Personalized peptide vaccine induced immune response associated with long-term survival of a metastatic cholangiocarcinoma patient

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Supplementary materials and methods

Clinical Specimens
Tumor (L06/10 [Primary tumor]; L03/11 [fist in loco recurrence]; L04/12 [second in loco recurrence]; P03/13 [lung metastasis]) and benign tissue samples that were resected during surgery, underwent routine histopathology, and were cryopreserved for further analysis (except for L03/11 for the latter). Peripheral blood was drawn during each vaccination visit (see Figure 1). Further DNA from 18 ml of peripheral venous blood was isolated as a healthy tissue reference in April 2012.

Isolation and storage of PBMCs
PBMCs were isolated from EDTA-blood within 6 h of blood drawing using standard density gradient centrifugation, by layering over Biocoll separating solution (Biochrom GmbH, Berlin, Germany). Cells were subsequently washed with PBS and counted using 0.1% Trypan blue solution. 5-10 x 10^6 cells were frozen/ml of freezing solution (heat-inactivated FCS containing 10% DMSO) and stored in the gaseous phase of liquid nitrogen.

Pre-stimulation and expansion of PBMCs
PBMCs were thawed (Day 0) and 4-6 x 10^5 cells were seeded per well in a 24 well plate. Culture medium was Iscove's modified Dulbecco's medium (IMDM; Lonza, Basel, Switzerland) containing 10% heat-inactivated human AB serum (Life Technologies, Carlsbad, CA), 1% penicillin/streptomycin (PAA, Pasching, Austria), and 50μM β-mercaptoethanol. For HLA class I peptide stimulations 5 ng/ml IL-4 (R&D, Minneapolis, MN) and 5 ng/ml IL-7 (Promokine, Heidelberg, Germany) were added. After overnight resting later (Day 1), cells were separately stimulated in triplicates (duplicates for pre-vaccination ‘scr’ time point), with peptide pool I* (1 μg/ml per
peptide) and peptide pool II** (5 µg/ml per peptide). After each 48 h interval, recombinant human IL-2 (R&D) was replenished at a final concentration of 2 ng/ml. On day 12 cells were harvested for functional testing. *Pool I: RGS-5, ADFP2, ADFP3, MMP7-(1) and HIV-A03. **Pool II: CCND1, IGFBP3, MMP7-(2), Filamin-A. HIV-A03 (KIRLRPGGK) and Filamin-A (ETVITVDTKAAGKGK) peptides were the negative control peptides for pool I and pool II respectively.

**IFN-\(\gamma\) ELISPOT**

IFN-\(\gamma\) secretion by PBMCs in response to peptide re-stimulation was determined using ELISPOT assay, as described previously (1). Briefly, cells were re-stimulated using peptides (5 µg/ml peptides from pool I and 2.5 µg/ml peptides from pool II) in a 96 well ELISPOT plate (MSHAN4B50, Millipore, Darmstadt, Germany), which was pre-coated with anti-IFN-\(\gamma\) antibody (clone 1-D1K, Mabtech, Nacka Strand, Sweden). Phytohaemagglutinin-L (PHA-L) (for pool I stimulated cells) or Staphylococcus enterotoxin B (SEB) (for pool II stimulated cells) were used as a positive controls at 10 µg/ml or 1 µg/ml respectively. Cells stimulated with HIV-A03 peptide or Filamin A peptide served as the relevant negative controls. 26 h later, the secreted IFN-\(\gamma\) was detected using biotinylated anti-IFN-\(\gamma\) antibody (clone 7-B6-1, Mabtech), Extravidin-phosphatase enzyme and BCIP/NBT tablets (Sigma-Aldrich, Hamburg, Germany). Spots were scanned and counted with an ImmunoSpot Series 6 Core ELISPOT Reader (C.T.L. Europe, Bonn, Germany). Responses were considered positive if the average no. of spots minus the no. of spots in the negative control wells were at least 8 spots/100,000 seeded cells and 2 fold above the average spots in negative control wells.

**HLA-peptide multimer staining**
Biotinylated MHC class I monomers containing vaccine peptides (RGS-5, ADFP2, ADFP3 and MMP7-(1)) were produced in-house using the conventional refolding technique (2, 3). Monomers were then co-incubated with streptavidin-PE or APC (Life-Technologies) to generate fluorescent HLA-peptide multimers (3). PBMCs were stained with HLA-peptide multimers adhering to the CIP–CIMT guidelines (3) (http://www.cimt.eu/workgroups/cip/publications). In short, PBMCs were incubated with HLA-peptide multimers (5 µg/ml), washed and then stained using a viability marker (Aqua Live Dead, Life Technologies), anti-CD4-FITC (clone HP2/6, in-house conjugated) and anti-CD8-PECy7 (clone SFCI21Thy2D3, Beckman Coulter, Krefeld, Germany). Cells were then acquired on a FACS Canto II (BD Biosciences) equipped with the DIVA software and analyzed using FlowJo 9.7.5 (Treestar, Ashland, USA). Responses were considered positive after vaccination if the percentage of living HLA-peptide multimer (+) CD8 (+) cells were at least 2-fold above the percentages in the scr or 1V time point.

**Intra-cellular cytokine staining (ICS)**

TNF-α and IFN-γ production was detected using ICS essentially as reported earlier (1). Briefly, cells were stimulated with individual peptides (10 µg/ml) in the presence of GolgiStop (BD Biosciences, Heidelberg, Germany) and Brefeldin A (Sigma-Aldrich, 10 µg/ml). Cells stimulated with HIV peptide or Filamin A peptide served as the relevant negative controls. After a 12 h stimulation period, cells were washed and stained with a viability marker (Aqua Live Dead; Life Technologies), CD4-APC-Cy7 and CD8-PE-Cy7 mAb (Beckman Coulter, Fullerton, CA) for 20 min at 4° C, fixed and permeabilized in Cytoperm/Cyto fix (BD Biosciences) for 20 min at 4° C and further stained with anti-IFN-γ-FITC (BD Biosciences) and anti-TNF-Pacific-blue (Biolegend, San Diego, CA) for 30 min at 4° C. At least 200,000 CD4+/CD8+ cells were acquired and analyzed.
Responses were considered positive if the percentage of cytokine producing cells were two-fold above the corresponding negative control peptide stimulated cells.

*Serum IL-10 assessment*

Serum samples were drawn at different vaccination time points (S-Monovette, Sarstedt, Nümbrecht, Germany). Blood samples were left for 4 hours at room temperature and centrifuged (5 min. at 4°C/ 1900 rpm). Serum was collected and centrifuged twice before freezing aliquots at -80°C until further use.

An in-house developed Luminex-based multiplexed sandwich immunoassay (Luminex, Austin, TX) was used to determine IL-10 levels in serum samples but detected sample values consistently ranged below the lower limit of quantification (LLoQ) of the assay.

Subsequently, an in-house developed ultra-sensitive IL-10 single molecule array (SIMOA) immunoassay was applied to determine serum IL-10 levels at different vaccination time points. The assay was validated, considering the recommendations for assay validation, put forward in respective guidelines from health authorities (e.g. European Medicine Agency (EMA), 2009; and Food and Drug Administration (FDA), 2013). The limit of detection (LoD) of the assay was found to be at 0.44 fg·mL⁻¹, the limit of quantification (LoQ) at 6.3 fg·mL⁻¹ (not considering any sample dilution factor). Inter-assay precision (4 samples, different analyte levels; 7 runs) was 8.4 to 17.8 %CV [coefficient of variation], intra-assay precision (3 samples, different analyte levels; 20 replicates each) was 3.4 to 11.2 %CV.

Purified recombinant IL-10 protein was used as a calibrator for the SIMOA immunoassay. A different standard protein (ThermoFisher Scientific, Bremen, Germany, Order# SIL10) calibrated against the NIBSC/WHO (92/516) IL-10 standard was additionally evaluated with this in-house developed assay. The dose response
curve of this NIBSC/WHO calibrated standard paralleled the applied IL-10 standard curve. To convert sample values measured by the mentioned IL-10 SIMOA assay to respective WHO standard concentrations, the given analyte concentrations (as shown in supplementary Table 20) should be divided by a factor of 0.77.

*Exome- (WES) and Transcriptome- (WTS) sequencing*

As part of the *IndividuaLIVER* project, whole exome sequencing (WES) was performed for L06/10 (tumor vs. liver) after exome enrichment using the SeqCap EZ Exome Enrichment Kit v2.0 (Roche NimbleGen, Mannheim, Germany), covering 44.1 megabases of coding sequence. For L06/10 and P03/13, combined WES (tumor vs. blood) and WTS (tumor) was done, which used the RNA Sample Preparation Kit v2 (illumina, Eindhoven, Netherlands). As part of a validation procedure for the first sequencing approach all somatic variants of the coding region found in the tumor sample L06/10 were validated by deep sequencing (average read depth 1330x) using an amplicon based approach (Haloplex custom panel; Agilent, Waldbronn, Germany). Only variants validated in the sample L06/10 by the deep sequencing approach were used for subsequent peptide prediction. All samples and venous blood were sequenced on a GAIIx (Illumina) as paired-end sequencing. Respective results are given below. This yielded a mean coverage depth of 90x for the tumor samples with 70 % of regions of interest covered with at least 30x and 58 % of the regions covered with at least 50x. On average 18 somatic variants were found, which is consistent with previous reports for CCC (4-7). Out of these somatic variants 7 were identified in 5 well known/potential tumor suppressor (TSG) or oncogenes.

*Bioinformatic analysis*

Adapters were trimmed using SeqPurge (manuscript under review, https://github.com/marc-sturm/ngs-bits), DNA-reads were mapped using BWA (v.
0.7.12, (8)) to hg19. Duplicates are marked by samblaster (v. 0.1.21, (9)). Overlapping reads were trimmed to reduce false-positive variants with very low allele-frequencies by an in-house tool. strelka (v. 1.0.14, (10)) was used for variant calling and SnpEff/SnpSift (v. 4.1c, (11, 12)), vcflib (last accessed 06/23/2015, https://github.com/ekg/vcflib) and dbNFSP (v. 3.0, (13)) were used for annotation. Custom filter criteria were used to extract high-confidence variants. Trimmed RNA-reads were mapped using STAR (v. 2.4.2a, (14)). Duplicates were removed by picard tools (v. 1.122, http://broadinstitute.github.io/picard/). QC parameters were collected by in-house scripts, all variants were annotated by in-house variant frequencies. Processing of amplicon-based deep-sequencing data ended after mapping.

Peptide prediction

Both lists of tumor and patient specific (hg19 divergent) mutations were handled in machine-readable tab-separated format to keep a minimum of manual inspection possible. The variations start and stop positions were recorded with their chromosomal base position according to hg19. They were linked with the respective mRNA positions to keep track of all splicing variants of a gene. These transcript sequences were fetched from UCSC’s GenomeBrowser Database (https://genome.ucsc.edu/). The tumor specific variations were then applied to this sequence with the possible combinations of patient specific variations on the transcript.

The possible combinations can be as follows:

- Tumor specific only or tumor specific with close homozygous patient specific variation, which results in a single variation sequence.

- Tumor specific variation with close heterozygous patient specific variation(s), which is fanned out according to the number of variations close.
- Interleaving insertions/deletions, which have to be processed in order of occurrence from 3’ to 5’ on the template strand.

Whether the tumor specific variation is heterozygous is irrelevant in this particular aspect as it is indeterminable if the heterozygous patient specific variation resides on the same allele as the tumor specific variation and both patient specific variation and regular genotype have to be considered with only the tumor specific since we are only interested in resulting peptides which are tumor specific.

From these combinations we derived the respective protein sequences with the translation of the mRNA in the according reading frame.

The binding prediction was then conducted in a sliding window fashion over the resulting protein sequences around the tumor-specific variations with SYFPEITHI and NetMHC (15, 16). The sequence slices were annotated each with their predicted binding score, the HLA allele for which the prediction is valid, and when available as with nucleotide exchange variations, with their wildtype counterpart and the respective score. Also connected were the chromosomal position of the mutation and the quality parameters of the sequencing experiments. This list was filtered for binding scores above the halfmax score of their respective HLA allele.

A fasta file was created from the protein sequences in addition to the predictions. This fasta file served as foundation of the individualized search database for LC-MS/MS validation via Spectra ID. From the filtered list also an inclusion list was created, which contained the respective mass-to-charge ratios for which a targeted search in the mass spectrometer could be conducted.

*Mass Spectrometry*
HLA-ligands were immunoprecipitated from cryopreserved tumor tissues and liver tissue (L06/10) as previously described (17) using the pan-HLA-class I antibody W6/32. Subsequently HLA-ligands were purified using 3 kDa cutoff centrifugal filters (Amicon, Merck Millipore, Carrigtwohill, Ireland), desalted (C18 ZipTip; Merck Millipore, Darmstadt, Germany) and concentrated (vacuum centrifuge; Bachofer, München, Germany). HLA-ligandomes were assessed by LC-MS/MS as previously described (18).

In short, samples were separated by reverse phase liquid chromatography on a 75µm trapping column and measured by an on-line coupled LTQ Orbitrap XL hybrid mass spectrometer (ThermoFisher Scientific, Bremen, Germany) by top 5 CID (collision induced dissociation) method. Raw data were processed against the human proteome (www.uniprot.org, as of 12/12/2012) as previously published (18) using MASCOT (v2.3.04 Matrix Science, Boston, MA) and Proteome Discoverer (v1.3 Thermo Fisher). Mass tolerance was set at 5ppm/ 0.5 Da for parent- and fragment masses respectively, filtering for Mascot Score<20; search rank 1 and peptide lengths of 8-12 AA at a target false discovery rate (FDR) q ≤ 5% using an inverse decoy database search.

An individualized database in FASTA format was produced for potential patient specific alterations in protein sequences derived from cancer-specific variations in WES/WTS and searched against respective data.
**Supplementary Table 1: Antibodies used for Immunohistochemistry**

Respective antibodies used for immunohistochemical stainings of diagnostic paraffin embedded sample material are listed with respective protein target, antibody clones used such as supplier and dilutions used for staining on an automated immunostainer following the manufacturer´s protocol (Benchmark, Ventana Medical Systems, Tucson, AZ).

| Antibody | Clone | Supplier | Dilution |
|----------|-------|----------|----------|
| CCR7     | clone Y59 | Abcam, Cambridge / UK | 1:200    |
| CD3      | SP7   | DCS, Hamburg / Germany | 1:100    |
| CD4      | SP 35 | Zytomed, Berlin / Germany | 1:50     |
| CD8      | C8/144B | DAKO, Glostrup / Denmark | 1:150    |
| CD25     | 4C9   | Novocastra, Nussloch / Germany | 1:100    |
| CD45     | mono mouse | DAKO, Glostrup / Denmark | 1:500    |
| CK7      | OV-TL12/30 | DAKO, Glostrup/ Denmark | 1:100    |
| CK20     | Ks20.8 | DAKO, Glostrup / Denmark | 1:200    |
| CCND1    | SP4   | DCS, Hamburg / Germany | 1:40     |
| EPCAM    | VU-1D9 | Novocastra, Nussloch / Germany | 1:50     |
| FOXP3    | mono mouse | Abcam, Cambridge / UK | 1:50     |
| Granzyme B | poly rabbit | Roche, Mannheim / Germany | ready to use |
| HLA DR   | DR antigen | DAKO, Glostrup / Denmark | 1:150    |
| HLA DQ   | DQ antigen | DAKO, Glostrup / Denmark | 1:200    |
| Napsin A | KCG1.1 | Zytomed, Berlin / Germany | 1:50     |
| MMP7     | ID-2  | Merck-Millipore, Darmstadt / Germany | 1:150    |
| Perforin | 5B10  | Novocastra, Nussloch / Germany | 1:20     |
| TTF1     | 8G7G3/1 | Zytomed, Berlin / Germany | 1:100    |
### Supplementary Table 2: Auxiliary Results: Immunohistochemistry

Counts per 10 high power fields (HPF) Stromal compartment

| Sample | CD3   | CD4   | CD8   | CD25 | FOX P3 | granzyme B | CD45 | HLA DR | HLA DQ |
|--------|-------|-------|-------|------|--------|------------|------|--------|--------|
| L06/10 | 45.1  | 8.9   | 9.3   | 9.8  | 0.5    | 0.3        | 44.8 | 48.0   | 48.0   |
| L03/11 | 16.5  | 4.2   | 3.3   | 32.8 | 2.4    | 1.1        | 7.6  | 13.3   | 16.6   |
| L04/12 | 78.0  | 59.7  | 36.2  | 18.4 | 5.2    | 1.5        | 67.2 | 122.5  | 95.0   |
| P03/13 | 119.3 | 47.7  | 24.5  | 21.2 | -      | 1.4        | 56.5 | 78.0   | 82.5   |

Counts per 10 high power fields (HPF) Epithelial compartment

| Sample | CD3 | CD4 | CD8 | CD25 | FOX P3 | granzyme B | CD45 | HLA DR | HLA DQ |
|--------|-----|-----|-----|------|--------|------------|------|--------|--------|
| L06/10 | 1.5 | 0.1 | 0.8 | 0.5  | 0.2    | 0.0        | 1.4  | 6.2    | 5.0    |
| L03/11 | 3.3 | 0.2 | 0.6 | 2.4  | 0.2    | 0.0        | 6.1  | 5.6    | 7.9    |
| L04/12 | 2.0 | 1.4 | 0.2 | 2.6  | 0.5    | 0.1        | 0.9  | 7.5    | 10.4   |
| P03/13 | 4.8 | 1.4 | 0.2 | 3.8  | -      | 0.1        | 0.3  | 35.5   | 29.5   |
Supplementary Figure 1-15: Selected Radiological Imaging Results

Selected Images: computed tomography (CT) / magnetic resonance imaging (MRI) / 18Fluorodeoxyglucose positron emission tomography (18FDG PET) CT

Diagnostic whole body CT scans/ MRI scans and 18FDG PET-CT scans were performed of the patient at various occasions during the course of disease. Here we show the pictures shown in Figure 1 for illustrative purposes in more detail, supplemented by further representative images that might be of interest.

L06/10 (Primary tumor) CT scan before surgery (Supplementary Figure 1 (left)/ 2 (right))

liver coronal (CT June/2010)  liver transversal (CT June/2010)
L06/10 (Primary tumor) CT scan after surgery (11/2010) (Supplementary Figure 3 (left)/ 4 (right))

liver coronal (CT November /2010)  
liver transversal (CT November/2010)
L03/11 (first local recurrence) CT / MRI scan before surgery (Supplementary Figure 5 (left)/ 6 (right))

liver (segment 5) transversal (CT February/2011)  liver (segment 3) transversal (MRI February/2011)
Supplementary Figure 7

liver (segment 5) transversal (MRI February/2011)
L04/12 (second local recurrence) CT scan after surgery (Supplementary Figure 8 (left)/ 9 (right))

liver coronal (CT September/2012)  liver transversal (CT September/2012)

Supplementary Figure 10

lung transversal (CT September/2012)
P03/13 (pulmonary metastasis) CT /$^{18}$FDG PET CT scan before surgery
(Supplementary Figure 11 (left)/ 12 (right))

Supplementary Figure 13

l lung transversal (CT March/2013) lung transversal (CT March/2013)

l lung transversal ($^{18}$FDG PET CT fusion March/2013)
Follow up (Supplementary Figure 14 (left)/ 15 (right))

- Lung transversal (CT February/2015)
- Liver transversal (CT July/2015)
Supplementary Table 3: Layout of the somatic Cancer Panel (V2)

The table lists all 336 genes included in the somatic cancer panel V2 (SureSelect XT; Agilent). The coding sequence of these genes was analyzed by NGS. Functional annotations (green: cell survival; blue: cell survival/ cell fate; yellow: cell fate; red: genome maintenance; orange: potential tumor suppressor or oncogene).

| Gene 1 | Gene 2 | Gene 3 | Gene 4 | Gene 5 | Gene 6 | Gene 7 |
|--------|--------|--------|--------|--------|--------|--------|
| ABL1   | PDGFRA | PTCH1  | ABCB1  | CSF3R  | HOXA3  | NAT2   |
| AKT1   | PIK3CA | PAX5   | ABL2   | CYP2A6 | HSP90AA1 | NTRK3 |
| AKT3   | PIK3R1 | PHF6   | ACE    | CYP2B6 | IGF2R  | PAK3   |
| ALK    | RB1    | RUNX1  | ADH1A  | CYP2C8 | INSR   | PDGFRB |
| BCL2   | RET    | SMARCA4| ADH1B  | CYP2C9 | JAG1   | PGR    |
| BCL2A1 | PTPN1  | SMARCB1| ADH1C  | CYP2E1 | JAG2   | PHLP2  |
| BCL2L1 | PTEN   | SMO    | ADRB1  | CYP2J2 | KCNH2  | PRAM1  |
| BRAF   | SMAD2  | SOX2   | ADRB2  | CYP3A4 | KCN11  | PTCH2  |
| CARD11 | STK11  | WT1    | AHR    | DDR2   | LRP1B  | PTPRD  |
| CASP8  | TSC1   | SRSF2  | AKT2   | Dicer1 | MAP2K2 | RAF1   |
| CBL    | TSC2   | TET2   | ALDH1A | Dll1   | GSTP1  | RGL1   |
| CCND1  | TGFB2  | ATM    | ALOX5  | Dll3   | IGF1R  | RGL2   |
| CCE1   | TP53   | BAP1   | ARAF   | DOT1L  | IKBKE  | PIK3CG |
| CDKN2A | VHL    | BRCA1  | ARFRP1 | Dpyd   | IR52   | PKHD1  |
| CDKN2B | SMAD4  | BRCA2  | ATR    | DRD2   | KDR    | PRKDC  |
| CEBPA  | TNFAIP3| MDM2   | AURKA  | EphA3  | LRP6   | PTG5S  |
| CRKL   | APC    | MLH1   | AURKB  | EphA5  | LTK    | RARA   |
| CRLF2  | AR     | MSH2   | BCL2L2 | EphA6  | GSTT1  | RICTOR |
| FLT3   | ARID1A | MSH6   | BCL6   | EphB1  | IKZF1  | RPTOR  |
| FGFR2  | ASXL1  | GNAS   | BTK    | Erbb3  | JUN    | SALL4  |
| FGFR3  | CDH1   | DDX3X  | CCND2  | ERF1L  | INHBA  | PLCG1  |
| GNAQ   | CTNBN1 | KMT2D  | CD38   | Fanca  | MDM4   | PMS2   |
| EGFR   | ERG    | MED1   | CD79A  | Flt1   | Mre11A | PTGIS  |
| ERBB2  | FBXW7  | IRF6   | CD79B  | G6PD   | Ms4A1  | Scn5a  |
| GNA11  | E2H2   | NRXN3  | CDH2   | Dll4   | Mthfr  | Slco1b1|
| Kras   | FOXL2  | PIK3AP1| CDH5   | EphA7  | Myb    | Smad3  |
| Jak3   | Gata1  | Ripk4  | CDH20  | EphB4  | Mycn   | Sox10   |
| Kit    | DNMT3A | RasA1  | Cdk6   | Ercc2  | Nrr12  | Tnk5   |
| MAP2K1 | Idh1   | Rimbp2 | Cdkn2c | Fgfr1  | Ntrk1  | Tnk5   |
| MAP2K4 | Idh2   | Rims2  | Chek2  | Fgfr4  | Mtor   | Vdr    |
| HRAS   | KDM6A  | RXFP3  | Comt   | Flt4   | Mycl   | Src    |
| Jak1   | Mitf   | Pclo   | Cux1   | Foxp4  | Notch4 | Sult1a1|
| Jak2   | Mll    | Prdm9  | Cyp1a2 | Ephb6  | Nqo1   | Top1   |
| Mcl1   | Notch1 | SynE1  | Cyp2c19| F5     | Nrxn2  | Tpmt   |
| Myd88  | Notch2 | SynE2  | Cyp2d6 | Erbb4  | Ntsc2  | Tyms   |
| Nras   | Men1   | Si     | Cyp3a5 | Esr1   | Ntrk2  | Ugt1a1 |
| NPM1   | Nf2    | Tp63   | Ccnd3  | Esr2   | P2ry1  | Usp9x  |
| Met    | Notch3 | Tbx22  | Cdk4   | Gpr124 | P2ry12 | Slc19a1|
| MPL    | Nkx2-1 | Vkorc1 | Cd8    | Gucy1a2| Muc1   | Stat3  |
| Nf1    | Myc    | Chek1  | Hmgcr  | Muthy  | Sufu   |
Supplementary Table 4: Overview of (potential) Tumor Suppressor (TSG) and Oncogenes (somatic Cancer Panel)  
(somatic Cancer Panel V2, 336 genes)

| Genes     | Variant Details | L06/10 Primary tumor | L03/11 1st Liver recurrence | L04/12 2nd Liver recurrence | P03/13 Pulmonary metastasis | Classification | Pathway | Core Pathway | Process |
|-----------|-----------------|----------------------|----------------------------|-----------------------------|----------------------------|----------------|---------|-------------|---------|
| IDH1      | missense variant | +                    | +                          | +                           | +                          | Oncogene       | chromatin modification | metabolism (hypermethylation), HIF1α stabilization | cell fate |
|           | NM_001282386.1 c.394C>T:p.Arg132Cys | (28.6%)               | (19.8%)                    | (18.9%)                     | (26.3%)                    |                |                     |                        |         |
| PBRM1     | stop gain       | +                    | +                          | +                           | +                          | TSG            | chromatin modification | chromatin SWI/SNF complex | cell fate |
|           | NM_018313.4 c.2128C>T:p.Arg710* | (19.9%)               | (13.3%)                    | (10.2%)                     | (18.3%)                    |                |                     |                        |         |
| KMT2C     | missense variant | +                    | +                          | +                           | +                          | TSG            | chromatin modification | chromatin histone methyltransferase | Cell Fate |
|           | NM_170606.2 c.12545A>G:p.As4182Gly | (11.6%)               | (8.1%)                     | (10.6%)                     | (15.3%)                    |                |                     |                        |         |
| PTGS2     | missense variant | +                    | -                          | -                           | +                          | probably oncogene | prostaglandine synthesis | N/A | angiogenesis |
|           | NM_000963.3 c.6304T:p.V102L | (14.4%)               |                            |                            | (10.6%)                    |                |                     |                        |         |
| NOTCH2    | missense variant | -                    | +                          | -                           | -                          | TSG            | notch-signaling       | NOTCH | cell fate |
|           | NM_024408.3 c.3410T>G:p.Leu1139Arg | (9.8%)               |                            |                            |                            |                |                     |                        |         |
| PIK3R1    | stop gain       | -                    | +                          | -                           | -                          | TSG            | PI3K-signaling        | PI3K   | cell survival |
|           | NM_181523.2 c.1493G>T:p.Glu485* | (10%)                |                            |                            |                            |                |                     |                        |         |
| PTPN11    | missense variant | -                    | -                          | -                           | +                          | oncogene        | RAS/MAPK sig.       | RAS    | cell Survival |
|           | NM_002834.3 c.1492C>T:p.Arg498Trp |                        |                            |                            | (18.1%)                    |                |                     |                        |         |

* N/A: Not applicable

**notes:**
1. Oncogene
2. TSG
3. Chromatin modification
4. Metabolism
5. HIF1α stabilization
6. SWI/SNF complex
7. Cell fate
8. PI3K signaling
9. RAS/MAPK signaling
10. Cell survival
11. Cell proliferation
12. Apoptosis
13. DNA repair
14. Cell cycle regulation
15. Signal transduction
16. Cell adhesion
17. Cell motility
18. Cell invasion
19. Cell migration
20. Cell death
21. Cell survival
22. Angiogenesis
23. Chromatin modification
24. Chromatin remodeling
25. Chromatin accessibility
26. Chromatin structure
27. Chromatin compaction
28. Chromatin assembly
29. Chromatin disassembly
30. Chromatin decondensation
31. Chromatin remodeling
32. Chromatin compaction
33. Chromatin accessibility
34. Chromatin structure
35. Chromatin modification
36. Chromatin remodeling
37. Chromatin accessibility
38. Chromatin structure
39. Chromatin modification
40. Chromatin remodeling
41. Chromatin accessibility
42. Chromatin structure
43. Chromatin modification
44. Chromatin remodeling
45. Chromatin accessibility
46. Chromatin structure
47. Chromatin modification
48. Chromatin remodeling
49. Chromatin accessibility
50. Chromatin structure
51. Chromatin modification
52. Chromatin remodeling
53. Chromatin accessibility
54. Chromatin structure
55. Chromatin modification
56. Chromatin remodeling
57. Chromatin accessibility
58. Chromatin structure
59. Chromatin modification
60. Chromatin remodeling
61. Chromatin accessibility
62. Chromatin structure
63. Chromatin modification
64. Chromatin remodeling
65. Chromatin accessibility
66. Chromatin structure
67. Chromatin modification
68. Chromatin remodeling
69. Chromatin accessibility
70. Chromatin structure
71. Chromatin modification
72. Chromatin remodeling
73. Chromatin accessibility
74. Chromatin structure
75. Chromatin modification
76. Chromatin remodeling
77. Chromatin accessibility
78. Chromatin structure
79. Chromatin modification
80. Chromatin remodeling
81. Chromatin accessibility
82. Chromatin structure
83. Chromatin modification
84. Chromatin remodeling
85. Chromatin accessibility
86. Chromatin structure
87. Chromatin modification
88. Chromatin remodeling
89. Chromatin accessibility
90. Chromatin structure
91. Chromatin modification
92. Chromatin remodeling
93. Chromatin accessibility
94. Chromatin structure
95. Chromatin modification
96. Chromatin remodeling
97. Chromatin accessibility
98. Chromatin structure
99. Chromatin modification
100. Chromatin remodeling
101. Chromatin accessibility
102. Chromatin structure
103. Chromatin modification
104. Chromatin remodeling
105. Chromatin accessibility
106. Chromatin structure
107. Chromatin modification
108. Chromatin remodeling
109. Chromatin accessibility
110. Chromatin structure
111. Chromatin modification
112. Chromatin remodeling
113. Chromatin accessibility
114. Chromatin structure
115. Chromatin modification
116. Chromatin remodeling
117. Chromatin accessibility
118. Chromatin structure
119. Chromatin modification
120. Chromatin remodeling
121. Chromatin accessibility
122. Chromatin structure
123. Chromatin modification
124. Chromatin remodeling
125. Chromatin accessibility
126. Chromatin structure
127. Chromatin modification
128. Chromatin remodeling
129. Chromatin accessibility
130. Chromatin structure
131. Chromatin modification
132. Chromatin remodeling
133. Chromatin accessibility
134. Chromatin structure
135. Chromatin modification
136. Chromatin remodeling
137. Chromatin accessibility
138. Chromatin structure
139. Chromatin modification
140. Chromatin remodeling
141. Chromatin accessibility
142. Chromatin structure
143. Chromatin modification
144. Chromatin remodeling
## Supplementary Table 5: Quality Scores: Somatic Cancer Panel

|                | L06/10 Primary Tumor | L03/11 1st Liver recurrence | L04/12 2nd Liver recurrence | P03/13 Pulmonary metastasis | Mean of all Tumor samples | Blood sample normal tissue reference |
|----------------|----------------------|-----------------------------|-----------------------------|-----------------------------|---------------------------|--------------------------------------|
| **Read count** | 36,259,368           | 43,976,922                  | 40,203,930                  | 39,160,748                  | 39,900,242                | 17,748,620                          |
| **Q30 percentage** | 85.78               | 85.43                       | 85.15                       | 85.1                        | 85.37                     | 85.24                               |
| **Read length** | 150                  | 150                         | 150                         | 150                         | 150                       | 150                                 |
| **Insert size** | 160.63               | 154.37                      | 158.21                      | 158.73                      | 157.99                    | 177.82                              |
| **Target region read depth** | 979.48               | 1172.31                     | 1058.96                     | 1051.85                     | 1065.65                   | 705.25                              |
| **Target region 100X [%]** | 97.71                | 97.95                       | 97.96                       | 97.72                       | 97.84                     | 98.25                               |
| **Target region 500X [%]** | 87.61                | 93.09                       | 90.78                       | 89.85                       | 90.33                     | 76.27                               |
| **Duplicate read [%]** | 34.24                | 36.78                       | 37.31                       | 32.24                       | 35.14                     | 16.01                               |
| **On-target read [%]** | 59.47                | 61.31                       | 62.25                       | 58.54                       | 60.39                     | 60.28                               |
## Supplementary Table 6: Overview of (potential) Tumor suppressor (TSG) and Oncogenes (WES)
(Analyzed by whole exome sequencing (WES) as described under Supplementary Materials and Methods above)

| Gene     | Variant Details | L06/10 Primary Tumor | L04/12 2nd Liver recurrence | P03/13 Pulmonary metastasis | Classification | Pathway | Process | Core pathway                                      |
|----------|-----------------|----------------------|----------------------------|-----------------------------|----------------|---------|---------|--------------------------------------------------|
| **PTGS2**|                 | +                    | -                          | -                           | probable oncogene | prostaglandine synthesis | angiogenesis<sup>(22)</sup> | n.a.                              |
| NM_000963 | c.G304T:p.V102L  |                      |                            |                             |                |         |         |                                                  |
| **IDH1** |                 | +                    | -                          | +                           | oncogene<sup>(19)</sup> | chromatin modification | cell fate<sup>(19)</sup> | metabolism (hypermethylation), HIF-1α stabilized<sup>(20)</sup> |
| NM_005896 | c.C394T:p.R132C |                      |                            |                             |                |         |         |                                                  |
| **PBRM1**|                 | +                    | -                          | -                           | TSG<sup>(19)</sup> | chromatin modification | cell fate<sup>(19)</sup> | chromatin SWI/SNF complex<sup>(21)</sup> |
| NM_018313 | c.C2128T:p.R710X |                      |                            |                             |                |         |         |                                                  |
| **KMT2C**|                 | +                    | +                          | -                           | TSG<sup>(19)</sup> | chromatin modification | cell fate<sup>(19)</sup> | chromatin histone methyltransferase<sup>(21)</sup> |
| NM_170606 | c.A12545G:p.D4182G |                      |                            |                             |                |         |         |                                                  |
| **KDM6B**|                 | -                    | +                          | -                           | probable TSG<sup>(39, 40)</sup> | chromatin modification | cell fate<sup>(42)</sup> | histone demethylase<sup>(43)</sup> |
| NM_001080424.1 | c.740C>T:p.Pro247Leu |                      |                            |                             |                |         |         |                                                  |
Supplementary Table 7: Quality Scores: Whole Exome Sequencing (WES) / Whole Transcriptome Sequencing (WTS)

|                      | WES L06/10 Primary Tumor | WES L04/12 2nd Liver recurrence | WES P03/13 Pulmonary metastasis | WES Mean of all Tumor samples | WES Normal Blood (reference) | WTS L06/10 Primary Tumor | WTS P03/13 Lung metastasis |
|----------------------|--------------------------|---------------------------------|---------------------------------|-------------------------------|-------------------------------|----------------------------|---------------------------|
| Read count           | 75,849,162               | 113,219,318                     | 87,341,796                      | 92,136,758.67                 | 114,787,500                   | 108,623,056                 | 78,955,014                 |
| Q30 percentage       | 73.11                    | 89.88                           | 92.44                           | 85.14                         | 90.93                         | 88.45                      | 90.06                     |
| Read length          | 151                      | 76                              | 76                              | 101.00                        | 76                            | 76                         | 76                        |
| Insert size          | 256.80                   | 104.57                          | 114.76                          | 158.71                        | 104.30                        | -                          | -                         |
| Target region read depth | 107.56             | 85.74                           | 76.11                           | 89.80                         | 105.90                        | -                          | -                         |
| Target region 10x [%] | 72.34                   | 91.99                           | 85.90                           | 83.41                         | 92.96                         | -                          | -                         |
| Target region 50x [%] | 58.53                   | 61.70                           | 52.84                           | 57.69                         | 69.02                         | -                          | -                         |
| Duplicate read [%]   | 7.18                     | 26.56                           | 20.96                           | 18.23                         | 12.31                         | 30.10                      | 21.41                     |
| On-target read [%]   | 72.34                   | 74.52                           | 79.58                           | 75.48                         | 74.90                         | -                          | -                         |
Supplementary Table 8: WES/WTS/Deep Sequencing Results (L06/10)

