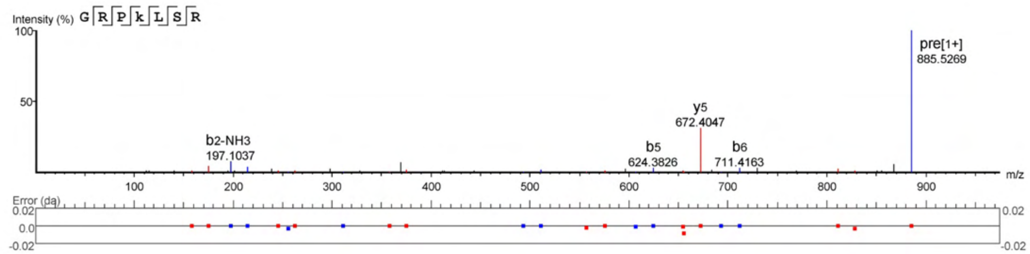


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	130.0504	112.0399	113.0234	65.5252	E					7
2	243.1339	225.1232	226.1075	122.0672	L	801.5192	783.5087	784.4922	401.2596	6
3	356.2185	338.2079	339.1915	178.6093	I	688.4344	670.4246	671.4082	344.7176	5
4	556.3346	538.3240	539.3076	278.6673	K(+72.02)	575.3513	557.3406	558.3242	288.1788	4
5	655.4030	637.3925	638.3760	328.2015	V	375.2350	357.2245	358.2080	188.1175	3
6	756.4507	738.4401	739.4237	378.7253	T	276.1665	258.1561	259.1387	138.5833	2
7					R	175.1189	157.1084	158.0919	88.0595	1

Figure S14_44

MSMS assignment of K307ox in Bifunctional arginine demethylase and lysyl-hydroxylase JMJD6

JMJD6(304-310): GRPK*[O]LSR; -10lgP 34.77; Scan 3885 (MC320)

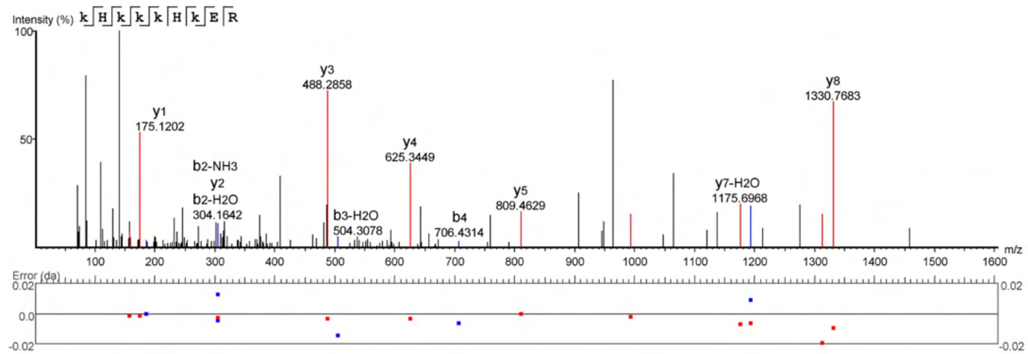


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	58.0293	40.0187	41.0023	29.5146	G					7
2	214.1300	196.1198	197.1037	107.5652	R	828.5083	810.4944	811.4780	414.7525	6
3	311.1833	293.1726	294.1562	156.0916	P	672.4047	654.3952	655.3856	336.7019	5
4	511.2985	493.2892	494.2722	256.1534	K(+72.02)	575.3521	557.3434	558.3241	288.1755	4
5	624.3826	606.3746	607.3563	312.6917	L	375.2355	357.2245	358.2088	188.1175	3
6	711.4163	693.4056	694.3883	356.2076	S	262.1515	244.1404	245.1248	131.5755	2
7					R	175.1192	157.1084	158.0928	88.0595	1

Figure S14_45

MSMS assignment of K360ox in La-related protein 7

LARP7(358-366): K*HK*[O]K*K*HK*ER; -10lgP 18.52; Scan 3999 (MC275)

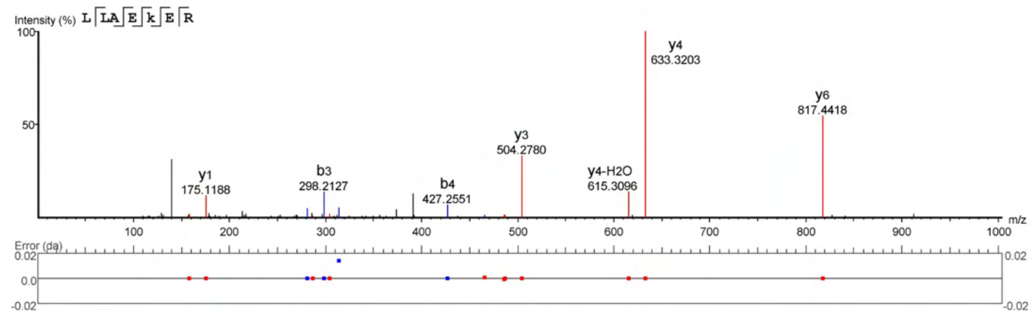


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	185.1295	167.1184	168.1020	93.0645	K(+56.03)					9
2	322.1879	304.1642	305.1656	161.5939	H	1330.7683	1312.7676	1313.7319	665.8795	8
3	522.3040	504.3078	505.2770	261.6520	K(+72.02)	1193.7063	1175.6968	1176.6731	597.3500	7
4	706.4314	688.4146	689.3982	353.7126	K(+56.03)	993.5858	975.5734	976.5569	497.2920	6
5	890.5463	872.5358	873.5193	445.7732	K(+56.03)	809.4629	791.4522	792.4358	405.2314	5
6	1027.6052	1009.5947	1010.5782	514.3026	H	625.3449	607.3311	608.3146	313.1708	4
7	1211.7264	1193.7063	1194.6995	606.3632	K(+56.03)	488.2858	470.2721	471.2557	244.6413	3
8	1340.7690	1322.7585	1323.7421	670.8845	E	304.1642	286.1509	287.1345	152.5807	2
9					R	175.1202	157.1084	158.0935	88.0595	1

Figure S14_46

MSMS assignment of K341ox in Prelamin-A/C

LMNA(337-343): LLAEK*[O]ER; -10lgP 22.86; Scan 9430 (MC306)

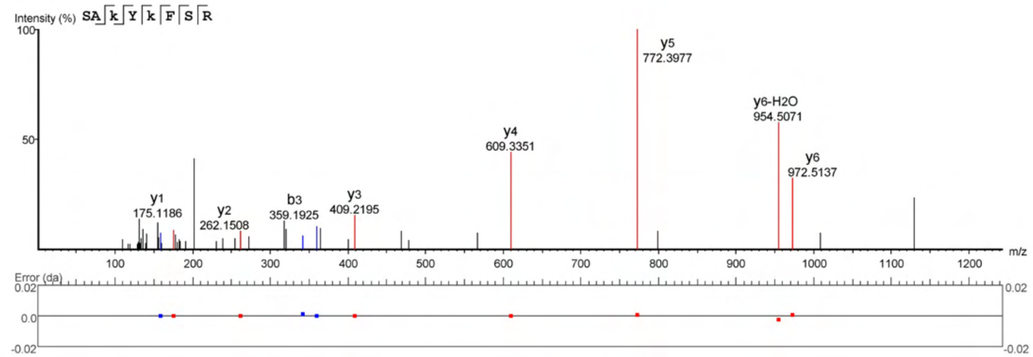


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	114.0919	96.0813	97.0649	57.5459	L					7
2	227.1759	209.1654	210.1489	114.0880	L	817.4418	799.4308	800.4144	409.2207	6
3	298.2127	280.2025	281.1859	149.6065	A	704.3573	686.3467	687.3303	352.6786	5
4	427.2551	409.2451	410.2286	214.1278	E	633.3203	615.3096	616.2932	317.1601	4
5	627.3717	609.3611	610.3447	314.1713	K(+72.02)	504.2780	486.2679	487.2504	252.6388	3
6	756.4143	738.4037	739.3873	378.7072	E	304.1617	286.1509	287.1351	152.5807	2
7					R	175.1188	157.1084	158.0924	88.0595	1

Figure S14_47

MSMS assignment of K323ox, K325ox in Putative RNA-binding protein Luc7-like 1

LUC7L(321-328): SAK*[O]YK*[O]FSR; -10lgP 36.68; Scan 9323 (MC317)

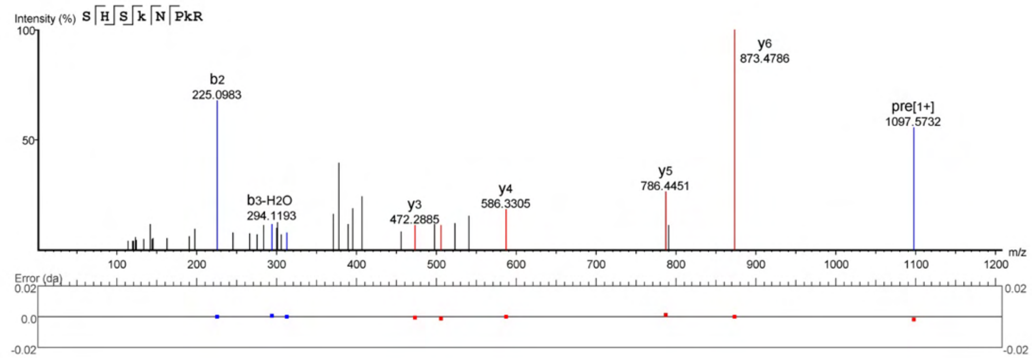


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	88.0399	70.0293	71.0129	44.5199	S					8
2	159.0766	141.0664	142.0500	80.0385	A	1043.5520	1025.5415	1026.5250	522.2760	7
3	359.1925	341.1811	342.1661	180.0965	K(+72.02)	972.5137	954.5071	955.4879	486.7574	6
4	522.2563	504.2458	505.2294	261.6282	Y	772.3977	754.3882	755.3718	386.6994	5
5	722.3724	704.3619	705.3455	361.6862	K(+72.02)	609.3351	591.3249	592.3085	305.1677	4
6	869.4409	851.4303	852.4139	435.2204	F	409.2195	391.2088	392.1924	205.1097	3
7	956.4729	938.4623	939.4459	478.7365	S	262.1508	244.1404	245.1240	131.5755	2
8					R	175.1186	157.1084	158.0919	88.0595	1

Figure S14_48

MSMS assignment of K266ox, K269ox in Putative RNA-binding protein Luc7-like 2

LUC7L2(263-270): SHSK*[O]NPK*[O]R; -10lgP 64.15; Scan 3234 (MC318)

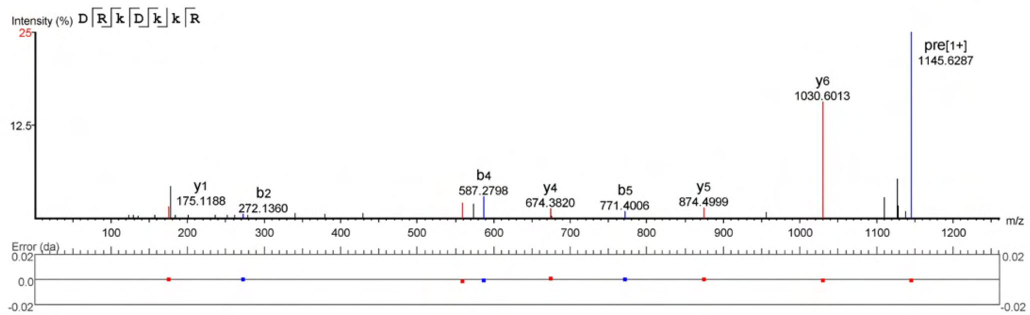


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	88.0399	70.0293	71.0129	44.5199	S					8
2	225.0983	207.0882	208.0718	113.0494	H	1010.5377	992.5272	993.5107	505.7702	7
3	312.1310	294.1193	295.1038	156.5654	S	873.4786	855.4683	856.4518	437.2394	6
4	512.2469	494.2363	495.2199	256.6234	K(+72.02)	786.4451	768.4362	769.4198	393.7234	5
5	626.2898	608.2792	609.2628	313.6449	N	586.3305	568.3201	569.3037	293.6653	4
6	723.3425	705.3320	706.3156	362.1713	P	472.2885	454.2772	455.2608	236.6439	3
7	923.4586	905.4481	906.4316	462.2293	K(+72.02)	375.2350	357.2245	358.2080	188.1175	2
8					R	175.1189	157.1084	158.0919	88.0595	1

Figure S14_49

MSMS assignment of K365ox, K368ox in Putative RNA-binding protein Luc7-like 2

LUC7L2(363-369): DRK*[O]DK*K*[O]R; -10lgP 26.30; Scan 5119 (MC312)

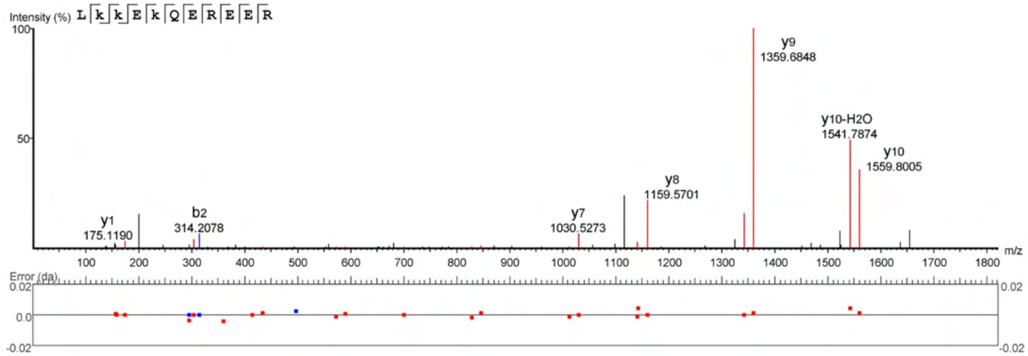


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	88.0399	70.0293	71.0129	44.5199	S					8
2	225.0983	207.0882	208.0718	113.0494	H	1010.5377	992.5272	993.5107	505.7702	7
3	312.1310	294.1193	295.1038	156.5654	S	873.4786	855.4683	856.4518	437.2394	6
4	512.2469	494.2363	495.2199	256.6234	K(+72.02)	786.4451	768.4362	769.4198	393.7234	5
5	626.2898	608.2792	609.2628	313.6449	N	586.3305	568.3201	569.3037	293.6653	4
6	723.3425	705.3320	706.3156	362.1713	P	472.2885	454.2772	455.2608	236.6439	3
7	923.4586	905.4481	906.4316	462.2293	K(+72.02)	375.2350	357.2245	358.2080	188.1175	2
8					R	175.1189	157.1084	158.0919	88.0595	1

Figure S14_50

MSMS assignment of K248ox and K249ox in Luc7-like protein 3

LUC7L3(247-257): LK*[O]K*[O]EK*QEREER; -10lgP 30.58; Scan 6968 (MC303)

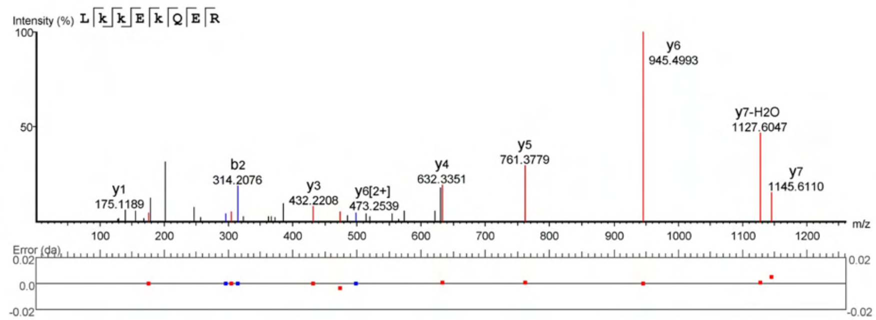


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	114.0919	96.0813	97.0649	57.5459	L					11
2	314.2078	296.1971	297.1810	157.6040	K(+72.02)	1559.8005	1541.7874	1542.7753	780.4011	10
3	514.3240	496.3110	497.2971	257.6620	K(+72.02)	1359.6848	1341.6753	1342.6593	680.3431	9
4	643.3666	625.3561	626.3397	322.1833	E	1159.5701	1141.5610	1142.5386	580.2850	8
5	827.4878	809.4772	810.4608	414.2439	K(+56.03)	1030.5273	1012.5170	1013.5021	515.7638	7
6	955.5464	937.5358	938.5194	478.2732	Q	846.4048	828.3958	829.3815	423.7032	6
7	1084.5890	1066.5785	1067.5620	542.7945	E	718.3478	700.3372	701.3204	359.6782	5
8	1240.6901	1222.6796	1223.6631	620.8450	R	589.3044	571.2946	572.2798	295.1563	4
9	1369.7327	1351.7222	1352.7057	685.3663	E	433.2025	415.1941	416.1771	217.1021	3
10	1498.7753	1480.7648	1481.7483	749.8876	E	304.1616	286.1509	287.1345	152.5807	2
11					R	175.1190	157.1077	158.0925	88.0595	1

Figure S14_51

MSMS assignment for K251ox in Luc7-like protein 3

LUC7L3(247-254): LK*[O]K*EK*[O]QER; -10lgP 24.43; Scan 6492 (MC317)

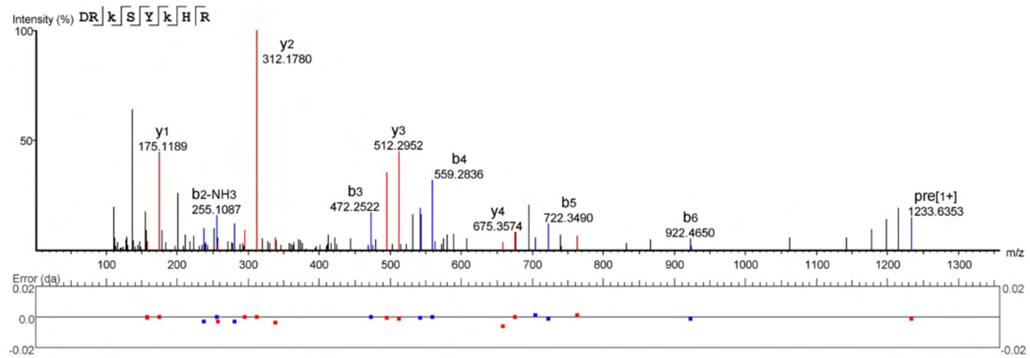


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	114.0919	96.0813	97.0649	57.5459	L					8
2	314.2076	296.1969	297.1810	157.6040	K(+72.02)	1145.6110	1127.6047	1128.5890	573.3080	7
3	498.3293	480.3186	481.3022	249.6646	K(+56.03)	945.4993	927.4894	928.4730	473.2539	6
4	627.3717	609.3611	610.3447	314.1859	E	761.3779	743.3682	744.3518	381.1894	5
5	827.4878	809.4772	810.4608	414.2439	K(+72.02)	632.3351	614.3256	615.3092	316.6681	4
6	955.5464	937.5358	938.5194	478.2732	Q	432.2208	414.2095	415.1931	216.6100	3
7	1084.5890	1066.5785	1067.5620	542.7945	E	304.1613	286.1509	287.1345	152.5807	2
8					R	175.1189	157.1084	158.0919	88.0595	1

Figure S14_52

MSMS assignment for K359ox, K362ox in Luc7-like protein 3

LUC7L3(357-364): DRK*[O]SYK*[O]HR; -10lgP 41.89; Scan 5575 (MC315)

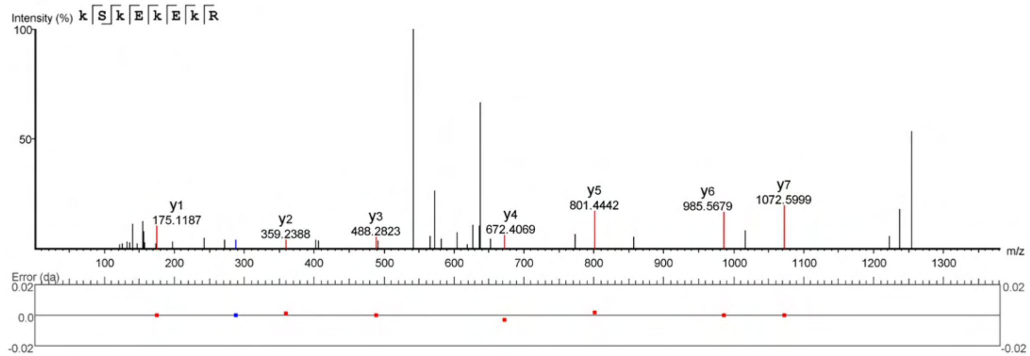


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	116.0348	98.0242	99.0078	58.5174	D					8
2	272.1359	254.1253	255.1087	136.5679	R	1118.6064	1100.5959	1101.5795	559.8032	7
3	472.2522	454.2414	455.2250	236.6295	K(+72.02)	962.5054	944.4948	945.4784	481.7527	6
4	559.2836	541.2740	542.2570	280.1452	S	762.3878	744.3787	745.3623	381.6946	5
5	722.3490	704.3351	705.3203	361.6736	Y	675.3574	657.3467	658.3365	338.1828	4
6	922.4650	904.4528	905.4364	461.7317	K(+72.02)	512.2952	494.2842	495.2670	256.6505	3
7	1059.5223	1041.5118	1042.4954	530.2612	H	312.1780	294.1670	295.1514	156.5889	2
8					R	175.1189	157.1084	158.0926	88.0595	1

Figure S14_53

MSMS assignment of K375ox in Luc7-like protein 3

LUC7L3(375-382): K*[O]SK*EK*EK*R; -10lgP 29.52; Scan 9691 (MC303)

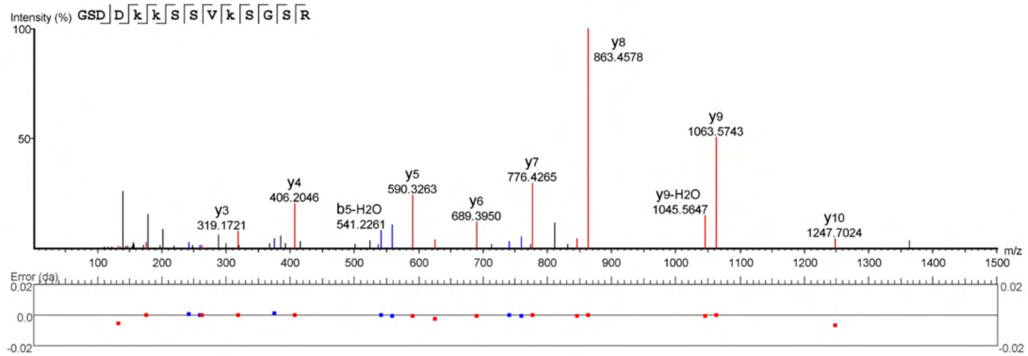


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	201.1239	183.1134	184.0969	101.0620	K(+72.02)					8
2	288.1557	270.1454	271.1290	144.5780	S	1072.5999	1054.5891	1055.5726	536.7998	7
3	472.2771	454.2665	455.2501	236.6385	K(+56.03)	985.5679	967.5571	968.5406	493.2838	6
4	601.3197	583.3091	584.2927	301.1599	E	801.4442	783.4359	784.4194	401.2232	5
5	785.4409	767.4303	768.4139	393.2204	K(+56.03)	672.4069	654.3933	655.3769	336.7019	4
6	914.4835	896.4729	897.4565	457.7417	E	488.2823	470.2721	471.2557	244.6413	3
7	1098.6046	1080.5941	1081.5776	549.8023	K(+56.03)	359.2388	341.2296	342.2131	180.1201	2
8					R	175.1187	157.1084	158.0919	88.0595	1

Figure S14_54

MSMS assignment for K388ox in Luc7-like protein 3

LUC7L3(383-396): GSDDK*K*[O]SSVK*SGSR; -10lgP 60.68; Scan 9889 (MC311)

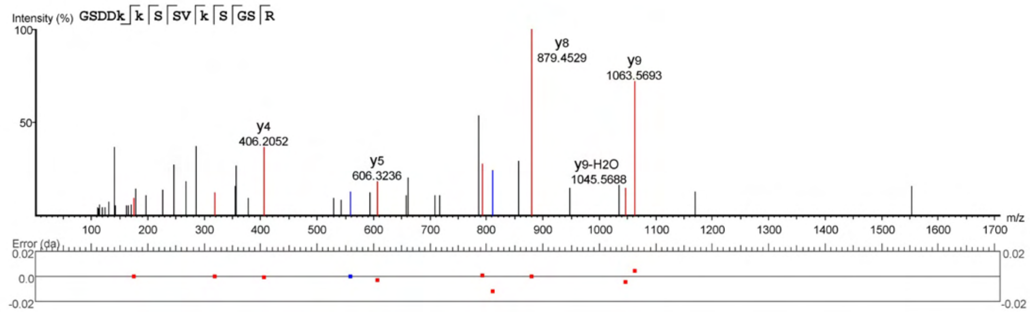


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	58.0293	40.0187	41.0023	29.5146	G					14
2	145.0613	127.0508	128.0343	73.0307	S	1564.7812	1546.7708	1547.7543	782.8906	13
3	260.0880	242.0770	243.0613	130.5441	D	1477.7493	1459.7388	1460.7223	739.3746	12
4	375.1136	357.1046	358.0882	188.0576	D	1362.7223	1344.7118	1345.6953	681.8611	11
5	559.2371	541.2261	542.2094	280.1182	K(+56.03)	1247.7024	1229.6848	1230.6683	624.3505	10
6	759.3535	741.3418	742.3254	380.1762	K(+72.02)	1063.5743	1045.5647	1046.5472	532.2871	9
7	846.3845	828.3739	829.3575	423.6922	S	863.4578	845.4485	846.4311	432.2290	8
8	933.4165	915.4059	916.3895	467.2083	S	776.4265	758.4155	759.3990	388.7130	7
9	1032.4849	1014.4743	1015.4579	516.7424	V	689.3950	671.3835	672.3671	345.1970	6
10	1216.6061	1198.5956	1199.5791	608.8030	K(+56.03)	590.3263	572.3151	573.2986	295.6628	5
11	1303.6381	1285.6276	1286.6111	652.3190	S	406.2046	388.1939	389.1775	203.6022	4
12	1360.6595	1342.6490	1343.6326	680.8298	G	319.1721	301.1619	302.1454	160.0862	3
13	1447.6917	1429.6812	1430.6647	724.3458	S	262.1514	244.1404	245.1240	131.5812	2
14					R	175.1189	157.1084	158.0919	88.0595	1

Figure S14_55

MSMS assignment of K392ox in Luc7-like protein 3

LUC7L3(383-396): GSDDK*K*SSVK*[O]SGSR; -10lgP 37.15; Scan 10322 (MC305)

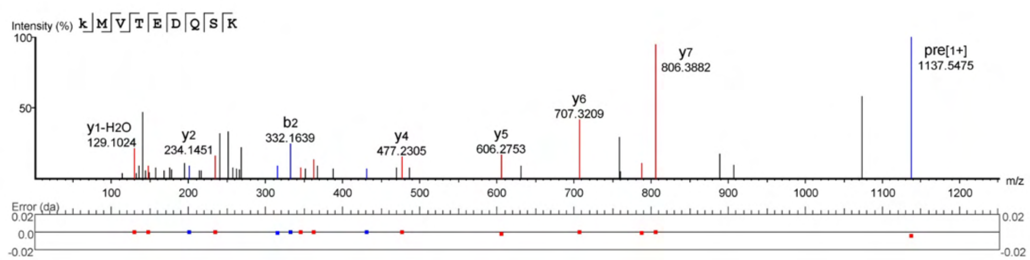


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	58.0293	40.0187	41.0023	29.5146	G					14
2	145.0613	127.0508	128.0343	73.0307	S	1564.7812	1546.7708	1547.7543	782.8906	13
3	260.0883	242.0777	243.0613	130.5441	D	1477.7493	1459.7388	1460.7223	739.3746	12
4	375.1152	357.1046	358.0882	188.0576	D	1362.7223	1344.7118	1345.6953	681.8611	11
5	559.2363	541.2258	542.2094	280.1182	K(+56.03)	1247.6953	1229.6848	1230.6683	624.3477	10
6	743.3575	725.3470	726.3306	372.1788	K(+56.03)	1063.5693	1045.5688	1046.5472	532.2871	9
7	830.3895	812.3790	813.3625	415.6948	S	879.4529	861.4424	862.4260	440.2265	8
8	917.4216	899.4110	900.3946	459.2108	S	792.4198	774.4104	775.3940	396.7105	7
9	1016.4900	998.4794	999.4630	508.7450	V	705.3889	687.3784	688.3619	353.1945	6
10	1216.6061	1198.5956	1199.5791	608.8030	K(+72.02)	606.3236	588.3100	589.2936	303.6603	5
11	1303.6381	1285.6276	1286.6111	652.3190	S	406.2052	388.1939	389.1775	203.6022	4
12	1360.6595	1342.6490	1343.6326	680.8298	G	319.1725	301.1619	302.1454	160.0862	3
13	1447.6917	1429.6812	1430.6647	724.3458	S	262.1510	244.1404	245.1240	131.5755	2
14					R	175.1190	157.1084	158.0919	88.0595	1

Figure S14_56

MSMS assignment of K322ox in 39S ribosomal protein L39, mitochondrial

MRPL39(322-330): K*[O]MVTEDQSK; -10lgP 42.04; Scan 6031 (MC314)

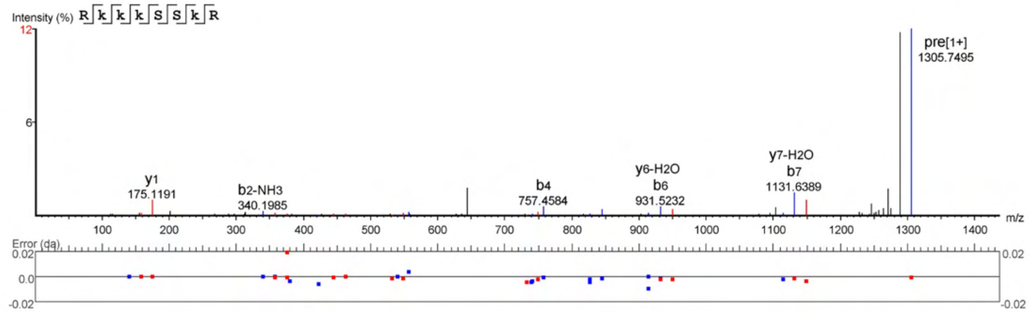


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	201.1239	183.1134	184.0969	101.0620	K(+72.02)					9
2	332.1639	314.1538	315.1392	166.5822	M	937.4295	919.4189	920.4025	469.2148	8
3	431.2319	413.2223	414.2058	216.1164	V	806.3882	788.3802	789.3621	403.6945	7
4	532.2805	514.2700	515.2535	266.6403	T	707.3209	689.3101	690.2936	354.1603	6
5	661.3231	643.3125	644.2961	331.1615	E	606.2753	588.2623	589.2459	303.6364	5
6	776.3500	758.3395	759.3231	388.6750	D	477.2305	459.2198	460.2033	239.1152	4
7	904.4086	886.3980	887.3816	452.7043	Q	362.2026	344.1928	345.1765	181.6017	3
8	991.4406	973.4301	974.4136	496.2203	S	234.1451	216.1343	217.1178	117.5724	2
9					K	147.1133	129.1024	130.0858	74.0564	1