Shown are sequencing results obtained by WES (whole exome sequencing) and WTS (whole transcriptome sequencing) and deep sequencing of altered regions evidenced in WES (for validation) of lesion L06/10 (primary tumor), yielding basic somatic variants. Complex variants are excluded as being unsuitable for the subsequent prediction of HLA-ligands. In sequential order of columns from left to right: serial number; chromosome number; start and end position of somatic variant, ref.: reference base; obs.: observed base at respective chromosomal location; allele frequency and depth of somatic variant as sequenced by WES in tumor and reference tissue (normal); frequency and depth of somatic variant as sequenced by WTS in tumor material; frequency and depth of somatic variant as sequenced by deep sequencing in tumor and reference tissue (normal); Ref. Seq. (NCBI Reference Sequence) such as variant type (MV: missense variant; DV: downstream gene variant; SG: stop gain variant; UV: upstream gene variant; SV: splice region variant)and putative AA (amino acid) alteration introduced by somatic variant; n.d. no data; ± variant excluded for peptide prediction.

| #  | chr  | start | end   | gene     | ref. | obs. | WES allele freq. | allele depth | WTS allele freq. | allele depth | deep sequencing allele freq. | allele depth | Ref. Seq. variant type [AA alteration] |
|----|------|-------|-------|----------|------|------|-----------------|--------------|-----------------|--------------|-----------------------------------|--------------|--------------------------------------|
| 1  | chr1 | 153633713 | 153633713 | SNAPIN\(^a\), ILF2\(^b\) | A    | G    | 0.12            | 186          | 0.00            | 84           | 0.04    | 203   | 0.09    | 2064 | 0.00    | 1378 | ^a NM_012437.5 MV [Q116G] ^b NM_004515.3 DV [n.d.] |

\(^a\)\(^b\)
### WES WTS deep sequencing

| Ref. Seq. | variant type | [AA alteration] |
|-----------|--------------|-----------------|
| NM_001267809.1 | DV [n.d.]] | |
| NM_000963.3 | MV [V102L] | |
| NM_178123.4 | MV [E346V] | |
| NM_001282386.1; NM_001282387.1; NM_005896.3 | MV [R132C] | |
| NM_018313.4 | SG [R710*] | |
| NM_001358.2 | MV [R31G] | |
| NM_001171976.1; NM_017675.4 | MV [V773I] | |
| NM_016020.3 | MV [V225M] | |
| NM_001001346.3 | UV [n.d.]] | |
| NM_012454.3; NM_001010927.2 | DV [n.d.]] | |
| NM_207111.3; NM_207116.2 | MV [N817K] | |

| # | #chr | start | end | gene | ref. | obs. | allele freq. | depth | allele freq. | depth |
|---|------|-------|-----|------|------|------|-------------|-------|-------------|-------|
| 2 | chr1 | 186648199 | 186648199 | *PTGS2* | C | A | 0.16 | 125 | 0.00 | 22 |
| 3 | chr2 | 179989221 | 179989221 | *SESTD1* | T | A | 0.22 | 161 | 0.00 | 99 |
| 4 | chr2 | 209113113 | 209113113 | *IDH1* | G | A | 0.23 | 229 | 0.00 | 33 |
| 5 | chr3 | 52643768 | 52643768 | *PBRM1* | G | A | 0.18 | 146 | 0.00 | 55 |
| 6 | chr4 | 24578282 | 24578282 | *DHX15* | G | C | 0.14 | 177 | 0.00 | 45 |
| 7 | chr5 | 176011599 | 176011599 | *CDHR2* | G | A | 0.06 | 105 | 0.00 | 31 |
| 8 | chr6 | 155581528 | 155581528 | *TFB1M*, *CLDN20*, *TIAM2* | C | T | 0.16 | 160 | 0.00 | 115 |
| 9 | chr7 | 5662641 | 5662641 | *RNF216* | G | T | 0.14 | 118 | 0.00 | 109 |
| #  | #chr | start   | end     | gene    | ref. | allele | depth | allele | depth | freq. | depth | freq. | depth | freq. | depth | Ref. Seq. variant type [AA alteration] |
|----|------|---------|---------|---------|------|--------|-------|--------|-------|-------|-------|-------|-------|-------|--------------------------------------|
| 10 | chr7 | 84671487| 84671487| SEMA3D  | G    | A      | 0.10  | 297    | 0.00  | 66    | 0.00  | 9     | 0.14  | 447   | 0.00  | 252                       NM_152754.2 SG [Q326*] |
|    |      |         |         |         |      |        |       |        |       |       |       |       |       |       |                                      |
| 11 | chr7 | 127669812| 127669812| LRRC4\(^a\), SND1\(^b\) | C    | G      | 0.12  | 485    | 0.00  | 47    | 0.00  | 6     | 0.12  | 4338  | 0.00  | 2558                       aNM_022143.4 MV [E294D]  
|    |      |         |         |         |      |        |       |        |       |       |       |       |       |       |                                      |
| 12 | chr7 | 151848648| 151848648| KMT2C   | T    | C      | 0.16  | 136    | 0.00  | 49    | 0.00  | 42    | 0.14  | 1730  | 0.00  | 1007                       NM_170606.2 MV [D4182G]       |
| 13 | chr10 | 6067959 | 6067959 | IL2RA   | G    | A      | 0.10  | 276    | 0.00  | 249   | 0.00  | 14    | 0.14  | 1711  | 0.00  | 1210                       NM_000417.2 MV [P32S]          |
| 14 | chr10 | 93668078| 93668078| FGFBP3  | C    | T      | 0.20  | 75     | 0.00  | 166   | 0.00  | 8     | 0.06  | 2125  | 0.00  | 1625                       NM_152429.4 MV [E217K]       |
| 15 | chr10 | 131665491| 131665491| EBF3    | C    | T      | 0.09  | 169    | 0.00  | 144   | 0.00  | 2     | 0.13  | 2878  | 0.00  | 1653                       NM_001005463.2 MV [R309K]    |
| 16 | chr14 | 20854241| 20854241| TEP1    | A    | G      | 0.28  | 129    | 0.00  | 74    | 0.07  | 14    | 0.27  | 2336  | 0.00  | 1632                       NM_007110.4 MV [F992S]        |
| 17 | chr14 | 91636435| 91636435| C14orf159 | G    | A      | 0.34  | 61     | 0.00  | 106   | 0.31  | 35    | 0.36  | 2538  | 0.00  | 2575                       NM_001102368.2; NM_001102366.2; NM_001102369.2; NM_001286470.1; NM_001286472.1; NM_024952.7; NM_001102367.2; NM_001286471.1 MV [D116N] NM_001286473.1 DV [n.d.] |
| #  | #chr | start   | end     | gene       | ref. | obs. | allele | freq. | depth | allele | freq. | depth | freq. | depth | Ref. Seq. | variant type |
|----|------|---------|---------|------------|------|------|--------|-------|-------|--------|-------|-------|-------|-------|-----------|--------------|
| 18 | chr15 | 45440569| 45440569| DUOX1      | A    | C    | 0.11   | 214   | 0.00  | 156    | 0.00  | 10    | 0.13  | 3081 | 0.00  | 1724 | NM_017434.4; NM_175940.2 [E914D] |
| 19 | chr17 | 3101176 | 3101176 | OR1A2      | C    | T    | 0.39   | 277   | 0.00  | 158    | n/a   | 0     | 0.35  | 1838 | 0.00  | 1397 | NM_012352.1 [R122*] |
| 20 | chr17 | 74005271| 74005271| EVPL<sup>a</sup>, CDK3<sup>b</sup> | C    | A    | 0.23   | 26    | 0.00  | 28     | n/a   | 0     | 0.32  | 3560 | 0.00  | 2705 | NM_001988.2 [E1339*]; NM_001258.2 [n.d.] |
| 21 | chr22 | 17072027| 17072027| CCT8L2     | G    | T    | 0.09   | 205   | 0.00  | 86     | n/a   | 0     | 0.16  | 862  | 0.00  | 676  | NM_014406.4 [Q472K] |
| 22 | chrX  | 21674105| 21674105| KLHL34<sup>a</sup>, CNKSR2<sup>b</sup> | C    | T    | 0.22   | 89    | 0.00  | 65     | n/a   | 0     | 0.32  | 981  | 0.00  | 652  | NM_153270.1 [R601H]; NM_014927.3 [n.d.]; NM_001168647.1 [n.d.] |
| 23 | chrX  | 27998815| 27998815| DCAF8L1    | T    | A    | 0.14   | 99    | 0.00  | 63     | n/a   | 0     | 0.07  | 2357 | 0.00  | 1619 | NM_001017930.1 [S213C] |
| 24 | chrX  | 48661274| 48661274| HDAC6      | A    | G    | 0.15   | 72    | 0.00  | 46     | 0.00  | 5     | 0.13  | 1973 | 0.00  | 1073 | NM_006044.2 [n.d.] |
| 25 | chrX  | 70467293| 70467293| ZMYM3      | A    | G    | 0.13   | 134   | 0.00  | 68     | 0.00  | 12    | 0.13  | 3349 | 0.00  | 2348 | NM_005096.3; NM_201599.2; NM_001171162.1 [I739T]; NM_001171163.1 [n.d.]; NM_001171164.1 [n.d.]; NM_001171165.1 [n.d.] |
Supplementary Table 9: Epitope Prediction of mutated Ligands (L06/10) at first vaccination

Shown are *in silico* predicted HLA class I peptide ligands (amino acid alterations in peptide sequences are underlined) based on mutations provided in Suppl. Table 8. Predictions encompass 9-12mer peptides and have been predicted using dedicated software available before September 2012 previous to starting vaccinations. Further information regarding bioinformatics analyses is given under Suppl. Material and Methods. Scoring of putative HLA binding peptides according to the used software algorithms together with predicted HLA alleles matching the patient given in nM for NetMHCpan 2.4 (42, 43) and NetMHC 3.0 (44-46) respectively or % of maximal binding (50% max.) for SYFPEITHI (16). Respective cut offs were predefined at <500nM for NetMHCpan 2.4 and NetMHC 3.0 or >50%max. for SYFPEITHI. As matrices for HLA allele B*07:05 were not always available closely related HLA allele B*07:02 was additionally used when available. Further gene identifiers (Gene ID) according to the National Center for Biotechnology Information (NCBI) are listed.

| #  | Peptide Sequence | mer | Method          | Score  | HLA          | Gene ID |
|----|------------------|-----|-----------------|--------|--------------|---------|
| 1  | EISHATFK         | 8   | netMHC 3.0      | 256 nM | A*03:01      | IL2RA   |
| 2  | HSHWAQQY         | 8   | netMHCpan 2.4   | 278 nM | A*29:01      | TEP1    |
|    |                  |     | netMHC 3.0      | 323 nM | B*35:01      |         |
| 3  | IIIGCHAY         | 8   | netMHCpan 2.4   | 17 nM  | A*29:01      | IDH1    |
|    |                  |     | netMHCpan 2.4   | 119 nM | B*35:01      |         |
|    |                  |     | netMHC 3.0      | 198 nM | B*35:01      |         |
| 4  | KAALVPNK         | 8   | netMHC 3.0      | 114 nM | A*03:01      | FGFBP3  |
|    |                  |     | netMHCpan 2.4   | 285 nM | A*03:01      |         |
| 5  | LPDHPHSH         | 8   | netMHCpan 2.4   | 488 nM | B*35:01      | TEP1    |
| 6  | MSYLLTSSR        | 8   | netMHC 3.0      | 55 nM  | A*03:01      | PTGS2   |
|    |                  |     | netMHCpan 2.4   | 280 nM |              |         |
| 7  | QPIFNLTV         | 8   | netMHCpan 2.4   | 306 nM | B*35:01      | CDHR2   |
|    |                  |     | netMHCpan 2.4   | 318 nM | B*07:02      |         |
| 8  | VPNKERPM         | 8   | netMHC 3.0      | 18 nM  | B*07:02      | FGFBP3  |
|    |                  |     | netMHCpan 2.4   | 27 nM  | B*07:02      |         |
| #  | Peptide Sequence | mer | Method       | Score   | HLA      | Gene ID |
|----|------------------|-----|--------------|---------|----------|---------|
| 9  | YLVDLHLH         | 8   | netMHCpan 2.4 | 101 nM  | B*07:05  | LRRC4   |
|    |                  |     | netMHC 2.4   | 110 nM  | B*35:01  |         |
|    |                  |     | netMHCpan 2.4| 115 nM  | B*35:01  |         |
| 10 | AIRVQTPPK        | 9   | netMHCpan 2.4| 185 nM  | A*03:01  | EBF3    |
|    |                  |     | netMHC 3.0   | 304 nM  | A*03:01  |         |
|    |                  |     | SYFPEITHI    | 55%     | A*03:01  |         |
| 11 | ALLNAGDVE        | 9   | SYFPEITHI    | 52%     | A*03:01  | SESTD1  |
| 12 | DPPEISHAT        | 9   | netMHC 3.0   | 83 nM   | B*35:01  | IL2RA   |
|    |                  |     | SYFPEITHI    | 52%     | B*07:02  |         |
| 13 | EQLKNMVAF        | 9   | netMHCpan 2.4| 153 nM  | B*35:01  | C14orf159|
| 14 | IMSYLLTSR        | 9   | netMHC 3.0   | 177 nM  | A*03:01  | PTGS2   |
|    |                  |     | netMHCpan 2.4| 492 nM  | A*03:01  |         |
| 15 | KGTARRRAM        | 9   | netMHC 3.0   | 350 nM  | B*07:02  | SNAPIN  |
|    |                  |     | netMHCpan 2.4| 467 nM  | B*07:02  |         |
| 16 | KPEVDMGVV        | 9   | netMHC 3.0   | 186 nM  | B*07:02  | TFB1M   |
|    |                  |     | SYFPEITHI    | 55%     | B*07:02  |         |
| 17 | KPIIIGCHA        | 9   | netMHC 3.0   | 313 nM  | B*07:02  | IDH1    |
|    |                  |     | SYFPEITHI    | 55%     | B*07:02  |         |
| 18 | MGVVHFTPL        | 9   | netMHC 3.0   | 278 nM  | B*35:01  | TFB1M   |
|    |                  |     | netMHCpan 2.4| 467 nM  | B*35:01  |         |
| 19 | PIIGCHAY         | 9   | netMHCpan 2.4| 220 nM  | A*29:01  | IDH1    |
| 20 | PPEISHATF        | 9   | netMHC 3.0   | 238 nM  | B*35:01  | IL2RA   |
|    |                  |     | SYFPEITHI    | 52%     | B*07:02  |         |
| 21 | PPKHIPGVV        | 9   | SYFPEITHI    | 52%     | B*07:02  | EBF3    |
| 22 | RPVFKNFPL        | 9   | netMHCpan 2.4| 4 nM    | B*07:02  | RNF216  |
|    |                  |     | netMHC 3.0   | 7 nM    | B*07:02  |         |
|    |                  |     | netMHCpan 2.4| 8 nM    | B*07:05  |         |
|    |                  |     | netMHC 3.0   | 196 nM  | B*35:01  |         |
|    |                  |     | netMHCpan 2.4| 207 nM  | B*35:01  |         |
|    |                  |     | SYFPEITHI    | 67%     | B*07:02  |         |
| 23 | SVAKGTARR        | 9   | netMHC 3.0   | 476 nM  | A*03:01  | SNAPIN  |
| 24 | TJHWRGQTR        | 9   | netMHC 3.0   | 350 nM  | A*03:01  | ZMYM3   |
| 25 | TPLRYLVDL        | 9   | SYFPEITHI    | 67%     | B*07:02  | LRRC4   |
| 26 | TPPKHIPGV        | 9   | SYFPEITHI    | 55%     | B*07:02  | EBF3    |
| 27 | YLVDLHLHH        | 9   | netMHCpan 2.4| 162 nM  | A*29:01  | LRRC4   |
| 28 | AIMSYLLTSR       | 10  | netMHC 3.0   | 71 nM   | A*03:01  | PTGS2   |
|    |                  |     | netMHCpan 2.4| 239 nM  | A*03:01  |         |
| 29 | DPPEISHATF       | 10  | netMHC 3.0   | 20 nM   | B*35:01  | IL2RA   |
|    |                  |     | netMHCpan 2.4| 239 nM  | B*35:01  |         |
|    |                  |     | SYFPEITHI    | 57%     | B*07:02  |         |
| 30 | EISHATFKAM       | 10  | netMHC 3.0   | 256 nM  | B*35:01  | IL2RA   |
|    |                  |     | netMHCpan 2.4| 274 nM  | B*35:01  |         |
| 31 | GLSGYKGSSH       | 10  | SYFPEITHI    | 57%     | A*03:01  | KMT2C   |
| #  | Peptide Sequence | mer | Method     | Score  | HLA     | Gene ID |
|----|------------------|-----|------------|--------|---------|---------|
| 32 | HAIRVQTPPK       | 10  | netMHCpan 2.4 | 497 nM | A*03:01 | EBF3    |
| 33 | HPHSHWAQQY       | 10  | netMHC 3.0   | 28 nM  | B*35:01 | TEP1    |
|     |                  |     | netMHCpan 2.4 | 14 nM  | B*35:01 |
| 34 | KPEVDMGVVH       | 10  | netMHC 3.0   | 418 nM | B*35:01 | TFB1M   |
| 35 | KPIIIGCHAY       | 10  | netMHCpan 2.4 | 19 nM  | B*35:01 | IDH1    |
|     |                  |     | netMHC 3.0   | 24 nM  | B*35:01 |
| 36 | LPDHPHSHWA       | 10  | SYFPEITHI   | 193 nM | A*03:01 | TEP1    |
|     |                  |     |              |        |         | RNF216  |
| 37 | PLPPVRPVVFK      | 10  | netMHC 3.0   | 193 nM | A*03:01 |         |
|     |                  |     |              |        |         |         |
| 38 | QPJFLNTVSA       | 10  | netMHC 3.0   | 264 nM | B*07:02 | CDHR2   |
|     |                  |     | netMHCpan 2.4 | 279 nM | B*35:01 |
|     |                  |     | netMHCpan 2.4 | 406 nM | B*07:02 |
|     |                  |     | SYFPEITHI   | 63%    | B*07:02 |
| 39 | ŠHATFKAMAY       | 10  | netMHCpan 2.4 | 328 nM | A*29:01 | IL2RA   |
| 40 | TPPKHIPGVV       | 10  | SYFPEITHI   | 31 nM  | A*03:01 | EBF3    |
| 41 | VMAEMSGVHK       | 10  | netMHCpan 2.4 | 31 nM  | A*03:01 |         |
|     |                  |     | netMHC 3.0   | 79 nM  | A*03:01 |
| 42 | VPKPEVDMGV       | 10  | SYFPEITHI   | 57%    | B*07:02 | TFB1M   |
| 43 | VPNKERPMGT       | 10  | SYFPEITHI   | 57%    | B*07:02 |         |
| 44 | IIIC3HAYGDQY     | 11  | netMHCpan 2.4 | 225 nM | A*29:01 | IDH1    |
| 45 | İŞHATFKAMAY      | 11  | netMHCpan 2.4 | 102 nM | A*29:01 | IL2RA   |
|     |                  |     | netMHC 3.0   | 209 nM | A*03:01 |
|     |                  |     | netMHCpan 2.4 | 247 nM | B*35:01 |
| 46 | KPEVDMGVVH       | 11  | netMHC 3.0   | 341 nM | B*07:02 | TFB1M   |
|     |                  |     | netMHC 3.0   | 248 nM | B*35:01 |
| 47 | MSYLTSRSHL       | 11  | netMHCpan 2.4 | 169 nM | C15:05  | PTG52   |
| 48 | NMVAFFLGCSF      | 11  | netMHCpan 2.4 | 131 nM | B*35:01 | C14orf159 |
|     |                  |     | netMHC 3.0   | 16 nM  | B*07:02 |
|     |                  |     | netMHCpan 2.4 | 12 nM  | B*07:02 |
|     |                  |     | netMHCpan 2.4 | 32 nM  | B*07:05 |
|     |                  |     | netMHCpan 2.4 | 173 nM | B*35:01 |
|     |                  |     | netMHC 3.0   | 273 nM | B*35:01 |
| 50 | VAKGTARRRAM      | 11  | netMHC 3.0   | 201 nM | B*07:02 | SNAPIN  |
|     |                  |     | netMHCpan 2.4 | 322 nM | B*07:02 |
| 51 | YSEQLKNMVAF      | 11  | netMHC 3.0   | 86 nM  | B*35:01 | C14orf159 |
|     |                  |     | netMHCpan 2.4 | 230 nM | B*35:01 |
| 52 | DVSLDYETQPIF     | 12  | netMHC 3.0   | 292 nM | B*35:01 | CDHR2   |
| 53 | İŞHATFKAMAY      | 12  | netMHC 3.0   | 93 nM  | B*35:01 | IL2RA   |
| 54 | EVDGVMVHF        | 12  | netMHC 3.0   | 483 nM | B*35:01 | TFB1M   |
| 55 | IPFLRNAIMSY       | 12  | netMHC 3.0   | 53 nM  | B*07:02 | PTG52   |
| 56 | İŞHATFKAMAY      | 12  | netMHC 3.0   | 21 nM  | A*03:01 | IL2RA   |
| 57 | KAALVPNKERPM     | 12  | netMHC 3.0   | 426 nM | B*07:02 | FGFBP3  |
| 58 | PPEİŞHATFKAM     | 12  | netMHC 3.0   | 233 nM | B*07:02 | IL2RA   |
| #  | Peptide Sequence | mer | Method         | Score | HLA     | Gene ID |
|----|------------------|-----|---------------|-------|---------|---------|
| 59 | PPVRPVFKNFPL     | 12  | netMHC 3.0    | 451 nM| B*07:02 | RNF216  |
| 60 | RLNHSVAKGTAR     | 12  | netMHC 3.0    | 56 nM | A*03:01 | SNAPIN  |
| 61 | RPVFKNFPLNMG     | 12  | netMHC 3.0    | 407 nM| B*07:02 | RNF216  |
| 62 | SVAKGTARRRAM     | 12  | netMHC 3.0    | 35 nM | B*07:02 | SNAPIN  |
| 63 | TPLRYLVDLHLH     | 12  | netMHC 3.0    | 441 nM| B*35:01 | LRRC4   |
| 64 | VPKPEVDMGVVH     | 12  | netMHC 3.0    | 477 nM| B*35:01 | TFB1M   |
| 65 | WVKPIIIGCHAY     | 12  | netMHC 3.0    | 37 nM | B*35:01 | IDH1    |
| 66 | YSEQLKNMVAFF     | 12  | netMHC 3.0    | 233 nM| B*35:01 | C14orf159 |
Supplementary Table 10: Epitope Prediction of mutated Ligands (L06/10)
current

Shown are *in silico* predicted HLA class I peptide ligands (amino acid alterations in peptide sequences are underlined) based on mutations provided in Suppl. Table 8. Predictions encompass 9-12mer peptides and have been predicted using respective dedicated currently available software. Further information regarding bioinformatics analyses is given under Suppl. Material and Methods. Scoring of putative HLA binding peptides according to the used software algorithms together with predicted HLA alleles matching the patient given in nM for NetMHCpan 2.8 (42, 43) and NetMHC 3.4 (15, 45, 46) respectively or % of maximal binding (50% max.) for SYFPEITHI* 2015 (in house version). Respective cut offs were predefined at <500nM for NetMHCpan 2.8 and NetMHC 3.4 or >50%max. for SYFPEITHI*. As matrices for HLA allele B*07:05 were not always available closely related HLA allele B*07:02 was additionally used when available. Further gene identifiers (Gene ID) according to the National Center for Biotechnology Information (NCBI) are listed.

| # | Peptide      | Mer | Method      | Score  | HLA       | Gene  |
|---|--------------|-----|-------------|--------|-----------|-------|
| 1 | AGDVEDLV     | 8   | SYFPEITHI*  | 51%    | C*04:01   | SESTD1|
| 2 | EISHATFK     | 8   | netMHC 3.4  | 366 nM | A*03:01   | IL2RA |
| 3 | GFQDKEDL     | 8   | SYFPEITHI*  | 54%    | C*04:01   | DUOX1 |
| 4 | GYDLDDLH     | 8   | SYFPEITHI*  | 54%    | C*04:01   | KLHL34|
| 5 | HPHSHWAAQ    | 8   | netMHC 3.4  | 83 nM  | B*35:01   | TEP1  |
|    |              |     | netMHCpan 2.8| 351 nM | C*15:05   |       |
| 6 | HSHWAQQY     | 8   | netMHC 3.4  | 58 nM  | B*35:01   | TEP1  |
|    |              |     | netMHCpan 2.8| 139 nM | C*04:01   |       |
|    |              |     | netMHCpan 2.8| 272 nM | A*29:01   |       |
| 7 | IIIGCHAY     | 8   | netMHCpan 2.8| 13 nM  | A*29:01   | IDH1  |
|    |              |     | netMHC 3.4  | 65 nM  | B*35:01   |       |
|    |              |     | netMHCpan 2.8| 84 nM  | C*04:01   |       |
| 8 | KAAVVPNK     | 8   | netMHC 3.4  | 99 nM  | A*03:01   | FGFBP3|
|    |              |     | netMHCpan 2.8| 204 nM | A*03:01   |       |
| 9 | MSYLLTSR     | 8   | netMHC 3.4  | 120 nM | A*03:01   | PTGS2 |
| #  | Peptide        | Method          | Score     | HLA          | Gene  |
|----|----------------|-----------------|-----------|--------------|-------|
| 10 | QPIFNLTV       | netMHCpan 2.8   | 175 nM    | A*03:01     |       |
|    |                | netMHCpan 2.8   | 289 nM    | C*15:05     | CDHR2 |
|    |                | netMHCpan 2.8   | 462 nM    | C*04:01     |       |
|    |                | netMHCpan 2.8   | 483 nM    | B*35:01     |       |
| 11 | RYLVDLHL       | SYFPEITHI*      | 59%       | C*04:01     | LRRC4 |
|    |                | netMHCpan 2.8   | 22 nM     | B*35:01     |       |
|    |                | netMHCpan 2.8   | 22 nM     | C*15:01     |       |
|    |                | netMHC 3.4      | 56 nM     | B*35:01     |       |
|    |                | netMHCpan 2.8   | 78 nM     | C*04:01     |       |
|    |                | netMHC 3.4      | 193 nM    | B*07:02     |       |
| 12 | VPNKERPM       | SYFPEITHI*      | 52%       | B*07:02     | IL2RA |
|    |                | netMHCpan 2.8   | 22 nM     | B*35:01     |       |
|    |                | netMHCpan 2.8   | 22 nM     | C*15:01     |       |
|    |                | netMHC 3.4      | 107 nM    | A*03:01     | EBF3  |
|    |                | SYFPEITHI*      | 68%       | A*03:01     |       |
| 13 | YLVDLHLH       | netMHCpan 2.8   | 267 nM    | A*29:01     | LRRC4 |
|    |                | netMHCpan 2.8   | 103 nM    | A*03:01     |       |
|    |                | netMHC 3.4      | 107 nM    | A*03:01     |       |
|    |                | SYFPEITHI*      | 61%       | C*04:01     |       |
|    |                | netMHCpan 2.8   | 316 nM    | C*04:01     | C14orf159 |
| 14 | AIRVQTPPK      | SYFPEITHI*      | 61%       | C*04:01     |       |
|    |                | netMHCpan 2.8   | 103 nM    | A*03:01     |       |
|    |                | netMHC 3.4      | 107 nM    | A*03:01     |       |
|    |                | SYFPEITHI*      | 68%       | A*03:01     |       |
| 15 | DPPEISHAT      | SYFPEITHI*      | 52%       | B*07:02     | IL2RA |
| 16 | DVEDLVELK      | SYFPEITHI*      | 74%       | A*03:01     | SESTD1|
| 17 | EQLKNMVAF      | netMHCpan 2.8   | 316 nM    | C*04:01     |       |
|    |                | netMHCpan 2.8   | 316 nM    | C*04:01     |       |
| 18 | EVDGTVHF       | SYFPEITHI*      | 61%       | C*04:01     |       |
| 19 | GDVEVLVEL      | SYFPEITHI*      | 54%       | B*35:01     | SESTD1|
| 20 | GYDDLDLHW      | SYFPEITHI*      | 61%       | C*04:01     | KLHL34|
| 21 | HPHSHWAQQQ     | SYFPEITHI*      | 74%       | A*03:01     |       |
|    |                | netMHC 3.4      | 354 nM    | B*35:01     |       |
| 22 | HWEDIGCAL      | SYFPEITHI*      | 57%       | B*35:01     | KLHL34|
| 23 | IMSYLLTSR      | netMHC 3.4      | 414 nM    | A*03:01     | PTGS2 |
|    |                | netMHCpan 2.8   | 497 nM    | A*03:01     |       |
| 24 | ISHATFKAM      | netMHCpan 2.8   | 477 nM    | C*04:01     | IL2RA |
| 25 | KEDLTWEDF      | SYFPEITHI*      | 58%       | C*04:01     | DUOX1 |
| 26 | KPEVDMGVV      | SYFPEITHI*      | 55%       | B*07:02     |       |
|    |                | netMHC 3.4      | 96 nM     | B*07:02     | TFB1M |
|    |                | netMHCpan 2.8   | 150 nM    | C*15:05     |       |
|    |                | netMHCpan 2.8   | 410 nM    | B*35:01     |       |
|    |                | SYFPEITHI*      | 55%       | B*07:02     |       |
| 27 | KPIIIQCHCHA     | SYFPEITHI*      | 55%       | B*07:02     | IDH1  |
| 28 | MGVVHFTPL      | netMHCpan 2.8   | 385 nM    | C*04:01     | TFB1M |
| 29 | NLPDHPSH       | SYFPEITHI*      | 61%       | A*03:01     | TEP1  |
| 30 | PIIGCHAY       | SYFPEITHI*      | 52%       | A*03:01     | IDH1  |
|    |                | netMHCpan 2.8   | 134 nM    | A*29:01     |       |
|    |                | SYFPEITHI*      | 52%       | A*03:01     |       |
| 31 | PLRLYVLDLH     | SYFPEITHI*      | 58%       | A*03:01     |       |
|    |                | SYFPEITHI*      | 71%       | B*35:01     |       |
|    |                | SYFPEITHI*      | 52%       | B*07:02     |       |
| 32 | PPEISHATF      | SYFPEITHI*      | 52%       | B*07:02     | IL2RA |
|    |                | SYFPEITHI*      | 52%       | B*07:02     |       |
|    |                | SYFPEITHI*      | 52%       | B*07:02     |       |
| 33 | PKKHIPGVV      | SYFPEITHI*      | 52%       | B*07:02     | EBF3  |
| 34 | QYSEQLKNM      | SYFPEITHI*      | 56%       | C*04:01     | C14orf159 |
| 35 | RKAALVPNK      | SYFPEITHI*      | 52%       | A*03:01     | FGBP3 |
|    |                | netMHCpan 2.8   | 6  nM      | C*15:02     |       |
|    |                | netMHC 3.4      | 9  nM      | B*07:02     |       |
|    |                | netMHCpan 2.8   | 213 nM    | C*04:01     | RNF216|
| #  | Peptide     | mer | Method     | Score   | HLA       | Gene  |
|----|-------------|-----|------------|---------|-----------|-------|
| 37 | RVQTPPKHI   | 9   | SYFPEITHI* | 75%     | B*35:01   | EBF3  |
| 38 | SVAKGTARR   | 9   | SYFPEITHI* | 55%     | A*03:01   | SNAPIN|
| 39 | TIHWRGQTR   | 9   | SYFPEITHI* | 52%     | A*03:01   | ZMYM3 |
| 40 | TPLRYLVDL   | 9   | netMHCpan 2.8 | 214 nM | C*15:05   | LRRC4 |
|     |             |     | netMHC 3.4 | 264 nM | B*07:02   |       |
|     |             |     | netMHCpan 2.8 | 401 nM | B*35:01   |       |
|     |             |     | SYFPEITHI* | 86%     | B*35:01   |       |
|     |             |     | SYFPEITHI* | 67%     | B*07:02   |       |
| 41 | TPPKHIPGV   | 9   | SYFPEITHI* | 55%     | B*07:02   | EBF3  |
| 42 | VFKNFPLNM   | 9   | SYFPEITHI* | 53%     | C*04:01   | RNF216|
| 43 | YLVD_LHLHH  | 9   | netMHCpan 2.8 | 178 nM | A*29:01   | LRRC4 |
|     |             |     | SYFPEITHI* | 61%     | A*03:01   |       |
| 44 | AGDV_EDLVEL | 10  | SYFPEITHI* | 56%     | C*04:01   | SESTD1|
| 45 | AIMSYLITSR  | 10  | netMHC 3.4 | 130 nM | A*03:01   | PTGS2 |
|     |             |     | netMHCpan 2.8 | 175 nM | A*03:01   |       |
| 46 | DPPEISHATF  | 10  | netMHCpan 2.8 | 201 nM | C*04:01   | IL2RA |
|     |             |     | SYFPEITHI* | 77%     | B*35:01   |       |
|     |             |     | SYFPEITHI* | 57%     | B*07:02   |       |
| 47 | DYETQPIFNFL | 10  | SYFPEITHI* | 51%     | C*04:01   | CDHR2 |
| 48 | EI7HATFKAM  | 10  | netMHCpan 2.8 | 486 nM | C*04:01   | IL2RA |
| 49 | FLRNAIMSYL  | 10  | netMHCpan 2.8 | 310 nM | C*15:05   | PTGS2 |
| 50 | GYDLDDLHWE  | 10  | SYFPEITHI* | 54%     | C*04:01   | KLHL34|
| 51 | HAIRVQTPPK  | 10  | netMHC 3.4 | 422 nM | A*03:01   | EBF3  |
| 52 | HPHŞHWAQQY  | 10  | netMHCpan 2.8 | 11 nM  | C*04:01   | TEP1  |
|     |             |     | netMHC 3.4 | 37 nM   | B*35:01   |       |
|     |             |     | SYFPEITHI* | 85%     | B*35:01   |       |
| 53 | KPIIIGCHAY  | 10  | netMHCpan 2.8 | 31 nM  | C*04:01   | IDH1  |
|     |             |     | netMHC 3.4 | 34 nM   | B*35:01   |       |
|     |             |     | SYFPEITHI* | 81%     | B*35:01   |       |
| 54 | LDHPHŞHWA   | 10  | SYFPEITHI* | 57%     | B*07:02   | TEP1  |
| 55 | PLPPVRPVF   | 10  | SYFPEITHI* | 71%     | A*03:01   | RNF216|
| 56 | PPVRPVFKN   | 10  | SYFPEITHI* | 77%     | B*35:01   |       |
|     |             |     | SYFPEITHI* | 57%     | B*07:02   |       |
| 57 | QPIFNLTVSA  | 10  | netMHCpan 2.8 | 297 nM | C*15:05   | CDHR2 |
|     |             |     | netMHCpan 2.8 | 338 nM | C*04:01   |       |
|     |             |     | netMHCpan 2.8 | 485 nM | B*35:01   |       |
|     |             |     | SYFPEITHI* | 63%     | B*07:02   |       |
| 58 | RLAŞGDDLR   | 10  | SYFPEITHI* | 52%     | A*03:01   | DCAF8L1|
| 59 | RVQTPPKHIP  | 10  | SYFPEITHI* | 52%     | A*03:01   | EBF3  |
| 60 | ŞHATFKAMAY  | 10  | netMHCpan 2.8 | 479 nM | A*29:01   | IL2RA |
| 61 | SLDYETQPIF  | 10  | SYFPEITHI* | 51%     | C*04:01   | CDHR2 |
| #  | Peptide          | mer | Method         | Score     | HLA             | Gene   |
|----|------------------|-----|----------------|-----------|------------------|--------|
| 62 | SYLLTSRSRSL     | 10  | SYFPEITHI*     | 62%       | C*04:01          | PTGS2  |
| 63 | TPPKHIPGVV       | 10  | SYFPEITHI*     | 60%       | B*07:02          | EBF3   |
| 64 | VEDLVELKSL       | 10  | SYFPEITHI*     | 62%       | C*04:01          | SESTD1 |
| 65 | VMAEMSGVHK       | 10  | netMHC 3.4     | 42 nM     | A*03:01          | CCT8L2 |
|     |                  |     | netMHCpan 2.8  | 72 nM     | A*03:01          |        |
| 66 | VPKPEVDMSGV      | 10  | SYFPEITHI*     | 57%       | B*07:02          | TFB1M  |
| 67 | VPNKERPMTG       | 10  | SYFPEITHI*     | 57%       | B*07:02          | FGFBP3 |
| 68 | DVMASGTVHS       | 11  | SYFPEITHI*     | 69%       | A*03:01          | CCT8L2 |
| 69 | IIGCHAYGDQY      | 11  | netMHCpan 2.8  | 163 nM    | A*29:01          | IL2RA  |
|     |                  |     | netMHC 3.4     | 79 nM     | C*04:01          | IL2RA  |
|     |                  |     | netMHCpan 2.8  | 80 nM     | A*29:01          |        |
|     |                  |     | netMHC 3.4     | 133 nM    | B*35:01          |        |
| 70 | ISHATFKAMAY      | 11  | SYFPEITHI*     | 67%       | B*07:02          | TFB1M  |
| 71 | KPEVDMSGVHF      | 11  | SYFPEITHI*     | 57%       | B*07:02          | RNF216 |
| 72 | LPPVRPFKgNf      | 11  | SYFPEITHI*     | 57%       | B*07:02          |        |
| 73 | MSYLLTSSRSL      | 11  | netMHCpan 2.8  | 229 nM    | B*07:05          | PTGS2  |
|     |                  |     | netMHC 3.4     | 268 nM    | C*04:01          | C14orf159 |
|     |                  |     | netMHC 3.4     | 447 nM    | B*35:01          |        |
| 74 | NMVAFGLGCSF      | 11  | SYFPEITHI*     | 63%       | B*07:02          | IL2RA  |
|     |                  |     | netMHCpan 2.8  | 192 nM    | B*07:02          |        |
|     |                  |     | netMHC 3.4     | 291 nM    | B*35:01          |        |
|     |                  |     | netMHCpan 2.8  | 363 nM    | C*04:01          |        |
| 75 | PPEISHATFKA      | 11  | SYFPEITHI*     | 63%       | B*07:02          | EBF3   |
| 76 | PPKHIPGVVVEV     | 11  | SYFPEITHI*     | 63%       | B*07:02          |        |
|     |                  |     | netMHCpan 2.8  | 25 nM     | B*07:02          |        |
|     |                  |     | netMHC 3.4     | 26 nM     | B*35:01          |        |
|     |                  |     | netMHCpan 2.8  | 29 nM     | C*15:05          |        |
|     |                  |     | netMHC 3.4     | 291 nM    | B*35:01          |        |
|     |                  |     | netMHCpan 2.8  | 363 nM    | C*04:01          |        |
|     |                  |     | SYFPEITHI*     | 63%       | B*07:02          |        |
| 77 | RPVFKNFPLNM      | 11  | netMHCpan 2.8  | 275 nM    | C*15:05          | RNF216 |
|     |                  |     | netMHC 3.4     | 449 nM    | B*35:01          |        |
|     |                  |     | SYFPEITHI*     | 73%       | B*07:02          |        |
| 78 | TPLRYLVDLHL      | 11  | netMHCpan 2.8  | 337 nM    | C*15:05          | LRR4   |
|     |                  |     | netMHC 3.4     | 344 nM    | B*35:01          | SNAPIN |
|     |                  |     | netMHCpan 2.8  | 430 nM    | B*35:01          |        |
| 79 | VAKGTARRRAM      | 12  | SYFPEITHI*     | 53%       | B*07:02          | TFB1M  |
|     |                  |     | netMHCpan 2.8  | 401 nM    | C*15:05          |        |
|     |                  |     | netMHC 3.4     | 595 nM    | B*35:01          |        |
|     |                  |     | SYFPEITHI*     | 60%       | B*07:02          |        |
| 80 | VDMGVVHTPL       | 11  | netMHCpan 2.8  | 172 nM    | B*35:01          | C14orf159 |
|     |                  |     | netMHC 3.4     | 309 nM    | C*04:01          |        |
| 81 | VPKPEVDMSGV      | 12  | netMHC 3.4     | 414 nM    | B*35:01          | CDHR2  |
| 82 | YSEQKLNMVAF      | 12  | netMHC 3.4     | 91 nM     | B*35:01          | IL2RA  |
|     |                  |     | netMHCpan 2.8  | 89 nM     | B*35:01          | TEP1   |
| 83 | DVSDLDEYTPJF     | 12  | netMHCpan 2.8  | 398 nM    | B*35:01          | IDH1   |
| 84 | EIJSHTFKAMAY     | 12  | netMHC 3.4     | 72 nM     | B*07:02          | PTGS2  |
| 85 | HPHSWHAQOYPS     | 12  | netMHC 3.4     | 52 nM     | A*03:01          | IL2RA  |
| 86 | IIGCHAYGDQY      | 12  | netMHC 3.4     | 149 nM    | B*07:02          | RNF216 |
| #  | Peptide        | mer | Method      | Score | HLA     | Gene   |
|----|----------------|-----|-------------|-------|---------|--------|
| 90 | RLNHSVAKGTAR   | 12  | netMHC 3.4  | 98 nM | A*03:01 | SNAPIN |
| 91 | SVAKGTARRRAM   | 12  | netMHC 3.4  | 17 nM | B*07:02 | SNAPIN |
|    |                |     | netMHC 3.4  | 357 nM| B*35:01 |        |
| 92 | WVKPIIGCHAY    | 12  | netMHC 3.4  | 43 nM | B*35:01 | IDH1   |
Supplementary Table 11: WES Results (L04/12)

Shown are sequencing results obtained by WES (whole exome sequencing) of lesion L04/12 (*in loco* recurrent tumor), yielding basic somatic variants. Complex variants are excluded as being unsuitable for the subsequent prediction of HLA-ligands. In sequential order of columns from left to right: serial number; chromosome number; start and end position of somatic variant, ref.: reference base; obs.: observed base at respective chromosomal location; allele frequency and depth of somatic variant as sequenced by WES in tumor and reference tissue (normal); Ref. Seq. (NCBI Reference Sequence) such as variant type (MV: missense variant; DV: downstream gene variant; SG: stop gain variant) and putative AA (amino acid) alteration introduced by somatic variant; n.d. no data; ± variant excluded for peptide prediction.

| #  | chr | start    | end      | gene | ref. | obs. | allele freq. | depth | allele freq. | depth | Ref. Seq. variant type [AA alteration] |
|----|-----|----------|----------|------|------|------|--------------|-------|--------------|-------|----------------------------------------|
| 1  | chr2| 25358435 | 25358435 | EFR3B| C    | T    | 0.18         | 108   | 0.00         | 130   | NM_014971.1 SG [R471*]                  |
| 2  | chr2| 179989221| 179989221| SESTD1| T    | A    | 0.15         | 68    | 0.00         | 99    | NM_178123.4 MV [E346V]                  |
| 3  | chr5| 71494779 | 71494779 | MAP1B| G    | A    | 0.14         | 50    | 0.00         | 40    | NM_005909.3 MV [G866D]                 |
| 4  | chr6| 90499570 | 90499570 | MDN1 | T    | G    | 0.27         | 26    | 0.02         | 43    | NM_014611.2 MV [T387P]                  |
| #  | #chr | start   | end     | gene   | ref. | obs.  | allele freq. | depth | allele freq. | depth | Ref. Seq. variant type [AA alteration] |
|----|------|---------|---------|--------|------|-------|--------------|-------|--------------|-------|---------------------------------------|
| 5  | chr7 | 151848648 | 151848648 | KMT2C  | T    | C     | 0.08         | 50    | 0.00         | 49    | NM_170606.2 MV [D4182G]                |
| 6  | chr8 | 41476225  | 41476225  | AGPAT6 | C    | T     | 0.06         | 119   | 0.00         | 166   | NM_178819.3 MV [A59V]                  |
| 7  | chr10| 6067959   | 6067959   | IL2RA  | G    | A     | 0.06         | 233   | 0.00         | 249   | NM_000417.2 MV [P32S]                  |
| 8  | chr10| 118386393 | 118386393 | PNLIPRP2 | A    | G     | 0.08         | 84    | 0.00         | 129   | NM_005396.4 MV [K117E]                 |
| 9  | chr11| 1270922   | 1270922   | MUC5B  | C    | G     | 0.11         | 96    | 0.01         | 133   | NM_002458.2 MV [S4271C]                |
| 10 | chr14| 20854241  | 20854241  | TEP1   | A    | G     | 0.08         | 59    | 0.00         | 74    | NM_007110.4 MV [F992S]                 |
| 11 | chr14| 91636435  | 91636435  | C14orf159 | G    | A     | 0.07         | 90    | 0.00         | 106   | NM_001102368.2; NM_001102366.2; NM_001102369.2; NM_001286470.1; NM_001286472.1; NM_024952.7; NM_001102367.2; NM_001286471.1 MV[D116N]; NM_001286473.1 DV [n.d.]; NM_012352.1 SG [R122*]; NM_012352.1 SG [R122*] |
| 12 | chr17| 3101176   | 3101176   | OR1A2  | C    | T     | 0.15         | 108   | 0.00         | 158   | NM_012352.1 SG [R122*]                 |
| 13 | chr17| 7750165   | 7750165   | KDM6B  | C    | T     | 0.08         | 65    | 0.00         | 71    | NM_001080424.1 MV [P247L]              |
| # | #chr | start   | end     | gene       | ref. | obs. allele freq. | tumor depth | allele freq. | normal depth | Ref. Seq. variant type [AA alteration] |
|---|------|---------|---------|------------|------|------------------|-------------|--------------|-------------|--------------------------------------|
| 14 | chr19 | 43920102 | 43920102 | TEX101     | A    | 0.11             | 45          | 0.00         | 46          | NM_031451.4 MV [I29F]                 |
|    |       |         |         |            |      |                  |             |              |             | NM_0011300111.1 MV [I11F]             |
| 15 | chr22 | 17072027 | 17072027 | CCT8L2     | G    | 0.07             | 68          | 0.00         | 86          | NM_014406.4 MV [Q472K]               |
| 16 | chrX  | 21674105 | 21674105 | KLHL34\(^a\), CNKSR2\(^b\) | C    | 0.17             | 63          | 0.00         | 65          | ^a NM_153270.1 MV [R601H] \(^b\) NM_014927.3; \(^b\) NM_001168647.1 DV [n.d.] \(^c\) |
| 17 | chrX  | 91873547 | 91873547 | PCDH11X    | G    | 0.06             | 271         | 0.00         | 393         | NM_032968.4 MV [A1218T] \(^b\) NM_001168360.1 MV [A1210T] \(^b\) NM_001168362.1 MV [A1181T] \(^b\) NM_001168363.1 MV [A1200T] \(^b\) NM_032969.4 MV [A1208T] |
Supplementary Table 12: Epitope Prediction of mutated Ligands (L04/12) at first vaccination

Shown are *in silico* predicted HLA class I peptide ligands (amino acid alterations in peptide sequences are underlined) based on mutations provided in Suppl. Table 11. Predictions encompass 9-12mer peptides and have been predicted using dedicated software available before September 2012 previous to starting vaccinations. Further information regarding bioinformatics analyses is given under Suppl. Material and Methods. Scoring of putative HLA binding peptides according to the used software algorithms together with predicted HLA alleles matching the patient given in nM for NetMHCpan 2.4 (42, 43) and NetMHC 3.0 NetMHC 3.0 (44-46) respectively or % of maximal binding (50% max.) for SYFPEITHI SYFPEITHI (16). Respective cut offs were predefined at <500nM for NetMHCpan 2.4 and NetMHC 3.0 or >50%max. for SYFPEITHI. As matrices for HLA allele B*07:05 were not always available closely related HLA allele B*07:02 was additionally used when available. Further gene identifiers (Gene ID) according to the National Center for Biotechnology Information (NCBI) are listed.

| #  | Peptide   | mer | Method       | Score | HLA       | Gene   |
|----|-----------|-----|--------------|-------|-----------|--------|
| 1  | DPQFGDVVF | 8   | netMHC 3.0   | 15 nM | B*35:01  | AGPAT6 |
|    |           |     | netMHCpan 2.4| 161 nM| B*35:01   |         |
| 2  | EISHATFK  | 8   | netMHCpan 2.4| 256 nM| A*03:01  | IL2RA  |
| 3  | FVWQPQGPL | 8   | netMHC 3.0   | 74 nM | B*35:01  | MDN1   |
|    |           |     | netMHCpan 2.4| 279 nM| B*35:01  |         |
|    |           |     | netMHC 3.0   | 499 nM| B*07:02  |         |
| 4  | HSHWAQQY  | 8   | netMHCpan 2.4| 278 nM| A*29:01  | TEP1   |
|    |           |     | netMHCpan 2.4| 323 nM| B*35:01  |         |
|    |           |     | netMHC 3.0   | 359 nM| B*35:01  |         |
| 5  | KTPDFSYY  | 8   | netMHCpan 2.4| 331 nM| A*29:01  | MAP1B  |
| 6  | LPDPHSH   | 8   | netMHCpan 2.4| 448 nM| B*35:01  | TEP1   |
| 7  | LPLLPPPL  | 8   | netMHCpan 2.4| 34 nM | B*07:02  | KDM6B  |
|    |           |     | netMHC 3.0   | 79 nM | B*07:02  |         |
| #  | Peptide     | mer | Method        | Score  | HLA        | Gene   |
|----|-------------|-----|---------------|--------|------------|--------|
| 8  | VFWNSSKY    | 8   | netMHCpan 2.4 | 113 nM | B*35:01    | AGPAT6 |
|    |             |     | netMHCpan 2.4 | 115 nM | B*07:05    |        |
|    |             |     | netMHC 3.0   | 140 nM | B*35:01    |        |
| 9  | ALLNAGDVIE  | 9   | SYFPEITHI    | 52%    | A*03:01    | SESTD1 |
| 10 | DPPEISHAT   | 9   | netMHC 3.0   | 83 nM  | B*35:01    | IL2RA  |
|    |             |     | SYFPEITHI    | 52%    | B*07:02    |        |
| 11 | DPQFGDVFW    | 9   | netMHC 3.0   | 318 nM | B*35:01    | AGPAT6 |
| 12 | DVFWNSSKY   | 9   | netMHCpan 2.4| 93 nM  | B*35:01    | AGPAT6 |
|    |             |     | netMHC 3.0   | 100 nM | B*35:01    |        |
|    |             |     | netMHCpan 2.4| 111 nM | A*29:01    |        |
| 13 | EFVWQPGL    | 9   | netMHC 3.0   | 201 nM | B*35:01    | MDN1   |
| 14 | EQLKNMVAF   | 9   | netMHCpan 2.4| 153 nM | B*35:01    | C14orf159 |
|    |             |     | netMHCpan 2.4| 93 nM  | B*35:01    |        |
|    |             |     | netMHC 3.0   | 100 nM | B*35:01    |        |
|    |             |     | netMHC 3.0   | 406 nM | B*07:05    |        |
|    |             |     | netMHC 3.0   | 489 nM | B*07:02    |        |
|    |             |     | SYFPEITHI    | 52%    | B*07:02    |        |
| 15 | GPLTQAATM   | 9   | netMHC 3.0   | 41 nM  | B*35:01    | MDN1   |
|    |             |     | netMHCpan 2.4| 116 nM | B*07:02    |        |
|    |             |     | netMHCpan 2.4| 138 nM | B*35:01    |        |
|    |             |     | netMHCpan 2.4| 406 nM | B*07:05    |        |
|    |             |     | netMHC 3.0   | 489 nM | B*07:02    |        |
|    |             |     | SYFPEITHI    | 52%    | B*07:02    |        |
| 16 | PPEISHATF   | 9   | netMHC 3.0   | 238 nM | B*35:01    | IL2RA  |
|    |             |     | SYFPEITHI    | 52%    | B*07:02    |        |
| 17 | PPGLPLPP    | 9   | SYFPEITHI    | 52%    | B*07:02    | KDM6B  |
| 18 | PPPIQVSTL   | 9   | SYFPEITHI    | 64%    | B*07:02    | PCDH11X |
| 19 | QPGPLTQAA   | 9   | netMHC 3.0   | 271 nM | B*35:01    | MDN1   |
|    |             |     | SYFPEITHI    | 61%    | B*07:02    |        |
| 20 | SPPIQVST    | 9   | SYFPEITHI    | 58%    | B*07:02    | PCDH11X |
| 21 | STLHHSPPL   | 9   | netMHCpan 2.4| 442 nM | B*07:02    | PCDH11X |
| 22 | TPDDFSYAY   | 9   | netMHC 3.0   | 4 nM   | B*35:01    | MAP1B  |
|    |             |     | netMHCpan 2.4| 5 nM   | B*35:01    |        |
| 23 | TPRIQHLLF   | 9   | netMHC 3.0   | 40 nM  | B*07:02    | TEX101 |
|    |             |     | netMHCpan 2.4| 154 nM | B*07:02    |        |
|    |             |     | netMHC 3.0   | 209 nM | B*35:01    |        |
|    |             |     | netMHCpan 2.4| 210 nM | B*35:01    |        |
|    |             |     | SYFPEITHI    | 61%    | B*07:02    |        |
| 24 | TPSCTPGTA   | 9   | SYFPEITHI    | 55%    | B*07:02    | MUC5B  |
| 25 | CTGATAPPKK  | 10  | netMHC 3.0   | 418 nM | A*03:01    | MUC5B  |
| 26 | DPPEISHATF  | 10  | netMHC 3.0   | 20 nM  | B*35:01    | IL2RA  |
|    |             |     | netMHCpan 2.4| 239 nM | B*35:01    |        |
|    |             |     | SYFPEITHI    | 57%    | B*07:02    |        |
| 27 | EISHATFKAM  | 10  | netMHC 3.0   | 256 nM | B*35:01    | IL2RA  |
|    |             |     | netMHCpan 2.4| 274 nM | B*35:01    |        |
| 28 | GLSGYKGSSS  | 10  | SYFPEITHI    | 57%    | A*03:01    | KMT2C  |
| 29 | HPHSHWAQQY  | 10  | netMHC 3.0   | 14 nM  | B*35:01    | TEP1   |
| #  | Peptide            | mer | Method          | Score  | HLA       | Gene      |
|----|--------------------|-----|-----------------|--------|-----------|-----------|
| 30 | KTPDDFSYAY         | 10  | netMHCpan 2.4   | 28 nM  | B*35:01   |           |
|    |                    |     |                 |        |           |           |
| 31 | LPDHPHSHWA         | 10  | SYFPEITHI      | 80 nM  | A*29:01   | MAP1B     |
|    |                    |     |                 |        |           |           |
| 32 | QPGPLTQAAT         | 10  | netMHC 3.0     | 262 nM | B*35:01   | MDN1      |
|    |                    |     |                 |        |           |           |
| 33 | SHATFKAMAY         | 10  | netMHCpan 2.4  | 328 nM | A*29:01   | IL2RA     |
| 34 | SPPIQVSTL          | 10  | netMHCpan 2.4  | 82 nM  | B*07:02   | PCDH11X   |
|    |                    |     |                 |        |           |           |
| 35 | TPRIQHLLFL         | 10  | netMHCpan 2.4  | 23 nM  | B*07:02   | TEX101    |
|    |                    |     |                 |        |           |           |
| 36 | VMAEMSGVHK         | 10  | netMHC 3.0     | 31 nM  | A*03:01   | CCT8L2    |
|    |                    |     |                 |        |           |           |
| 37 | DVFNNSSKYGM        | 11  | netMHCpan 2.4  | 132 nM | B*35:01   | AGPAT6    |
|    |                    |     |                 |        |           |           |
| 38 | ISHATFKAMAY        | 11  | netMHCpan 2.4  | 102 nM | A*29:01   | IL2RA     |
|    |                    |     |                 |        |           |           |
| 39 | NMVAFFLGCSF        | 11  | netMHCpan 2.4  | 131 nM | B*35:01   | C14orf159 |
| 40 | QPGPLTQAATM        | 11  | netMHCpan 2.4  | 70 nM  | B*35:01   | MDN1      |
|    |                    |     |                 |        |           |           |
| 41 | TPRIQHLLFL         | 11  | netMHCpan 2.4  | 149 nM | B*07:02   | TEX101    |
|    |                    |     |                 |        |           |           |
| 42 | VSTLHHSPPLV        | 11  | netMHCpan 2.4  | 247 nM | C*15:05   | PCDH11X   |
|    |                    |     |                 |        |           |           |
| 43 | YSEQKNNMVAF        | 11  | netMHC 3.0     | 86 nM  | B*35:01   | C14orf159 |
|    |                    |     |                 |        |           |           |
| 44 | EISHATFKAMAY       | 12  | netMHC 3.0     | 93 nM  | B*35:01   | IL2RA     |
| 45 | FVWQPPLTQAAT       | 12  | netMHC 3.0     | 157 nM | B*35:01   | MDN1      |
| 46 | ISHATFKAMAYK       | 12  | netMHC 3.0     | 21 nM  | A*03:01   | IL2RA     |
| 47 | KTPDDFSYAYK        | 12  | netMHC 3.0     | 332 nM | A*03:01   | MAP1B     |
|    |                    |     |                 |        |           |           |
| 48 | LPPGLPLLPPPL       | 12  | netMHC 3.0     | 164 nM | B*35:01   | KDM6B     |
|    |                    |     |                 |        |           |           |
| 49 | PPEISHATFKAM       | 12  | netMHC 3.0     | 223 nM | B*35:01   | IL2RA     |
|    |                    |     |                 |        |           |           |
| 50 | TPRIQHLLFLLV       | 12  | netMHC 3.0     | 122 nM | B*07:02   | TEX101    |
| 51 | VPGFVWQPPLG        | 12  | netMHC 3.0     | 83 nM  | B*35:01   | MDN1      |
|    |                    |     |                 |        |           |           |
| 52 | YSEQKNNMVAFF       | 12  | netMHC 3.0     | 233 nM | B*35:01   | C14orf159 |
Supplementary Table 13: Epitope Prediction of mutated Ligands (L04/12) current

Shown are in silico predicted HLA class I peptide ligands (amino acid alterations in peptide sequences are underlined) based on mutations provided in Suppl. Table 11. Predictions encompass 9-12mer peptides and have been predicted using respective dedicated currently available software. Further information regarding bioinformatics analyses is given under Suppl. Material and Methods. Scoring of putative HLA binding peptides according to the used software algorithms together with predicted HLA alleles matching the patient given in nM for NetMHCpan 2.8 (42, 43) and NetMHC 3.4 (15, 45, 46) respectively or % of maximal binding (50% max.) for SYFPEITHI* 2015 (in house version). Respective cut offs were predefined at <500nM for NetMHCpan 2.8 and NetMHC 3.4 or >50%max. for SYFPEITHI*. As matrices for HLA allele B*07:05 were not always available closely related HLA allele B*07:02 was additionally used when available. Further gene identifiers (Gene ID) according to the National Center for Biotechnology Information (NCBI) are listed.