Figure S14_57

MSMS assignment of K198ox, K19ox, K200ox, K203ox in NF-kappa-B-activating protein

NKAP(197-204): RK*[O]K*[O]K*[O]SSK*[O]R; -10lgP 21.51; Scan 4675 (MC309)

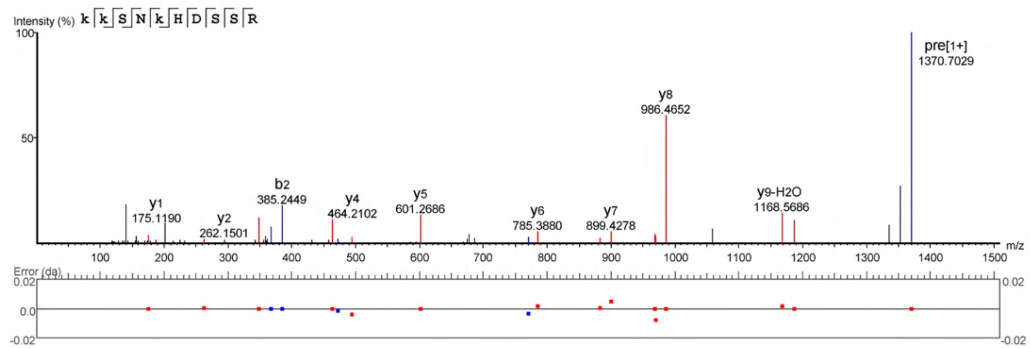


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	157.1089	139.0984	140.0815	79.0545	R					8
2	357.2254	339.2144	340.1985	179.1125	K(+72.02)	1149.6514	1131.6389	1132.6204	575.3237	7
3	557.3372	539.3305	540.3146	279.1705	K(+72.02)	949.5339	931.5232	932.5043	475.2656	6
4	757.4584	739.4514	740.4343	379.2327	K(+72.02)	749.4174	731.4046	732.3929	375.1883	5
5	844.4913	826.4812	827.4669	422.7505	S	549.3009	531.2885	532.2742	275.1495	4
6	931.5232	913.5112	914.5046	466.2606	S	462.2676	444.2565	445.2412	231.6335	3
7	1131.6389	1113.6268	1114.6130	566.3187	K(+72.02)	375.2363	357.2254	358.2095	188.1175	2
8					R	175.1191	157.1084	158.0924	88.0595	1

Figure S14_58

MSMS assignment of K199ox in Histone-lysine N-methyltransferase NSD3

NSD3(198-207): K*K*[O]SNK*HDSSR; -10lgP 33.37; Scan 5486 (MC361)

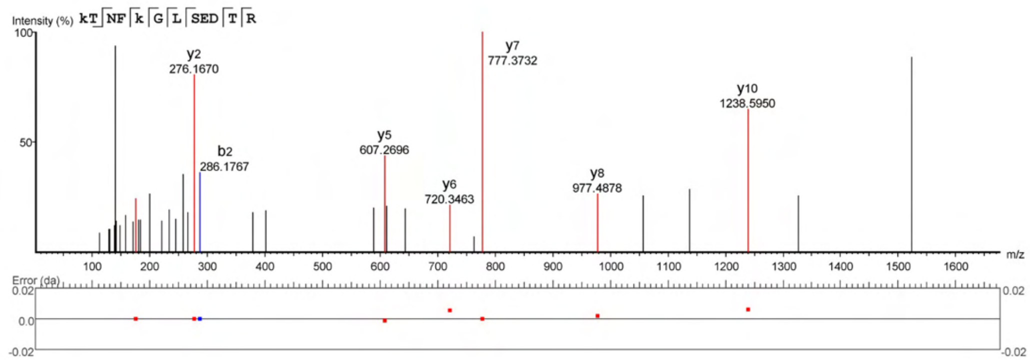


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	185.1290	167.1184	168.1020	93.0645	K(+56.03)					10
2	385.2449	367.2341	368.2181	193.1225	K(+72.02)	1186.5806	1168.5686	1169.5541	593.7905	9
3	472.2788	454.2665	455.2501	236.6385	S	986.4652	968.4546	969.4462	493.7368	8
4	586.3200	568.3094	569.2930	293.6600	N	899.4278	881.4224	882.4052	450.2165	7
5	770.4446	752.4307	753.4142	385.7206	K(+56.03)	785.3880	767.3795	768.3630	393.1950	6
6	907.5001	889.4896	890.4731	454.2501	H	601.2686	583.2583	584.2419	301.1344	5
7	1022.5270	1004.5165	1005.5001	511.7635	D	464.2102	446.1994	447.1830	232.6050	4
8	1109.5591	1091.5486	1092.5321	555.2795	S	349.1830	331.1724	332.1560	175.0915	3
9	1196.5911	1178.5806	1179.5641	598.7955	S	262.1501	244.1404	245.1240	131.5755	2
10					R	175.1190	157.1084	158.0919	88.0595	1

Figure S14_59

MSMS assignment of K173 in PHD finger protein 6

PHF6(169-180): K*TNFK*[O]GLSEDTR; -10lgP 41.15; Scan 12215 (MC319)

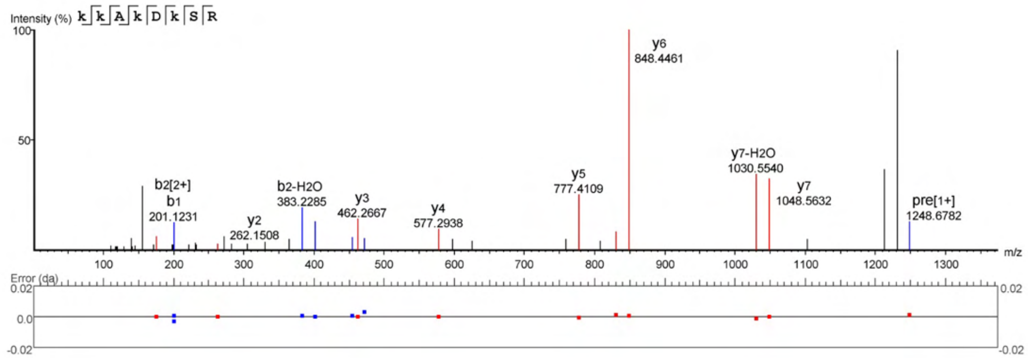


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	185.1290	167.1184	168.1020	93.0645	K(+56.03)					12
2	286.1767	268.1661	269.1497	143.5883	T	1339.6488	1321.6383	1322.6218	670.3244	11
3	400.2196	382.2090	383.1926	200.6098	N	1238.5950	1220.5906	1221.5741	619.8005	10
4	547.2880	529.2775	530.2610	274.1440	F	1124.5582	1106.5477	1107.5312	562.7791	9
5	747.4041	729.3936	730.3771	374.2021	K(+72.02)	977.4878	959.4792	960.4628	489.2449	8
6	804.4255	786.4150	787.3986	402.7128	G	777.3732	759.3631	760.3467	389.1868	7
7	917.5096	899.4991	900.4827	459.2548	L	720.3463	702.3417	703.3253	360.6761	6
8	1004.5416	986.5311	987.5146	502.7708	S	607.2696	589.2576	590.2412	304.1341	5
9	1133.5842	1115.5737	1116.5573	567.2921	E	520.2361	502.2256	503.2092	260.6181	4
10	1248.6112	1230.6007	1231.5842	624.8056	D	391.1935	373.1830	374.1666	196.0968	3
11	1349.6588	1331.6483	1332.6318	675.3294	T	276.1670	258.1561	259.1396	138.5833	2
12					R	175.1189	157.1084	158.0919	88.0595	1

Figure S14_60

MSMS assignment of K1068ox, K1069ox, K1071ox, K1073ox in PHD and RING finger domain-containing protein 1

PHRF1(1068-1075): K*[O]K*[O]AK*[O]DK*[O]SR; -10lgP 18.49; Scan 54671 (MC301)

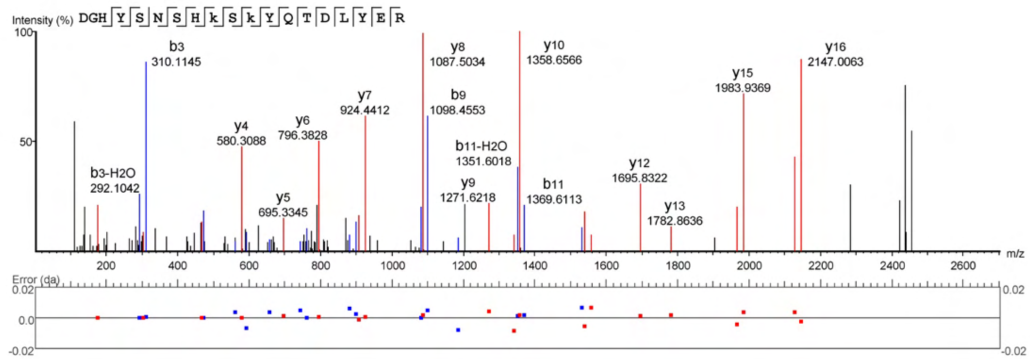


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	201.1231	183.1134	184.0969	101.0620	K(+72.02)					8
2	401.2394	383.2285	384.2130	201.1231	K(+72.02)	1048.5632	1030.5540	1031.5363	524.7816	7
3	472.2738	454.2659	455.2501	236.6385	A	848.4461	830.4349	831.4202	424.7236	6
4	672.3932	654.3826	655.3662	336.6966	K(+72.02)	777.4109	759.3995	760.3831	389.2050	5
5	787.4201	769.4095	770.3931	394.2101	D	577.2938	559.2834	560.2670	289.1470	4
6	987.5362	969.5256	970.5092	494.2681	K(+72.02)	462.2667	444.2565	445.2401	231.6335	3
7	1074.5682	1056.5577	1057.5413	537.7841	S	262.1508	244.1404	245.1240	131.5755	2
8					R	175.1187	157.1084	158.0919	88.0595	1

Figure S14_61

MSMS assignment for K458ox in Peptidyl-prolyl cis-trans isomerase-like 4

PPIL4(450-468): DGHYSNSHK*[O]SK*YQTDLYER; -10lgP 74.89; Scan 10653 (MC302)

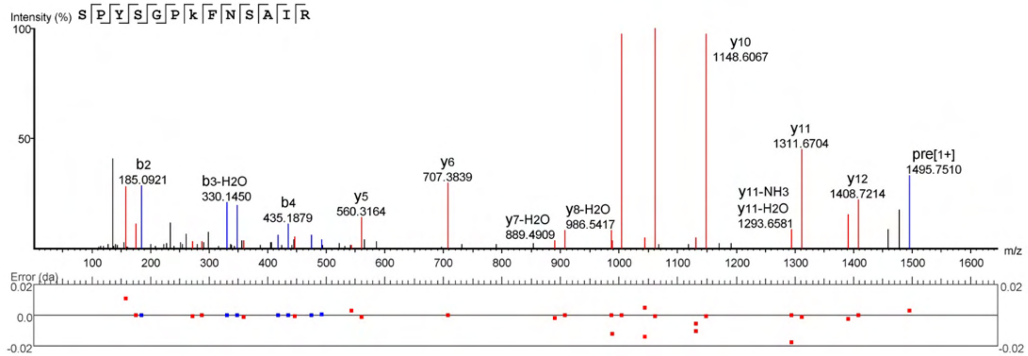


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	116.0348	98.0242	99.0078	58.5174	D					19
2	173.0562	155.0457	156.0292	87.0281	G	2341.0842	2323.0737	2324.0571	1171.0421	18
3	310.1145	292.1042	293.0881	155.5576	H	2284.0627	2266.0522	2267.0356	1142.5314	17
4	473.1781	455.1679	456.1515	237.0892	Y	2147.0063	2128.9897	2129.9768	1074.0020	16
5	560.2067	542.1999	543.1835	280.6052	S	1983.9369	1965.9302	1966.9185	992.4703	15
6	674.2534	656.2391	657.2264	337.6267	N	1896.9086	1878.8981	1879.8816	948.9543	14
7	761.2855	743.2695	744.2585	381.1427	S	1782.8636	1764.8551	1765.8386	891.9328	13
8	898.3419	880.3271	881.3174	449.6722	H	1695.8322	1677.8231	1678.8066	848.4168	12
9	1098.4553	1080.4500	1081.4335	549.7302	K(+72.02)	1558.7675	1540.7700	1541.7477	779.8873	11
10	1185.5009	1167.4819	1168.4655	593.2534	S	1358.6566	1340.6481	1341.6405	679.8293	10
11	1369.6113	1351.6018	1352.5867	685.3068	K(+56.03)	1271.6218	1253.6161	1254.5996	636.3133	9
12	1532.6698	1514.6665	1515.6500	766.8385	Y	1087.5034	1069.4949	1070.4784	544.2527	8
13	1660.7356	1642.7251	1643.7086	830.8678	Q	924.4412	906.4315	907.4165	462.7210	7
14	1761.7832	1743.7727	1744.7562	881.3916	T	796.3828	778.3730	779.3566	398.6918	6
15	1876.8102	1858.7997	1859.7832	938.9051	D	695.3345	677.3253	678.3088	348.1679	5
16	1989.8943	1971.8838	1972.8673	995.4471	L	580.3088	562.2983	563.2819	290.6544	4
17	2152.9575	2134.9470	2135.9304	1076.9788	Y	467.2250	449.2143	450.1979	234.1124	3
18	2282.0002	2263.9897	2264.9731	1141.5001	E	304.1611	286.1509	287.1345	152.5807	2
19					R	175.1189	157.1084	158.0919	88.0595	1

Figure S14_62

MSMS assignment of K103ox in RNA-binding protein 39

RBM39(97-109): SPYSGPK*[O]FNSAIR; -10lgP 54.47; Scan 14607 (MC315)

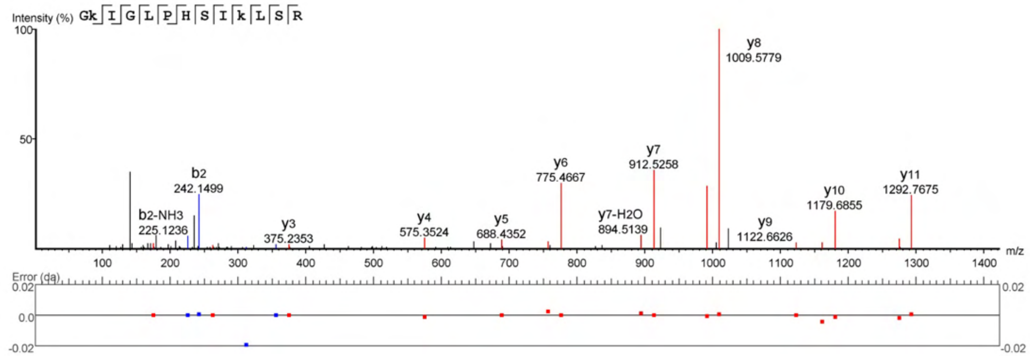


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	88.0399	70.0293	71.0129	44.5199	S					13
2	185.0921	167.0820	168.0656	93.0463	P	1408.7214	1390.7139	1391.6949	704.8610	12
3	348.1558	330.1450	331.1289	174.5780	Y	1311.6704	1293.6581	1294.6599	656.3345	11
4	435.1879	417.1774	418.1610	218.0940	S	1148.6067	1130.6011	1131.5895	574.8029	10
5	492.2085	474.1989	475.1824	246.6047	G	1061.5746	1043.5580	1044.5610	531.2869	9
6	589.2621	571.2516	572.2352	295.1311	P	1004.5529	986.5417	987.5375	502.7762	8
7	789.3782	771.3677	772.3513	395.1891	K(+72.02)	907.4990	889.4909	890.4726	454.2498	7
8	936.4467	918.4361	919.4197	468.7233	F	707.3839	689.3729	690.3565	354.1917	6
9	1050.4896	1032.4791	1033.4626	525.7448	N	560.3164	542.3045	543.2850	280.6575	5
10	1137.5216	1119.5111	1120.4946	569.2608	S	446.2728	428.2616	429.2451	223.6361	4
11	1208.5587	1190.5482	1191.5317	604.7794	A	359.2416	341.2296	342.2131	180.1201	3
12	1321.6428	1303.6323	1304.6158	661.3214	I	288.2031	270.1924	271.1767	144.6015	2
13					R	175.1189	157.0971	158.0919	88.0595	1

Figure S14_63

MSMS assignment of K119ox in RNA-binding protein 39

RBM39(110-122): GK*IGLPHSIK*[O]LSR; -10lgP 54.51; Scan 16858 (MC315)

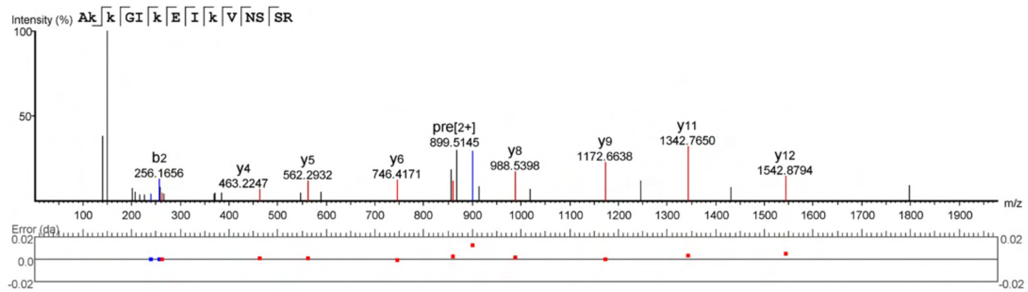


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	58.0293	40.0187	41.0023	29.5146	G					13
2	242.1499	224.1399	225.1236	121.5752	K(+56.03)	1476.8896	1458.8792	1459.8627	738.9448	12
3	355.2340	337.2239	338.2075	178.1172	I	1292.7675	1274.7598	1275.7415	646.8842	11
4	412.2560	394.2454	395.2290	206.6280	G	1179.6855	1161.6782	1162.6573	590.3422	10
5	525.3400	507.3295	508.3130	263.1700	L	1122.6626	1104.6525	1105.6360	561.8315	9
6	622.3928	604.3822	605.3658	311.7162	P	1009.5779	991.5690	992.5519	505.2894	8
7	759.4517	741.4412	742.4247	380.2259	H	912.5258	894.5139	895.4991	456.7631	7
8	846.4837	828.4731	829.4567	423.7419	S	775.4667	757.4537	758.4402	388.2336	6
9	959.5678	941.5573	942.5408	480.2839	I	688.4352	670.4246	671.4082	344.7176	5
10	1159.6838	1141.6733	1142.6569	580.3419	K(+72.02)	575.3524	557.3405	558.3241	288.1755	4
11	1272.7679	1254.7574	1255.7410	636.8840	L	375.2353	357.2245	358.2080	188.1175	3
12	1359.7999	1341.7894	1342.7729	680.4000	S	262.1513	244.1404	245.1240	131.5755	2
13					R	175.1190	157.1084	158.0919	88.0595	1

Figure S14_64

MSMS assignment of K38ox in Replication factor C subunit 1

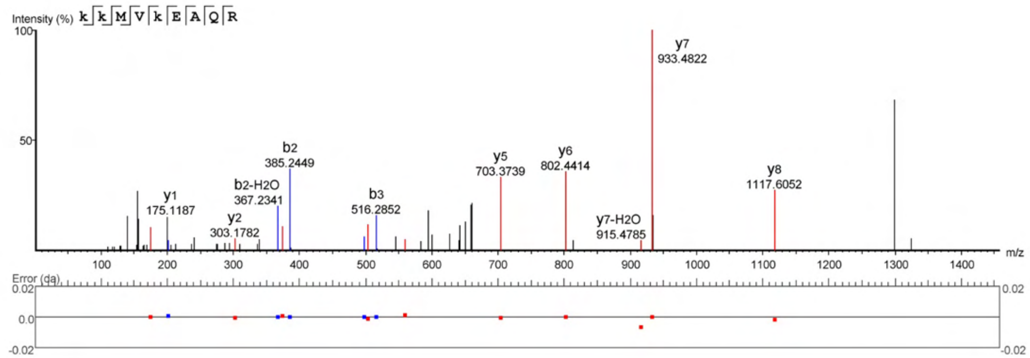
RFC1(36-49): AK*K*[O]GIK*EIK*VNSSR; -10lgP 40.41; Scan 42314 (MC358)



#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	72.0449	54.0344	55.0179	36.5225	A					14
2	256.1656	238.1555	239.1399	128.5831	K(+56.03)	1727.0061	1708.9956	1709.9791	864.0031	13
3	456.2822	438.2716	439.2552	228.6411	K(+72.02)	1542.8794	1524.8744	1525.8579	771.9424	12
4	513.3036	495.2931	496.2767	257.1518	G	1342.7650	1324.7583	1325.7418	671.8844	11
5	626.3877	608.3771	609.3607	313.6938	I	1285.7473	1267.7368	1268.7203	643.3737	10
6	810.5089	792.4983	793.4819	405.7544	K(+56.03)	1172.6638	1154.6528	1155.6364	586.8317	9
7	939.5515	921.5409	922.5245	470.2757	E	988.5398	970.5316	971.5151	494.7711	8
8	1052.6355	1034.6250	1035.6085	526.8177	I	859.4969	841.4890	842.4726	430.2498	7
9	1236.7567	1218.7462	1219.7297	618.8784	K(+56.03)	746.4171	728.4050	729.3885	373.7078	6
10	1335.8251	1317.8146	1318.7981	668.4125	V	562.2932	544.2838	545.2673	281.6472	5
11	1449.8680	1431.8575	1432.8411	725.4340	N	463.2247	445.2154	446.1989	232.1130	4
12	1536.9000	1518.8895	1519.8730	768.9500	S	349.1830	331.1724	332.1560	175.0915	3
13	1623.9321	1605.9216	1606.9052	812.4661	S	262.1507	244.1404	245.1240	131.5755	2
14					R	175.1189	157.1084	158.0919	88.0595	1

Figure S14_65

MSMS assignment of K535ox, K539ox in Serine/threonine-protein kinase RIO1
RIOK1(535-543): TK*[O]K*MVK*[O]EAQR; -10lgP 28.22; Scan 9331 (MC316)

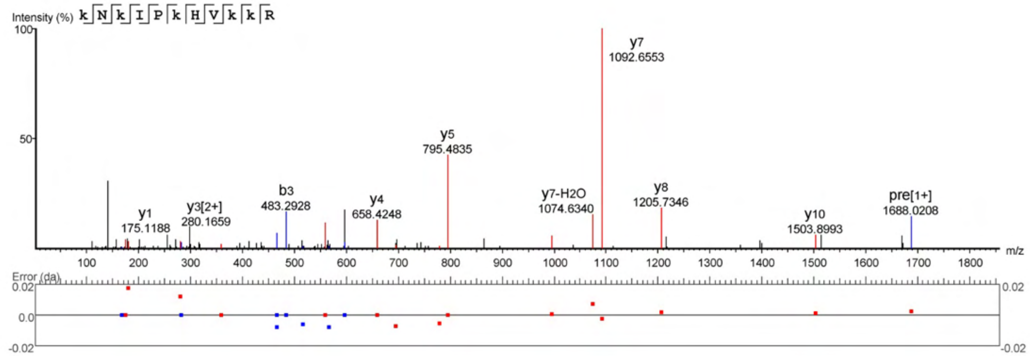


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	201.1231	183.1134	184.0969	101.0620	K(+72.02)					9
2	385.2449	367.2341	368.2181	193.1225	K(+56.03)	1117.6052	1099.5929	1100.5764	559.3003	8
3	516.2852	498.2745	499.2586	258.6428	M	933.4822	915.4785	916.4552	467.2411	7
4	615.3540	597.3434	598.3270	308.1770	V	802.4414	784.4312	785.4147	401.7209	6
5	815.4701	797.4595	798.4431	408.2350	K(+72.02)	703.3739	685.3627	686.3463	352.1866	5
6	944.5126	926.5021	927.4857	472.7563	E	503.2585	485.2466	486.2302	252.1286	4
7	1015.5497	997.5392	998.5228	508.2749	A	374.2140	356.2040	357.1876	187.6073	3
8	1143.6084	1125.5979	1126.5814	572.3042	Q	303.1782	285.1669	286.1505	152.0887	2
9					R	175.1187	157.1084	158.0919	88.0595	1

Figure S14_66

MSMS assignment of K552ox, K555ox in Serine/threonine-protein kinase RIO1

RIOK1(547-557): K*NK*IPK*[O]HVK*[O]K*R; -10lgP 40.00; Scan 13202 (MC315)

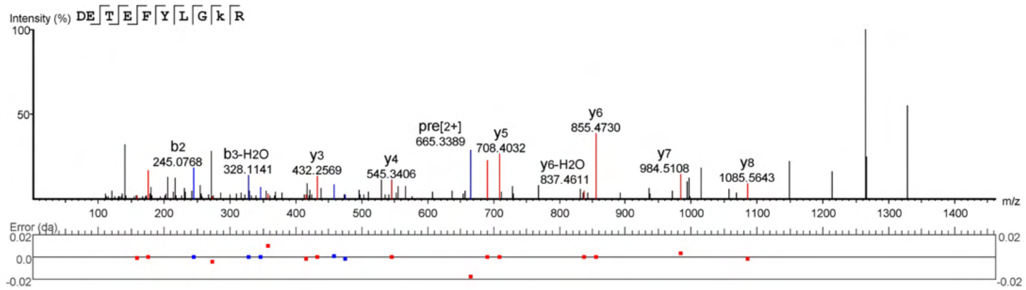


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	185.1290	167.1184	168.1022	93.0645	K(+56.03)					11
2	299.1719	281.1613	282.1454	150.0860	N	1503.8993	1485.8900	1486.8735	752.4503	10
3	483.2928	465.2820	466.2745	242.1465	K(+56.03)	1389.8575	1371.8470	1372.8306	695.4366	9
4	596.3766	578.3666	579.3502	298.6886	I	1205.7346	1187.7260	1188.7095	603.3682	8
5	693.4299	675.4194	676.4030	347.2150	P	1092.6553	1074.6340	1075.6254	546.8262	7
6	893.5460	875.5355	876.5190	447.2730	K(+72.02)	995.5986	977.5891	978.5726	498.2998	6
7	1030.6049	1012.5943	1013.5779	515.8090	H	795.4835	777.4730	778.4622	398.2418	5
8	1129.6733	1111.6628	1112.6464	565.3450	V	658.4248	640.4141	641.3976	329.7123	4
9	1329.7894	1311.7789	1312.7625	665.3947	K(+72.02)	559.3567	541.3456	542.3292	280.1659	3
10	1513.9105	1495.9000	1496.8835	757.4553	K(+56.03)	359.2401	341.2296	342.2131	180.1019	2
11					R	175.1188	157.1084	158.0919	88.0595	1

Figure S14_67

MSMS assignment of K45ox in 60S ribosomal protein L35a

RPL35A(37-46): DETEFYLGK*[O]R; -10lgP 30.99; Scan 14742 (MC326)

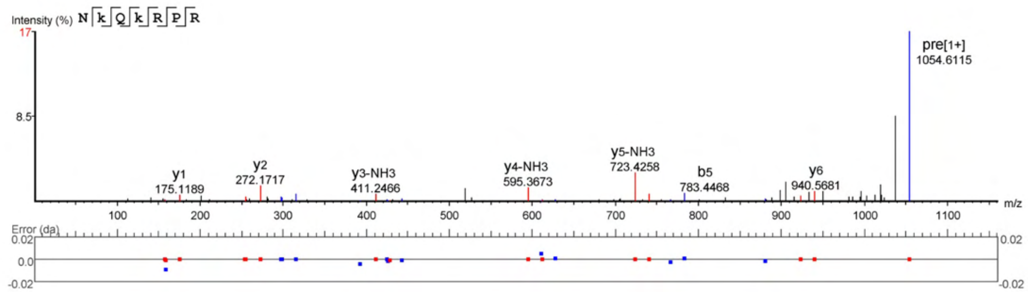


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	116.0348	98.0242	99.0078	58.5174	D					10
2	245.0768	227.0668	228.0503	123.0387	E	1214.6051	1196.5946	1197.5781	607.8026	9
3	346.1246	328.1141	329.0981	173.5625	T	1085.5643	1067.5520	1068.5355	543.2812	8
4	475.1693	457.1561	458.1406	238.0838	E	984.5108	966.5043	967.4879	492.7574	7
5	622.2360	604.2255	605.2090	311.6180	F	855.4730	837.4611	838.4453	428.2361	6
6	785.2993	767.2888	768.2723	393.1497	Y	708.4032	690.3928	691.3769	354.7019	5
7	898.3834	880.3729	881.3564	449.6917	L	545.3406	527.3300	528.3135	273.1746	4
8	955.4048	937.3943	938.3779	478.2024	G	432.2569	414.2459	415.2319	216.6282	3
9	1155.5210	1137.5105	1138.4940	578.2605	K(+72.02)	375.2350	357.2141	358.2080	188.1175	2
10					R	175.1188	157.1084	158.0928	88.0595	1

Figure S14_68

MSMS assignment of K113ox in 40S ribosomal protein S7

RPS7(112-118): NK*[O]QK*RPR; -10lgP 23.54; Scan3701 (MC330)

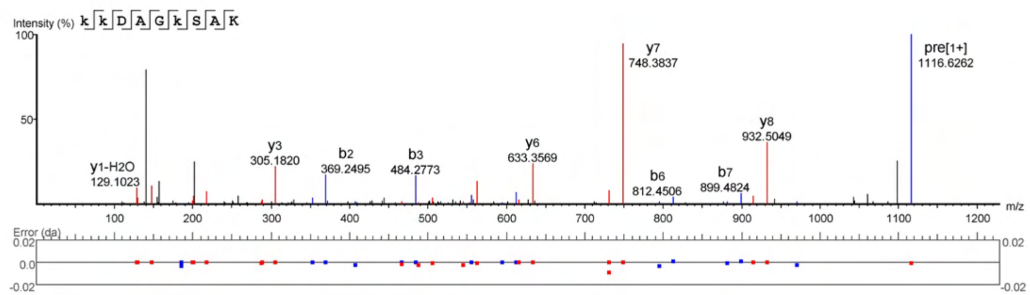


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	115.0508	97.0402	98.0238	58.0254	N					7
2	315.1664	297.1559	298.1396	158.0928	K(+72.02)	940.5681	922.5580	923.5416	470.7843	6
3	443.2263	425.2144	426.2002	222.1127	Q	740.4531	722.4420	723.4258	370.7263	5
4	627.3455	609.3360	610.3145	314.1733	K(+56.03)	612.3944	594.3834	595.3673	306.6970	4
5	783.4468	765.4371	766.4236	392.2286	R	428.2741	410.2622	411.2466	214.6364	3
6	880.5022	862.4899	863.4734	440.7502	P	272.1717	254.1614	255.1450	136.5858	2
7					R	175.1189	157.1081	158.0928	88.0595	1