| #  | Peptide     | mer | Method                        | Score  | HLA     | Gene   |
|----|-------------|-----|-------------------------------|--------|---------|--------|
| 1  | AGDVEDLV    | 8   | SYFPEITHI*                    | 51%    | C*04:01 | SESTD1 |
| 2  | DPQFGDVF    | 8   | netMHCpan 2.8                 | 91 nM  | C*04:01 | AGPAT6 |
|    |             |     | netMHC 3.4                    | 155 nM | B*35:01 |
| 3  | EISHATFK    | 8   | netMHC 3.4                    | 366 nM | A*03:01 | IL2RA  |
| 4  | FVWQPGPL    | 8   | netMHCpan 2.8                 | 140 nM | C*15:05 | MDN1   |
|    |             |     | netMHC 3.4                    | 174 nM | B*35:01 |
|    |             |     | netMHCpan 2.8                 | 207 nM | C*04:01 |
|    |             |     | netMHCpan 2.8                 | 343 nM | B*35:01 |
| 5  | GYDLLDLDH   | 8   | SYFPEITHI*                    | 54%    | C*04:01 | KLHL34 |
| 6  | HPHSHWAQ    | 8   | netMHC 3.4                    | 83 nM  | B*35:01 | TEP1   |
|    |             |     | netMHCpan 2.8                 | 351 nM | C*15:05 |
| 7  | KTPDDFSY    | 8   | netMHCpan 2.8                 | 314 nM | A*29:01 | MAP1B  |
| 8  | LPLLPPPL    | 8   | netMHCpan 2.8                 | 22 nM  | C*15:05 | KDM6B  |
|    |             |     | netMHCpan 2.8                 | 29 nM  | B*35:01 |
|    |             |     | netMHCpan 2.8                 | 66 nM  | C*04:01 |
| #  | Peptide      | mer | Method    | Score     | HLA       | Gene      |
|----|--------------|-----|-----------|-----------|-----------|-----------|
| 9  | PPIQVSTL     | 8   | netMHC 3.4| 67 nM     | B*35:01   | PDCDHX11  |
| 10 | VFWNSSKY     | 8   | netMHC 3.4| 487 nM    | B*35:01   | AGPAT6    |
| 11 | DPPEISHAT    | 9   | SYFPEITHI*| 52%       | B*07:02   | IL2RA     |
| 12 | DVEDDLVFK    | 9   | SYFPEITHI* | 74%   | A*03:01   | SESTD1    |
| 13 | DVFWNSSKY    | 9   | netMHC 3.4| 18 nM     | B*35:01   | AGPAT6    |
| 14 | EFVWQPGLPL   | 9   | SYFPEITHI* | 56%   | C*04:01   | MDN1      |
| 15 | EQKLMVFAF     | 9   | netMHCpan 2.8| 316 nM | C*04:01   | C14orf159 |
| 16 | GDVSDLVELK   | 9   | SYFPEITHI* | 54%   | B*35:01   | SESTD1    |
| 17 | GPLTQAATM    | 9   | netMHCpan 2.8| 122 nM | C*15:05   | MDN1      |
| 18 | GYDDLQDHW     | 9   | SYFPEITHI* | 61%   | C*04:01   | KLHL34    |
| 19 | HPHSHWAQQ     | 9   | SYFPEITHI* | 354 nM  | B*35:01   | TEP1      |
| 20 | HWDIGICAL    | 9   | SYFPEITHI* | 57%    | B*35:01   | KLHL34    |
| 21 | ISHATFKAM    | 9   | netMHCpan 2.8| 477 nM | C*04:01   | IL2RA     |
| 22 | KYDPQFGDV     | 9   | SYFPEITHI* | 81%    | C*04:01   | AGPAT6    |
| 23 | NLDPHSH      | 9   | SYFPEITHI* | 61%    | C*04:01   | TEP1      |
| 24 | PIQVSTLHH     | 9   | SYFPEITHI* | 58%    | A*03:01   | PCDH11X   |
| 25 | PLLPPPLPP     | 9   | SYFPEITHI* | 52%    | A*03:01   | KDM6B     |
| 26 | PPEISHATF     | 9   | SYFPEITHI* | 71%    | B*35:01   | IL2RA     |
| 27 | PPGLPLLPP     | 9   | SYFPEITHI* | 52%    | B*07:02   | KDM6B     |
| 28 | PPPIQVSTL     | 9   | SYFPEITHI* | 75%    | B*35:01   | PCDH11X   |
| 29 | QPGPLTQAAM    | 9   | netMHCpan 2.8| 206 nM | C*15:05   | MDN1      |
| 30 | QYSEQLKNM     | 9   | SYFPEITHI* | 56%    | C*04:01   | C14orf159 |
| 31 | RIOHLLFL      | 9   | SYFPEITHI* | 52%    | A*03:01   | TEX101    |
| 32 | SPPPIQVST     | 9   | SYFPEITHI* | 58%    | B*07:02   | PCDH11X   |
| 33 | TPDDFSYAY     | 9   | netMHC 3.4| 2 nM     | B*35:01   | MAP1B     |
| 34 | TPRIQHLLF     | 9   | netMHC 3.4| 53 nM    | B*07:02   | TEX101    |
| #  | Peptide     | mer | Method          | Score  | HLA       | Gene      |
|----|-------------|-----|-----------------|--------|-----------|-----------|
| 35 | TPSCTPGTA   | 9   | netMHCpan 2.8   | 215 nM | C*15:05   | MUC5B     |
|    |             |     | netMHCpan 2.8   | 255 nM | C*04:01   |           |
|    |             |     | netMHC 3.4      | 343 nM | B*35:01   |           |
|    |             |     | SYFPEITHI*      | 61%    | B*07:02   |           |
|    |             |     | SYFPEITHI*      | 68%    | B*35:01   |           |
| 36 | AGDVEDLVEL  | 10  | SYFPEITHI*      | 56%    | C*04:01   | SESTD1    |
| 37 | CTPGTAPPPK  | 10  | SYFPEITHI*      | 65%    | A*03:01   | MUC5B     |
| 38 | DPPEISHATF  | 10  | SYFPEITHI*      | 77%    | B*35:01   | IL2RA     |
|    |             |     | SYFPEITHI*      | 57%    | B*07:02   |           |
| 39 | EISHATFKAM  | 10  | SYFPEITHI*      | 54%    | B*35:01   | IL2RA     |
| 40 | FLLVLGASL   | 10  | SYFPEITHI*      | 54%    | C*04:01   | TEX101    |
| 41 | GYDLDLDHWE  | 10  | SYFPEITHI*      | 54%    | C*04:01   | KLHL34    |
| 42 | HPHSHWAQQY  | 10  | SYFPEITHI*      | 85%    | B*35:01   | TEP1      |
|    |             |     | netMHCpan 2.8   | 201 nM | C*04:01   |           |
|    |             |     | netMHC 3.4      | 37 nM  | B*35:01   |           |
| 43 | KTPDDFSYAY  | 10  | SYFPEITHI*      | 79%    | C*04:01   | AGPAT6    |
| 44 | KYDPQFGDVF  | 10  | SYFPEITHI*      | 54%    | C*04:01   | TEX101    |
| 45 | LFLVLGASL   | 10  | SYFPEITHI*      | 81%    | B*35:01   |           |
|    |             |     | SYFPEITHI*      | 73%    | B*07:02   |           |
| 46 | LPDHPHSHWA  | 10  | SYFPEITHI*      | 57%    | B*07:02   | TEP1      |
| 47 | QPGPLTQAAT  | 10  | SYFPEITHI*      | 67%    | B*07:02   | MDN1      |
| 48 | RIQHLLLFLV  | 10  | SYFPEITHI*      | 52%    | A*03:01   | TEX101    |
| 49 | SHTFKAMAY   | 10  | netMHCpan 2.8   | 479 nM | A*29:01   | IL2RA     |
| 50 | SPPIQVSTL   | 10  | netMHCpan 2.8   | 46 nM  | C*15:05   | PCDH11X   |
|    |             |     | netMHCpan 2.8   | 56 nM  | B*35:01   |           |
|    |             |     | netMHC 3.4      | 82 nM  | B*07:02   |           |
|    |             |     | SYFPEITHI*      | 81%    | B*35:01   |           |
|    |             |     | SYFPEITHI*      | 73%    | B*07:02   |           |
| 51 | TPRIQHLLLFL| 10  | netMHCpan 2.8   | 30 nM  | B*35:01   | TEX101    |
|    |             |     | netMHC 3.4      | 41 nM  | B*07:02   |           |
|    |             |     | netMHCpan 2.8   | 44 nM  | C*15:05   |           |
|    |             |     | SYFPEITHI*      | 83%    | B*07:02   |           |
|    |             |     | SYFPEITHI*      | 81%    | B*35:01   |           |
| 52 | VEDLVELKSL  | 10  | SYFPEITHI*      | 62%    | C*04:01   | SESTD1    |
| 53 | VMAEMSGVHK  | 10  | SYFPEITHI*      | 69%    | A*03:01   | CCT8L2    |
| 54 | DVFWNSSSKYGM| 11  | SYFPEITHI*      | 69%    | A*03:01   | AGPAT6    |
|    |             |     | netMHC 3.4      | 123 nM | B*35:01   |           |
|    |             |     | netMHCpan 2.8   | 211 nM | C*04:01   |           |
| 55 | DVMAEMSGVHK| 11   | SYFPEITHI*      | 69%    | A*03:01   | CCT8L2    |
| 56 | FGDVFWNSSKY| 11   | SYFPEITHI*      | 69%    | A*03:01   | AGPAT6    |
| 57 | HSPPPIQVSTL | 11   | SYFPEITHI*      | 69%    | A*03:01   | PCDH11X   |
| 58 | ISSHATFKAMAY| 11  | SYFPEITHI*      | 69%    | A*03:01   | IL2RA     |
| #  | Peptide    | Method       | Score | HLA     | Gene      |
|----|------------|--------------|-------|---------|-----------|
| 59 | NMVAFFLGCSF| netMHCpan 2.8| 80 nM | A*29:01 | C14orf159 |
|    |            | netMHC 3.4   | 133 nM| B*35:01 |           |
|    |            | netMHCpan 2.8| 268 nM| C*04:01 |           |
|    |            | netMHC 3.4   | 447 nM| B*35:01 |           |
|    |            | netMHCpan 2.8| 550 nM| A*29:01 |           |
| 60 | PPEIŠHATFKA| netMHC 3.4   | 77 nM | B*07:02 | IL2RA     |
|    |            | SYFPEITHI*   | 57%   | B*07:02 |           |
| 61 | PPGLPLLPPPL| netMHC 3.4   | 64 nM | B*35:01 | KDM6B     |
|    |            | SYFPEITHI*   | 263 nM| B*07:02 |           |
| 62 | QPGPLTQAATM| netMHC 3.4   | 64 nM | B*35:01 | MDN1      |
|    |            | netMHCpan 2.8| 64 nM | C*04:01 |           |
|    |            | netMHC 3.4   | 153 nM| B*07:02 |           |
|    |            | netMHCpan 2.8| 169 nM| B*35:01 |           |
|    |            | SYFPEITHI*   | 63%   | B*07:02 |           |
| 63 | TPRIQHLLFL | netMHC 3.4   | 32 nM | B*07:02 | TEX101    |
|    |            | netMHCpan 2.8| 55 nM | B*07:02 |           |
|    |            | netMHC 3.4   | 67 nM | C*15:05 |           |
|    |            | SYFPEITHI*   | 73%   | B*07:02 |           |
| 64 | YSEQKLMVAF  | netMHC 3.4   | 172 nM| B*35:01 | C14orf159 |
|    |            | netMHCpan 2.8| 309 nM| C*04:01 |           |
| 65 | EISHATFKAMAY| netMHC 3.4   | 91 nM | B*35:01 | IL2RA     |
| 66 | FVWQPGPLTQA| netMHC 3.4   | 397 nM| B*35:01 | MDN1      |
| 67 | HPHŠHWÁQQYPS| netMHC 3.4   | 89 nM | B*35:01 | TEP1      |
| 68 | IŠHATFKAMAYK| netMHC 3.4   | 52 nM | A*03:01 | IL2RA     |
| 69 | LPPGLPLLPPPL| netMHC 3.4   | 111 nM| B*07:02 | KDM6B     |
|    |            | netMHC 3.4   | 192 nM| B*35:01 |           |
| 70 | TPRIQHLLFLV| netMHC 3.4   | 83 nM | B*07:02 | TEX101    |
| 71 | VPGEFVWQPGPL| netMHC 3.4   | 72 nM | B*07:02 | MDN1      |
Supplementary Table 14: WES/WTS Results (P03/13)

Shown are sequencing results obtained by WES (whole exome sequencing) and WTS (whole transcriptome sequencing) of lesion P03/13 (lung metastasis), yielding basic somatic variants. Complex variants are excluded as being unsuitable for the subsequent prediction of HLA-ligands. In sequential order of columns from left to right: serial number; chromosome number; start and end position of somatic variant, ref.: reference base; obs.: observed base at respective chromosomal location; allele frequency and depth of somatic variant as sequenced by WES in tumor and reference tissue (normal); frequency and depth of somatic variant as sequenced by WTS in tumor material; Ref. Seq. (NCBI Reference Sequence) such as variant type (MV: missense variant; DV: downstream gene variant; SG: stop gain variant; UV: upstream gene variant; SV: splice region variant) and putative AA (amino acid) alteration introduced by somatic variant; n.d. no data; ± variant excluded for peptide prediction.

| #  | #chr | start    | end      | gene            | ref. | obs. | allele freq. | depth | allele freq. | depth | freq. | depth |
|----|------|----------|----------|-----------------|------|------|--------------|-------|--------------|-------|-------|-------|
| 1  | chr1 | 186277277| 186277277| PRG4<sup>a</sup>, TPR<sup>b</sup> | G    | A    | 0.06         | 89    | 0.00         | 217   | 0.00  | 1.00  |

<sup>a</sup> NM_005807.3  
MV [G809E]<sup>a</sup>

<sup>b</sup> NM_001127708.1  
MV [G768E]<sup>b</sup>

<sup>c</sup> NM_001127709.1  
MV [G716E]<sup>c</sup>
| #  | #chr | start | end    | gene | ref. | obs. | allele freq. | depth | allele freq. | depth | freq. | depth |
|----|------|-------|--------|------|------|------|-------------|-------|-------------|-------|-------|-------|
| 2  | chr2 | 25358435 | 25358435 | EFR3B | C    | T    | 0.08        | 85    | 0.00        | 130   | n/a   | 0.00  |
| 3  | chr2 | 179989221 | 179989221 | SESTD1 | T    | A    | 0.11        | 80    | 0.00        | 99    | 0.56  | 32.00 |
| 4  | chr2 | 209113113 | 209113113 | IDH1  | G    | A    | 0.17        | 36    | 0.00        | 33    | 0.42  | 237.00 |
| 5  | chr5 | 58289248  | 58289248  | PDE4D | C    | A    | 0.07        | 54    | 0.00        | 48    | 0.20  | 5.00  |

**Ref. Seq. variant type [AA alteration]**

- NM_001127710.1
- MV [G675E]²
- NM_003292.2
- DV [n.d.]²
- NM_014971.1
- SG [R471*]²
- NM_178123.4
- MV [E346V]
- NM_001282386.1
- NM_001282387.1
- NM_005896.3
- MV [R132C]
- NM_001104631.1
- MV [M322I]²
- NM_001197223.1
- MV [M311]²
- NM_001197221.1
- MV [M201]²
- NM_001197222.1
- MV [M981]²
- NM_001197220.1
- MV [M192I]²
- NM_001197219.1
- MV [M200I]²
- NM_006203.4
- MV [M186I]²
- NM_001197218.1
- MV [M258I]²
| #  | #chr | start  | end    | gene         | ref. gene | obs. | allele | freq. | depth | allele | freq. | depth | freq. | depth | Ref. Seq. variant type [AA alteration] |
|----|------|--------|--------|--------------|-----------|------|--------|-------|-------|--------|-------|-------|-------|-------|-------------------------------------|
| 6  | chr7 | 99313514 | 99313514 | CYP3A7-CYP3AP1, CYP3A7 | G         | T    | 0.06   | 114   | 0.00  | 111    | 0.15  | 20.00 |       | NM_001165899.1 MV [M261I]^c       |
| 7  | chr7 | 140710306 | 140710306 | MRPS33       | G         | A    | 0.06   | 180   | 0.00  | 159    | 0.21  | 292.00 |       | NM_016071.3; NM_053035.2 MV [A43V] |
| 8  | chr10 | 6067959  | 6067959  | IL2RA        | G         | A    | 0.05   | 114   | 0.00  | 249    | 0.00  | 13.00  |       | NM_000417.2 MV [P325]             |
| 9  | chr12 | 55039476 | 55039476 | DCD          | G         | A    | 0.05   | 111   | 0.00  | 154    | n/a   | 0.00   |       | NM_001300854.1; NM_053283.3 MV [S38L] |
| 10 | chr14 | 91636435 | 91636435 | C14orf159    | G         | A    | 0.22   | 23    | 0.00  | 106    | 0.80  | 51.00  |       | NM_001102368.2; NM_001102366.2; NM_001102369.2; NM_001286470.1; NM_001286472.1; NM_024952.7; NM_001102367.2; NM_001286471.1 MV [D116N] |
| 11 | chr17 | 3101176  | 3101176  | OR1A2        | C         | T    | 0.14   | 111   | 0.00  | 158    | n/a   | 0.00   |       | NM_012352.1 SG [R122]*^c           |
| 12 | chr22 | 17072027 | 17072027 | CCT8L2       | G         | T    | 0.10   | 63    | 0.00  | 86     | n/a   | 0.00   |       | NM_014406.4 MV [Q472K]            |
**Supplementary Table 15: Epitope Prediction of mutated Ligand (P03/13) at first vaccination**

Shown are *in silico* predicted HLA class I peptide ligands (amino acid alterations in peptide sequences are underlined) based on mutations provided in Suppl. **Table 14**. Predictions encompass 9-12mer peptides and have been predicted using dedicated software available before September 2012 previous to starting vaccinations. Further information regarding bioinformatics analyses is given under **Suppl. Material and Methods**. Scoring of putative HLA binding peptides according to the used software algorithms together with predicted HLA alleles matching the patient given in nM for NetMHCpan 2.4 (42, 43) and NetMHC 3.0 (44-46) respectively or % of maximal binding (50% max.) for SYFPEITHI (16). Respective cut offs were predefined at <500nM for NetMHCpan 2.4 and NetMHC 3.0 or >50%max. for SYFPEITHI. As matrices for HLA allele B*07:05 were not always available closely related HLA allele B*07:02 was additionally used when available. Further gene identifiers (Gene ID) according to the National Center for Biotechnology Information (NCBI) are listed.

| #  | Peptide     | mer | Method           | Score  | HLA     | Gene      |
|----|-------------|-----|-----------------|--------|---------|-----------|
| 1  | EISHATFK    | 8   | netMHC 3.0      | 256 nM | A*03:01 | IL2RA     |
|    |             |     | netMHC 3.0      | 222 nM | B*35:01 |           |
| 2  | IIIGCHAY    | 8   | netMHCpan 2.4   | 17 nM  | A*29:01 | IDH1      |
|    |             |     | netMHCpan 2.4   | 119 nM | B*35:01 |           |
|    |             |     | netMHC 3.0      | 198 nM | B*35:01 |           |
| 3  | ALLNAGDVE   | 9   | SYFPEITHI       | 52%    | A*03:01 | SESTD1    |
| 4  | DPPEISHAT   | 9   | netMHC 3.0      | 83 nM  | B*35:01 | IL2RA     |
|    |             |     | SYFPEITHI       | 52%    | B*07:02 |           |
| 5  | EQKLNMVAF   | 9   | netMHCpan 2.4   | 153 nM | B*35:01 | C14orf159 |
| 6  | KPIIGCHHA   | 9   | netMHC 3.0      | 313 nM | B*07:02 | IDH1      |
|    |             |     | SYFPEITHI       | 55%    | B*07:02 |           |
| 7  | NPCHEALAA   | 9   | netMHCpan 2.4   | 238 nM | B*35:01 | DCD       |
|    |             |     | netMHC 3.0      | 287 nM | B*35:01 |           |
|    |             |     | SYFPEITHI       | 58%    | B*07:02 |           |
| 8  | PIIIGCHAY   | 9   | netMHCpan 2.4   | 220 nM | A*29:01 | IDH1      |
| #  | Peptide       | mer | Method         | Score    | HLA     | Gene    |
|----|---------------|-----|----------------|----------|---------|---------|
| 9  | PPEIȘHATF     | 9   | netMHC 3.0     | 238 nM   | B*35:01 | IL2RA   |
|    |               |     | SYFPEITHI     | 52%      | B*07:02 |         |
|    |               |     | netMHC 3.0     | 20 nM    | B*35:01 | IL2RA   |
|    |               |     | netMHCpan 2.4  | 239 nM   | B*35:01 |         |
|    |               |     | SYFPEITHI     | 57%      | B*07:02 |         |
| 10 | DPPEIȘHATF    | 10  | netMHC 3.0     | 256 nM   | B*35:01 | IL2RA   |
|    |               |     | SYFPEITHI     | 74%      | A*03:01 |         |
| 11 | EiȘHATFKAM    | 10  | netMHC 3.0     | 19 nM    | B*35:01 | IL2RA   |
|    |               |     | netMHCpan 2.4  | 24 nM    | B*35:01 |         |
|    |               |     | netMHCpan 2.4  | 18 nM    | A*03:01 |         |
|    |               |     | netMHC 3.0     | 75 nM    | B*35:01 | MRPS33  |
|    |               |     | netMHCpan 2.4  | 120 nM   | B*35:01 |         |
| 12 | KLFSELPLVK    | 10  | netMHC 3.0     | 31 nM    | A*03:01 |         |
|    |               |     | SYFPEITHI     | 74%      | A*03:01 |         |
| 13 | KPIIIGÇHAY    | 10  | netMHCpan 2.4  | 225 nM   | A*29:01 | IDH1    |
|    |               |     | netMHC 3.0     | 402 nM   | B*35:01 | DCD     |
|    |               |     | netMHCpan 2.4  | 328 nM   | A*29:01 | IL2RA   |
| 14 | LPLVKKKETY    | 10  | netMHC 3.0     | 31 nM    | A*03:01 |         |
|    |               |     | netMHCpan 2.4  | 79 nM    | A*03:01 | CCT8L2  |
| 15 | NPCHEALAAQ    | 10  | netMHC 3.0     | 86 nM    | B*35:01 |         |
|    |               |     | netMHCpan 2.4  | 131 nM   | B*35:01 | C14orf159|
| 16 | ŞHATFKAMAY    | 10  | netMHCpan 2.4  | 102 nM   | A*29:01 | IL2RA   |
|    |               |     | netMHC 3.0     | 209 nM   | A*03:01 |         |
|    |               |     | netMHCpan 2.4  | 247 nM   | B*35:01 |         |
| 17 | VMAEMSGVHK    | 10  | netMHC 3.0     | 7 nM     | A*03:01 | MRPS33  |
|    |               |     | netMHCpan 2.4  | 23 nM    | A*03:01 |         |
| 18 | IIGÇHAYGDQY   | 11  | netMHCpan 2.4  | 382 nM   | A*29:01 | IDH1    |
|    |               |     | netMHC 3.0     | 30 nM    | B*07:02 | DCD     |
| 19 | IȘHATFKAMAY   | 11  | netMHCpan 2.4  | 30 nM    | B*07:02 |         |
|    |               |     | netMHC 3.0     | 93 nM    | B*35:01 | IL2RA   |
| 20 | KLFSELPLVKK   | 11  | netMHC 3.0     | 11 nM    | A*03:01 | MRPS33  |
|    |               |     | netMHCpan 2.4  | 303 nM   | B*07:02 |         |
| 21 | NMVAFFLGCSF   | 11  | netMHCpan 2.4  | 223 nM   | B*35:01 | MRPS33  |
|    |               |     | netMHC 3.0     | 233 nM   | B*35:01 | C14orf159|
| 22 | YSEQŁKNMVAF   | 11  | netMHC 3.0     | 382 nM   | A*03:01 | MRPS33  |
|    |               |     | netMHCpan 2.4  | 86 nM    | B*35:01 |         |
| 23 | APGSNPCHEALé  | 12  | netMHC 3.0     | 86 nM    | B*35:01 | C14orf159|
|    |               |     | netMHCpan 2.4  | 30 nM    | B*07:02 | DCD     |
| 24 | EȘHATFKAMAYK  | 12  | netMHC 3.0     | 21 nM    | A*03:01 |         |
|    |               |     | netMHCpan 2.4  | 21 nM    | A*03:01 | IL2RA   |
| 25 | IȘHATFKAMAYK  | 12  | netMHC 3.0     | 11 nM    | A*03:01 | IL2RA   |
| 26 | KLFSELPLVKKK  | 12  | netMHC 3.0     | 233 nM   | B*35:01 |         |
|    |               |     | netMHCpan 2.4  | 382 nM   | A*03:01 | MRPS33  |
| 27 | PPEIȘHATFKAM  | 12  | netMHC 3.0     | 37 nM    | B*35:01 | IDH1    |
|    |               |     | netMHCpan 2.4  | 37 nM    | B*35:01 |         |
| 28 | VVKLFSELVK    | 12  | netMHC 3.0     | 233 nM   | B*35:01 |         |
|    |               |     | netMHCpan 2.4  | 382 nM   | A*03:01 | MRPS33  |
| 29 | WVKPIIIGÇHAY  | 12  | netMHC 3.0     | 233 nM   | B*35:01 |         |
|    |               |     | netMHCpan 2.4  | 382 nM   | A*03:01 | MRPS33  |
| 30 | YSEQŁKNMVAFF  | 12  | netMHC 3.0     | 233 nM   | B*35:01 | C14orf159|
Supplementary Table 16: Epitope Prediction of mutated Ligands (P03/13) current

Shown are in silico predicted HLA class I peptide ligands (amino acid alterations in peptide sequences are underlined) based on mutations provided in Suppl. Table 14. Predictions encompass 9-12mer peptides and have been predicted using respective dedicated currently available software. Further information regarding bioinformatics analyses is given under Suppl. Material and Methods. Scoring of putative HLA binding peptides according to the used software algorithms together with predicted HLA alleles matching the patient given in nM for NetMHCpan 2.8 (42, 43) and NetMHC 3.4 (15, 45, 46) respectively or % of maximal binding (50% max.) for SYFPEITHI* 2015 (in house version). Respective cut offs were predefined at <500nM for NetMHCpan 2.8 and NetMHC 3.4 or >50%max. for SYFPEITHI*. As matrices for HLA allele B*07:05 were not always available closely related HLA allele B*07:02 was additionally used when available. Further gene identifiers (Gene ID) according to the National Center for Biotechnology Information (NCBI) are listed.

| #  | Peptide   | mer | Method            | Score  | HLA       | Gene     |
|----|-----------|-----|-------------------|--------|-----------|----------|
| 1  | AGDVEDLV  | 8   | SYFPEITHI*        | 51%    | C*04:01   | SESTD1   |
| 2  | EISHATFK  | 8   | netMHC 3.4        | 366 nM | A*03:01   | IL2RA    |
| 3  | IIIGCHAY  | 8   | netMHCpan 2.8     | 13 nM  | A*29:01   | IDH1     |
|    |           |     | netMHC 3.4        | 65 nM  | B*35:01   |          |
|    |           |     | netMHCpan 2.8     | 84 nM  | C*04:01   |          |
| 4  | LFSELPVL  | 8   | SYFPEITHI*        | 51%    | C*04:01   | MRPS33   |
| 5  | DPPEISHAT | 9   | SYFPEITHI*        | 52%    | B*07:02   | IL2RA    |
| 6  | DVEDLVELK | 9   | SYFPEITHI*        | 74%    | A*03:01   | SESTD1   |
| 7  | EQLKNMVAF | 9   | netMHCpan 2.8     | 316 nM | C*04:01   | C14orf159|
| 8  | GDVEDLVEL | 9   | SYFPEITHI*        | 54%    | B*35:01   | SESTD1   |
| 9  | IŞHATFKAM | 9   | netMHCpan 2.8     | 477 nM | C*04:01   | IL2RA    |
| 10 | KLFSELPLV | 9   | SYFPEITHI*        | 58%    | A*03:01   | MRPS33   |
| 11 | KPİİIGÇHA | 9   | SYFPEITHI*        | 55%    | B*07:02   | IDH1     |
| 12 | NPCHEALAA | 9   | netMHC 3.4        | 412 nM | B*35:01   | DCD      |
| 13 | IIIİİİÇHA | 9   | netMHCpan 2.8     | 134 nM | A*29:01   | IDH1     |
|    |     |     | SYFPEITHI* |     |     |     |
|----|-----|-----|------------|-----|-----|-----|
| 14 | PLVKKETY | 9 | SYFPEITHI* | 52% | A*03:01 | MRPS33 |
| 15 | PPEI\text{\textregistered}HATF | 9 | SYFPEITHI* | 55% | A*03:01 | IL2RA |
| 16 | QYSEQ\text{\textregistered}K\text{\textregistered}NM | 9 | SYFPEITHI* | 71% | B*35:01 | IL2RA |
| 17 | AGDVEDLEVEL | 10 | SYFPEITHI* | 71% | C*04:01 | C14orf159 |
| 18 | DPPEI\text{\textregistered}HATF | 10 | SYFPEITHI* | 56% | C*04:01 | SESTD1 |
| 19 | EI\text{\textregistered}HATFKAM | 10 | SYFPEITHI* | 55% | A*03:01 | IL2RA |
| 20 | KLFSELPLVK | 10 | SYFPEITHI* | 56% | C*04:01 | MRPS33 |
| 21 | KPIIIG\text{\textregistered}HAY | 10 | SYFPEITHI* | 56% | A*03:01 | IL2RA |
| 22 | LLPLVKKKETY | 10 | SYFPEITHI* | 56% | A*03:01 | MRPS33 |
| 23 | SHATFKKAMAYK | 10 | SYFPEITHI* | 56% | A*03:01 | C14orf159 |
| 24 | VEDLVELKSL | 10 | SYFPEITHI* | 57% | B*35:01 | SESTD1 |
| 25 | VMAEMSGVH\text{\textregistered}K | 10 | SYFPEITHI* | 57% | B*35:01 | MRPS33 |
| 26 | DVM\text{\textregistered}EMSGVH\text{\textregistered}K | 11 | SYFPEITHI* | 57% | B*35:01 | MRPS33 |
| 27 | IIG\text{\textregistered}HAYGDQY | 11 | SYFPEITHI* | 57% | B*35:01 | MRPS33 |
| 28 | I\text{\textregistered}HATFKKAMAYK | 11 | SYFPEITHI* | 57% | B*35:01 | MRPS33 |
| 29 | KLFSELPLVKK | 11 | SYFPEITHI* | 57% | B*35:01 | MRPS33 |
| 30 | NMVAFFLGCSF | 11 | SYFPEITHI* | 57% | B*35:01 | MRPS33 |
| 31 | PPEI\text{\textregistered}HATFKA | 11 | SYFPEITHI* | 57% | B*35:01 | MRPS33 |
| 32 | YSEQ\text{\textregistered}KNMVAF | 11 | SYFPEITHI* | 57% | B*35:01 | MRPS33 |
| 33 | APGSGNPCHEAL | 12 | SYFPEITHI* | 57% | B*35:01 | MRPS33 |
| 34 | EI\text{\textregistered}HATFKKAMAYK | 12 | SYFPEITHI* | 57% | B*35:01 | MRPS33 |
Supplementary Figure 16-21: Comparison mass spectra of immunopeptidome (L06/10) and respective synthetic peptides

Analysis of the Major Histocompatibility Complex (MHC) immunopeptidome by uHPLC coupled tandem mass spectrometry

Mass spectrometric analysis of the HLA Class I ligandome on L06/10 yielded 375 unique peptides (3,811 peptide spectrum matches) (see below) (adjacent liver tissue: 1,169 peptides (19,462 peptide spectrum matches)). Three out of four HLA class I epitopes contained in the vaccine cocktail were confirmed to be presented as natural HLA-ligands on the patient’s tumor tissue; GLASFKSFLK (RGS-5)/ TSALPIIQK (ADFP-3)/ SLLTSSKGQLQK (ADFP-2).
Supplementary Figure 16 (RGS-5 peptide immunopeptidome: autologous tumor mass spectrum)

Supplementary Figure 17 (RGS-5 synthetic peptide mass spectrum)
Supplementary Figure 18 (ADFP-3 immunopeptidome: autologous tumor mass spectrum)

T|S|A|L|P|I|Q|K (Tumor L06/10)

Supplementary Figure 19 (ADFP-3 synthetic peptide mass spectrum)

T|S|A|L|P|I|Q|K (synthetic peptide)
Supplementary Figure 20 (ADFP-2) immunopeptidome: autologous tumor mass spectrum