Figure S14_69

MSMS assignment of K14ox in 40S ribosomal protein S25

RPS25(9-17): K*K*DAGK*[O]SAK; -10lgP 29.45; Scan 4813 (MC328)

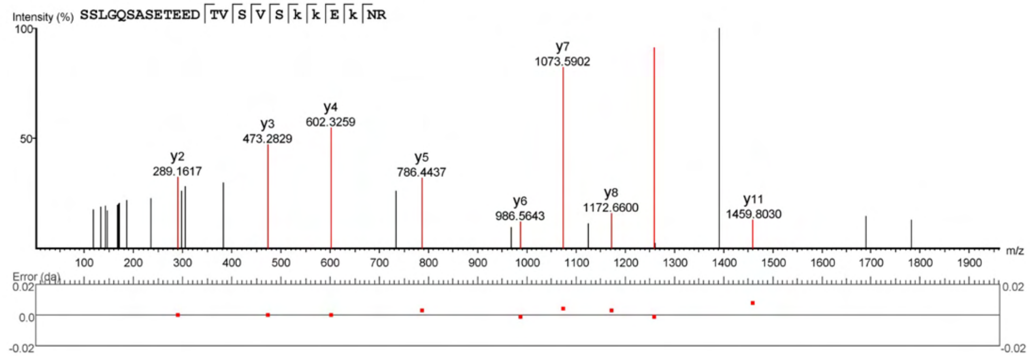


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	185.1289	167.1184	168.1020	93.0645	K(+56.03)					9
2	369.2495	351.2396	352.2238	185.1289	K(+56.03)	932.5049	914.4938	915.4777	466.7547	8
3	484.2773	466.2670	467.2501	242.6385	D	748.3837	730.3732	731.3663	374.6918	7
4	555.3141	537.3036	538.2872	278.1571	A	633.3569	615.3456	616.3296	317.1783	6
5	612.3352	594.3247	595.3087	306.6678	G	562.3205	544.3114	545.2925	281.6597	5
6	812.4506	794.4447	795.4248	406.7292	K(+72.02)	505.2992	487.2903	488.2710	253.1490	4
7	899.4824	881.4745	882.4568	450.2419	S	305.1820	287.1724	288.1551	153.0910	3
8	970.5239	952.5103	953.4939	485.7604	A	218.1499	200.1396	201.1234	109.5750	2
9					K	147.1127	129.1023	130.0861	74.0564	1

Figure S14_70

MSMS assignment of K320ox in Splicing factor 3B subunit 2

SF3B2(302-325): SSLGQSASETEEDTVSVSK*[O]K*EK*NR; -10lgP 52.86; Scan 16763 (MC304)

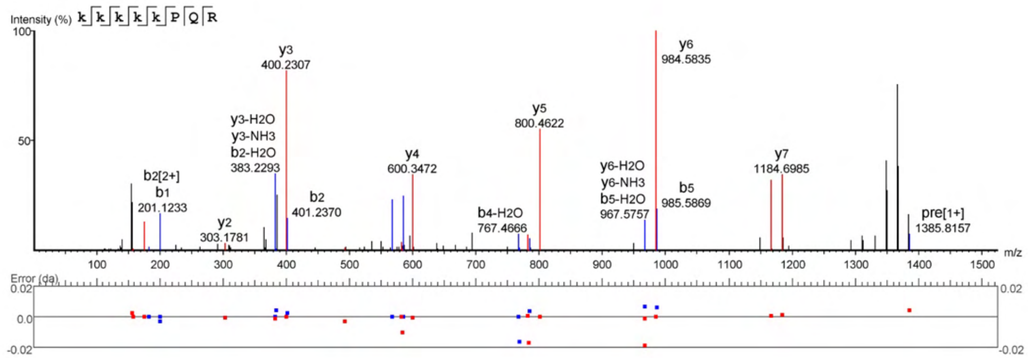


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	88.0399	70.0293	71.0129	44.5199	S					24
2	175.0719	157.0613	158.0449	88.0359	S	2693.3110	2675.3005	2676.2839	1347.1555	23
3	288.1559	270.1454	271.1290	144.5780	L	2606.2791	2588.2686	2589.2520	1303.6395	22
4	345.1774	327.1668	328.1504	173.0887	G	2493.1951	2475.1846	2476.1680	1247.0975	21
5	473.2360	455.2254	456.2090	237.1180	Q	2436.1736	2418.1631	2419.1465	1218.5868	20
6	560.2680	542.2574	543.2410	280.6340	S	2308.1150	2290.1045	2291.0879	1154.5575	19
7	631.3051	613.2946	614.2781	316.1526	A	2221.0830	2203.0725	2204.0559	1111.0415	18
8	718.3372	700.3266	701.3102	359.6686	S	2150.0459	2132.0354	2133.0188	1075.5229	17
9	847.3797	829.3691	830.3527	424.1898	E	2063.0139	2045.0033	2045.9868	1032.0070	16
10	948.4274	930.4169	931.4005	474.7137	T	1933.9712	1915.9607	1916.9442	967.4856	15
11	1077.4700	1059.4595	1060.4430	539.2350	E	1832.9236	1814.9131	1815.8966	916.9618	14
12	1206.5126	1188.5021	1189.4856	603.7563	E	1703.8810	1685.8705	1686.8540	852.4405	13
13	1321.5396	1303.5291	1304.5126	661.2698	D	1574.8384	1556.8279	1557.8114	787.9192	12
14	1422.5872	1404.5767	1405.5602	711.7936	T	1459.8030	1441.8009	1442.7844	730.4057	11
15	1521.6556	1503.6451	1504.6287	761.3278	V	1358.7638	1340.7533	1341.7368	679.8819	10
16	1608.6876	1590.6771	1591.6606	804.8438	S	1259.6969	1241.6848	1242.6683	630.3477	9
17	1707.7561	1689.7456	1690.7291	854.3781	V	1172.6600	1154.6528	1155.6364	586.8317	8
18	1794.7881	1776.7776	1777.7611	897.8940	S	1073.5902	1055.5844	1056.5679	537.2974	7
19	1994.9042	1976.8937	1977.8772	997.9521	K(+72.02)	986.5643	968.5523	969.5359	493.7814	6
20	2179.0254	2161.0149	2161.9983	1090.0127	K(+56.03)	786.4437	768.4362	769.4198	393.7234	5
21	2308.0679	2290.0574	2291.0408	1154.5339	E	602.3259	584.3151	585.2986	301.6628	4
22	2492.1892	2474.1787	2475.1621	1246.5946	K(+56.03)	473.2829	455.2725	456.2560	237.1415	3
23	2606.2319	2588.2214	2589.2048	1303.6160	N	289.1617	271.1513	272.1349	145.0809	2
24					R	175.1189	157.1084	158.0919	88.0595	1

Figure S14_71

MSMS assignment of K331ox, K332ox, K334ox, K335ox in Splicing factor 3B subunit 2

SF3B2(331-338): K*[O]K*[O]K*K*[O]K*PQR; -10lgP 26.70; Scan 8477 (MC304)

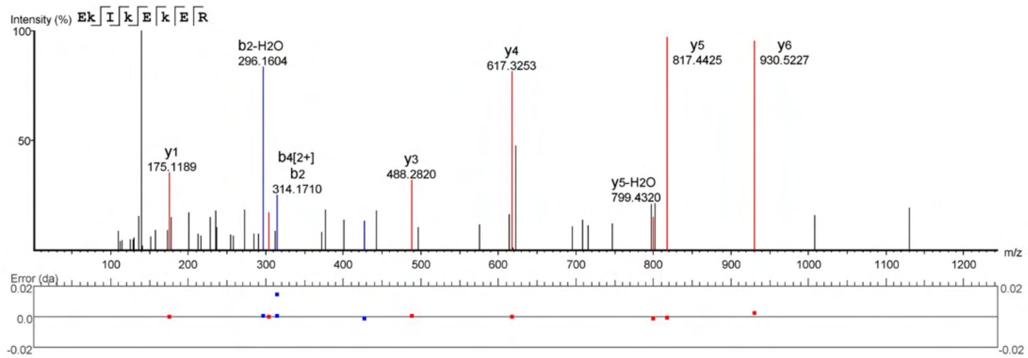


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	201.1233	183.1129	184.0969	101.0620	K(+72.02)					8
2	401.2370	383.2293	384.2085	201.1233	K(+72.02)	1184.6985	1166.6882	1167.6727	592.8499	7
3	585.3613	567.3503	568.3342	293.1806	K(+56.03)	984.5835	966.5745	967.5757	492.7953	6
4	785.4735	767.4666	768.4672	393.2386	K(+72.02)	800.4622	782.4512	783.4526	400.7312	5
5	985.5869	967.5757	968.5663	493.2967	K(+72.02)	600.3472	582.3356	583.3298	300.6732	4
6	1082.6461	1064.6356	1065.6191	541.8231	P	400.2307	382.2214	383.2046	200.6151	3
7	1210.7047	1192.6942	1193.6777	605.8524	Q	303.1781	285.1669	286.1505	152.0887	2
8					R	175.1192	157.1056	158.0922	88.0595	1

Figure S14_72

MSMS assignment for K269ox in Splicing regulatory glutamine/lysine-rich protein 1

SREK1(266-273): EK*IK*[O]EK*ER; -10lgP 24.73; Scan 10897 (MC315)

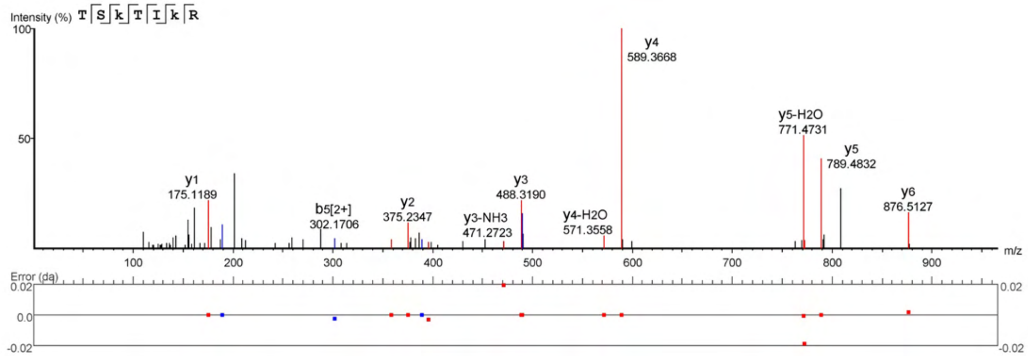


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	130.0504	112.0399	113.0234	65.5252	E					8
2	314.1710	296.1604	297.1446	157.5858	K(+56.03)	1114.6466	1096.6361	1097.6196	557.8233	7
3	427.2570	409.2451	410.2286	214.1278	I	930.5227	912.5148	913.4984	465.7627	6
4	627.3717	609.3611	610.3447	314.1710	K(+72.02)	817.4425	799.4320	800.4144	409.2207	5
5	756.4143	738.4037	739.3873	378.7072	E	617.3253	599.3147	600.2983	309.1626	4
6	940.5355	922.5249	923.5085	470.7677	K(+56.03)	488.2820	470.2721	471.2557	244.6413	3
7	1069.5781	1051.5676	1052.5511	535.2891	E	304.1610	286.1509	287.1345	152.5807	2
8					R	175.1189	157.1084	158.0919	88.0595	1

Figure S14_73

MSMS assignment of K397ox, K400ox in Splicing regulatory glutamine/lysine-rich protein 1

SREK1(395-401): TSK*[O]TIK*[O]R; -10lgP 34.43; Scan 6860 (MC315)



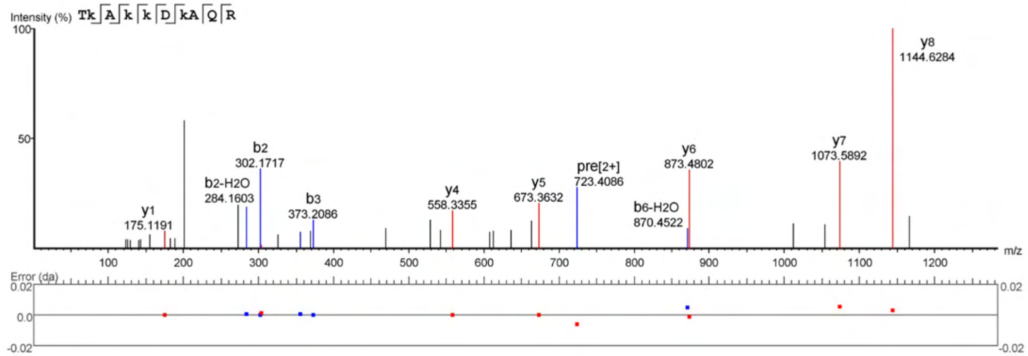
#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	102.0555	84.0450	85.0285	51.5278	T					7
2	189.0871	171.0770	172.0605	95.0438	S	876.5127	858.5043	859.4879	438.7574	6
3	389.2031	371.1931	372.1766	195.1018	K(+72.02)	789.4832	771.4731	772.4751	395.2449	5
4	490.2513	472.2407	473.2243	245.6256	T	589.3668	571.3558	572.3398	295.1834	4
5	603.3353	585.3248	586.3083	302.1706	I	488.3190	470.3085	471.2723	244.6595	3
6	803.4514	785.4409	786.4244	402.2257	K(+72.02)	375.2347	357.2245	358.2077	188.1175	2
7					R	175.1189	157.1084	158.0919	88.0595	1

Figure S14_74

Figure S14_76

MSMS assignment of K16ox, K18ox, K19ox in SRSF protein kinase 1

SRPK1(15-24): TK*[O]AK*[O]K*[O]DK*AQR; -10lgP 32.05; Scan 7719 (MC306)

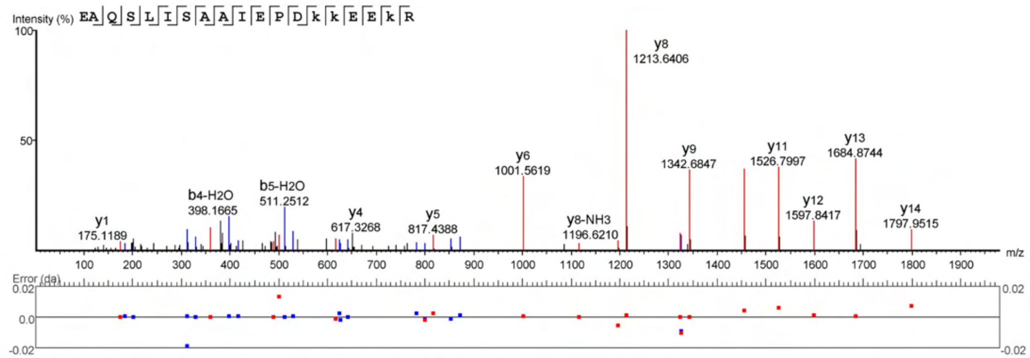


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	102.0555	84.0450	85.0285	51.5278	T					10
2	302.1717	284.1603	285.1446	151.5858	K(+72.02)	1344.7480	1326.7375	1327.7211	672.8740	9
3	373.2086	355.1972	356.1817	187.1043	A	1144.6284	1126.6215	1127.6050	572.8160	8
4	573.3248	555.3142	556.2978	287.1624	K(+72.02)	1073.5892	1055.5844	1056.5679	537.2974	7
5	773.4409	755.4303	756.4139	387.2204	K(+72.02)	873.4802	855.4683	856.4518	437.2394	6
6	888.4678	870.4522	871.4409	444.7339	D	673.3632	655.3522	656.3358	337.1814	5
7	1072.5890	1054.5785	1055.5620	536.7945	K(+56.03)	558.3355	540.3253	541.3088	279.6679	4
8	1143.6261	1125.6156	1126.5991	572.3130	A	374.2146	356.2040	357.1876	187.6073	3
9	1271.6847	1253.6742	1254.6577	636.3423	Q	303.1757	285.1669	286.1505	152.0887	2
10					R	175.1191	157.1084	158.0919	88.0595	1

Figure S14_77

MSMS assignment of K242ox in Serine/arginine-rich splicing factor 11

SRSF11(228-246): EAQSLISAAIEPDK*K*[O]EEK*R; -10lgP 65.23; Scan 21298 (MC303)

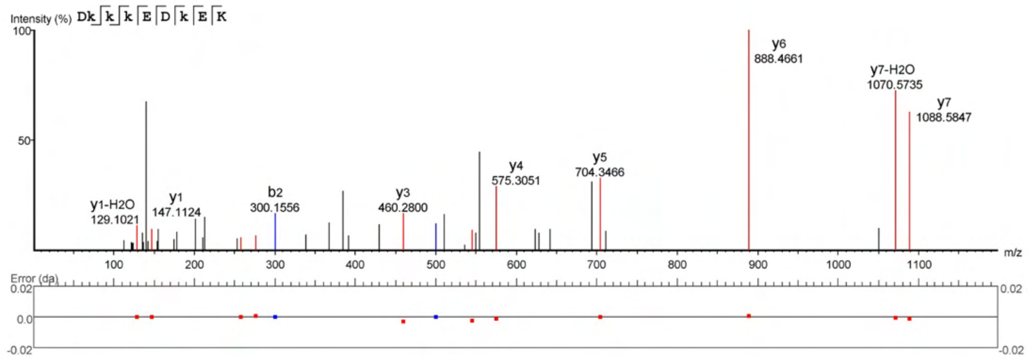


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	130.0504	112.0399	113.0234	65.5252	E					19
2	201.0872	183.0761	184.0605	101.0438	A	2197.1709	2179.1604	2180.1438	1099.0854	18
3	329.1457	311.1346	312.1381	165.0730	Q	2126.1338	2108.1233	2109.1067	1063.5669	17
4	416.1769	398.1665	399.1511	208.5891	S	1998.0753	1980.0648	1981.0483	999.5377	16
5	529.2615	511.2512	512.2352	265.1311	L	1911.0432	1893.0327	1894.0162	956.0216	15
6	642.3464	624.3329	625.3216	321.6731	I	1797.9515	1779.9487	1780.9323	899.4796	14
7	729.3783	711.3677	712.3513	365.1891	S	1684.8744	1666.8646	1667.8481	842.9376	13
8	800.4166	782.4020	783.3884	400.7077	A	1597.8417	1579.8326	1580.8162	799.4216	12
9	871.4507	853.4434	854.4255	436.2263	A	1526.7997	1508.7955	1509.7791	763.9030	11
10	984.5366	966.5260	967.5096	492.7683	I	1455.7645	1437.7584	1438.7419	728.3845	10
11	1113.5791	1095.5686	1096.5521	557.2896	E	1342.6847	1324.6748	1325.6685	671.8424	9
12	1210.6318	1192.6213	1193.6049	605.8159	P	1213.6406	1195.6317	1196.6210	607.3211	8
13	1325.6685	1307.6483	1308.6318	663.3294	D	1116.5896	1098.5790	1099.5625	558.7947	7
14	1509.7800	1491.7695	1492.7531	755.3900	K(+56.03)	1001.5619	983.5519	984.5355	501.2673	6
15	1709.8961	1691.8856	1692.8691	855.4481	K(+72.02)	817.4388	799.4308	800.4166	409.2207	5
16	1838.9387	1820.9282	1821.9117	919.9694	E	617.3268	599.3147	600.2983	309.1626	4
17	1967.9812	1949.9707	1950.9542	984.4906	E	488.2826	470.2721	471.2557	244.6413	3
18	2152.1025	2134.0920	2135.0754	1076.5513	K(+56.03)	359.2399	341.2296	342.2131	180.1201	2
19					R	175.1189	157.1084	158.0919	88.0595	1

Figure S14_78

MSMS assignment of K314ox in Serine/arginine-rich splicing factor 11

SRSF11(312-320): DK*K*[O]K*EDK*EK; -10lgP 22.49; Scan 10961 (MC304)

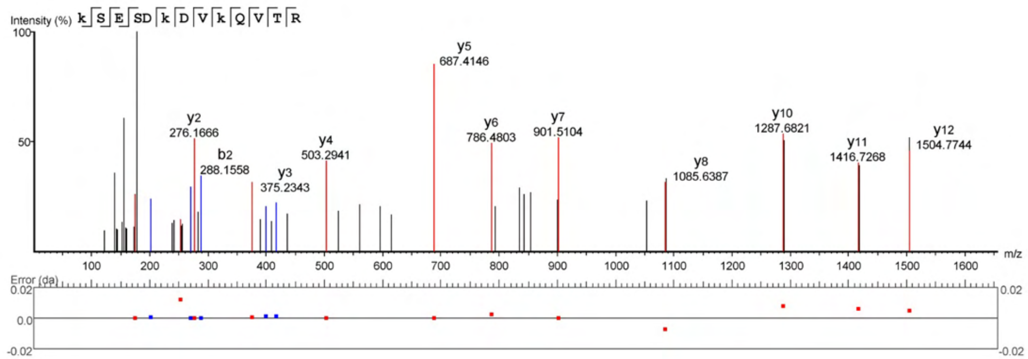


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	116.0348	98.0242	99.0078	58.5174	D					9
2	300.1556	282.1454	283.1289	150.5780	K(+56.03)	1272.7045	1254.6940	1255.6775	636.8522	8
3	500.2722	482.2614	483.2450	250.6360	K(+72.02)	1088.5847	1070.5735	1071.5564	544.7943	7
4	684.3932	666.3826	667.3662	342.6966	K(+56.03)	888.4661	870.4567	871.4402	444.7336	6
5	813.4358	795.4252	796.4088	407.2179	E	704.3466	686.3355	687.3191	352.6730	5
6	928.4627	910.4521	911.4357	464.7314	D	575.3051	557.2929	558.2765	288.1517	4
7	1112.5839	1094.5734	1095.5569	556.7919	K(+56.03)	460.2800	442.2660	443.2496	230.6383	3
8	1241.6265	1223.6160	1224.5995	621.3132	E	276.1547	258.1449	259.1284	138.5777	2
9					K	147.1124	129.1021	130.0858	74.0564	1

Figure S14_79

MSMS assignment of K411ox in Serine/arginine-rich splicing factor 11

SRSF11(411-423): K*[O]SESDK*DVK*QVTR; -10lgP 44.25; Scan 12062 (MC301)

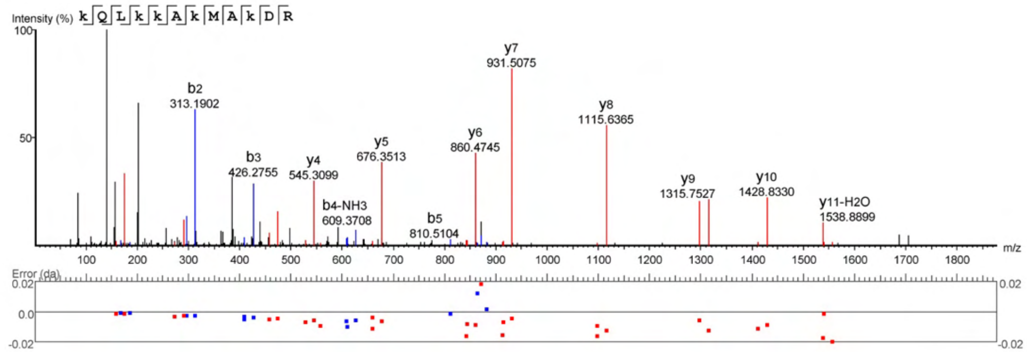


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	201.1230	183.1134	184.0969	101.0620	K(+72.02)					13
2	288.1558	270.1453	271.1290	144.5780	S	1503.7600	1485.7544	1486.7379	752.3824	12
3	417.1973	399.1866	400.1715	209.0993	E	1416.7268	1398.7224	1399.7059	708.8665	11
4	504.2305	486.2200	487.2036	252.6153	S	1287.6821	1269.6798	1270.6633	644.3452	10
5	619.2575	601.2469	602.2305	310.1288	D	1200.6582	1182.6477	1183.6312	600.8291	9
6	803.3787	785.3681	786.3517	402.1893	K(+56.03)	1085.6387	1067.6208	1068.6044	543.3157	8
7	918.4056	900.3950	901.3786	459.7028	D	901.5104	883.4996	884.4832	451.2551	7
8	1017.4740	999.4634	1000.4470	509.2370	V	786.4803	768.4726	769.4562	393.7416	6
9	1201.5952	1183.5847	1184.5682	601.2976	K(+56.03)	687.4146	669.4042	670.3878	344.2074	5
10	1329.6538	1311.6433	1312.6268	665.3269	Q	503.2941	485.2831	486.2666	252.1347	4
11	1428.7222	1410.7117	1411.6952	714.8611	V	375.2343	357.2245	358.2080	188.1175	3
12	1529.7699	1511.7594	1512.7429	765.3849	T	276.1666	258.1561	259.1396	138.5833	2
13					R	175.1188	157.1084	158.0919	88.0595	1

Figure S14_80

MSMS assignment of K521ox in FACT complex subunit SSRP1

SSRP1(518-529): K*QLK*[O]K*AK*MAK*DR; -10lgP 47.56; Scan 25968 (MC275)

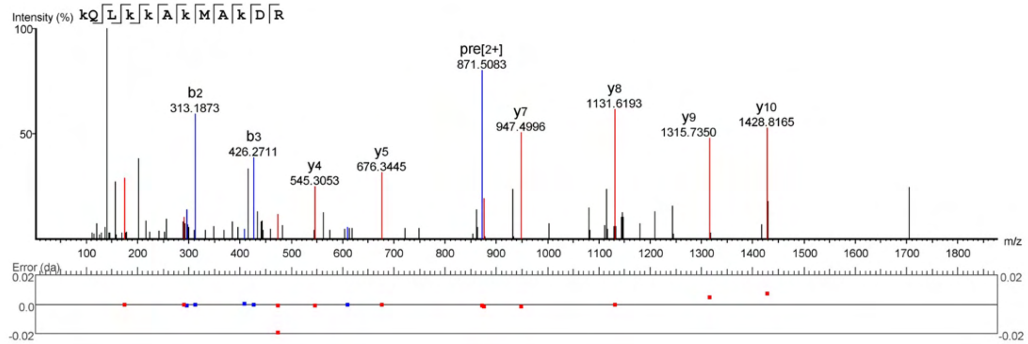


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	185.1299	167.1184	168.1027	93.0645	K(+56.03)					12
2	313.1902	295.1770	296.1635	157.0938	Q	1556.9026	1538.8899	1539.8572	778.9414	11
3	426.2755	408.2645	409.2497	213.6358	L	1428.8330	1410.8252	1411.7972	714.9121	10
4	626.3938	608.3837	609.3708	313.6938	K(+72.02)	1315.7527	1297.7354	1298.7133	658.3812	9
5	810.5104	792.4984	793.4819	405.7545	K(+56.03)	1115.6365	1097.6302	1098.6068	558.3219	8
6	881.5438	863.5230	864.5190	441.2730	A	931.5075	913.5080	914.4832	466.2515	7
7	1065.6671	1047.6566	1048.6401	533.3336	K(+56.03)	860.4745	842.4717	843.4471	430.7329	6
8	1196.7076	1178.6971	1179.6807	598.8538	M	676.3513	658.3341	659.3216	338.6723	5
9	1267.7448	1249.7343	1250.7178	634.3724	A	545.3099	527.2936	528.2840	273.1521	4
10	1451.8660	1433.8555	1434.8390	726.4330	K(+56.03)	474.2717	456.2565	457.2451	237.6335	3
11	1566.8928	1548.8823	1549.8658	783.9464	D	290.1489	272.1353	273.1220	145.5729	2
12					R	175.1204	157.1084	158.0938	88.0595	1

Figure S14_81

MSMS assignment of K524ox in FACT complex subunit SSRP1

SSRP1(518-529): K*QLK*K*AK*[O]MAK*DR; -10lgP 32.58; Scan 39541 (MC362)

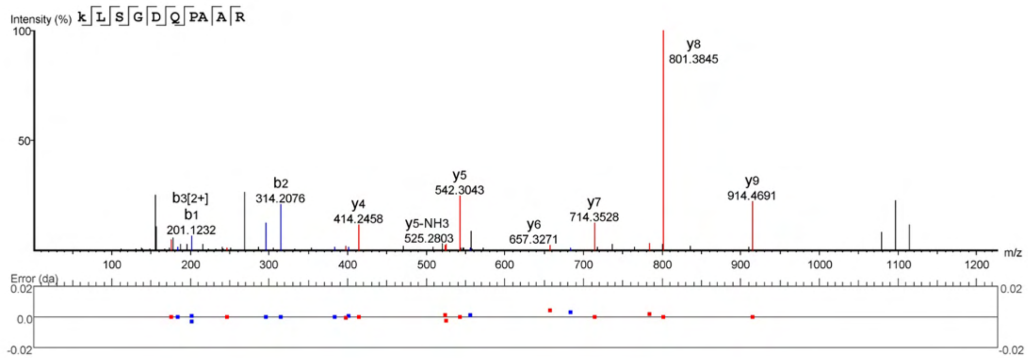


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	185.1290	167.1184	168.1020	93.0645	K(+56.03)					12
2	313.1873	295.1770	296.1612	157.0938	Q	1556.8828	1538.8723	1539.8558	778.9414	11
3	426.2711	408.2610	409.2434	213.6358	L	1428.8165	1410.8137	1411.7972	714.9121	10
4	610.3934	592.3823	593.3658	305.6964	K(+56.03)	1315.7350	1297.7297	1298.7133	658.3701	9
5	794.5140	776.5034	777.4870	397.7570	K(+56.03)	1131.6193	1113.6085	1114.5920	566.3095	8
6	865.5511	847.5405	848.5241	433.2755	A	947.4996	929.4873	930.4709	474.2682	7
7	1065.6671	1047.6566	1048.6401	533.3336	K(+72.02)	876.4622	858.4502	859.4338	438.7304	6
8	1196.7076	1178.6971	1179.6807	598.8538	M	676.3445	658.3341	659.3177	338.6723	5
9	1267.7448	1249.7343	1250.7178	634.3724	A	545.3053	527.2936	528.2772	273.1521	4
10	1451.8660	1433.8555	1434.8390	726.4330	K(+56.03)	474.2682	456.2565	457.2401	237.6335	3
11	1566.8928	1548.8823	1549.8658	783.9464	D	290.1463	272.1353	273.1189	145.5729	2
12					R	175.1190	157.1084	158.0919	88.0595	1