Supplementary Figure 21 (ADFP-2) synthetic peptide mass spectrum
| #  | Sequence          | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area     | q-Value | PEP   | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|----|------------------|-------|------------|--------------------------|-----------|----------|---------|-------|----------|------------|-----|----------|---------|---------|
| 1  | mPVGPDAILRY      | 70    | 1          | P46379                   | M1        | 8,331E7  | 0       | 0,0004028 | 81        | 3,90559E-06 | 2    | 1247,64556 | 0,18     | 113,36   |
| 2  | RVQEAVESMVK      | 2     | 1          | Q96C01                   |           | 1,889E7  | 0       | 0,007824  | 78        | 6,71881E-06 | 2    | 1275,67204 | -0,45    | 62,74    |
| 3  | VFVATFLRY        | 127   | 1          | O00767                   |           | 5,690E7  | 0       | 0,00013264 | 73        | 1,40465E-05 | 2    | 1115,62444 | -0,35    | 132,09   |
| 4  | MPVGPDAILRY      | 81    | 1          | P46379                   |           | 1,666E8  | 0       | 0,001035  | 72        | 2,83352E-05 | 2    | 1231,65007 | -0,28    | 126,17   |
| 5  | IYADLSKY         | 74    | 1          | Q9Y320                   |           | 5,009E7  | 0       | 0,0005538 | 70        | 3,48954E-05 | 2    | 1085,58769 | -0,06    | 113,47   |
| 6  | VLSQKVIAH        | 1     | 1          | P49914                   |           | 4,878E6  | 0       | 0,005591  | 68        | 1,50778E-05 | 2    | 994,60430  | -0,14    | 45,54    |
| 7  | AVIVLVENFYK      | 38    | 1          | Q96FQ6                   |           | 1,038E7  | 0       | 0,002223  | 67        | 2,8677E-05  | 2    | 1294,74101 | 0,32     | 135,31   |
| 8  | SIGDIFLKY        | 84    | 1          | Q9H8V3                   |           | 2,856E8  | 0       | 0,00232   | 66        | 6,76553E-05 | 2    | 1055,57659 | -0,59    | 139,39   |
| 9  | TPAGVNVNY        | 1     | 1          | Q9UBM7                   |           | 1,255E7  | 0       | 0,01179   | 64        | 0,000146998 | 2    | 948,51750  | 2,70     | 51,79    |
| 10 | ATLEVILRPK       | 2     | 1          | Q9NQT4                   |           | 3,189E6  | 0       | 0,01259   | 63        | 2,95149E-05 | 2    | 1139,71599 | 1,10     | 84,14    |
| 11 | NVIRDAVTY        | 106   | 1          | P62805                   |           | 1,675E9  | 0       | 0,01914   | 63        | 0,000199808 | 2    | 1050,55742 | -0,43    | 80,14    |
| 12 | IPNEIHAL         | 27    | 1          | P52272                   |           | 7,137E7  | 0       | 0,01284   | 63        | 0,000135869 | 2    | 1019,59081 | 2,31     | 106,09   |
| 13 | YNIQKESTL        | 80    | 4          | P62987;P62979;P0CG47;P0CG48 |           | 1,211E9  | 0       | 0,005369  | 63        | 0,000188119 | 2    | 1095,56963 | 1,40     | 66,57    |
| 14 | IVALILSTK        | 62    | 1          | P27449                   |           | 8,402E5  | 0       | 0,02427   | 62        | 1,98552E-05 | 2    | 957,63390  | -0,46    | 107,74   |
| 15 | NPNEEVARFY       | 1     | 2          | P14207;P15328            |           | 4,510E6  | 0       | 0,009627  | 61        | 0,000228239 | 2    | 1238,58318 | 2,51     | 87,25    |
| 16 | FFGETSHNY        | 86    | 1          | P43243                   |           | 4,915E8  | 0       | 0,006809  | 60        | 9,98175E-05 | 2    | 1101,46294 | -0,62    | 75,76    |
| 17 | NAFEVAEKY        | 1     | 1          | Q43707                   |           | 3,797E7  | 0       | 0,008389  | 60        | 0,000345799 | 2    | 1070,51897 | 3,39     | 83,20    |
| #  | Sequence    | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area  | q-Value | PEP       | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|----|-------------|--------|------------|--------------------------|-----------|-------|---------|-----------|-----------|-----------|-----|---------|----------|---------|
| 18 | YSLKVMLSY  | 68     | 1          | P50416                   |           | 2,24E7    | 0       | 0,001692 | 60        | 0,000282864 | 2  | 1085,62419 | 0,05     | 129,62  |
| 19 | APAARFNSQF | 1      | 1          | Q99967                   |           | 5,873E6    | 0       | 0,02573  | 59        | 0,000530133 | 2  | 1222,59783 | 1,17     | 69,75   |
| 20 | KVYDKAINR  | 1      | 1          | Q6KC79                   |           | 4,810E6    | 0       | 0,005298 | 59        | 0,000222925 | 2  | 1106,63432 | 2,36     | 31,23   |
| 21 | TAADIFQFY  | 1      | 1          | Q8N3U4                   |           | 1,643E7    | 0       | 0,007845 | 59        | 0,000406553 | 2  | 1056,53887 | 2,65     | 96,58   |
| 22 | ALDGSNVVFK | 34     | 1          | O15212                   |           | 9,182E7    | 0       | 0,006907 | 59        | 0,000396864 | 2  | 1162,64604 | -0,57    | 117,94  |
| 23 | APILHVSY   | 1      | 1          | Q98ZZ2                   |           | 1,727E7    | 0       | 0,02026  | 59        | 0,000464974 | 2  | 986,53368  | 3,14     | 94,84   |
| 24 | TFDLQRIGF  | 20     | 1          | Q13454                   |           | 1,006E7    | 0       | 0,002194 | 59        | 0,000416636 | 2  | 1096,58257 | 3,60     | 131,57  |
| 25 | SFARLSLTY  | 61     | 1          | Q15904                   |           | 1,896E8    | 0       | 0,01804  | 58        | 0,000610223 | 2  | 1057,56767 | -0,03    | 108,10  |
| 26 | APASALVRIPL| 1      | 1          | P07339                   |           | 3,745E6    | 0       | 0,00826  | 58        | 6,1592E-05  | 2  | 1107,69231 | 3,42     | 117,68  |
| 27 | ALYDKALGY  | 22     | 1          | QSTAA0                   |           | 1,192E8    | 0       | 0,02003  | 58        | 0,00056772 | 2  | 1013,52983 | -0,41    | 98,98   |
| 28 | RPAPPISGGY | 2      | 1          | P02675                   |           | 2,615E7    | 0       | 0,003001 | 58        | 0,000573284 | 2  | 1168,61260 | 1,37     | 69,77   |
| 29 | SVAKTILKR  | 20     | 2          | Q9H8S9;Q7L9L4            |           | 3,257E5    | 0       | 0,02647  | 58        | 5,15772E-05  | 2  | 1015,66155 | -0,73    | 34,79   |
| 30 | NVADVVIKF  | 39     | 1          | P04844                   |           | 1,312E8    | 0       | 0,008159 | 58        | 0,000498269 | 2  | 1004,57720 | -0,36    | 124,14  |
| 31 | VLQADILLYK | 4      | 1          | Q9UGM6                   |           | 1,259E7    | 0       | 0,002853 | 57        | 0,00188188 | 2  | 1246,74443 | 3,07     | 123,89  |
| 32 | SVSDQPYRY  | 53     | 1          | P55010                   |           | 1,097E8    | 0       | 0,005652 | 57        | 0,000690279 | 2  | 1164,53740 | 4,61     | 88,10   |
| 33 | AAVIKAMAK  | 3      | 2          | P63241;Q6I514            |           | 4,872E7    | 0       | 0,01599  | 57        | 0,000284904 | 2  | 902,54949  | 0,26     | 40,59   |
| 34 | SVAQVVLFSR | 16     | 1          | Q92482                   |           | 1,129E8    | 0       | 0,02423  | 57        | 0,00058382 | 2  | 958,56774  | -0,33    | 75,08   |
| 35 | AIDQLHLEY  | 61     | 1          | O43707                   |           | 5,835E8    | 0       | 0,002211 | 56        | 0,001071324 | 2  | 1101,55730 | -0,21    | 110,03  |
| #  | Sequence     | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area     | q-Value | PEP    | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|----|--------------|--------|------------|--------------------------|-----------|----------|---------|--------|----------|------------|-----|----------|----------|----------|
| 36 | LPSPVTAQKY   | 20     | 1          | P13639                   |           | 1,092E8  | 0       | 0,02165| 55       | 0,001493953| 2   | 1103,60918| -0,36    | 73,53    |
| 37 | KLFDHAVSKF   | 15     | 1          | O60488                   |           | 1,105E8  | 0       | 0,004928| 55       | 0,001028478| 2   | 1191,65166| -0,39    | 66,26    |
| 38 | GVHGGILNK    | 52     | 1          | P60673                   |           | 1,684E9  | 0       | 0,025  | 55       | 0,000630373| 2   | 894,51543| -0,22    | 34,37    |
| 39 | RISSAAASK    | 1      | 1          | P28074                   |           | 1,684E7  | 0       | 0,0287 | 54       | 0,001013752| 2   | 902,54137| -0,52    | 30,36    |
| 40 | ALFLTLTTK    | 16     | 1          | P00403                   |           | 4,884E5  | 0       | 0,01998| 53       | 0,000296397| 2   | 1007,61272| -0,88    | 117,60   |
| 41 | SVFNHARH     | 5      | 1          | Q7L576                   |           | 5,062E7  | 0       | 0,01561| 53       | 0,002075005| 2   | 1080,57085| 1,00     | 40,41    |
| 42 | GLFEVGAGWIGK | 1      | 1          | P51659                   |           | 7,035E6  | 0       | 0,00628| 53       | 0,001943166| 2   | 1233,66692| 3,41     | 136,19   |
| 43 | KILDIGLAY    | 16     | 1          | P49754                   |           | 2,281E7  | 0       | 0,01741| 53       | 0,000779671| 2   | 1005,59691| -1,04    | 128,10   |
| 44 | IPATITERY    | 1      | 1          | O15075                   |           | 1,171E7  | 0       | 0,00877| 53       | 0,002043581| 2   | 1063,58122| 2,78     | 76,03    |
| 45 | TFMDHVLRY    | 1      | 1          | P53396                   |           | 3,834E7  | 0       | 0,002752| 53       | 0,001794864| 2   | 1181,58049| 2,76     | 102,70   |
| 46 | FPNIPGKSL    | 15     | 1          | O15121                   |           | 2,121E8  | 0       | 0,02343| 52       | 0,002460573| 2   | 972,54869| -2,72    | 94,63    |
| 47 | APAPSTVHF    | 3      | 1          | Q13118                   |           | 1,133E8  | 0       | 0,01277| 52       | 0,001504637| 2   | 926,47527| 2,36     | 72,70    |
| 48 | SYINFELRY    | 51     | 1          | Q98210                   |           | 2,914E7  | 0       | 0,00154| 52       | 0,003055891| 2   | 1204,55966| -0,05    | 125,19   |
| 49 | ALASLVSAPK   | 13     | 2          | P55011;Q13621            |           | 1,625E5  | 0       | 0,01319| 52       | 0,001433343| 2   | 956,57695| -0,64    | 81,20    |
| 50 | KLLNYAPPLEK  | 6      | 1          | P62875                   |           | 1,114E8  | 0       | 0,008789| 52      | 0,001205105| 2   | 1188,69817| -0,47    | 75,48    |
| 51 | DPDVGNHY     | 1      | 1          | O15379                   |           | 1,055E7  | 0       | 0,01068| 52       | 0,001373676| 2   | 1063,45146| 3,27     | 95,16    |
| 52 | NVTQVRAPY    | 14     | 1          | P04040                   |           | 3,958E7  | 0       | 0,01702| 52       | 0,001737742| 2   | 1097,57695| 2,82     | 83,38    |
| 53 | EVLGLILRY    | 56     | 1          | P78527                   |           | 1,771E7  | 0       | 0,00264| 52       | 0,000785608| 2   | 1075,65093| -0,12    | 143,31   |
| #  | Sequence       | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area    | q-Value | PEP    | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|----|----------------|--------|------------|--------------------------|-----------|---------|---------|--------|----------|------------|-----|----------|----------|----------|
| 54 | KIADRFLLY      | 91     | 1          | P61968                   | 0         | 1,16E9  | 0       | 0,007001 | 52       | 0,001113642 | 2   | 1138,66167 | -0,25    | 100,77   |
| 55 | IMLPGVLRY      | 22     | 1          | O60832                   | 0         | 1,64E7  | 0       | 0,009831 | 52       | 0,001167049 | 2   | 1061,62041 | 2,60     | 124,05   |
| 56 | SSITASLRF      | 35     | 9          | P68363;Q9H853;A6NHLL2;Q71U36;Q9BQE3;P68366;Q13748;Q6PEY2;Q9NY65 | 0         | 7,72E7  | 0       | 0,01526  | 51       | 0,002099281 | 2   | 981,53600 | -0,42    | 101,47   |
| 57 | ILmEHIHKL      | 81     | 1          | P84098                   | M3        | 1,17E6  | 0       | 0,02045  | 51       | 0,001361965 | 2   | 1149,64482 | -0,09    | 47,71    |
| 58 | YFDPANGKF      | 38     | 1          | P13639                   | 0         | 7,80E7  | 0       | 0,02192  | 51       | 0,002201027 | 2   | 1058,49358 | -0,60    | 97,82    |
| 59 | NVADLHEKY      | 20     | 1          | P28074                   | 0         | 1,52E8  | 0       | 0,01262  | 51       | 0,004208725 | 2   | 1088,54180 | 4,28     | 53,51    |
| 60 | FLLEIVVRY      | 41     | 1          | Q8TF05                   | 0         | 9,00E6  | 0       | 0,004628 | 50       | 0,000499782 | 2   | 1119,69243 | -0,08    | 151,59   |
| 61 | RPVPPEVAQGY    | 1      | 1          | Q6P1N0                   | 0         | 6,62E6  | 0       | 0,01064  | 50       | 0,00274834  | 2   | 1283,67742 | 2,42     | 72,03    |
| 62 | DPLGGSAAIHLY   | 1      | 1          | P07333                   | 0         | 3,57E6  | 0       | 0,002838 | 50       | 0,00354963  | 2   | 1213,62358 | 1,95     | 119,62   |
| 63 | VSYSHISQSK     | 1      | 1          | P27816                   | 0         | 1,51E7  | 0       | 0,01693  | 50       | 0,004061982 | 2   | 1048,54375 | 1,48     | 31,99    |
| 64 | YPNVNIHNF      | 76     | 1          | Q01082                   | 0         | 2,18E8  | 0       | 0,004369 | 50       | 0,003534404 | 2   | 1117,54265 | 0,10     | 96,38    |
| 65 | VLAPEGSVANK    | 1      | 1          | Q13283                   | 0         | 1,73E7  | 0       | 0,02275  | 50       | 0,003128748 | 2   | 1084,60271 | 2,72     | 53,66    |
| 66 | NPVEDKDAVAF    | 16     | 3          | P13688;P31997;P40199     | 0         | 9,13E7  | 0       | 0,01202  | 49       | 0,004944626 | 2   | 1204,58403 | -0,40    | 88,21    |
| 67 | ImLPGVLRY      | 36     | 1          | O60832                   | M2        | 9,94E7  | 0       | 0,002583 | 49       | 0,00226304  | 2   | 1077,61601 | 3,20     | 118,80   |
| 68 | AFHISTAY       | 30     | 1          | Q96K12                   | 0         | 9,23E7  | 0       | 0,01317  | 49       | 0,005465851 | 2   | 1022,53032 | -0,25    | 102,28   |
| 69 | DAARLQAAY      | 1      | 1          | Q01082                   | 0         | 4,84E7  | 0       | 0,02443  | 49       | 0,005510418 | 2   | 978,50017 | -0,20    | 68,25    |
| 70 | LPSEIEVKY      | 23     | 1          | Q9UX3                    | 0         | 5,80E7  | 0       | 0,005831 | 49       | 0,004344253 | 2   | 1077,58281 | 0,11     | 97,72    |
| 71 | VVYPWTQRF      | 66     | 5          | P68871;P02042;P02100;P69891;P69892 | 0         | 9,71E7  | 0       | 0,003099 | 49       | 0,004135558 | 2   | 1195,62566 | -0,20    | 115,60   |
| #  | Sequence | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area | q-Value | PEP | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|----|----------|--------|------------|--------------------------|----------|------|---------|-----|----------|------------|-----|----------|----------|---------|
| 72 | AVANIVNSVK | 1      | 1          | Q9BRQ8                  |          | 2,949E6 | 0      | 0,01461 | 49   | 0,004582272  | 2   | 1014,59484 | 0,56     | 69,97   |
| 73 | PSLRLAIAGTR | 15     | 1          | Q6P1M3                  |          | 2,543E6 | 0      | 0,025   | 48   | 0,000588776  | 2   | 1196,75090 | 2,90     | 104,70  |
| 74 | RVQEAVEsMVK | 2      | 1          | Q96C01                  |          | 4,951E6 | 0      | 0,00352 | 48   | 0,008203671  | 2   | 1291,66936 | 1,41     | 43,29   |
| 75 | KITDVIIGF   | 30     | 1          | P35579                  |          | 3,638E7 | 0      | 0,007497 | 48   | 0,002257602  | 2   | 1005,59740 | -0,56    | 139,00  |
| 76 | KVYENYPTY   | 34     | 1          | P35659                  |          | 1,677E8 | 0      | 0,01908 | 48   | 0,005139569  | 2   | 1176,55669 | -0,41    | 71,06   |
| 77 | YEVSNLKD    | 1      | 1          | Q96KP4                  |          | 3,783E7 | 0      | 0,01983 | 48   | 0,00521753   | 2   | 981,49138  | 2,65     | 62,52   |
| 78 | SPAEWGQRL   | 1      | 1          | Q9NPR9                  |          | 1,257E7 | 0      | 0,01252 | 48   | 0,004840486  | 2   | 1043,52971 | 2,67     | 79,17   |
| 79 | FLNDSYLKY   | 33     | 2          | Q8WVM7;Q8N3U4           |          | 3,037E7 | 0      | 0,01198 | 48   | 0,007192722  | 2   | 1162,57817 | 0,22     | 112,17  |
| 80 | ILMEHIIKL   | 32     | 1          | P84098                  |          | 4,160E5 | 0      | 0,01391 | 48   | 0,002460726  | 2   | 1133,64995 | -0,05    | 62,05   |
| 81 | VLRDNIQGITK | 1      | 1          | P62805                  |          | 3,630E6 | 0      | 0,02136 | 48   | 0,003371183  | 2   | 1256,73625 | 3,25     | 62,17   |
| 82 | NSSPLFLHY   | 19     | 1          | Q63HR2                  |          | 1,091E8 | 0      | 0,0206  | 48   | 0,007617103  | 2   | 1077,53618 | -0,20    | 108,79  |
| 83 | VPDSSGPERIL | 20     | 1          | P61978                  |          | 7,165E7 | 0      | 0,01999 | 48   | 0,006033006  | 2   | 1169,62004 | 3,34     | 83,75   |
| 84 | RLFVGSIPK   | 20     | 2          | Q60506;Q43390           |          | 9,109E8 | 0      | 0,01537 | 47   | 0,002031211  | 2   | 1016,62438 | -0,79    | 69,68   |
| 85 | APVLLSQKF   | 1      | 1          | Q8IY21                  |          | 7,455E6 | 0      | 0,02782 | 47   | 0,002425019  | 2   | 1002,60039 | 2,09     | 96,74   |
| 86 | QTYGGQQLQK  | 1      | 1          | P20591                  |          | 1,473E7 | 0      | 0,02011 | 47   | 0,007976071  | 2   | 1093,56499 | 1,20     | 42,43   |
| 87 | HVIDKFLY    | 106    | 1          | Q16531                  |          | 7,529E7 | 0      | 0,004834| 47   | 0,006327291  | 2   | 1133,63518 | -0,19    | 111,15  |
| 88 | HNYPYSDEY   | 32     | 1          | P42330                  |          | 7,847E7 | 0      | 0,02422 | 47   | 0,001358547  | 2   | 1284,51677 | 0,01     | 75,05   |
| 89 | RSYVTTSTR   | 1      | 1          | P08670                  |          | 1,034E7 | 0      | 0,008945| 47   | 0,005801723  | 2   | 1070,56072 | 1,68     | 29,82   |