Figure S14_82

MSMS assignment of K1348ox in Treacle protein

TCOF1(1348-1357): K*[O]LSGDQPAAR; -10lgP 37.48; Scan 5589 (MC301)

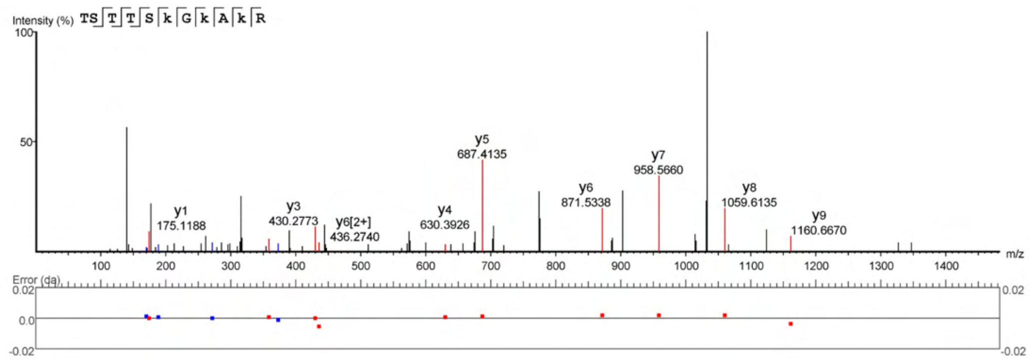


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	201.1232	183.1128	184.0969	101.0620	K(+72.02)					10
2	314.2076	296.1970	297.1810	157.6040	L	914.4691	896.4584	897.4420	457.7345	9
3	401.2390	383.2291	384.2130	201.1232	S	801.3845	783.3724	784.3579	401.1924	8
4	458.2614	440.2509	441.2345	229.6307	G	714.3528	696.3423	697.3259	357.6765	7
5	573.2884	555.2766	556.2614	287.1442	D	657.3271	639.3209	640.3044	329.1657	6
6	701.3470	683.3334	684.3200	351.1735	Q	542.3043	524.2927	525.2803	271.6523	5
7	798.3997	780.3892	781.3727	399.6999	P	414.2458	396.2354	397.2200	207.6230	4
8	869.4368	851.4263	852.4099	435.2184	A	317.1931	299.1826	300.1662	159.0966	3
9	940.4739	922.4634	923.4470	470.7370	A	246.1564	228.1455	229.1290	123.5780	2
10					R	175.1189	157.1084	158.0919	88.0595	1

Figure S14_83

MSMS assignment of K1389ox in Treacle protein

TCOF1(1382-1392): TSTTSK*GK*[O]AK*R; -10lgP 31.46; Scan 6621 (MC301)

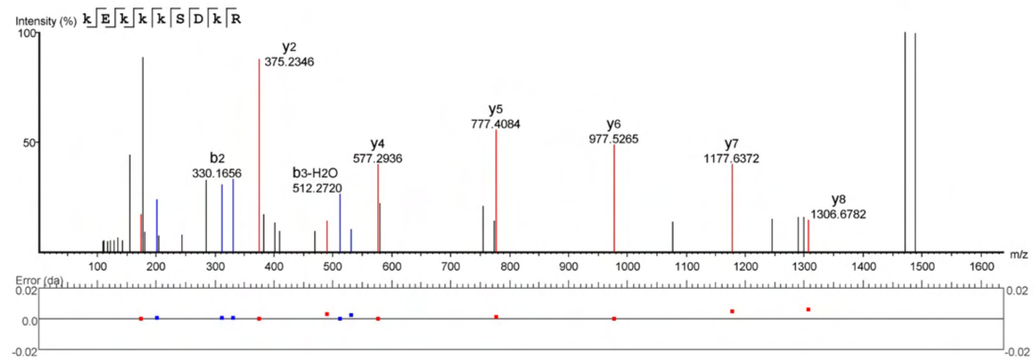


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	102.0555	84.0450	85.0285	51.5278	T					11
2	189.0868	171.0756	172.0605	95.0438	S	1247.6953	1229.6848	1230.6683	624.3477	10
3	290.1352	272.1248	273.1082	145.5676	T	1160.6670	1142.6528	1143.6364	580.8317	9
4	391.1829	373.1740	374.1559	196.0914	T	1059.6135	1041.6051	1042.5886	530.3078	8
5	478.2149	460.2043	461.1879	239.6075	S	958.5660	940.5574	941.5410	479.7840	7
6	662.3361	644.3255	645.3091	331.6680	K(+56.03)	871.5338	853.5254	854.5090	436.2740	6
7	719.3575	701.3470	702.3306	360.1788	G	687.4135	669.4042	670.3878	344.2074	5
8	919.4736	901.4631	902.4467	460.2368	K(+72.02)	630.3926	612.3828	613.3663	315.6967	4
9	990.5107	972.5002	973.4838	495.7554	A	430.2773	412.2667	413.2502	215.6386	3
10	1174.6320	1156.6215	1157.6050	587.8160	K(+56.03)	359.2393	341.2296	342.2131	180.1201	2
11					R	175.1188	157.1084	158.0919	88.0595	1

Figure S14_84

MSMS assignment of K1440ox, K1442ox, K1443ox, K1444ox, K1447ox in Treacle protein

TCOF1(1440-1448): K*[O]EK*[O]K*[O]K*[O]SDK*[O]R; -10lgP 22.72; Scan 6898 (MC302)

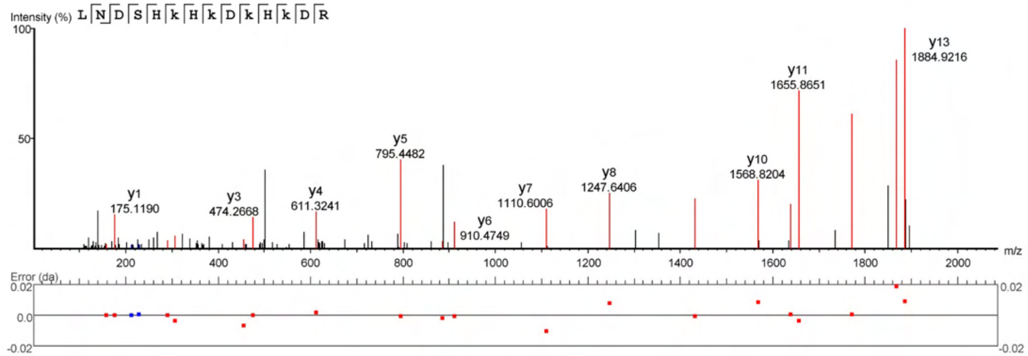


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	201.1233	183.1134	184.0969	101.0620	K(+72.02)					9
2	330.1656	312.1548	313.1395	165.5833	E	1306.6782	1288.6743	1289.6578	653.8424	8
3	530.2797	512.2720	513.2556	265.6413	K(+72.02)	1177.6372	1159.6317	1160.6152	589.3211	7
4	730.3987	712.3881	713.3717	365.6993	K(+72.02)	977.5265	959.5156	960.4992	489.2631	6
5	930.5148	912.5042	913.4878	465.7574	K(+72.02)	777.4084	759.3995	760.3831	389.2050	5
6	1017.5468	999.5362	1000.5198	509.2734	S	577.2936	559.2834	560.2670	289.1470	4
7	1132.5737	1114.5632	1115.5468	566.7869	D	490.2589	472.2514	473.2350	245.6310	3
8	1332.6898	1314.6793	1315.6628	666.8449	K(+72.02)	375.2346	357.2245	358.2080	188.1175	2
9					R	175.1187	157.1084	158.0919	88.0595	1

Figure S14_85

MSMS assignment of K25ox in DNA topoisomerase 1

TOP1(18-31): LNDSHK*HK*[O]DK*HK*DR; -10lgP 52.38; Scan 10714 (MC315)

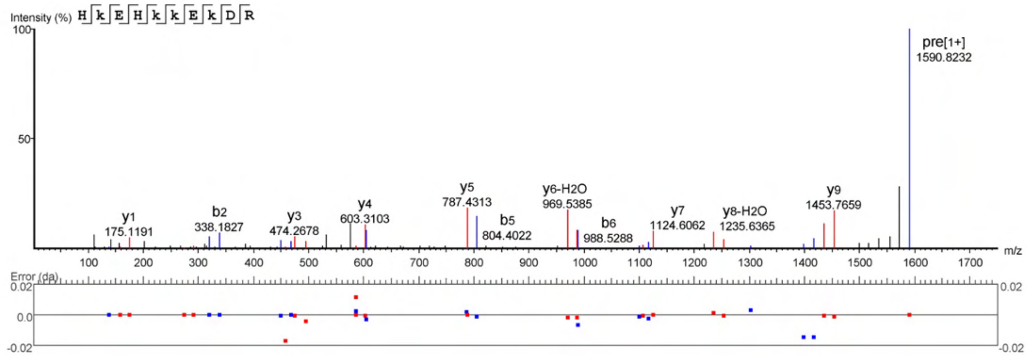


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	114.0919	96.0813	97.0649	57.5459	L					14
2	228.1338	210.1243	211.1075	114.5674	N	1884.9216	1866.9016	1867.9041	942.9655	13
3	343.1617	325.1512	326.1348	172.0809	D	1770.8873	1752.8776	1753.8611	885.9462	12
4	430.1938	412.1832	413.1668	215.5969	S	1655.8651	1637.8499	1638.8342	828.4306	11
5	567.2527	549.2421	550.2257	284.1263	H	1568.8204	1550.8186	1551.8021	784.9146	10
6	751.3738	733.3633	734.3469	376.1869	K(+56.03)	1431.7714	1413.7598	1414.7433	716.3851	9
7	888.4327	870.4222	871.4058	444.7164	H	1247.6406	1229.6385	1230.6221	624.3245	8
8	1088.5488	1070.5383	1071.5219	544.7744	K(+72.02)	1110.6006	1092.5796	1093.5631	555.7950	7
9	1203.5758	1185.5653	1186.5488	602.2879	D	910.4749	892.4635	893.4471	455.7437	6
10	1387.6970	1369.6865	1370.6700	694.3485	K(+56.03)	795.4482	777.4366	778.4202	398.2236	5
11	1524.7559	1506.7454	1507.7289	762.8779	H	611.3241	593.3154	594.2990	306.1672	4
12	1708.8771	1690.8666	1691.8501	854.9385	K(+56.03)	474.2668	456.2565	457.2401	237.6335	3
13	1823.9041	1805.8936	1806.8771	912.4520	D	290.1461	272.1353	273.1189	145.5729	2
14					R	175.1190	157.1084	158.0923	88.0595	1

Figure S14_86

MSMS assignment of K36ox, K39ox in DNA topoisomerase 1

TOP1(35-44): HK*[O]EHK*[O]K*EK*DR; -10lgP 47.29; Scan 5788 (MC306)

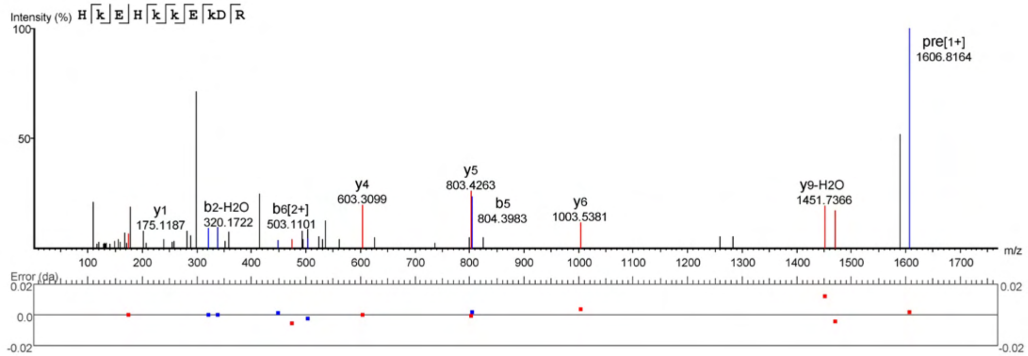


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	138.0664	120.0562	121.0397	69.5334	H					10
2	338.1827	320.1719	321.1558	169.5914	K(+72.02)	1453.7659	1435.7546	1436.7375	727.3823	9
3	467.2256	449.2156	450.1984	234.1127	E	1253.6490	1235.6365	1236.6215	627.3242	8
4	604.2874	586.2711	587.2573	302.6422	H	1124.6062	1106.5962	1107.5789	562.8029	7
5	804.4022	786.3880	787.3734	402.7002	K(+72.02)	987.5487	969.5385	970.5199	494.2782	6
6	988.5288	970.5110	971.4946	494.7608	K(+56.03)	787.4313	769.4202	770.4038	394.2154	5
7	1117.5667	1099.5554	1100.5372	559.2821	E	603.3103	585.2988	586.2711	302.1548	4
8	1301.6821	1283.6748	1284.6583	651.3427	K(+56.03)	474.2678	456.2565	457.2572	237.6335	3
9	1416.7274	1398.7164	1399.6853	708.8561	D	290.1460	272.1353	273.1186	145.5729	2
10					R	175.1191	157.1084	158.0925	88.0595	1

Figure S14_87

MSMS assignment of K40ox in DNA topoisomerase 1

TOP1(35-44): HK*[O]EHK*[O]K*[O]EK*DR; -10lgP 33.51; Scan 5452 (MC306)

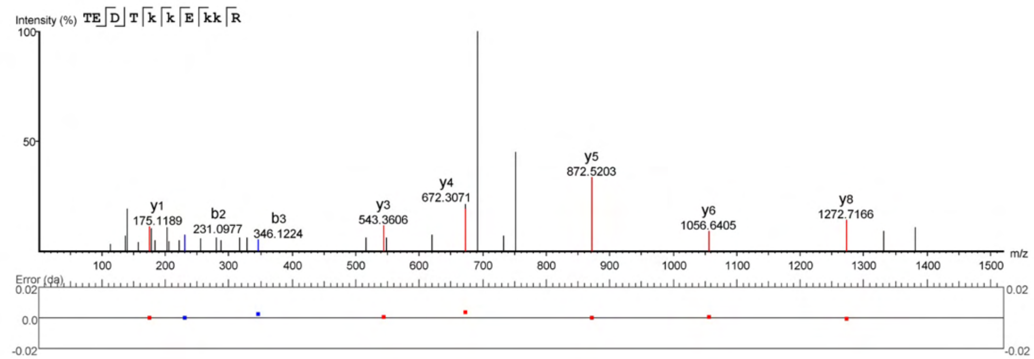


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	138.0667	120.0562	121.0397	69.5334	H					10
2	338.1823	320.1722	321.1558	169.5914	K(+72.02)	1469.7638	1451.7366	1452.7324	735.3797	9
3	467.2254	449.2135	450.1984	234.1127	E	1269.6433	1251.6328	1252.6163	635.3217	8
4	604.2843	586.2737	587.2573	302.6422	H	1140.6007	1122.5902	1123.5737	570.8004	7
5	804.3983	786.3898	787.3734	402.7002	K(+72.02)	1003.5381	985.5312	986.5148	502.2709	6
6	1004.5165	986.5059	987.4895	502.7608	K(+72.02)	803.4263	785.4152	786.3987	402.2129	5
7	1133.5591	1115.5486	1116.5321	567.2795	E	603.3099	585.2991	586.2827	302.1548	4
8	1317.6803	1299.6698	1300.6533	659.3401	K(+56.03)	474.2725	456.2565	457.2401	237.6335	3
9	1432.7072	1414.6967	1415.6802	716.8536	D	290.1459	272.1353	273.1189	145.5729	2
10					R	175.1187	157.1084	158.0919	88.0595	1