63
| #   | Sequence       | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area  | q-Value | PEP   | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|----------------|--------|------------|--------------------------|-----------|-------|--------|-------|----------|-----------|-----|---------|----------|---------|
| 90  | ILNDmVWKY      | 1      | 1          | Q9ULK4                   | M5        | 4,076E6 | 0      | 0,0139 | 47       | 0,007272462 | 2   | 1197,6012 | 3,19     | 105,12  |
| 91  | KKKKTETQEK     | 26     | 3          | P63313;O14604;P62328     |           | 6,074E6 | 0      | 0,005257 | 46       | 0,003613992 | 2   | 1232,72075 | -0,15    | 21,06   |
| 92  | TPAIJAIRY      | 3      | 4          | P52895;Q04828;P42330;P17516 | 1,439E7 | 0      | 0,009127 | 46       | 0,003059072 | 2   | 1017,61211 | 2,88     | 110,18  |
| 93  | FPDKPTQY       | 87     | 1          | P39656                   |           | 3,008E8 | 0      | 0,02301 | 46       | 0,011631075 | 2   | 1108,56719 | -0,17    | 89,16   |
| 94  | SAVDVHINm      | 5      | 1          | P46379                   | M9        | 2,442E7 | 0      | 0,01407 | 46       | 0,007773757 | 2   | 1001,47197 | -0,13    | 67,13   |
| 95  | RTLSDYNIQQK    | 1      | 4          | P62987;P62979;P0CG47;P0CG48 | 6,988E6 | 0      | 0,02813 | 46       | 0,009412414 | 2   | 1237,65764 | 3,30     | 54,96   |
| 96  | VTYNGVDNNK     | 1      | 1          | Q16181                   |           | 6,963E6 | 0      | 0,01575 | 45       | 0,012565796 | 2   | 1123,53984 | 1,76     | 40,21   |
| 97  | TPAFFAERL      | 7      | 1          | P50995                   |           | 2,148E7 | 0      | 0,01788 | 45       | 0,009403176 | 2   | 1051,56035 | 3,03     | 109,69  |
| 98  | RIAGQVAAANK    | 1      | 1          | P39019                   |           | 9,127E6 | 0      | 0,00633 | 45       | 0,005855147 | 2   | 1098,63933 | 1,32     | 30,25   |
| 99  | QVDPRLSALKY    | 1      | 1          | Q9UL63                   |           | 4,122E6 | 0      | 0,01913 | 45       | 0,011251222 | 2   | 1133,62395 | 3,36     | 116,21  |
| 100 | RSDTPLIYK      | 4      | 1          | P41252                   |           | 5,146E6 | 0      | 0,02754 | 45       | 0,010794989 | 2   | 1092,60454 | -0,26    | 53,57   |
| 101 | IINSSITTK      | 1      | 1          | P49368                   |           | 1,349E8 | 0      | 0,02576 | 45       | 0,00685152 | 2   | 976,56822 | 0,87     | 51,94   |
| 102 | YFSDPFLKY      | 44     | 1          | Q15165                   |           | 6,673E6 | 0      | 0,005473 | 45       | 0,014883852 | 2   | 1179,57219 | 0,07     | 128,30  |
| 103 | IMADIRAQY      | 13     | 1          | P05783                   |           | 2,645E5 | 0      | 0,0108 | 45       | 0,011547402 | 2   | 1080,55071 | 0,01     | 88,19   |
| 104 | RVFSGLVSTGLK   | 4      | 1          | P13639                   |           | 2,540E7 | 0      | 0,001831 | 44       | 0,004235324 | 2   | 1263,74578 | 2,98     | 84,61   |
| 105 | RISVSAASK      | 1      | 1          | P28062                   |           | 5,703E7 | 0      | 0,02817 | 44       | 0,009068957 | 2   | 918,53710 | 0,38     | 29,78   |
| 106 | NAFKEITIIm     | 1      | 1          | Q00403                   | M9        | 2,081E7 | 0      | 0,02277 | 44       | 0,012713533 | 2   | 1070,51836 | -0,34    | 68,53   |
| 107 | FYPELKLAY      | 31     | 2          | Q9UMR2;Q9NUU7            |           | 5,491E7 | 0      | 0,01295 | 44       | 0,014785756 | 2   | 1143,60832 | -0,16    | 127,93  |
| #   | Sequence     | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area     | q-Value | PEP     | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|--------------|--------|------------|--------------------------|-----------|----------|---------|---------|----------|------------|-----|----------|----------|--------|
| 108 | VLLDYHLNY    | 34     | 1          | Q06787                   | 6,092E7   | 0        | 0,003115| 44      | 0,018945097| 1149,59355 | -0,30 | 123,74   |
| 109 | VFNEKGWNY    | 12     | 1          | P43490                   | 5,202E7   | 0        | 0,01057 | 44      | 0,012404932| 1156,54570 | 3,01  | 90,33    |
| 110 | AITTHLQY     | 24     | 1          | Q96845                   | 1,337E8   | 0        | 0,02876 | 44      | 0,021324574| 1059,58306 | -0,27 | 92,51    |
| 111 | QIFVKTTLTGK  | 25     | 4          | P62978;P62979;P0CG47;P0CG48| 2,430E8   | 0        | 0,01116 | 44      | 0,003614351| 1134,68779 | -0,33 | 68,26    |
| 112 | AQYSPQQLAGK  | 1       | 1          | Q01581                   | 2,378E7   | 0        | 0,01099 | 44      | 0,022471835| 1190,62139 | 4,14  | 61,86    |
| 113 | ISNPIPIK      | 1       | 1          | Q92614                   | 8,240E6   | 0        | 0,02065 | 44      | 0,002202774| 980,61553 | 1,62  | 102,29   |
| 114 | GPGSRISSSF   | 37     | 1          | P05787                   | 5,348E8   | 0        | 0,02765 | 44      | 0,01520025 | 1081,52703 | -0,26 | 58,68    |
| 115 | TVSDAILRY    | 1       | 1          | Q9Y5W9                   | 5,589E7   | 0        | 0,01036 | 43      | 0,013926929| 1037,56462 | 1,93  | 96,09    |
| 116 | TPLEEAIKF    | 1       | 1          | Q98X19                   | 5,689E6   | 0        | 0,01895 | 43      | 0,01453644 | 1047,57463 | 2,38  | 113,39   |
| 117 | VIYNEQMASK   | 1       | 1          | Q9H8H3                   | 5,683E6   | 0        | 0,01225 | 43      | 0,022564524| 1182,58464 | 1,91  | 58,12    |
| 118 | IVSSLRLAY    | 26     | 1          | Q9NP61                   | 1,123E8   | 0        | 0,01895 | 43      | 0,00669272 | 1021,60399 | -0,10 | 99,93    |
| 119 | RTQNVLGEK    | 1       | 1          | P23396                   | 2,070E7   | 0        | 0,02252 | 43      | 0,018507177| 1044,57891 | -0,74 | 29,96    |
| 120 | VFLPIHITY    | 10     | 1          | Q99788                   | 2,204E7   | 0        | 0,0244  | 43      | 0,0137483  | 1102,62883 | -0,67 | 139,98   |
| 121 | FIDASRLVY    | 43     | 2          | P35221;P26232           | 1,009E8   | 0        | 0,00229 | 43      | 0,018261169| 1083,58269 | -0,62 | 119,06   |
| 122 | AFTDLHLRY    | 16     | 1          | P04114                   | 7,399E7   | 0        | 0,01742 | 43      | 0,016694992| 1135,59197 | 2,17  | 95,86    |
| 123 | VTFPEFLRY    | 13     | 1          | Q98NC0                   | 3,031E7   | 0        | 0,01765 | 43      | 0,017258717| 1171,61443 | -0,20 | 138,94   |
| 124 | RSPDFASSFK   | 1       | 1          | Q99828                   | 2,574E7   | 0        | 0,01341 | 43      | 0,019529788| 1141,56218 | -1,33 | 64,48    |
| 125 | RIFAPNHVVAK  | 1       | 1          | Q02543                   | 1,284E7   | 0        | 0,004994| 43      | 0,006177735| 1251,73161 | -0,40 | 48,76    |
| #  | Sequence       | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area     | q-Value | PEP      | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|----|----------------|--------|------------|--------------------------|----------|----------|---------|----------|----------|-----------|-----|----------|----------|---------|
| 126| KIFNVAIPRF     | 1      | 1          | Q9UK99                   |          | 9,34E6   | 0       | 0,02165  | 42       | 0,003205486 | 2   | 1204,72344 | 2,73    | 115,71  |
| 127| KIWADIPAPK     | 1      | 1          | P49419                   |          | 5,58E6   | 0       | 0,02787  | 42       | 0,007563925 | 2   | 1138,66435 | 2,09    | 84,50   |
| 128| TIFSTARLYY     | 28     | 2          | Q8IU4X4;Q8NRW3           |          | 4,70E7   | 0       | 0,01886  | 42       | 0,025030325 | 2   | 1147,61846 | 3,32    | 116,40  |
| 129| DPFKDIILY      | 52     | 1          | Q7L1Q6                   |          | 2,04E6   | 0       | 0,02284  | 42       | 0,017848762 | 2   | 1123,60356 | 0,12    | 155,32  |
| 130| SPVFTSRSAF     | 1      | 1          | P08729                   |          | 3,08E7   | 0       | 0,007637 | 42       | 0,019794711 | 2   | 1169,59844 | 2,94    | 86,28   |
| 131| FSIYDVKY       | 32     | 1          | Q9UF9                    |          | 4,99E7   | 0       | 0,01364  | 42       | 0,02708793  | 2   | 1131,57524 | 2,77    | 117,86  |
| 132| FPEEDKTY       | 2      | 1          | Q95298                   |          | 3,43E7   | 0       | 0,0126   | 42       | 0,023134765 | 2   | 1156,55193 | -0,17   | 47,99   |
| 133| RTNEVVAIK      | 1      | 1          | Q7L7X3                   |          | 9,99E6   | 0       | 0,02441  | 42       | 0,019896508 | 2   | 1029,60747 | 2,23    | 40,83   |
| 134| QLYWSHPRK      | 11     | 1          | P62273                   |          | 1,07E8   | 0       | 0,008521 | 41       | 0,037871535 | 2   | 1214,64311 | 0,15    | 38,25   |
| 135| YWNASDLRY      | 1      | 1          | P20929                   |          | 3,16E7   | 0       | 0,005677 | 41       | 0,019650264 | 2   | 1187,55107 | 2,57    | 102,43  |
| 136| AIAQAEELRYK    | 1      | 1          | P23396                   |          | 3,61E6   | 0       | 0,01073  | 41       | 0,020932698 | 2   | 1249,69426 | 3,44    | 58,38   |
| 137| SPIDVVEKY      | 9      | 1          | Q53G59                   |          | 5,12E7   | 0       | 0,01455  | 41       | 0,028466101 | 2   | 1049,55364 | 2,14    | 97,37   |
| 138| HGYENPTYK      | 1      | 1          | Q06481                   |          | 1,11E7   | 0       | 0,02756  | 41       | 0,023313427 | 2   | 1108,50810 | 2,07    | 34,88   |
| 139| SPVNSSQPSY     | 1      | 1          | P05496                   |          | 1,02E7   | 0       | 0,007354 | 41       | 0,031226593 | 2   | 1193,58025 | 0,44    | 44,59   |
| 140| AFDLTEQRY      | 1      | 1          | Q86UE8                   |          | 2,89E6   | 0       | 0,01551  | 41       | 0,03008209  | 2   | 1142,54924 | 1,35    | 92,69   |
| 141| VLFEHAVGY      | 1      | 1          | O00567                   |          | 4,12E7   | 0       | 0,02315  | 41       | 0,042488455 | 2   | 1034,53362 | 2,92    | 99,24   |
| 142| EVYAGSHQY      | 1      | 1          | Q9H3P7                   |          | 5,65E7   | 0       | 0,01348  | 41       | 0,018649422 | 2   | 1053,46391 | 0,29    | 49,75   |
| 143| RQTGIVLNUR     | 1      | 1          | Q13435                   |          | 8,75E6   | 0       | 0,01653  | 40       | 0,019926272 | 2   | 1056,62663 | -0,63   | 44,43   |
| #   | Sequence  | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area  | q-Value | PEP       | IonScore  | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|-----------|--------|------------|--------------------------|-----------|-------|---------|----------|-----------|-----------|-----|---------|----------|----------|
| 144 | LLSPILARY | 1      | 1          | Q96JH7                   |           | 8,507E6 | 0       | 0,02899  | 40        | 0,007150436 | 2    | 1045,64299 | 2,40     | 112,36   |
| 145 | SIFDGRVVAK| 25     | 1          | Q9UM00                   |           | 3,098E8 | 0       | 0,02089  | 40        | 0,025069842 | 2    | 1091,62041 | -0,39    | 75,68    |
| 146 | GVLDTELRY | 1      | 1          | P18583                   |           | 1,543E7 | 0       | 0,02574  | 40        | 0,045717391 | 2    | 1065,55986 | 2,18     | 105,45   |
| 147 | YPVEIHEY  | 30     | 1          | Q13901                   |           | 6,595E7 | 0       | 0,01885  | 40        | 0,042735405 | 2    | 1049,49333 | -0,49    | 86,68    |
| 148 | VLYDRVLYK | 27     | 1          | Q9UH89                   |           | 6,729E7 | 0       | 0,0121   | 40        | 0,021859226 | 2    | 1168,67266 | 0,13     | 88,03    |
| 149 | NLAEDImRL | 29     | 1          | P08670                   | M7        | 3,312E5 | 0       | 0,007073 | 40        | 0,050495036 | 2    | 1090,55571 | -0,44    | 114,27   |
| 150 | AVIADTWHY | 36     | 1          | Q15800                   |           | 7,221E7 | 0       | 0,01348  | 39        | 0,046293828 | 2    | 1133,52971 | 3,07     | 102,44   |
| 151 | SPNAKEFVY | 1      | 1          | Q14106                   |           | 4,743E6 | 0       | 0,0286   | 39        | 0,05092105  | 2    | 1054,52275 | 2,21     | 74,04    |
| 152 | STVSRFKLY | 31     | 1          | Q969X6                   |           | 6,275E7 | 0       | 0,0267   | 39        | 0,062949608 | 2    | 1119,58599 | 2,35     | 118,67   |
| 153 | DPADIIHDF | 1      | 1          | Q9NQX7                   |           | 4,761E6 | 0       | 0,0162   | 39        | 0,037889772 | 2    | 1042,48772 | 3,52     | 131,97   |
| 154 | DPIERLVSY | 1      | 1          | Q7LGA3                   |           | 1,892E6 | 0       | 0,01837  | 39        | 0,0581567   | 2    | 1091,57598 | 2,55     | 112,03   |
| 155 | VVQGITLTIK | 1      | 1          | P13010                   |           | 4,898E6 | 0       | 0,01557  | 39        | 0,023898328 | 2    | 1186,70683 | 2,20     | 94,88    |
| 156 | DPEGSRITY | 2      | 1          | Q9Y530                   |           | 6,769E6 | 0       | 0,02166  | 39        | 0,04884619  | 2    | 1037,49004 | 0,18     | 65,72    |
| 157 | ALAYEVYR  | 3      | 1          | Q9H2K2                   |           | 2,032E7 | 0       | 0,01252  | 39        | 0,03700539  | 2    | 1097,60259 | 3,27     | 99,58    |
| 158 | FPRHIEPEL | 1      | 1          | P86790                   |           | 5,757E7 | 0       | 0,01933  | 38        | 0,038986811 | 2    | 1137,60735 | 1,91     | 79,42    |
| 159 | YPSRFGDGT | 1      | 1          | Q9H3H5                   |           | 3,676E6 | 0       | 0,02652  | 38        | 0,056740581 | 2    | 1287,63945 | 2,01     | 108,48   |
| 160 | KIADFGLAR | 2      | 14         | P07948;P11362;P21802;P22607;P22455;P09769;P20794;P51451;P06239;Q9UPZ9;P06241;P07947;Q8IZL9;P08631;P50750 | 3,113E7 | 0       | 0,01074  | 38        | 0,030571075 | 2    | 990,57543  | 2,30     | 77,40    |
| #   | Sequence     | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area     | q-Value | PEP    | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|--------------|--------|------------|--------------------------|-----------|----------|---------|--------|----------|------------|-----|----------|----------|---------|
| 161 | NPIDHVSFY    | 13     | 1          | Q9Y323                   |           | 6,697E7  | 0       | 0,01041| 38       | 0,061055908 | 2   | 1091,51567 | 0,01   | 107,47  |
| 162 | RQIPYTmmK    | 2      | 1          | Q00325                   |           | 2,550E7  | 0       | 0,02618| 38       | 0,066184118 | 2   | 1199,59392 | 2,28   | 41,05   |
| 163 | YYYEYPSRY    | 27     | 1          | Q14511                   |           | 4,054E7  | 0       | 0,01391| 38       | 0,051095523 | 2   | 1239,56792 | -0,12  | 83,63   |
| 164 | NPDDVFREF    | 1      | 1          | O75190                   |           | 8,903E6  | 0       | 0,01334| 37       | 0,048036046 | 2   | 1138,51970 | 2,88   | 117,63  |
| 165 | YPDRIMNTF    | 20     | 5          | Q13885;Q98VA1;P68371;P07437;Q13509 | 4,337E7 | 0       | 0,0162  | 37       | 0,053054664 | 2   | 1156,54485 | -0,65  | 104,56  |
| 166 | SLYDRPASY    | 1      | 1          | P16234                   |           | 2,346E7  | 0       | 0,008717| 37       | 0,059976111 | 2   | 1071,51323 | 2,48   | 73,34   |
| 167 | RIYGESADAVK  | 1      | 1          | P51114                   |           | 3,371E7  | 0       | 0,02813| 37       | 0,068269756 | 2   | 1208,62810 | 0,88   | 44,62   |
| 168 | KVADmALHY    | 7      | 1          | P50990                   |           | 7,125E7  | 0       | 0,02859| 37       | 0,089903234 | 2   | 1063,52715 | 2,83   | 54,13   |
| 169 | AVYGGFHKSK   | 1      | 1          | P00325                   |           | 3,757E7  | 0       | 0,02317| 37       | 0,077941463 | 2   | 956,52068 | 0,68   | 40,70   |
| 170 | ILELAGNAARDN | 1      | 14         | P04908;Q93077;P20671;Q96KK5;Q99878;P0C058;Q6F113;Q81UE6;Q16777;Q7L7L0;Q9BTM1;Q9P0M6;P16104;O75367 | 1,487E6 | 0       | 0,005699| 36       | 0,089012645 | 2   | 1256,66277 | 2,67   | 79,61   |
| 171 | TFMdHVLRY    | 4      | 1          | P53396                   |           | 2,134E7  | 0       | 0,01179| 36       | 0,069298746 | 2   | 1197,57585 | 3,10   | 77,13   |
| 172 | VPVSTINHAF   | 3      | 1          | O75410                   |           | 3,499E7  | 0       | 0,01314| 36       | 0,063201492 | 2   | 1084,58245 | 3,53   | 83,40   |
| 173 | VELDDLGKDEL  | 1      | 1          | Q15084                   |           | 5,624E6  | 0       | 0,01991| 36       | 0,089568347 | 2   | 1245,62493 | 3,18   | 113,03  |
| 174 | ALPSRILLWK   | 42     | 1          | Q98RK3                   |           | 7,094E8  | 0       | 0,01212| 36       | 0,009930018 | 2   | 1196,75127 | -0,15  | 104,80  |
| 175 | FSPSILKIQY   | 1      | 1          | Q15291                   |           | 2,193E6  | 0       | 0,01929| 36       | 0,048369603 | 2   | 1191,68083 | 3,00   | 117,69  |
| 176 | KWTDLALQY    | 20     | 1          | Q98S18                   |           | 4,733E7  | 0       | 0,02609| 36       | 0,102717159 | 2   | 1137,59392 | 0,00   | 123,21  |
| 177 | LPAGWILSHL   | 1      | 1          | P10176                   |           | 8,054E5  | 0       | 0,01048| 36       | 0,031325356 | 2   | 1106,63835 | 2,36   | 145,43  |
| #  | Sequence       | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area    | q-Value | PEP  | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM  [ppm] | RT  [min] |
|----|----------------|-------|------------|--------------------------|-----------|---------|---------|------|----------|------------|-----|----------|-----------|---------|
| 178| YVHDGRVSY     | 1     | 1          | O60234                   |           | 1,427E7 | 0       | 0,01072 | 36       | 0,07011458 | 2   | 1210,54961 | 0,71    | 49,43   |
| 179| RLPSPSQQR     | 1     | 1          | P02545                   |           | 1,174E8 | 0       | 0,00835 | 36       | 0,0850875  | 2   | 1128,61406 | 1,79    | 30,47   |
| 180| KPFQTTIL      | 9     | 1          | Q15417                   |           | 6,366E5 | 0       | 0,02051 | 36       | 0,105583562 | 2   | 1149,61528 | 0,19    | 108,09  |
| 181| KTLDQAKAVLK   | 1     | 1          | Q9H0A0                   |           | 1,726E6 | 0       | 0,02079 | 36       | 0,025683933 | 2   | 1214,74883 | 1,70    | 48,37   |
| 182| KVFGIPPPPY    | 9     | 2          | P40429;Q6NVV1            |           | 9,361E7 | 0       | 0,01271 | 36       | 0,118285218 | 2   | 1132,60796 | 3,70    | 107,88  |
| 183| KLFDAPLSISK   | 1     | 5          | Q9NQA3;C4AMC7;A8K023;Q6VEQ5;A8MWX3 | | 4,112E6 | 0       | 0,00587 | 35       | 0,05164459 | 2   | 1218,71135 | 1,67    | 98,23   |
| 184| YYIIPSKF      | 17    | 1          | Q9H054                   |           | 2,052E7 | 0       | 0,01219 | 35       | 0,10886775 | 2   | 1177,63298 | 3,19    | 135,72  |
| 185| SYQIKVHR      | 1     | 1          | Q14204                   |           | 1,892E6 | 0       | 0,01174 | 35       | 0,082301875 | 2   | 1129,64800 | 0,28    | 45,71   |
| 186| RLSYNTASNK    | 1     | 1          | P49207                   |           | 1,327E7 | 0       | 0,01089 | 35       | 0,120945642 | 2   | 1153,59587 | -0,15   | 29,97   |
| 187| AVYSHIQKL     | 1     | 1          | P20132                   |           | 1,442E7 | 0       | 0,02426 | 35       | 0,065922643 | 2   | 1157,67156 | 3,29    | 73,68   |
| 188| AYNASDLRY     | 1     | 1          | P20929                   |           | 6,166E6 | 0       | 0,01094 | 34       | 0,124954264 | 2   | 1258,58953 | 3,48    | 106,99  |
| 189| LPIPVDKVGY    | 1     | 1          | Q13615                   |           | 3,185E6 | 0       | 0,01689 | 34       | 0,117138743 | 2   | 1171,67510 | 2,48    | 110,97  |
| 190| TYAPVAFRY     | 1     | 3          | O60331;A2A3N6;Q99755     |           | 1,509E7 | 0       | 0,02124 | 34       | 0,198773986 | 2   | 1087,55950 | 2,17    | 98,64   |
| 191| APFQGDQRL     | 4     | 1          | Q00978                   |           | 3,776E7 | 0       | 0,01676 | 34       | 0,175535943 | 2   | 1118,56011 | 1,03    | 67,29   |
| 192| SFEQFLFY      | 2     | 1          | P16885                   |           | 9,649E6 | 0       | 0,005867| 34       | 0,149673556 | 2   | 1217,56706 | 3,66    | 139,67  |
| 193| YPFHKQPPTY    | 2     | 1          | Q98U23                   |           | 1,598E7 | 0       | 0,005553| 33       | 0,237225869 | 2   | 1277,63494 | 2,81    | 60,60   |
| 194| VLYNGFTGR     | 1     | 1          | P30876                   |           | 3,050E6 | 0       | 0,02471 | 33       | 0,101194498 | 2   | 1026,53838 | 1,59    | 79,76   |
| 195| NFDKLSLY     | 2     | 1          | P53621                   |           | 6,972E6 | 0       | 0,01641 | 33       | 0,212938787 | 2   | 1146,58708 | 3,54    | 132,41  |
| #   | Sequence     | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area    | q-Value | PEP  | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|--------------|--------|------------|--------------------------|-----------|---------|---------|------|----------|------------|-----|---------|----------|---------|
| 196 | IPDPKFITY    | 15     | 1          | Q8N7H5                   |           | 5,652E7 | 0       | 0,02085 | 33       | 0,191398254 | 2   | 1240,66631 | 4,05    | 134,55  |
| 197 | IPIYADKDV    | 1      | 1          | Q15181                   |           | 3,655E6 | 0       | 0,02755 | 33       | 0,191522904 | 2   | 1180,62688 | 1,67    | 111,39  |
| 198 | KVLDKIVHY    | 1      | 2          | Q2NKO1;Q75897            |           | 1,017E7 | 0       | 0,02058 | 32       | 0,128171203 | 2   | 1114,66191 | -0,03   | 68,38   |
| 199 | RTYLPQVSR    | 1      | 1          | P35606                   |           | 1,214E7 | 0       | 0,01861 | 32       | 0,185857085 | 2   | 1206,66460 | 4,66    | 55,41   |
| 200 | VPESSLAGHSF  | 1      | 1          | P5S854                   |           | 2,297E7 | 0       | 0,01183 | 32       | 0,228972554 | 2   | 1130,54949 | 1,57    | 78,39   |
| 201 | FPDPAGKLNQF  | 1      | 2          | Q98T22;Q6GMV1            |           | 7,883E6 | 0       | 0,02564 | 32       | 0,279750886 | 2   | 1233,62895 | 2,14    | 108,01  |
| 202 | KVHAYIISY    | 1      | 1          | Q9H223                   |           | 8,874E6 | 0       | 0,02653 | 31       | 0,109536107 | 2   | 1093,60576 | 1,54    | 78,36   |
| 203 | SFVWHALDY    | 1      | 1          | P49792                   |           | 1,459E7 | 0       | 0,02038 | 31       | 0,312589564 | 2   | 1137,53972 | 2,92    | 123,71  |
| 204 | mPRVQTQYY    | 1      | 1          | O94979                   | M1        | 1,211E6 | 0       | 0,02783 | 31       | 0,268295697 | 2   | 1166,56255 | 0,21    | 45,70   |
| 205 | RWNPLPSY     | 21     | 1          | Q9UPW6                   |           | 4,813E7 | 0       | 0,0203  | 31       | 0,487737076 | 2   | 1145,61040 | 0,14    | 124,14  |
| 206 | VPTDEARAF    | 1      | 2          | P62491;Q15907            |           | 2,300E5 | 0       | 0,01999 | 30       | 0,435712077 | 2   | 1005,49834 | -1,69   | 68,40   |
| 207 | YFVTGNHEY    | 6      | 1          | Q6ZT21                   |           | 1,821E7 | 0       | 0,01989 | 30       | 0,189415877 | 2   | 1129,49748 | 2,28    | 73,60   |
| 208 | SFAARSFYY    | 14     | 1          | P49327                   |           | 2,267E5 | 0       | 0,01713 | 30       | 0,244407311 | 2   | 1111,52056 | -0,17   | 93,88   |
| 209 | LPQHQVPAY    | 1      | 1          | P17535                   |           | 1,079E8 | 0       | 0,02554 | 30       | 0,326283684 | 2   | 1052,55156 | -0,78   | 64,54   |
| 210 | APSLHLNTL    | 1      | 1          | Q96Q81                   |           | 1,304E7 | 0       | 0,02853 | 30       | 0,239164958 | 2   | 1112,61272 | 2,52    | 122,18  |
| 211 | FFPSYDVKY    | 8      | 1          | Q9UFF9                   |           | 6,921E6 | 0       | 0,02259 | 30       | 0,447088018 | 2   | 1278,64055 | 0,02    | 137,44  |
| 212 | YSIITPNILR   | 1      | 1          | P01024                   |           | 2,979E6 | 0       | 0,01669 | 29       | 0,202138498 | 2   | 1189,69731 | 2,81    | 118,12  |
| 213 | FPASFPNRQY   | 11     | 1          | Q8TCT9                   |           | 4,412E7 | 0       | 0,02402 | 29       | 0,411411895 | 2   | 1226,59758 | 1,84    | 89,08   |
| #   | Sequence   | # PSMs | # Proteins | Protein Group Accessions | Area (ox) | q-Value | PEP     | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|------------|--------|------------|--------------------------|-----------|---------|---------|----------|-----------|-----|----------|----------|----------|
| 214 | RLFNAIHR   | 1      | 1          | Q15149                   | 2,958E6   | 0       | 0,02424 | 29       | 0,131336786 | 2   | 1139,68401 | 3,80     | 69,27    |
| 215 | IPYHSEVPVS | 19     | 1          | Q01082                   | 3,817E8   | 0       | 0,01374 | 29       | 0,455760887 | 2   | 1240,65752 | 0,22     | 107,18   |
| 216 | KLIGEYGLRNK| 1      | 1          | P46781                   | 5,265E6   | 0       | 0,01292 | 29       | 0,173225211 | 2   | 1290,75701 | 3,18     | 54,54    |
| 217 | YLNEKAFSY  | 1      | 1          | O60641                   | 6,640E6   | 0       | 0,02777 | 28       | 0,696644816 | 2   | 1134,54766 | 0,91     | 88,92    |
| 218 | APFHQLRISY | 1      | 1          | O60264                   | 4,039E6   | 0       | 0,01358 | 28       | 0,544315001 | 2   | 1231,66142 | 2,58     | 85,31    |
| 219 | YPFKPPKVAF | 1      | 3          | P62837;P61077;Q9Y2X8     | 8,120E7   | 0       | 0,01548 | 27       | 0,363806029 | 2   | 1193,67546 | 3,08     | 99,12    |
| 220 | LPYNQHQHLY | 1      | 1          | Q9Y5Q0                   | 1,875E7   | 0       | 0,01551 | 27       | 0,811488986 | 2   | 1175,58647 | 1,77     | 78,99    |
| 221 | YYVYPYKLKY | 1      | 1          | Q982Z9                   | 3,808E7   | 0       | 0,01146 | 27       | 0,588791578 | 2   | 1236,66948 | 2,56     | 83,81    |
| 222 | RFDHVITNm  | 2      | 1          | P02746                   | 1,137E7   | 0       | 0,01788 | 27       | 0,780769964 | 2   | 1148,55559 | 3,34     | 60,02    |
| 223 | FAVDLEHHSY | 1      | 1          | Q01780                   | 6,471E6   | 0       | 0,01914 | 26       | 0,717340546 | 2   | 1217,56023 | 1,34     | 85,35    |
| 233 | IPIELRYVY  | 5      | 1          | P49588                   | 1,242E7   | 0       | 0,00724 | 26       | 0,459335087 | 2   | 1266,71294 | 2,89     | 116,44   |
| 225 | MPAVKAIYQY | 1      | 1          | P37268                   | 6,500E6   | 0       | 0,02432 | 26       | 0,893462026 | 2   | 1296,70439 | 1,77     | 112,31   |
| 226 | FYSEVPHQY  | 5      | 1          | Q98RR6                   | 3,146E7   | 0       | 0,02666 | 26       | 0,655101578 | 2   | 1178,52715 | 0,51     | 64,07    |
| 227 | RQIPYTMMK  | 1      | 1          | Q00325                   | 5,336E6   | 0       | 0,01725 | 25       | 1,682820378 | 2   | 1167,60613 | 4,09     | 63,82    |
| 228 | RQYENFINR  | 1      | 1          | O60437                   | 3,436E6   | 0       | 0,01165 | 25       | 1,30598054  | 2   | 1239,62847 | 4,46     | 59,34    |
| 229 | YYSNKAYQY  | 1      | 1          | Q6P9H5                   | 3,679E7   | 0       | 0,01699 | 25       | 0,815266813 | 2   | 1199,53911 | 1,97     | 59,92    |
| 230 | TPLSQAIHQY | 1      | 1          | Q9NQS7                   | 7,076E6   | 0       | 0,01135 | 24       | 1,253531607 | 2   | 1270,68218 | 2,47     | 98,70    |
| 231 | VVYSGLENIKK| 1      | 1          | Q9H8L8                   | 5,186E6   | 0       | 0,009705 | 24      | 0,848896004  | 2   | 1249,71623 | 0,90     | 67,33    |
| #   | Sequence          | PSMs | Proteins | Protein Group Accessions | Mod. (ox) | Area     | q-Value | PEP     | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|-------------------|------|----------|--------------------------|-----------|----------|---------|---------|----------|------------|-----|----------|----------|---------|
| 232 | KLIKDGILIIRK      | 2    | 1        | P84098                   |           | 3,958E7  | 0       | 0,01687 | 23       | 0,015706089 | 2   | 1296,87639 | 2,89     | 56,96   |
| 233 | YPDRimNTF        | 11   | 5        | Q13885;Q987VA1;P68371;P07437;Q13509 | M6        | 8,527E7  | 0       | 0,02364 | 23       | 1,842428776 | 2   | 1172,54228 | 1,51     | 85,71   |
| 234 | LPDEIYHVIY       | 2    | 1        | Q987V86                  |           | 2,257E7  | 0       | 0,01657 | 23       | 2,373228755 | 2   | 1148,56584 | 3,11     | 106,97  |
| 235 | YFELVQHEY        | 1    | 1        | P21580                   |           | 4,817E6  | 0       | 0,01143 | 22       | 2,155694913 | 2   | 1227,57182 | 3,05     | 105,10  |
| 236 | EAFREHQQY        | 1    | 1        | Q96788                   |           | 3,111E7  | 0       | 0,02638 | 21       | 2,502083317 | 2   | 1207,55034 | 1,03     | 40,95   |
| 237 | VYDLLKTNL        | 1    | 1        | Q99460                   |           | 5,565E6  | 0,001   | 0,03446 | 52       | 0,001202743 | 2   | 1078,61846 | 3,83     | 113,15  |
| 238 | VPWSNNGY         | 16   | 2        | Q8NHW5;P05388            |           | 6,221E5  | 0,001   | 0,03406 | 51       | 0,003034349 | 2   | 999,52501 | -0,82    | 80,21   |
| 239 | KTLDHVLTTH       | 1    | 1        | Q987TW9                  |           | 9,545E6  | 0,001   | 0,03648 | 51       | 0,002680802 | 2   | 1063,58989 | 0,37     | 42,62   |
| 240 | KGDFGGLTK        | 3    | 2        | P60674;P23458            |           | 3,521E5  | 0,001   | 0,03591 | 51       | 0,002047457 | 2   | 978,56145 | -0,47    | 70,69   |
| 241 | AVAVALDRAARR     | 1    | 1        | Q14697                   |           | 3,428E6  | 0,001   | 0,03909 | 50       | 0,001681852 | 2   | 884,54436 | 2,08     | 28,87   |
| 242 | GLASFKSFLK       | 3    | 1        | Q15539                   |           | 5,876E7  | 0,001   | 0,02945 | 49       | 0,002287782 | 2   | 1097,63786 | 2,24     | 97,20   |
| 243 | KVAVATPAK        | 1    | 1        | P19338                   |           | 4,508E6  | 0,001   | 0,03087 | 48       | 0,002053328 | 2   | 884,55528 | -1,30    | 29,44   |
| 244 | STNNWVLK         | 1    | 1        | Q14617                   |           | 6,576E6  | 0,001   | 0,04381 | 47       | 0,006628142 | 2   | 1074,59636 | 1,95     | 96,18   |
| 245 | APPPPPAHAL       | 2    | 1        | Q967R1                   |           | 1,203E9  | 0,001   | 0,03952 | 47       | 0,00255727 | 2   | 870,48375 | 0,56     | 51,74   |
| 246 | VFDEAIRAV        | 7    | 3        | P63000;P15153;P60763     |           | 1,016E5  | 0,001   | 0,03314 | 47       | 0,009201701 | 2   | 1019,55150 | -0,57    | 104,03  |
| 247 | LPDTLKVTY        | 24   | 1        | P05107                   |           | 8,663E7  | 0,001   | 0,04315 | 44       | 0,008910269 | 2   | 1049,58745 | -0,31    | 102,19  |
| 248 | YPVDLQDFK        | 1    | 1        | P52434                   |           | 1,207E7  | 0,001   | 0,03676 | 44       | 0,014925366 | 2   | 1053,52837 | 3,02     | 105,06  |
| 249 | SVNKLKVSPK       | 1    | 1        | O75475                   |           | 7,953E6  | 0,001   | 0,04293 | 44       | 0,009642509 | 2   | 971,58806 | -0,40    | 44,93   |
| #  | Sequence       | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area    | q-Value | PEP   | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|----|----------------|--------|------------|--------------------------|-----------|---------|---------|-------|----------|------------|-----|----------|----------|---------|
| 250| NAIHAILLY      | 2      | 1          | P50416                   |           | 1,230E7 | 0,001   | 0,03796| 44       | 0,010684719 | 2   | 1027,59282 | -0,68    | 115,86  |
| 251| NAAKVFNLY     | 1      | 1          | Q16555                   |           | 2,926E7 | 0,001   | 0,03247| 43       | 0,013936875 | 2   | 1039,55925 | 2,03     | 96,48   |
| 252| KIGEVSSPK     | 1      | 1          | P35251                   |           | 1,659E7 | 0,001   | 0,04276| 43       | 0,022422799 | 2   | 944,54137 | 0,21     | 32,07   |
| 253| SIIIDVYHKY     | 1      | 1          | P05109                   |           | 7,602E6 | 0,001   | 0,02921| 42       | 0,031334174 | 2   | 1137,59551 | 1,41     | 84,91   |
| 254| VFDKTLAEL     | 1      | 1          | Q6VMQ6                   |           | 4,335E7 | 0,001   | 0,0398  | 42       | 0,016101296 | 2   | 1035,57390 | 1,70     | 107,62  |
| 255| AVmGAYVLLK    | 2      | 1          | Q98Y50                   | M3        | 5,271E6 | 0,001   | 0,03823| 42       | 0,011600163 | 2   | 1080,61162 | -0,57    | 92,04   |
| 256| VIKKAALVQQ     | 1      | 1          | Q99715                   |           | 9,581E4 | 0,001   | 0,03374| 42       | 0,00346448  | 2   | 1097,70342 | -0,68    | 97,94   |
| 257| GLLDVGLRY     | 2      | 1          | Q4AC94                   |           | 1,405E7 | 0,001   | 0,03195| 42       | 0,020779396 | 2   | 1005,57555 | 2,73     | 125,94  |
| 258| KPSLPFTSL     | 6      | 1          | P31785                   |           | 9,883E7 | 0,001   | 0,04251| 41       | 0,027360559 | 2   | 989,56633  | -0,32    | 112,49  |
| 259| TPYGGQFERm     | 1      | 1          | Q9NR30                   | M10       | 3,773E6 | 0,001   | 0,03331| 41       | 0,018820914 | 2   | 1201,53459 | 3,25     | 63,25   |
| 260| SLGVAALYK      | 1      | 1          | P09669                   |           | 9,610E6 | 0,001   | 0,03818| 41       | 0,014073547 | 2   | 921,54277  | 2,54     | 88,05   |
| 261| SPMSADRVVAF    | 2      | 2          | P10589;P24468            |           | 1,030E7 | 0,001   | 0,03299| 40       | 0,04380575  | 2   | 1179,58586 | 2,65     | 98,13   |
| 262| RPAPVEVTY     | 43     | 1          | Q93096                   |           | 6,234E8 | 0,001   | 0,04174| 40       | 0,051912263 | 2   | 1031,55156 | -0,48    | 70,96   |
| 263| ALYGVVNVK     | 1      | 1          | Q94952                   |           | 1,292E7 | 0,001   | 0,03005| 40       | 0,022283322 | 2   | 962,56822  | 1,29     | 84,17   |
| 264| ALKNPPINTK    | 6      | 1          | O15511                   |           | 8,171E7 | 0,001   | 0,04242| 39       | 0,014624623 | 2   | 1095,65203 | -0,09    | 39,74   |
| 265| IPIAGRDITY     | 1      | 3          | Q9P1U1;Q9C0K3;P61158     |           | 2,251E7 | 0,001   | 0,03711| 38       | 0,055606503 | 2   | 1118,62236 | 1,68     | 97,26   |
| 266| AVNAHSNILK    | 6      | 1          | Q16891                   |           | 5,693E7 | 0,001   | 0,03976| 38       | 0,036270272 | 2   | 1066,59966 | -0,71    | 38,96   |
| 267| VLAALRLQY     | 1      | 1          | Q9HD67                   |           | 5,762E4 | 0,001   | 0,03855| 37       | 0,020938857 | 2   | 1046,63506 | -0,64    | 111,87  |
|   | Sequence   | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area    | q-Value | PEP     | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|---|------------|--------|------------|--------------------------|-----------|---------|---------|---------|----------|-----------|-----|----------|----------|---------|
| 268| SVMRLTISY  | 10     | 1          | Q16665                   |           | 4,613E5 | 0,001  | 0,04377 | 37       | 0,060524282 | 2   | 1069,57060 | -0,45   | 106,48  |
| 269| LPQGIVREL  | 10     | 1          | P63272                   |           | 6,906E7 | 0,001  | 0,03158 | 37       | 0,022722128 | 2   | 1024,61785 | 2,77    | 96,24   |
| 270| RAYPHVFTK  | 1      | 1          | O14949                   |           | 5,811E6 | 0,001  | 0,03262 | 36       | 0,083618525 | 2   | 1118,61125 | 0,61    | 44,62   |
| 271| TSDFKFYKY  | 1      | 1          | P45985                   |           | 9,712E6 | 0,001  | 0,04366 | 36       | 0,085394087 | 2   | 1198,58049 | 2,14    | 84,99   |
| 272| RSADLTGLEK | 1      | 1          | Q13751                   |           | 2,151E6 | 0,001  | 0,03947 | 36       | 0,124508541 | 2   | 1089,59209 | 1,99    | 51,59   |
| 273| KIZEHVRSK  | 1      | 1          | O15205                   |           | 2,794E6 | 0,001  | 0,0304  | 36       | 0,015033133 | 2   | 1124,68938 | -0,46   | 18,19   |
| 274| KNLSSVRQVK | 1      | 1          | Q9UBE8                   |           | 1,507E5 | 0,001  | 0,0397  | 35       | 0,032815579 | 2   | 1158,69902 | 3,14    | 59,10   |
| 275| VPVWIIHYY  | 1      | 1          | O95139                   |           | 2,795E6 | 0,001  | 0,04286 | 35       | 0,106676396 | 2   | 1189,64324 | 2,33    | 134,58  |
| 276| MTHNLLNY   | 10     | 2          | Q92769;Q13547            |           | 2,588E5 | 0,001  | 0,03841 | 35       | 0,132655477 | 2   | 1118,56609 | -0,21   | 103,52  |
| 277| SWIQNVDKYL | 1      | 1          | P04114                   |           | 1,644E7 | 0,001  | 0,03992 | 35       | 0,125746105 | 2   | 1253,61858 | 1,97    | 97,64   |
| 278| SPEPGQRTF  | 1      | 1          | O14867                   |           | 9,168E6 | 0,001  | 0,02959 | 35       | 0,129753835 | 2   | 1018,49578 | 0,48    | 50,52   |
| 279| AIQNPTmINK | 2      | 1          | Q02086                   | M7        | 1,371E7 | 0,001  | 0,03822 | 35       | 0,160328746 | 2   | 1145,60295 | 3,99    | 55,14   |
| 280| KVAENVIRQK | 1      | 1          | Q6ZSC3                   |           | 6,155E6 | 0,001  | 0,03541 | 34       | 0,050429061 | 2   | 1184,71221 | 0,98    | 30,13   |
| 281| HPLYPFNDPY | 16     | 1          | P14550                   |           | 2,339E7 | 0,001  | 0,03894 | 34       | 0,112814089 | 2   | 1262,58391 | -0,13   | 113,20  |
| 282| RVFVGVGmTK | 3      | 1          | P22307                   | M9        | 6,331E6 | 0,001  | 0,03146 | 34       | 0,059114494 | 2   | 1208,68242 | 0,29    | 68,02   |
| 283| YVANEFLKY  | 6      | 1          | Q14314                   |           | 2,763E7 | 0,001  | 0,03585 | 34       | 0,164155225 | 2   | 1146,58672 | 3,23    | 104,41  |
| 284| SVYSGIRHK  | 1      | 1          | Q14642                   |           | 8,551E6 | 0,001  | 0,03425 | 34       | 0,139103092 | 2   | 1046,57634 | 2,06    | 28,93   |
| 285| LPAKDIQTNVY| 3      | 1          | P48556                   |           | 1,208E8 | 0,001  | 0,03277 | 34       | 0,163744746 | 2   | 1261,68169 | 2,35    | 77,64   |
| #  | Sequence      | PSMs | Proteins | Protein Group Accessions | Mod. (ox) | Area | q-Value | PEP  | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|----|---------------|------|----------|--------------------------|----------|------|---------|------|----------|------------|-----|----------|----------|---------|
| 286| YPFKPPKVTF    | 4    | 3        | Q96974;P51965;Q96LR5     |          | 3,085E8 | 0,001   | 0,02904 | 34       | 0,090006128 | 2   | 1223,68559 | 2,65     | 99,61   |
| 287| FPEHIFFPAL    | 1    | 1        | P61160                   |          | 0,00000 | 0,001   | 0,04136 | 33       | 0,157158191 | 2   | 1070,56999 | 2,80     | 133,78  |
| 288| FPFEKGSVQY    | 3    | 1        | P35659                   |          | 5,689E7 | 0,001   | 0,02996 | 33       | 0,190413151 | 2   | 1201,59294 | 3,41     | 99,22   |
| 289| RQTATQQLK     | 1    | 1        | P62424                   |          | 2,079E7 | 0,001   | 0,03672 | 33       | 0,112606448 | 2   | 1058,63213 | 0,39     | 41,09   |
| 290| HISNPNAIFK    | 1    | 1        | P48436                   |          | 4,282E6 | 0,001   | 0,03476 | 32       | 0,139688372 | 2   | 1026,57329 | 0,15     | 69,92   |
| 291| RIHGSPLQK     | 1    | 1        | O00566                   |          | 1,068E7 | 0,001   | 0,03331 | 32       | 0,08694361  | 2   | 1035,60625 | 0,40     | 28,31   |
| 292| IPQFIVDY      | 2    | 1        | P55774                   |          | 1,707E7 | 0,001   | 0,04132 | 32       | 0,192847563 | 2   | 1122,62261 | 2,85     | 103,02  |
| 293| KFYNGLLFY     | 1    | 1        | Q2M389                   |          | 1,607E5 | 0,001   | 0,03816 | 32       | 0,288663385 | 2   | 1164,60918 | 0,30     | 132,86  |
| 294| IQNDRQLQY     | 1    | 1        | Q9UB89                   |          | 5,532E7 | 0,001   | 0,04185 | 32       | 0,283655881 | 2   | 1177,59892 | 2,45     | 58,85   |
| 295| LSQNRAEF      | 1    | 1        | P48556                   |          | 4,070E6 | 0,001   | 0,03737 | 32       | 0,293138169 | 2   | 1063,55559 | 2,31     | 66,57   |
| 296| VVYTHSLQLK    | 1    | 7        | P0DJ0D;P49792;P0DJ1A6NKT7 Q7Z23J3;Q99666;O14715 |          | 5,611E6 | 0,001   | 0,04094 | 31       | 0,218765017 | 2   | 1187,67815 | -0,14    | 65,88   |
| 297| FPYGDASKF     | 1    | 5        | P61601;P37235;P62760;P84074; Q9UM19 |          | 8,176E6 | 0,001   | 0,03591 | 31       | 0,222107034 | 2   | 1031,48454 | 1,20     | 93,55   |
| 298| SLHLGALY      | 11   | 1        | O00767                   |          | 4,640E7 | 0,001   | 0,03025 | 31       | 0,229909111 | 2   | 986,56975 | 2,82     | 123,98  |
| 299| ASFDKAKLKL    | 1    | 1        | P63313                   |          | 2,135E7 | 0,001   | 0,0418  | 31       | 0,143028471 | 2   | 1007,58867 | 0,21     | 33,32   |
| 300| TPEEKIREY     | 1    | 1        | Q14103                   |          | 1,526E7 | 0,001   | 0,03576 | 30       | 0,414407173 | 2   | 1164,59099 | 1,22     | 49,22   |
| 301| KVTESFVYK     | 3    | 1        | P50395                   |          | 4,554E7 | 0,001   | 0,03561 | 30       | 0,322492676 | 2   | 1157,62444 | 3,71     | 55,32   |
| 302| SVLDSFLKCY    | 2    | 1        | Q96J7                    |          | 3,129E7 | 0,001   | 0,0299  | 30       | 0,321919233 | 2   | 1071,57536 | 3,03     | 139,76  |
| 303| YAIANNPLHY    | 14   | 1        | ASYKK6                   |          | 3,052E7 | 0,001   | 0,04353 | 30       | 0,402853429 | 2   | 1105,53105 | -0,22    | 109,45  |
| #  | Sequence                   | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area  | q-Value | PEP  | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|----|---------------------------|-------|-----------|--------------------------|-----------|-------|---------|------|----------|------------|-----|---------|----------|--------|
| 304| KTQDYVVGF                 | 1     | 1         | O14530                   |           | 3,805E6 | 0,001   | 0,03125 | 30       | 0,26744782 | 2   | 1056,53777 | 1,61    | 93,90  |
| 305| NFTEVHPDY                 | 8     | 1         | P04040                   |           | 4,020E7 | 0,001   | 0,04228 | 30       | 0,280601581 | 2   | 1121,49211 | 2,03    | 79,34  |
| 306| KTKEAVLLLK                | 1     | 1         | P36578                   |           | 2,825E6 | 0,001   | 0,03828 | 29       | 0,025648868 | 2   | 1142,75273 | 1,71    | 51,95  |
| 307| YPDLIHIY                  | 1     | 2         | Q9H930;P23497            |           | 2,065E6 | 0,001   | 0,03143 | 29       | 0,615390116 | 2   | 1033,53789 | 2,48    | 126,91 |
| 308| LPLEEAYRF                 | 1     | 1         | Q9H223                   |           | 8,051E6 | 0,001   | 0,03919 | 29       | 0,459921373 | 2   | 1137,59697 | 2,67    | 113,31 |
| 309| ALYETPTGWK                | 1     | 1         | P36871                   |           | 3,931E6 | 0,001   | 0,03643 | 29       | 0,555639835 | 2   | 1165,59197 | 2,68    | 90,71  |
| 310| HPRIITEGF                 | 1     | 1         | P40227                   |           | 5,329E7 | 0,001   | 0,04364 | 28       | 0,28190914  | 2   | 1069,58086 | 1,78    | 74,07  |
| 311| MAVDDFNLY                 | 1     | 1         | Q9C075                   |           | 7,874E6 | 0,001   | 0,03477 | 28       | 0,485611274 | 2   | 1215,57427 | 2,28    | 115,24 |
| 312| RPVPKGATY                 | 1     | 1         | P61313                   |           | 1,134E7 | 0,001   | 0,03637 | 28       | 0,412275901 | 2   | 988,55840  | 0,93    | 32,83  |
| 313| IPVNEKDTLY                | 1     | 1         | O75446                   |           | 8,063E6 | 0,001   | 0,03807 | 27       | 0,736658151 | 2   | 1292,67656 | 2,52    | 83,64  |
| 314| RPSLPLPHF                 | 1     | 1         | Q98V38                   |           | 1,579E7 | 0,001   | 0,04251 | 27       | 0,241955924 | 2   | 1063,60613 | 1,27    | 101,03 |
| 315| FPPYHVQGTF                | 4     | 1         | P16989                   |           | 1,452E6 | 0,001   | 0,03847 | 27       | 0,996366343 | 2   | 1192,58196 | 2,81    | 103,88 |
| 316| RLLPGNATISK               | 2     | 1         | Q460N5                   |           | 5,161E7 | 0,001   | 0,03165 | 27       | 0,288883199 | 2   | 1169,70232 | 1,86    | 61,28  |
| 317| KLYLPVQNK                 | 1     | 1         | Q9Y6A4                   |           | 5,633E6 | 0,001   | 0,03277 | 27       | 0,326837576 | 2   | 1102,66252 | 0,53    | 64,02  |
| 318| ALDTKIGRY                 | 1     | 1         | O60264                   |           | 4,064E6 | 0,001   | 0,04265 | 27       | 0,392953496 | 2   | 1164,67412 | 0,46    | 45,80  |
| 319| LPYNHQHEY                 | 12    | 1         | O95864                   |           | 1,682E8 | 0,001   | 0,03012 | 27       | 0,55193668  | 2   | 1200,54509 | 1,53    | 43,49  |
| 320| SPLPTAEKPPL               | 1     | 1         | Q16665                   |           | 7,100E6 | 0,001   | 0,04238 | 26       | 0,410518198 | 2   | 1250,70281 | 2,93    | 89,63  |
| 321| AIDSVHQLHY                | 1     | 1         | Q5VT25                   |           | 5,173E6 | 0,001   | 0,03733 | 26       | 0,764907553 | 2   | 1182,59258 | 1,99    | 68,17  |
| #  | Sequence       | PSMs | Proteins | Protein Group Accessions | Mod. (ox) | Area | q-Value | PEP   | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|----|----------------|------|----------|--------------------------|-----------|------|---------|-------|----------|------------|-----|----------|----------|----------|
| 322| LTTMGDRFTDE    | 5    | 3        | P19105;O14950;P24844     | 1,129E5   | 0,001| 0,03557 | 26    | 0,529946966 | 1285,57268 | 1285,57268 | 0,22    | 84,13    |
| 323| SVYDSVLQK      | 1    | 1        | Q8NF91                   | 2,498E7   | 0,001| 0,03056 | 26    | 0,780149096 | 1038,54802 | 1038,54802 | 1,34    | 81,65    |
| 324| LPFPFIGDRVT    | 3    | 1        | Q6H8Q1                   | 4,090E6   | 0,001| 0,03408 | 26    | 1,149104555 | 1245,66741 | 1245,66741 | 3,78    | 123,29   |
| 325| RTAVHLRY       | 2    | 1        | Q9UKV5                   | 3,285E7   | 0,001| 0,04213 | 26    | 0,665239401 | 1128,66460 | 1128,66460 | 0,82    | 49,21    |
| 326| SFIDVDDERWHY    | 1    | 1        | O14929                   | 1,748E7   | 0,001| 0,03913 | 25    | 0,70273335  | 1581,70017 | 1581,70017 | 2,07    | 116,16   |
| 327| LPIENNTK       | 1    | 1        | O00186                   | 2,575E6   | 0,001| 0,04033 | 25    | 1,377926824 | 1255,62602 | 1255,62602 | 4,38    | 87,48    |
| 328| FGRRPFDTF      | 1    | 1        | P25685                   | 7,455E6   | 0,001| 0,03878 | 25    | 0,818853749 | 1157,53679 | 1157,53679 | -0,61   | 113,62   |
| 329| RPPYTPNQL      | 1    | 1        | Q13310                   | 2,839E6   | 0,001| 0,03221 | 24    | 1,045581756 | 1219,67986 | 1219,67986 | 0,38    | 67,81    |
| 330| RLYPPTAR       | 1    | 1        | P49841                   | 2,839E6   | 0,001| 0,03221 | 24    | 1,365276701 | 1248,64031 | 1248,64031 | 2,51    | 82,79    |
| 331| KLGGVIKEK      | 1    | 1        | Q9Y2X3                   | 1,775E7   | 0,001| 0,03548 | 24    | 0,329621937 | 971,62462  | 971,62462  | -0,24   | 30,13    |
| 332| YLLPHILVY      | 11   | 1        | Q13535                   | 1,066E7   | 0,001| 0,03016 | 24    | 0,826284528 | 1130,66081 | 1130,66081 | -0,04   | 144,49   |
| 333| TPYPAILHEY     | 1    | 1        | Q9P2H3                   | 6,138E6   | 0,001| 0,04016 | 24    | 1,920807075 | 1203,60820 | 1203,60820 | 3,10    | 105,43   |
| 334| KTYHALSNLPK    | 1    | 1        | O00231                   | 2,016E6   | 0,001| 0,04255 | 23    | 1,62925834  | 1271,71221 | 1271,71221 | 1,20    | 45,98    |
| 335| LHLGYPNLQ     | 9     | 1        | Q92499                   | 3,982E7   | 0,001| 0,0313  | 23    | 1,251850787 | 1167,65239 | 1167,65239 | 0,25    | 120,05   |
| 336| LPEEHARFY      | 1     | 2        | Q05513;P41743            | 2,391E6   | 0,001| 0,03175 | 23    | 2,067840932 | 1161,57207 | 1161,57207 | 2,84    | 68,88    |
| 337| YPFDPGPNTLAH   | 1    | 1        | P09237                   | 5,898E6   | 0,001| 0,03604 | 21    | 1,956176473 | 1288,59831 | 1288,59831 | 2,01    | 96,12    |
| 338| KYFDEHYE       | 5     | 1        | P33552                   | 5,629E7   | 0,001| 0,03619 | 20    | 1,412222504 | 1293,54228 | 1293,54228 | 0,03    | 75,99    |
| 339| VVYQQWNTK      | 1    | 1        | Q8N766                   | 3,824E6   | 0,001| 0,03529 | 19    | 5,538911648 | 1200,60674 | 1200,60674 | 1,61    | 84,91    |
| # | Sequence     | # PSMs | # Proteins | Protein Group Accessions  | Mod. (ox) | Area     | q-Value | PEP    | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|---|--------------|--------|------------|---------------------------|-----------|----------|---------|--------|----------|------------|-----|----------|----------|---------|
| 340 | RVGDVYIPR    | 1      | 2          | Q9BRL6;Q01130             |           | 4,780E6  | 0,001   | 0,032  | 19       | 3,625350627 | 2   | 1074,60552 | 0,01    | 67,43   |
| 341 | FPAGIYDTKY   | 2      | 1          | Q96GM8                    |           | 4,195E6  | 0,001   | 0,03726 | 19       | 5,053834761 | 2   | 1174,58171 | 3,22    | 98,62   |
| 342 | RLIQEQLRY    | 1      | 2          | Q9Y2J4;Q8IY63             |           | 9,856E6  | 0,001   | 0,03446 | 17       | 3,569683192 | 2   | 1218,69853 | 2,60    | 75,75   |
| 343 | VYIVLDKAey   | 1      | 1          | Q43913                    |           | 2,031E6  | 0,001   | 0,03577 | 15       | 10,504999673 | 2   | 1212,65349 | 1,97    | 105,50  |
| 344 | YIYPKHLKY    | 1      | 1          | Q96BY6                    |           | 1,441E7  | 0,001   | 0,03448 | 14       | 8,327766102 | 2   | 1224,68010 | 2,07    | 58,31   |
| 345 | IVAGTTLNK    | 1      | 1          | Q75251                    |           | 3,878E7  | 0,002   | 0,05288 | 51       | 0,002451959 | 2   | 916,54686 | 0,67    | 50,56   |
| 346 | KAYHNSPAY    | 1      | 1          | Q969G3                    |           | 3,228E6  | 0,002   | 0,04452 | 49       | 0,004931102 | 2   | 1050,49980 | -0,50   | 29,11   |
| 347 | KPVDPIVGY    | 10     | 1          | Q99715                    |           | 4,556E7  | 0,002   | 0,04634 | 48       | 0,003275346 | 2   | 987,55235 | 1,37    | 83,79   |
| 348 | KLYIDIVAK    | 2      | 1          | P62750                    |           | 2,062E7  | 0,002   | 0,05682 | 48       | 0,004046751 | 2   | 1064,59819 | -0,46   | 71,52   |
| 349 | QTYGHFPSR    | 1      | 1          | O00482                    |           | 4,279E6  | 0,002   | 0,04405 | 48       | 0,008027117 | 2   | 1092,52165 | -0,45   | 47,61   |
| 350 | SPGGVYATRSS  | 1      | 1          | Q997915                    |           | 5,594E6  | 0,002   | 0,04851 | 46       | 0,009466981 | 2   | 1081,52971 | 2,23    | 41,22   |
| 351 | RLYLNGDGTGK  | 1      | 1          | Q13077                    |           | 3,967E6  | 0,002   | 0,04616 | 45       | 0,011518872 | 2   | 1193,63017 | 2,36    | 47,45   |
| 352 | ATGDMSSLK    | 4      | 1          | Q13685                    |           | 1,950E5  | 0,002   | 0,05338 | 45       | 0,00996079 | 2   | 992,51061 | 2,45    | 83,75   |
| 353 | SPALTISKVLL  | 2      | 5          | Q969T4;P62837;P61077;P51965;Q96LKR5 | 1,728E7  | 2,635E5  | 0,002   | 0,04934 | 45       | 0,002440742 | 2   | 1141,71904 | -0,09   | 126,46  |
| 354 | KLYEELPSK    | 1      | 1          | Q13355                    |           | 4,214E6  | 0,002   | 0,0545  | 44       | 0,009033489 | 2   | 1106,61382 | 4,13    | 55,73   |
| 355 | IPYGERITL    | 1      | 1          | P49750                    |           | 1,023E7  | 0,002   | 0,0454  | 44       | 0,011933683 | 2   | 1061,60137 | 2,22    | 98,61   |
| 356 | APYPLYPAEL   | 9      | 1          | Q93062                    |           | 9,943E5  | 0,002   | 0,04824 | 44       | 0,019114105 | 2   | 1133,58794 | 0,15    | 145,87  |
| 357 | RVGTIVGSKN   | 1      | 1          | P09874                    |           | 1,728E7  | 0,002   | 0,05701 | 43       | 0,012346882 | 2   | 1030,60076 | 0,32    | 32,08   |
| #   | Sequence       | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area     | q-Value | PEP     | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|----------------|--------|------------|--------------------------|-----------|----------|---------|---------|----------|------------|-----|----------|---------|---------|
| 358 | RSVDTVNTTF    | 1      | 1          | Q14579                   |           | 1,535E7  | 0,002   | 0,05739 | 43       | 0,022176828 | 2   | 1139,57085 | 1,47    | 75,68   |
| 359 | GIYVQDVKTGK   | 1      | 1          | Q14764                   |           | 3,049E6  | 0,002   | 0,0466  | 42       | 0,017422434 | 2   | 1207,67266 | 3,72    | 53,56   |
| 360 | KIYEGQVEV     | 2      | 1          | P46777                   |           | 4,871E7  | 0,002   | 0,05394 | 42       | 0,022987363 | 2   | 1064,56548 | 2,99    | 74,23   |
| 361 | RILSGVVTK     | 2      | 1          | P62280                   |           | 1,162E8  | 0,002   | 0,05686 | 41       | 0,006344392 | 2   | 972,61955 | -0,55   | 48,41   |
| 362 | RPSQNNLTVGL   | 1      | 1          | Q9H0H0                   |           | 3,362E6  | 0,002   | 0,04768 | 40       | 0,026425514 | 2   | 1099,58733 | 1,67    | 59,14   |
| 363 | SVYRTPVVLK    | 1      | 1          | P20929                   |           | 4,952E6  | 0,002   | 0,05211 | 40       | 0,014748922 | 2   | 1275,74590 | 3,06    | 72,45   |
| 364 | SFFDLNPKY     | 1      | 2          | Q98Q16;Q96AC1            |           | 3,745E6  | 0,002   | 0,05677 | 40       | 0,041335109 | 2   | 1130,55596 | 3,75    | 123,27  |
| 365 | FPANNIKF      | 4      | 1          | P43307                   |           | 4,298E5  | 0,002   | 0,05523 | 39       | 0,036599739 | 2   | 1049,57756 | -0,31   | 108,36  |
| 366 | SSYGGLTRY     | 1      | 1          | O15230                   |           | 1,633E6  | 0,002   | 0,0569  | 39       | 0,034555429 | 2   | 1003,48613 | 1,77    | 66,55   |
| 367 | miYASSKDAIK   | 2      | 3          | P23528;Q9Y281;P60981     | M1        | 6,272E6  | 0,002   | 0,04497 | 39       | 0,046233718 | 2   | 1242,63982 | -0,07   | 46,02   |
| 368 | GVIGQDGLFVK   | 1      | 1          | Q9NQ75                   |           | 5,442E6  | 0,002   | 0,05631 | 39       | 0,036282501 | 2   | 1146,65373 | 1,69    | 115,46  |
| 369 | GLTDVILHY     | 1      | 1          | O60506                   |           | 2,762E7  | 0,002   | 0,05449 | 39       | 0,058447508 | 2   | 1030,56035 | 3,44    | 120,38  |
| 370 | RTAVPSFLTK    | 5      | 1          | Q96Q09                   |           | 4,409E7  | 0,002   | 0,04858 | 38       | 0,026839336 | 2   | 1119,65532 | 2,86    | 73,78   |
| 371 | STFNVQLVK     | 1      | 1          | Q07020                   |           | 9,138E6  | 0,002   | 0,05007 | 38       | 0,044147802 | 2   | 1035,58354 | 0,18    | 78,81   |
| 372 | GTYQPLSTR     | 1      | 1          | O15213                   |           | 1,795E5  | 0,002   | 0,05742 | 38       | 0,069443478 | 2   | 1022,52629 | -0,26   | 54,68   |
| 373 | RVAPAHLFLK    | 1      | 1          | Q8N028                   |           | 3,739E6  | 0,002   | 0,04855 | 37       | 0,020083556 | 2   | 1208,73064 | 3,59    | 60,32   |
| 374 | KLEEQARAK     | 1      | 1          | Q14247                   |           | 2,177E6  | 0,002   | 0,05354 | 37       | 0,073563036 | 2   | 1072,61138 | 0,36    | 20,06   |
| 375 | GVAERSWLY     | 3      | 1          | O00255                   |           | 2,367E7  | 0,002   | 0,04529 | 36       | 0,074190929 | 2   | 1080,55058 | 3,03    | 95,48   |
| #   | Sequence      | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area   | q-Value | PEP    | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|---------------|--------|------------|--------------------------|-----------|--------|---------|--------|----------|------------|-----|----------|----------|---------|
| 376 | RLLQKVLAY    | 1      | 1          | Q5PRF9                  |           | 9,07E6 | 0,002   | 0,0439 | 36       | 0,009372159 | 2   | 1103,69585 | -2,05   | 86,08   |
| 377 | RPELVRPAL    | 11     | 3          | P52895;Q04828;P42330    |           | 1,10E6 | 0,002   | 0,04623| 35       | 0,017288068 | 2   | 1050,64128 | -0,59  | 67,85   |
| 378 | LPHAPGQVm    | 1      | 2          | Q92769;Q13547           | M9        | 1,18E7 | 0,002   | 0,05424| 35       | 0,142213884 | 2   | 965,49083  | 3,59   | 62,48   |
| 379 | RPPSITSQTSL  | 1      | 1          | Q9NY89                  |           | 4,04E6 | 0,002   | 0,04625| 35       | 0,139693612 | 2   | 1186,64531 | 2,22   | 71,70   |
| 380 | DVIRLIMQY    | 14     | 1          | Q2TAY7                  |           | 5,19E5 | 0,002   | 0,05145| 35       | 0,084681899 | 2   | 1150,62883 | -0,10  | 158,08  |
| 381 | RSNPYYIVK    | 1      | 1          | Q9UQE7                  |           | 4,59E6 | 0,002   | 0,04813| 35       | 0,092999026 | 2   | 1139,62505 | 3,73   | 54,92   |
| 382 | GVADKILKK    | 3      | 1          | Q13287                  |           | 2,10E5 | 0,002   | 0,05708| 34       | 0,032810746 | 2   | 971,62444  | -0,43  | 43,69   |
| 383 | RPYEPINSI    | 3      | 1          | Q8WUA4                  |           | 4,02E7 | 0,002   | 0,04425| 34       | 0,189992643 | 2   | 1088,57305 | -0,44  | 79,38   |
| 384 | KVQEQPLFY    | 10     | 1          | P07711                  |           | 2,68E5 | 0,002   | 0,04876| 34       | 0,13937499 | 2   | 1170,61907 | -0,29  | 117,36  |
| 385 | LPPPVFQmL    | 1      | 1          | Q15388                  | M8        | 2,68E7 | 0,002   | 0,04938| 34       | 0,140694657 | 2   | 1057,57854 | 3,23   | 136,59  |
| 386 | TPVDDRVDY    | 1      | 1          | P20929                  |           | 1,25E7 | 0,002   | 0,0483 | 34       | 0,163108241 | 2   | 1079,50163 | 1,12   | 68,11   |
| 387 | GVYSFQFNK    | 2      | 1          | Q15434                  |           | 1,68E5 | 0,002   | 0,04983| 33       | 0,182672514 | 2   | 1089,53606 | -0,31  | 94,43   |
| 388 | IFIEDAIKY    | 6      | 1          | O14791                  |           | 6,78E6 | 0,002   | 0,0483 | 33       | 0,137288765 | 2   | 1111,60283 | -0,54  | 127,57  |
| 389 | NPPVNYGRPY   | 1      | 1          | Q9UKX0                  |           | 1,79E6 | 0,002   | 0,05617| 33       | 0,189404277 | 2   | 1079,53069 | 3,52   | 63,41   |
| 390 | DPIGGHIHSY   | 1      | 1          | B0I1T2                  |           | 1,55E7 | 0,002   | 0,04501| 33       | 0,166108068 | 2   | 1095,52532 | 3,20   | 62,16   |
| 391 | DYDPLVVKL    | 1      | 1          | Q96A65                  |           | 9,58E6 | 0,002   | 0,05383| 32       | 0,159517277 | 2   | 1061,59172 | 3,71   | 130,22  |
| 392 | AVLTKQQLH    | 1      | 1          | Q14094                  |           | 8,67E6 | 0,002   | 0,05354| 32       | 0,034846951 | 2   | 1022,63487 | -0,84  | 64,60   |
| 393 | QSFDEKAVK    | 1      | 1          | P13073                  |           | 9,82E6 | 0,002   | 0,04617| 32       | 0,268302973 | 2   | 1237,62090 | -0,26  | 67,09   |
| #   | Sequence   | # PSMs | # Proteins | Protein Group Accessions       | Mod. (ox) | Area   | q-Value | PEP    | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|------------|--------|------------|------------------|----------|--------|---------|--------|----------|------------|-----|---------|----------|---------|
| 394 | RIEETLALK  | 1      | 1          | O15144           | 0,002    | 1,736E7| 0,04425 | 32     | 0,089725401 | 2       | 1185,72368| 2,93     | 82,61   |
| 395 | APAPIHNQF  | 16     | 1          | Q15011           | 0,002    | 2,304E8| 0,05239 | 32     | 0,173974943 | 2       | 994,51189| 1,36     | 62,94   |
| 396 | APEEPVULL  | 7      | 3          | P60709;P63261;A5A3E0 | 0,002    | 1,782E6| 0,0537  | 32     | 0,382228623 | 2       | 1004,54094| -0,23    | 83,52   |
| 397 | HPVPQPLQSF | 8      | 1          | Q95SQ3           | 0,002    | 2,368E5| 0,04969 | 31     | 0,255128686 | 2       | 1149,60491| -0,22    | 94,87   |
| 398 | NPYSGDLTKF | 2      | 1          | Q14157           | 0,002    | 1,513E7| 0,05109 | 31     | 0,265942785 | 2       | 1141,55254| 0,08     | 95,84   |
| 399 | RQNJVQFEF  | 5      | 3          | P52895;Q04828;P42330 | 0,002    | 2,320E5| 0,04396 | 31     | 0,275230463 | 2       | 1166,59502| -0,27    | 104,28  |
| 400 | GSHSmRYFY  | 3      | 35         | P01891;P10316;P13746;P18462;P30450;P30453;P30456;P30457;P01889;P30461;P30462;P30464;P30685;Q95365;P30475;P30480;P30481;P30484;P30485;P30486;P18464;P30490;P30491;P30492;P30493;P30495;P18465;P10319;Q29940;Q29836;P30498;Q31610;Q29718;P04222;Q95604 | M5       | 5,693E7| 0,05771 | 31     | 0,137402967 | 2       | 1163,49870| 4,15     | 53,54   |
| 401 | KVADMALHY  | 13     | 1          | P50990           | 0,002    | 1,086E8| 0,04983 | 31     | 0,433220222 | 2       | 1047,52873| -0,47    | 69,76   |
| 402 | YPVEIHEYL  | 2      | 1          | Q13901           | 0,002    | 2,253E7| 0,0551  | 31     | 0,380355256 | 2       | 1162,58196| 3,47     | 110,17  |
| 403 | LPYTVDHY   | 1      | 1          | Q95N08           | 0,002    | 7,379E6| 0,05192 | 30     | 0,316832566 | 2       | 1104,61138| 2,31     | 113,99  |
| 404 | GtTgMGlyK  | 3      | 2          | Q55RD1;Q14925    | 0,002    | 4,482E7| 0,04518 | 30     | 0,233171671 | 2       | 1033,47026| 0,90     | 43,67   |
| 405 | ATGSWDSFLK | 3      | 3          | P62879;P62873;P16520 | 0,002    | 2,540E7| 0,04695 | 30     | 0,359021291 | 2       | 1111,54399| 1,88     | 111,18  |
| 406 | QLYKEQALK  | 3      | 1          | P35579           | 0,002    | 8,672E7| 0,05263 | 30     | 0,238437242 | 2       | 1120,63689| 0,68     | 45,91   |
| 407 | VVVVGGILTK | 4      | 1          | Q16880           | 0,002    | 2,039E5| 0,04932 | 30     | 0,076524711 | 2       | 1048,64006| -0,08    | 99,66   |
| 408 | KPYNPIIGETF| 2      | 2          | Q98X85;Q98X84    | 0,002    | 1,478E7| 0,05236 | 30     | 0,375199153 | 2       | 1278,67729| 3,43     | 107,98  |
| #   | Sequence          | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area   | q-Value | PEP    | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|-------------------|--------|------------|--------------------------|-----------|--------|---------|--------|----------|------------|-----|----------|----------|----------|
| 409 | ILYDHAHVK         | 1      | 1          | P11926                   |           | 1,380E7| 0,002   | 0,04438| 30       | 0,285160192| 2   | 1095,59551| 0,84     | 41,09    |
| 410 | GPGVAFRPSI        | 1      | 1          | P08727                   |           | 6,094E6| 0,002   | 0,04876| 30       | 0,237301645| 2   | 1071,59807| 3,22     | 99,91    |
| 411 | KLNIPTKK          | 1      | 1          | Q7K285                   |           | 0,000E0| 0,002   | 0,04808| 30       | 0,080142285| 2   | 1042,66069| -1,21    | 29,38    |
| 412 | APLKSKMIY         | 1      | 3          | P23528;Q9Y281;P60981     |           | 2,341E7| 0,002   | 0,05764| 29       | 0,182066612| 2   | 1050,60588| 4,02     | 56,18    |
| 413 | NGFQEVHSF         | 1      | 1          | Q4VNC1                   |           | 3,757E6| 0,002   | 0,05065| 29       | 0,316127996| 2   | 1064,48039| 0,73     | 81,37    |
| 414 | LRYYNILF          | 6      | 1          | Q7Z232                   |           | 1,337E6| 0,002   | 0,05585| 29       | 0,366042537| 2   | 1101,60918| 0,02     | 133,06   |
| 415 | LDPKWQHDL         | 1      | 1          | Q86V81                   |           | 7,849E6| 0,002   | 0,0479 | 29       | 0,430287522| 2   | 1151,58684| 2,09     | 77,11    |
| 416 | RPPIGSISSm        | 1      | 1          | Q98QY9                   | M10       | 9,219E6| 0,002   | 0,04693| 29       | 0,756445315| 2   | 1060,54704| 1,35     | 60,77    |
| 417 | LAVASFPKQKE       | 1      | 1          | P14406                   |           | 4,869E6| 0,002   | 0,05613| 29       | 0,348302216| 2   | 1217,69267| 3,09     | 60,12    |
| 418 | RTFPPSLQY         | 2      | 1          | O7S159                   |           | 6,540E6| 0,002   | 0,04961| 29       | 0,555769427| 2   | 1158,59819| 3,40     | 122,84   |
| 419 | RVDSKTLTR         | 1      | 1          | Q969V3                   |           | 5,705E5| 0,002   | 0,04803| 29       | 0,289505185| 2   | 1075,62712| 4,87     | 27,20    |
| 420 | MPNPEGRYTF        | 1      | 1          | P04626                   |           | 2,350E6| 0,002   | 0,0506 | 28       | 0,365393002| 2   | 1211,55364| 1,83     | 88,85    |
| 421 | GTAPPTLALHY       | 1      | 1          | P12980                   |           | 8,134E6| 0,002   | 0,05584| 28       | 0,494406029| 2   | 1140,60735| 2,21     | 98,87    |