Figure S14_88

MSMS assignment of K159ox in DNA topoisomerase 1

TOP1(154-163): TEDTK*K*[O]EK*K*R; -10lgP 32.64; Scan 10327 (MC306)

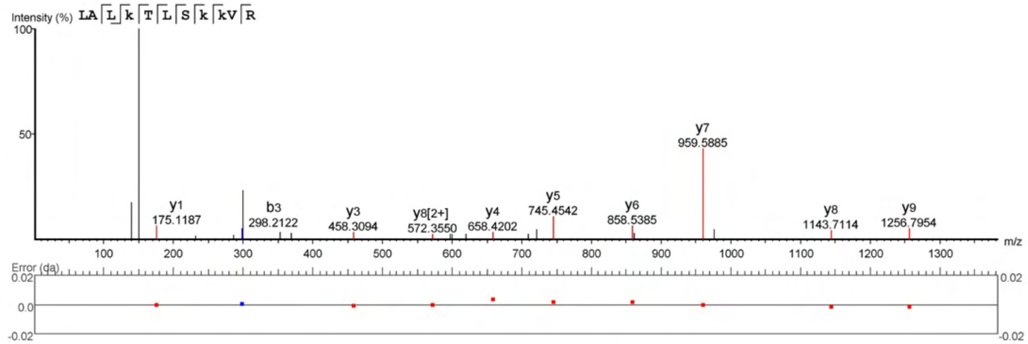


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	102.0555	84.0450	85.0285	51.5278	T					10
2	231.0977	213.0875	214.0711	116.0490	E	1401.7583	1383.7478	1384.7313	701.3792	9
3	346.1224	328.1145	329.0981	173.5625	D	1272.7166	1254.7052	1255.6887	636.8578	8
4	447.1727	429.1621	430.1457	224.0863	T	1157.6888	1139.6783	1140.6619	579.3444	7
5	631.2939	613.2833	614.2669	316.1469	K(+56.03)	1056.6405	1038.6306	1039.6141	528.8206	6
6	831.4100	813.3994	814.3830	416.2050	K(+72.02)	872.5203	854.5094	855.4930	436.7600	5
7	960.4526	942.4420	943.4256	480.7263	E	672.4001	654.3933	655.3769	336.7019	4
8	1144.5737	1126.5632	1127.5468	572.7869	K(+56.03)	543.3606	525.3507	526.3343	272.1806	3
9	1328.6949	1310.6844	1311.6680	664.8475	K(+56.03)	359.2401	341.2296	342.2131	180.1201	2
10					R	175.1189	157.1084	158.0919	88.0595	1

Figure S14_89

MSMS assignment of K42ox in Pre-rRNA-processing protein TSR1 homolog

TSR1(35-45): LALK*TLSK*[O]K*VR; -10lgP 24.97; Scan 50609 (MC357)

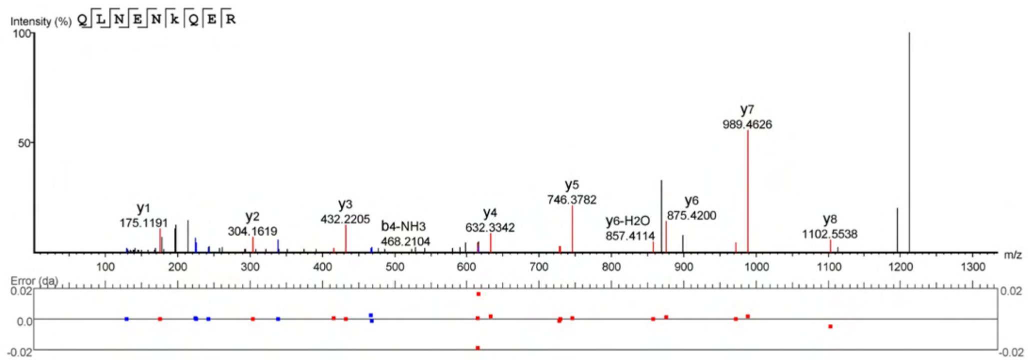


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	114.0919	96.0813	97.0649	57.5459	L					11
2	185.1290	167.1184	168.1020	93.0645	A	1327.8307	1309.8202	1310.8037	664.4153	10
3	298.2122	280.2025	281.1861	149.6065	L	1256.7954	1238.7831	1239.7666	628.8968	9
4	482.3342	464.3237	465.3073	241.6671	K(+56.03)	1143.7114	1125.6991	1126.6826	572.3550	8
5	583.3819	565.3713	566.3549	292.1909	T	959.5885	941.5778	942.5614	480.2942	7
6	696.4659	678.4554	679.4390	348.7330	L	858.5385	840.5302	841.5137	429.7704	6
7	783.4980	765.4874	766.4710	392.2490	S	745.4542	727.4460	728.4296	373.2283	5
8	983.6141	965.6035	966.5871	492.3070	K(+72.02)	658.4202	640.4141	641.3976	329.7123	4
9	1167.7352	1149.7247	1150.7083	584.3676	K(+56.03)	458.3094	440.2979	441.2815	229.6543	3
10	1266.8037	1248.7932	1249.7767	633.9019	V	274.1873	256.1768	257.1604	137.5937	2
11					R	175.1187	157.1084	158.0919	88.0595	1

Figure S14_90

MSMS assignment of K15ox in Splicing factor U2AF 65 kDa subunit

U2AF2(10-18): QLNENK*[O]QER; -10lgP 45.85; Scan 5669 (MC311)

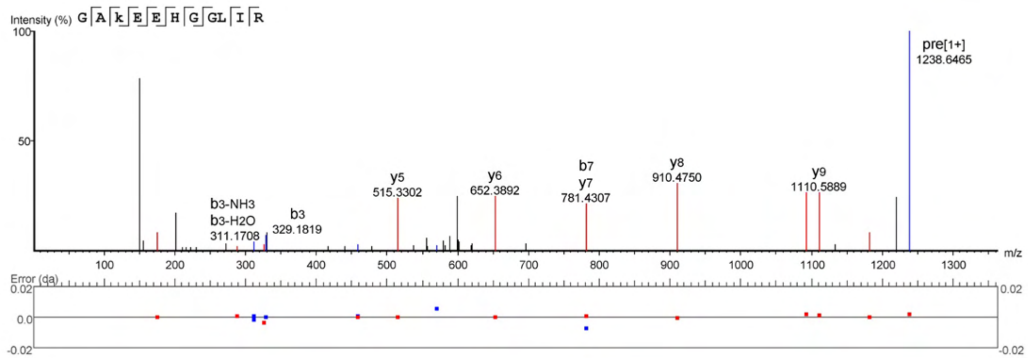


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	129.0661	111.0558	112.0394	65.0332	Q					9
2	242.1504	224.1390	225.1237	121.5752	L	1102.5538	1084.5382	1085.5217	551.7744	8
3	356.1934	338.1826	339.1665	178.5967	N	989.4626	971.4540	972.4381	495.2323	7
4	485.2360	467.2226	468.2104	243.1180	E	875.4200	857.4114	858.3947	438.2108	6
5	599.2789	581.2684	582.2520	300.1395	N	746.3782	728.3702	729.3519	373.6895	5
6	799.3950	781.3845	782.3680	400.1975	K(+72.02)	632.3342	614.3245	615.3284	316.6681	4
7	927.4536	909.4430	910.4266	464.2268	Q	432.2205	414.2095	415.1921	216.6100	3
8	1056.4961	1038.4856	1039.4691	528.7480	E	304.1619	286.1509	287.1345	152.5807	2
9					R	175.1191	157.1084	158.0919	88.0595	1

Figure S14_91

MSMS assignment of K70ox in Splicing factor U2AF 65 kDa subunit

U2AF2(68-78): GAK*[O]EEHGGLIR; -10lgP 48.53; Scan 6473 (MC317)

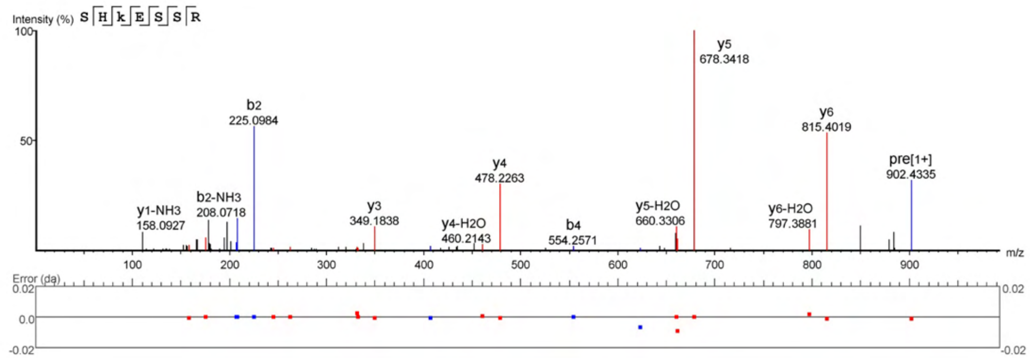


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	58.0293	40.0187	41.0023	29.5146	G					11
2	129.0664	111.0558	112.0394	65.0332	A	1181.6277	1163.6167	1164.6002	591.3136	10
3	329.1819	311.1708	312.1575	165.0912	K(+72.02)	1110.5889	1092.5776	1093.5631	555.7950	9
4	458.2239	440.2145	441.1981	229.6125	E	910.4750	892.4635	893.4471	455.7370	8
5	587.2676	569.2571	570.2350	294.1338	E	781.4307	763.4209	764.4045	391.2157	7
6	724.3265	706.3160	707.2996	362.6633	H	652.3892	634.3784	635.3619	326.6984	6
7	781.3553	763.3375	764.3210	391.1740	G	515.3302	497.3194	498.3030	258.1650	5
8	838.3695	820.3589	821.3425	419.6848	G	458.3085	440.2979	441.2815	229.6543	4
9	951.4536	933.4430	934.4266	476.2268	L	401.2870	383.2765	384.2601	201.1435	3
10	1064.5376	1046.5271	1047.5106	532.7688	I	288.2021	270.1924	271.1760	144.6015	2
11					R	175.1188	157.1084	158.0919	88.0595	1

Figure S14_92

MSMS assignment of K962ox in U2 snRNP-associated SURP motif-containing protein

SR140(960-966): SHK*[O]ESSR; -10lgP 35.97; Scan 3529 (MC310)

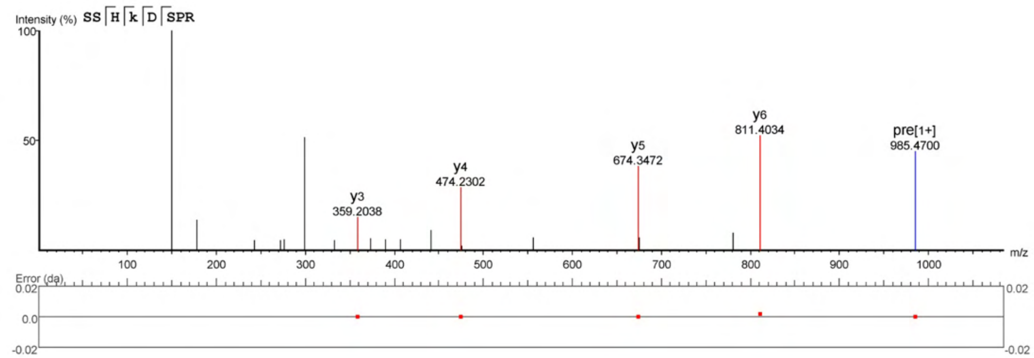


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	88.0399	70.0293	71.0129	44.5199	S					7
2	225.0984	207.0878	208.0718	113.0494	H	815.4019	797.3881	798.3736	408.2003	6
3	425.2148	407.2049	408.1879	213.1074	K(+72.02)	678.3418	660.3306	661.3242	339.6708	5
4	554.2571	536.2469	537.2305	277.6287	E	478.2263	460.2143	461.1986	239.6128	4
5	641.2894	623.2859	624.2625	321.1447	S	349.1838	331.1698	332.1561	175.0915	3
6	728.3215	710.3109	711.2945	364.6607	S	262.1516	244.1404	245.1245	131.5755	2
7					R	175.1191	157.1084	158.0927	88.0595	1

Figure S14_93

MSMS assignment of K972ox in U2 snRNP-associated SURP motif-containing protein

SR140(969-976): SSHK*[O]DSPR; -10lgP 34.55; Scan 4219 (MC310)

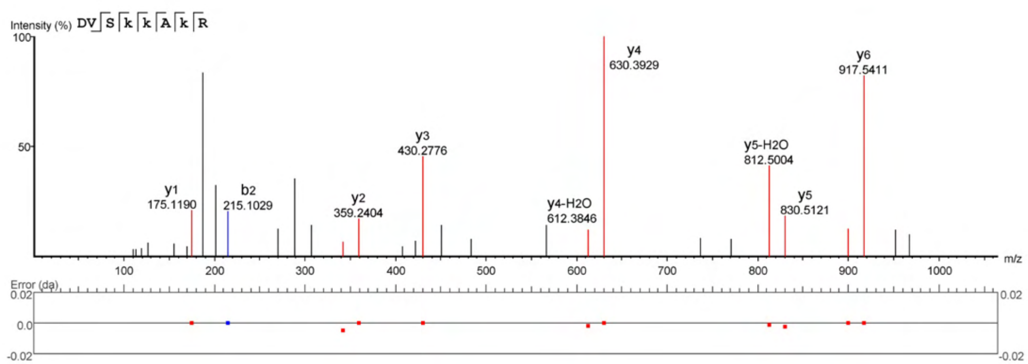


#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	88.0399	70.0293	71.0129	44.5199	S					8
2	175.0719	157.0613	158.0449	88.0359	S	898.4377	880.4271	881.4107	449.7188	7
3	312.1308	294.1202	295.1038	156.5654	H	811.4034	793.3951	794.3787	406.2028	6
4	512.2469	494.2363	495.2199	256.6234	K(+72.02)	674.3472	656.3362	657.3198	337.6734	5
5	627.2738	609.2632	610.2468	314.1369	D	474.2302	456.2201	457.2037	237.6153	4
6	714.3058	696.2953	697.2789	357.6529	S	359.2038	341.1931	342.1767	180.1019	3
7	811.3586	793.3480	794.3316	406.1793	P	272.1717	254.1611	255.1447	136.5858	2
8					R	175.1189	157.1084	158.0919	88.0595	1

Figure S14_94

MSMS assignment of K980ox, K981ox in U2 snRNP-associated SURP motif-containing protein

SR140(977-984): DVSK*[O]K*[O]AK*R; -10lgP 36.37; Scan 7728 (MC313)



#	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	116.0348	98.0242	99.0078	58.5174	D					8
2	215.1029	197.0926	198.0762	108.0516	V	1016.6098	998.5992	999.5828	508.8049	7
3	302.1352	284.1246	285.1082	151.5676	S	917.5411	899.5303	900.5144	459.2707	6
4	502.2513	484.2407	485.2243	251.6256	K(+72.02)	830.5121	812.5004	813.4824	415.7547	5
5	702.3674	684.3568	685.3404	351.6837	K(+72.02)	630.3929	612.3846	613.3663	315.6967	4
6	773.4045	755.3939	756.3775	387.2022	A	430.2776	412.2667	413.2502	215.6386	3
7	957.5256	939.5151	940.4987	479.2628	K(+56.03)	359.2404	341.2296	342.2182	180.1201	2
8					R	175.1190	157.1084	158.0919	88.0595	1