| 422 | VIHEKGFY          | 5      | 1          | P50591                   |           | 5,347E7| 0,002   | 0,04993| 28       | 0,602876869| 2   | 1155,58464| 1,13     | 66,47    |
| 423 | VIADLRNAFY        | 1      | 1          | P35575                   |           | 3,020E6| 0,002   | 0,05467| 28       | 0,523702913| 2   | 1181,63542| 3,42     | 116,57   |
| 424 | LPASGRSAEVTL      | 1      | 1          | O15533                   |           | 1,184E7| 0,002   | 0,0576 | 27       | 0,825773788| 2   | 1200,66167| 2,77     | 76,53    |
| 425 | EAIIKILGKEY       | 1      | 1          | Q92499                   |           | 1,674E7| 0,002   | 0,04862| 27       | 0,330112297| 2   | 1163,67082| 3,20     | 79,07    |
| 426 | YLPKEQLY          | 1      | 1          | Q9Y4W6                   |           | 3,621E7| 0,002   | 0,05712| 26       | 1,002520658| 2   | 1216,62871| 3,16     | 92,10    |
| #   | Sequence       | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area       | q-Value | PEP     | IonScore | Exp. Value | Ch. | MH+ [Da] | ∆M [ppm] | RT [min] |
|-----|----------------|--------|------------|--------------------------|-----------|------------|---------|---------|----------|------------|-----|----------|----------|---------|
| 427 | AFKAFLKSEY     | 1      | 1          | P49798                   |           | 2,347E7    | 0,002   | 0,05246 | 26       | 1,065897228 | 2   | 1203,64299 | 1,75     | 81,55   |
| 428 | QALLHPVTSGLK   | 1      | 1          | Q81WD5                   |           | 1,370E5    | 0,002   | 0,05026 | 26       | 0,337242824 | 2   | 1263,74211 | 0,09     | 81,72   |
| 429 | AVADKVLHLMYK   | 1      | 1          | Q142S8                   | M9        | 2,335E6    | 0,002   | 0,04532 | 25       | 1,302408873 | 2   | 1290,69390 | 4,93     | 53,85   |
| 430 | RVLPTGNQR      | 1      | 1          | P53814                   |           | 5,279E6    | 0,002   | 0,04552 | 25       | 0,391656295 | 2   | 1153,68193 | 1,61     | 51,34   |
| 431 | ATLSQFYINK     | 1      | 1          | Q96EK5                   |           | 5,703E6    | 0,002   | 0,04948 | 25       | 1,008366385 | 2   | 1184,63469 | 3,09     | 94,27   |
| 432 | AILDTAHOY      | 1      | 1          | Q5VSG8                   |           | 1,610E7    | 0,002   | 0,05194 | 25       | 1,17168781  | 2   | 1031,51738 | 1,67     | 76,88   |
| 433 | YREDIPELQGF    | 1      | 1          | Q86V21                   |           | 9,997E6    | 0,002   | 0,05723 | 25       | 1,246783116 | 2   | 1237,62432 | 2,51     | 116,18  |
| 434 | AIHALAI        | 1      | 1          | P42285                   |           | 0,000E0    | 0,002   | 0,05359 | 24       | 0,41098894  | 2   | 984,62419  | 4,16     | 63,68   |
| 435 | LFHDHAVSKF     | 1      | 1          | Q60488                   |           | 1,055E7    | 0,002   | 0,04744 | 24       | 1,626581233 | 2   | 1063,55828 | 1,06     | 81,86   |
| 436 | SLmHSFILK      | 6      | 1          | Q9NP97                   | M3        | 2,857E7    | 0,002   | 0,05625 | 24       | 1,278320688 | 2   | 1091,59368 | 1,69     | 71,64   |
| 437 | NPASNFRVL      | 12     | 1          | P13010                   |           | 7,976E7    | 0,002   | 0,04825 | 24       | 1,631126674 | 2   | 1059,55828 | 0,05     | 92,78   |
| 438 | SYTRPRHEY      | 3      | 1          | Q9UBR2                   |           | 9,151E7    | 0,002   | 0,05506 | 22       | 1,67267086  | 2   | 1149,53435 | 1,73     | 43,49   |
| 439 | YLWHILPY       | 7      | 1          | Q6P179                   |           | 1,314E7    | 0,002   | 0,04729 | 22       | 3,258811029 | 2   | 1205,63591 | 0,45     | 146,80  |
| 440 | RPIEDDQEVY     | 1      | 1          | Q1SS17                   |           | 8,002E6    | 0,002   | 0,04716 | 22       | 2,620655718 | 2   | 1263,58476 | -0,36    | 67,10   |
| 441 | LPLPNDKTLLY    | 1      | 1          | Q969X6                   |           | 1,150E7    | 0,002   | 0,05123 | 22       | 1,44097467  | 2   | 1286,73943 | 3,04     | 119,47  |
| 442 | YPDYAQHGIEY    | 2      | 1          | Q15147                   |           | 3,054E7    | 0,002   | 0,05302 | 21       | 0,445771467 | 2   | 1172,45622 | 2,66     | 70,57   |
| 443 | FPDRImNTF      | 1      | 2          | P04350;Q9BFU5            | M6        | 6,150E6    | 0,002   | 0,04875 | 21       | 2,681430011 | 2   | 1156,54924 | 3,13     | 97,02   |
| 444 | EVNKFGmAY      | 1      | 1          | P37108                   | M7        | 2,733E6    | 0,002   | 0,04933 | 19       | 3,447960747 | 2   | 1145,53020 | 0,51     | 64,06   |
| #   | Sequence           | PSMs | Proteins | Protein Group Accessions | Mod. (ox) | Area     | q-Value | PEP    | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|-------------------|------|----------|--------------------------|-----------|----------|---------|--------|----------|------------|-----|----------|----------|---------|
| 445 | IPYQDRESY         | 1    | 1        | Q9H2Y7                   |           | 8,685E6  | 0,002   | 0,04528| 19       | 4,08316201 | 2   | 1170,54204| -0,48    | 64,65   |
| 446 | FIANLFNRY         | 1    | 1        | P13796                   |           | 1,248E6  | 0,002   | 0,05156| 17       | 7,93244131 | 2   | 1157,61540| 4,46     | 120,84  |
| 447 | ImKFINDQY         | 1    | 1        | Q9UHD8                   | M2        | 2,981E6  | 0,002   | 0,05616| 16       | 8,030553348| 2   | 1187,58159| 4,23     | 83,40   |
| 448 | VTYNYPVHY         | 1    | 1        | Q9NV96                   |           | 3,908E6  | 0,002   | 0,05443| 16       | 10,82560606| 2   | 1155,54863| 1,47     | 86,13   |
| 449 | YYPEYKLLF         | 1    | 1        | P61421                   |           | 3,423E7  | 0,002   | 0,05739| 13       | 23,14325485| 2   | 1235,63970| 4,04     | 133,08  |
| 450 | FDPNVKVFY         | 1    | 1        | P22415                   |           | 6,499E6  | 0,002   | 0,04991| 13       | 20,29955256| 2   | 1225,62749| 1,84     | 122,56  |
| 451 | SPNQARAQAAL       | 1    | 1        | P26599                   |           | 1,299E7  | 0,003   | 0,05918| 54       | 0,001299536| 2   | 1126,59746| 0,94     | 45,32   |
| 452 | QARIEIESF         | 3    | 1        | P11021                   |           | 2,396E5  | 0,003   | 0,05984| 53       | 0,002530171| 2   | 1092,56816| -0,26    | 96,79   |
| 453 | IPKQVSISF         | 1    | 1        | Q96D46                   |           | 1,001E7  | 0,003   | 0,05957| 52       | 0,001566822| 2   | 1018,59374| 0,53     | 63,84   |
| 454 | RPPTAGSQF         | 2    | 1        | O43795                   |           | 1,341E5  | 0,003   | 0,06484| 51       | 0,003293061| 2   | 960,48992 | 0,12     | 45,86   |
| 455 | KPIITGGVTY        | 1    | 1        | Q14192                   |           | 8,987E7  | 0,003   | 0,06305| 49       | 0,003991781| 2   | 1036,56963| 2,18     | 62,57   |
| 456 | FVATAAAVHY        | 1    | 1        | Q15546                   |           | 0,000E0  | 0,003   | 0,06304| 49       | 0,004803767| 2   | 1049,54424| 2,62     | 83,59   |
| 457 | KVNIVPVIAK        | 5    | 1        | Q15019                   |           | 2,315E5  | 0,003   | 0,06259| 49       | 0,000175713| 2   | 1080,71282| -1,10    | 72,41   |
| 458 | LPAKILVEF         | 21   | 1        | O95229                   |           | 8,062E5  | 0,003   | 0,06224| 47       | 0,002872207| 2   | 1029,63371| -0,62    | 126,17  |
| 459 | KTFEGNLTTK        | 1    | 1        | Q6P2Q9                   |           | 2,472E7  | 0,003   | 0,05935| 47       | 0,007922879| 2   | 1138,61223| 1,69     | 43,50   |
| 460 | KVGEVIVTK         | 1    | 1        | P10809                   |           | 9,055E6  | 0,003   | 0,05967| 46       | 0,002744056| 2   | 972,60997 | 1,14     | 43,81   |
| 461 | GTYAPAEVPK        | 10   | 2        | P52895;Q04828            |           | 3,593E8  | 0,003   | 0,06344| 46       | 0,014193242| 2   | 1032,53594| -0,14    | 60,44   |
| 462 | SVLSPLLNK         | 4    | 1        | Q12929                   |           | 6,648E5  | 0,003   | 0,05959| 45       | 0,005361541| 2   | 970,59282 | -0,39    | 100,72  |
| # | Sequence | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area | q-Value | PEP | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|---|----------|-------|-----------|-------------------------|----------|------|---------|-----|----------|------------|-----|----------|----------|---------|
| 463 | LPLDPLKY | 1 | 1 | Q9NV79 | 6,81E6 | 0,003 | 0,05854 | 43 | 0,00768533 | 0,024628533 | 2 | 1055,61650 | -2,75 | 122,75 |
| 464 | RPINALDEL | 1 | 1 | Q8TCU6 | 1,982E7 | 0,003 | 0,06278 | 40 | 0,029651178 | 2 | 1040,57561 | 1,99 | 95,00 |
| 465 | FVQMMTAK | 1 | 1 | P62158 | 2,138E5 | 0,003 | 0,0582 | 40 | 0,032043779 | 2 | 955,47350 | -0,56 | 69,49 |
| 466 | RIYGIGVSR | 1 | 1 | Q96PD2 | 7,371E6 | 0,003 | 0,06296 | 39 | 0,028243377 | 2 | 1134,64031 | 2,15 | 56,82 |
| 467 | KVANIILSY | 13 | 1 | Q96JI7 | 1,079E8 | 0,003 | 0,06157 | 39 | 0,017234925 | 2 | 1107,72490 | -0,01 | 30,18 |
| 468 | KVAPAPAVKK | 1 | 1 | P62424 | 1,662E6 | 0,003 | 0,06074 | 38 | 0,00192799 | 2 | 1020,60857 | -0,27 | 102,79 |
| 469 | AIIDHIFASK | 1 | 1 | Q8TA51 | 3,082E7 | 0,003 | 0,06275 | 38 | 0,042080603 | 2 | 1114,62859 | 2,15 | 56,32 |
| 470 | KTYGEIFEK | 13 | 1 | O95298 | 1,883E8 | 0,003 | 0,0623 | 37 | 0,061949819 | 2 | 1114,58183 | 3,49 | 62,21 |
| 471 | STSQTFIYK | 1 | 1 | O60341 | 1,015E7 | 0,003 | 0,06072 | 37 | 0,111013902 | 2 | 1074,54607 | -0,51 | 65,32 |
| 472 | RLFPLRQR | 2 | 1 | Q8NB4M4 | 6,638E7 | 0,003 | 0,06047 | 36 | 0,021828089 | 2 | 1182,72576 | 3,28 | 61,40 |
| 473 | RVNPKTIGK | 1 | 1 | P80162 | 2,328E6 | 0,003 | 0,0582 | 36 | 0,024046446 | 2 | 1012,62975 | 3,46 | 25,12 |
| 474 | ALYPHVLVK | 1 | 1 | Q98UJ2 | 3,502E7 | 0,003 | 0,06098 | 36 | 0,016630153 | 2 | 1039,63249 | 2,48 | 75,35 |
| 475 | APYRDLPASL | 1 | 1 | P54259 | 2,171E7 | 0,003 | 0,05971 | 36 | 0,132209883 | 2 | 1102,59038 | 1,09 | 92,50 |
| 476 | FPmTHGNTGF | 3 | 1 | Q15366 | M3 | 4,112E7 | 0,003 | 0,05846 | 35 | 0,05193986 | 2 | 1124,48503 | 1,80 | 70,27 |
| 477 | IPYALRVEL | 1 | 1 | P02679 | 3,359E7 | 0,003 | 0,0587 | 34 | 0,077400668 | 2 | 1073,63799 | 2,41 | 120,07 |
| 478 | NPYHVVLIF | 12 | 1 | Q86X29 | 1,337E6 | 0,003 | 0,05923 | 31 | 0,208224372 | 2 | 1101,60906 | -0,10 | 133,42 |
| 479 | SPVIHPVSY | 1 | 1 | Q15904 | 1,133E7 | 0,003 | 0,05968 | 31 | 0,246516004 | 2 | 1095,58696 | 3,30 | 88,62 |
| 480 | STNTRVLYF | 8 | 1 | P49755 | 4,956E5 | 0,003 | 0,06395 | 30 | 0,376208259 | 2 | 1100,57341 | -0,09 | 93,27 |
| #    | Sequence  | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area  | q-Value | PEP  | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|------|-----------|--------|------------|--------------------------|-----------|-------|---------|------|----------|------------|-----|----------|----------|---------|
| 481  | ATAASSSLEKS | 1      | 7          | P60709;P63261;Q658J3;P62736;P68032;P63267;P68113 |           | 4,806E4 | 0,003  | 0,05884 | 30    | 0,42155  | 2          | 1138,55864 | -0,03 | 34,56    |
| 482  | GLYQDGVFK  | 1      | 1          | Q9H8T0                  |           | 5,458E6 | 0,003  | 0,06132 | 30    | 0,263438566 | 2       | 1026,52690 | 1,36   | 86,32    |
| 483  | GSHSmRYFFT | 5      | 7          | P01892;P30443;P04439;P10314;P30455;P30459;Q09160 | MS        | 4,958E7 | 0,003  | 0,05841 | 29    | 0,217085602 | 2       | 1248,54582 | -0,67  | 68,63    |
| 484  | PYNHQHEY   | 1      | 1          | Q95864                  |           | 3,545E6 | 0,003  | 0,0602  | 28    | 0,23116088  | 2       | 1087,46050 | 1,21   | 43,56    |
| 485  | IYSHVTAAY  | 1      | 1          | Q8WWM9                  |           | 2,305E7 | 0,003  | 0,06171 | 26    | 1,087482481 | 2       | 1024,51042 | 0,58   | 65,69    |
| 486  | ALNVPLHNR  | 1      | 1          | Q6ZMI0                  |           | 1,181E7 | 0,003  | 0,0598  | 26    | 0,600480579 | 2       | 1033,59282 | 2,55   | 54,53    |
| 487  | VPAPWLSVKL | 1      | 2          | Q95782;Q94973           |           | 2,590E6 | 0,003  | 0,06359 | 25    | 0,207419265 | 2       | 1109,67595 | 3,74   | 133,09   |
| 488  | FPQKIAGELY | 1      | 1          | Q9GZM5                  |           | 2,854E7 | 0,003  | 0,06333 | 25    | 1,012370024 | 2       | 1165,62798 | 2,36   | 98,66    |
| 489  | KINPTSSLYK | 1      | 1          | O75665                  |           | 3,580E6 | 0,003  | 0,06428 | 24    | 0,969897023 | 2       | 1150,65019 | 3,05   | 52,06    |
| 490  | AVIGADSVTLK| 1      | 1          | Q9NYH9                  |           | 1,476E7 | 0,003  | 0,05972 | 24    | 1,129968682 | 2       | 1073,62139 | 1,14   | 84,72    |
| 491  | YFIGRIYLY  | 5      | 1          | P41250                  |           | 9,637E4 | 0,003  | 0,06043 | 24    | 1,626925948 | 2       | 1207,65190 | 0,73   | 134,08   |
| 492  | FTIPANREF  | 1      | 1          | P01024                  |           | 1,964E7 | 0,003  | 0,05802 | 23    | 1,453047516 | 2       | 1094,56009 | 2,85   | 98,59    |
| 493  | FPVKGLKTGY | 1      | 1          | P19174                  |           | 9,963E6 | 0,003  | 0,05881 | 22    | 1,137353147 | 2       | 1109,63750 | 1,89   | 70,97    |
| 494  | ATYYGAFIKK | 1      | 3          | Q8N4C8;Q9UKES;Q95819    |           | 1,812E7 | 0,003  | 0,06226 | 22    | 2,724695296 | 2       | 1161,63262 | 1,99   | 71,57    |
| 495  | MPVRGPDVEAY| 1      | 1          | Q9NQ34                  |           | 9,347E6 | 0,003  | 0,06103 | 21    | 3,123309382 | 2       | 1233,59697 | 2,98   | 84,29    |
| 496  | mAVDDFNLKY | 2      | 1          | Q9C075                  | M1        | 5,842E6 | 0,003  | 0,06337 | 21    | 2,11240443  | 2       | 1231,57060 | 3,41   | 102,05   |
| 497  | SPEEGARVY  | 1      | 1          | Q8TE68                  |           | 1,141E7 | 0,003  | 0,06211 | 20    | 3,981407819 | 2       | 1007,48009 | 0,79   | 49,41    |
| 498  | GSHSMRYFY  | 1      | 35         | P01891;P10316;P13746;P18462;P30450;P30453;P30456;P30457;P01889;P30461;P30462;P30464; |           | 2,047E7 | 0,003  | 0,06203 | 19    | 2,087123159 | 2       | 1147,50066 | 1,48   | 65,50    |
| #   | Sequence   | PSMs | Proteins | Protein Group Accessions                                                                 | Mod. (ox) | Area | q-Value | PEP    | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|------------|------|----------|----------------------------------------------------------------------------------------|-----------|------|---------|--------|----------|------------|-----|----------|----------|---------|
| 499 | QPWEIIKTSY | 1    | 1        | P30685;Q95365;P30475;P30480;P30481;P30484;P30485;P30486;P18464;P30490;P30491;P30492 | P49961    | 2,219E7 | 0,003   | 0,05851 | 19       | 5,356432155 | 2   | 1280,61821 | 1,90     | 97,04   |
| 500 | AIYKTPGPIQK | 1    | 1        | Q6W2J9                                                                                   | Q16851    | 1,120E7 | 0,004   | 0,06737 | 51       | 0,002500008 | 2   | 1215,71355 | 3,22     | 57,03   |
| 501 | KLYEMILKR   | 1    | 1        | P56559                                                                                   | Q16851    | 1,120E7 | 0,004   | 0,06737 | 51       | 0,002500008 | 2   | 1215,71355 | 3,22     | 57,03   |
| 502 | LPVAKDVSY   | 1    | 1        | Q16851                                                                                   | Q16851    | 1,120E7 | 0,004   | 0,06737 | 51       | 0,002500008 | 2   | 1215,71355 | 3,22     | 57,03   |
| 503 | AVYSHVIQK   | 1    | 1        | P20132                                                                                   | Q16851    | 1,120E7 | 0,004   | 0,06737 | 51       | 0,002500008 | 2   | 1215,71355 | 3,22     | 57,03   |
| 504 | AVMGAYVLLK  | 7    | 1        | Q98Y50                                                                                   | Q16851    | 1,120E7 | 0,004   | 0,06737 | 51       | 0,002500008 | 2   | 1215,71355 | 3,22     | 57,03   |
| 505 | KVFERAVQY   | 1    | 1        | Q14690                                                                                   | Q14690    | 1,120E7 | 0,004   | 0,06737 | 51       | 0,002500008 | 2   | 1215,71355 | 3,22     | 57,03   |
| 506 | FNSHVHVEY   | 1    | 1        | Q14690                                                                                   | Q14690    | 1,120E7 | 0,004   | 0,06737 | 51       | 0,002500008 | 2   | 1215,71355 | 3,22     | 57,03   |
| 507 | VmAPRTLIL   | 11   | 8        | P04222;P30504;Q29963;P30508;P30510;Q29960;Q9TNN7;P30505;P30443;P04439;P13746;P16188;P10314;P30455;P30459 | M2        | 7,149E7 | 0,004   | 0,06773 | 32       | 0,109755735 | 2   | 1029,61162 | -0,93    | 101,07  |
| 508 | HPGFKDPVY   | 1    | 1        | P00439                                                                                   | P00439    | 7,852E7 | 0,004   | 0,06751 | 31       | 0,331847305 | 2   | 1059,52873 | 2,73     | 63,23   |
| 509 | KVLDAIQEQ   | 1    | 1        | Q9NTJ3                                                                                   | Q9NTJ3    | 4,504E6 | 0,004   | 0,06717 | 28       | 0,282357002 | 2   | 1156,69621 | 2,21     | 77,96   |
| 510 | SVYSPGVPVR  | 1    | 1        | Q9NS56                                                                                   | Q9NS56    | 9,128E6 | 0,004   | 0,06658 | 24       | 1,60363642  | 2   | 1162,58476 | -0,33    | 57,90   |
| 511 | LPWNITVHF   | 1    | 1        | Q9H1Y0                                                                                   | Q9H1Y0    | 1,151E6 | 0,004   | 0,06624 | 17       | 5,792315053 | 2   | 1126,60613 | 1,50     | 142,65  |
| 512 | MYDAAKLLY   | 2    | 1        | Q00610                                                                                   | Q00610    | 2,882E6 | 0,005   | 0,07097 | 51       | 0,0038332   | 2   | 1087,55315 | 3,56     | 110,97  |
| #  | Sequence   | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area | q-Value | PEP | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|----|------------|--------|------------|--------------------------|-----------|------|---------|-----|----------|------------|-----|----------|----------|---------|
| 513| LPAGWILSH  | 1      | 1          | P10176                   | 1,355E6   | 0,005| 0,07028 | 50  | 0,001129198 | 2          | 993,55370 | 2,04    | 115,92  |
| 514| GPGSRISSSFS| 1      | 1          | P05787                   | 6,983E6   | 0,005| 0,07183 | 49  | 0,004808194 | 2          | 1168,56340 | 3,48    | 58,73   |
| 515| VQSNARLLY  | 1      | 1          | P35869                   | 0,00000   | 0,005| 0,07121 | 44  | 0,01056081 | 2          | 1063,59136 | 1,74    | 72,50   |
| 516| RPVPLEQTY   | 1      | 1          | O75643                   | 2,058E7   | 0,005| 0,06869 | 43  | 0,018396129 | 2          | 1102,59087 | 1,54    | 70,82   |
| 517| IPDKFVVGY   | 1      | 1          | P00492                   | 1,947E7   | 0,005| 0,07224 | 41  | 0,022201038 | 2          | 1037,56938 | 2,63    | 103,75  |
| 518| IAVATLHK    | 1      | 1          | Q9P267                   | 5,111E5   | 0,005| 0,07127 | 40  | 0,008383446 | 2          | 852,53008 | -0,15   | 81,24   |
| 519| RLGOSQLVK   | 2      | 1          | Q16531                   | 3,226E7   | 0,005| 0,07311 | 34  | 0,126265355 | 2          | 1015,58843 | -1,08   | 47,68   |
| 520| FVQmMTAK    | 4      | 1          | P62158                   | 1,241E7   | 0,005| 0,06856 | 34  | 0,119074389 | 2          | 971,46941 | 0,48    | 50,16   |
| 521| SAEEGYRTY   | 1      | 1          | Q96Q6                    | 9,591E5   | 0,005| 0,07295 | 31  | 0,156067098 | 2          | 1075,46855 | -0,51   | 48,67   |
| 522| NPPKAPWSLL  | 1      | 1          | P52630                   | 2,336E7   | 0,005| 0,06871 | 31  | 0,155869419 | 2          | 1122,63298 | 2,07    | 122,03  |
| 523| VPYHGEVPVSL | 1      | 1          | O15020                   | 1,019E7   | 0,005| 0,07303 | 30  | 0,313535683 | 2          | 1196,63408 | 2,54    | 99,62   |
| 524| RLYDAYELK   | 1      | 1          | P08758                   | 9,843E6   | 0,005| 0,07112 | 30  | 0,383115281 | 2          | 1170,61992 | 3,88    | 74,38   |
| 525| GLHGVTFGY   | 1      | 1          | Q8NE71                   | 1,888E7   | 0,005| 0,0699  | 29  | 0,328107931 | 2          | 950,47490 | 1,93    | 93,24   |
| 526| KLYEmILKR   | 2      | 1          | P56559                   | 9,862E6   | 0,005| 0,07136 | 29  | 0,139823354 | 2          | 1209,70708 | 3,83    | 61,89   |
| 527| RVLPYFPFTH  | 1      | 1          | Q98VJ6                   | 1,656E5   | 0,005| 0,07038 | 29  | 0,417008928 | 2          | 1129,61455 | -0,68   | 87,78   |
| 528| SIGQVFLLLK  | 1      | 1          | Q9Y383                   | 5,543E6   | 0,005| 0,07042 | 29  | 0,145597538 | 2          | 1004,61504 | 1,09    | 114,13  |
| 529| RPFAFAERL   | 1      | 1          | P20073                   | 1,335E7   | 0,005| 0,07271 | 27  | 0,474084252 | 2          | 1106,61370 | 2,80    | 84,41   |
| 530| GSHSmRYFYT  | 2      | 35         | P01891;P10316;P13746;P18462;P30450;P30453;P30456;P30457;P01889;P30461;P30462;P30464; | M5        | 5,009E7 | 0,005| 0,07214 | 27  | 0,383059149 | 2          | 1264,54558 | 3,18    | 53,67   |
| #   | Sequence   | PSMs | Proteins | Protein Group Accessions | Mod. (ox) | Area | q-Value | PEP  | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|------------|------|----------|--------------------------|-----------|------|---------|------|----------|------------|-----|----------|----------|---------|
| 531 | LPDLRPWTS | 1    | 1        | Q03519                   |           | 9,802E6 | 0,005   | 0,06837 | 24   | 0,885910454 | 2    | 1197,66692 | 3,53   | 139,59  |
| 532 | AVVNKVPTL | 1    | 1        | Q8WUH6                   |           | 1,140E6 | 0,005   | 0,07262 | 23   | 0,396039557 | 2    | 1125,70293 | 3,42   | 54,94   |
| 533 | YPAYLGA   | 1    | 1        | P38606                   |           | 3,961E6 | 0,005   | 0,07293 | 21   | 1,12914272  | 2    | 1023,56352 | 1,27   | 97,93   |
| 534 | FVYEPEK   | 1    | 1        | Q16666                   |           | 5,393E6 | 0,005   | 0,07171 | 18   | 6,984296097 | 2    | 1167,60576 | 1,09   | 49,03   |
| 535 | RVFPYSV   | 1    | 1        | O15118                   |           | 1,369E7 | 0,005   | 0,07251 | 15   | 15,67709849 | 2    | 1177,60832 | 3,60   | 129,53  |
| 536 | LPIESNP    | 1    | 1        | Q8N3C0                   |           | 3,679E6 | 0,005   | 0,06959 | 14   | 13,45054736 | 2    | 1140,57146 | 2,65   | 83,81   |
| 537 | LHDPDLS    | 1    | 1        | Q9P217                   |           | 1,568E7 | 0,005   | 0,07029 | 13   | 16,30150036 | 2    | 1056,50237 | 2,54   | 84,34   |
| 538 | TPTGIKV    | 2    | 1        | Q9Y5R8                   | M9        | 1,095E7 | 0,006   | 0,07624 | 59   | 0,000460461 | 2    | 961,53716 | -1,64  | 64,48   |
| 539 | LPDPIIIHL  | 1    | 1        | Q7Z7G8                   |           | 3,511E6 | 0,006   | 0,07822 | 48   | 0,001767947 | 2    | 1030,63384 | 4,12   | 138,57  |
| 540 | KASEVFLQR  | 1    | 1        | Q9H0A0                   |           | 4,556E6 | 0,006   | 0,07835 | 47   | 0,005498887 | 2    | 1077,60942 | 3,95   | 53,26   |
| 541 | LLAKVFITK  | 1    | 1        | Q9H9Q4                   |           | 1,145E5 | 0,006   | 0,07385 | 47   | 0,00019286 | 2    | 1032,68083 | -0,77  | 77,92   |
| 542 | APVKPGP    | 1    | 1        | Q9U8P4                   |           | 3,294E7 | 0,006   | 0,07485 | 47   | 0,002359449 | 2    | 849,52098 | 1,96   | 56,89   |
| 543 | GVMDRGSY  | 5    | 1        | P28074                   |           | 2,079E5 | 0,006   | 0,08226 | 46   | 0,005115166 | 2    | 1047,45635 | -0,09  | 76,08   |
| 544 | ALSDLAL    | 1    | 1        | P50991                   |           | 5,216E6 | 0,006   | 0,07914 | 43   | 0,013002105 | 2    | 986,53246 | 1,88   | 132,60  |
| 545 | SIFKQPV    | 1    | 2        | Q9UB85;Q9S983            |           | 3,753E7 | 0,006   | 0,07654 | 42   | 0,010049135 | 2    | 1047,62285 | 2,96   | 52,76   |
| #   | Sequence     | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area  | q-Value | PEP   | IonScore | Exp. Value | Ch. | MH+ [Da]     | ΔM [ppm] | RT [min] |
|-----|--------------|--------|------------|--------------------------|-----------|-------|---------|-------|----------|------------|-----|--------------|---------|---------|
| 546 | KIFSGVFVK    | 3      | 1          | Q6DK11                   |           | 2,77E5 | 0,006   | 0,07597 | 40       | 0,011934721 | 2   | 1024,61882   | -0,20   | 77,68   |
| 547 | IFDGNVAHI    | 1      | 1          | P46939                   |           | 1,54E7 | 0,006   | 0,07331 | 39       | 0,035940534 | 2   | 985,51262    | 2,46    | 97,02   |
| 548 | KPYQGSAGF    | 1      | 1          | P22670                   |           | 5,19E6 | 0,006   | 0,08349 | 39       | 0,041281812 | 2   | 954,47081    | 2,95    | 51,86   |
| 549 | KPGPPGILAL   | 6      | 1          | P35579                   |           | 2,31E8 | 0,006   | 0,07752 | 38       | 0,010443302 | 2   | 1033,63970   | -0,79   | 107,70  |
| 550 | LPRQVILKF    | 1      | 1          | Q96GQ7                   |           | 1,35E7 | 0,006   | 0,07944 | 37       | 0,037962682 | 2   | 1072,64287   | 2,53    | 126,97  |
| 551 | IVAKHTSAL    | 1      | 2          | Q9Y490;Q9Y4G6            |           | 2,33E7 | 0,006   | 0,07693 | 36       | 0,034146846 | 2   | 939,56352    | 1,38    | 32,23   |
| 552 | LPSPFLRAL    | 1      | 1          | Q95456                   |           | 2,90E6 | 0,006   | 0,07751 | 36       | 0,012340137 | 2   | 1013,61595   | 1,65    | 121,94  |
| 553 | SPEETRAAL    | 1      | 1          | P78549                   |           | 4,98E6 | 0,006   | 0,07887 | 35       | 0,142698022 | 2   | 973,49498    | 0,03    | 49,47   |
| 554 | KLHDETLTY    | 1      | 2          | Q9N217;Q12800            |           | 8,59E6 | 0,006   | 0,07475 | 35       | 0,154816792 | 2   | 1119,57195   | 3,44    | 57,70   |
| 555 | NVYEVNPK     | 1      | 1          | Q86YQ8                   |           | 4,28E6 | 0,006   | 0,08337 | 33       | 0,261764263 | 2   | 1061,56218   | -0,41   | 68,59   |
| 556 | AYHGSFSTK    | 4      | 1          | P12111                   |           | 2,91E5 | 0,006   | 0,08344 | 33       | 0,167805873 | 2   | 1098,52068   | -0,72   | 34,53   |
| 557 | GLEAIQRTPK   | 1      | 1          | P61769                   |           | 3,15E6 | 0,006   | 0,08177 | 33       | 0,1095344   | 2   | 1112,64409   | 1,62    | 50,72   |
| 558 | AVAIKAmAK    | 2      | 2          | P63241;Q6I514            | M7        | 5,70E7 | 0,006   | 0,08008 | 32       | 0,100937808 | 2   | 918,54442    | 0,28    | 40,70   |
| 559 | FPPIEIVTY    | 3      | 1          | Q13409                   |           | 5,28E6 | 0,006   | 0,07443 | 32       | 0,203678393 | 2   | 1121,60198   | 2,64    | 97,70   |
| 560 | IVDGNAMTGL   | 1      | 1          | P43370                   |           | 2,64E6 | 0,006   | 0,0818  | 31       | 0,328041542 | 2   | 1061,56938   | 3,17    | 77,14   |
| 561 | HINGRVLYY    | 8      | 1          | Q13751                   |           | 3,69E7 | 0,006   | 0,07623 | 31       | 0,315587855 | 2   | 1134,60515   | -0,28   | 63,64   |
| 562 | YPSETTVKY    | 2      | 1          | P11047                   |           | 7,27E7 | 0,006   | 0,07876 | 31       | 0,279107855 | 2   | 1087,53179   | 1,06    | 66,01   |
| 563 | RTFGQGTKL    | 1      | 1          | P01593                   |           | 6,95E6 | 0,006   | 0,08185 | 29       | 0,287613578 | 2   | 1007,56377   | 0,46    | 43,68   |
| #   | Sequence     | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area     | q-Value  | PEP      | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|--------------|--------|------------|--------------------------|-----------|----------|----------|----------|----------|-----------|-----|----------|----------|---------|
| 564 | ALFSRIFGK    | 1      | 1          | P84085                   |           | 6,779E6  | 0,006    | 0,07852  | 29       | 0,096744081 | 2   | 1038,61174| 2,13     | 101,92  |
| 565 | FPAGKVPAF    | 1      | 1          | P26641                   |           | 1,134E7  | 0,006    | 0,07487  | 29       | 0,348134627 | 2   | 933,52074| 1,52     | 96,46   |
| 566 | SINDGFHVY    | 1      | 1          | Q04771                   |           | 1,281E7  | 0,006    | 0,07862  | 29       | 0,429959075 | 2   | 1051,48747| 2,96     | 94,99   |
| 567 | DIYKRFLE     | 1      | 1          | QSH8A3                   |           | 1,105E6  | 0,006    | 0,07369  | 28       | 0,43805794  | 2   | 1101,60881| -0,34    | 133,26  |
| 568 | HPNDDDVHF    | 1      | 1          | Q8IZH2                   |           | 1,755E7  | 0,006    | 0,07355  | 28       | 0,170371639 | 2   | 1095,45305| 3,65     | 53,87   |
| 569 | RSNEHIREL    | 1      | 1          | P50995                   |           | 2,171E7  | 0,006    | 0,08335  | 28       | 0,492216163 | 2   | 1153,60918| 1,64     | 30,63   |
| 570 | RLYQHAVEY    | 1      | 1          | Q9UN37                   |           | 2,098E7  | 0,006    | 0,08023  | 28       | 0,793589259 | 2   | 1178,59990| 3,90     | 55,13   |
| 571 | KTFPNTIEH    | 1      | 1          | Q9NUA8                   |           | 1,046E7  | 0,006    | 0,07683  | 28       | 0,705849208 | 2   | 1086,55876| 0,82     | 49,17   |
| 572 | GLYEFFRAK    | 1      | 1          | Q8IWX8                   |           | 1,515E5  | 0,006    | 0,07824  | 27       | 0,691846379 | 2   | 1130,59868| -0,59    | 97,76   |
| 573 | SISDKFFQK    | 1      | 1          | Q9BQS7                   |           | 1,854E7  | 0,006    | 0,07432  | 27       | 0,696951862 | 2   | 1099,58037| 1,90     | 73,96   |
| 574 | RVWDVESGLK   | 1      | 1          | Q9GZL7                   |           | 9,347E6  | 0,006    | 0,08335  | 27       | 0,88381211 | 2   | 1275,67241| 2,48     | 75,75   |
| 575 | SLYHRVLLY    | 1      | 1          | Q5TH69                   |           | 4,983E6  | 0,006    | 0,07905  | 26       | 0,52581804  | 2   | 1163,66167| 3,86     | 87,63   |
| 576 | ATYSVGMQK    | 2      | 2          | A8MT19;Q8IUC4            |           | 4,099E7  | 0,006    | 0,08266  | 26       | 0,836703188 | 2   | 984,48522| 3,34     | 52,46   |
| 577 | NPLKDPQY     | 1      | 1          | Q15435                   |           | 1,431E7  | 0,006    | 0,07706  | 26       | 1,156085038 | 2   | 1102,55412| 1,22     | 57,55   |
| 578 | RVFPWFSVK    | 1      | 1          | Q03164                   |           | 5,591E6  | 0,006    | 0,08167  | 25       | 0,622244208 | 2   | 1165,65422| 2,14     | 111,19  |
| 579 | HPVFQQESF    | 2      | 1          | P16455                   |           | 1,048E7  | 0,006    | 0,07681  | 25       | 1,097418137 | 2   | 1118,52922| 2,37     | 82,39   |
| 580 | APLPDGRSL    | 1      | 1          | Q15648                   |           | 1,587E7  | 0,006    | 0,0815   | 25       | 0,894805288 | 2   | 925,51232| 2,27     | 75,50   |
| 581 | FPNIVIKGSEL  | 1      | 1          | Q6P2Q9                   |           | 2,468E6  | 0,006    | 0,07881  | 25       | 0,906449412 | 2   | 1216,69682| 2,60     | 118,36  |
| #  | Sequence       | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area  | q-Value | PEP   | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|----|----------------|-------|------------|--------------------------|----------|-------|---------|-------|----------|------------|-----|----------|----------|---------|
| 582| KLIDIFQKY      | 1     | 1          | Q92484                   |          | 2,715E6 | 0,006   | 0,0738| 24       | 0,48906614 | 2   | 1167,68120| 3,37     | 110,18  |
| 583| KPSSWLRTL     | 1     | 1          | P12755                   |          | 1,541E7 | 0,006   | 0,08219| 24       | 1,097517994| 2   | 1087,62676| 0,79     | 79,51   |
| 584| SLAERSSLQK    | 1     | 1          | Q9UPN3                   |          | 6,841E6 | 0,006   | 0,07387| 22       | 1,503141887| 2   | 1231,70281| 1,85     | 58,19   |
| 585| ALYDATYETK     | 1     | 2          | P23528;Q9Y281            |          | 2,713E6 | 0,006   | 0,08058| 22       | 1,845659152| 2   | 1174,56609| 2,91     | 73,76   |
| 586| KVIDRILYK     | 1     | 1          | O75533                   |          | 4,429E6 | 0,006   | 0,07996| 22       | 0,204432866| 2   | 1147,72331| 3,06     | 62,61   |
| 587| APFDWKILY     | 1     | 1          | Q96RK4                   |          | 7,136E5 | 0,006   | 0,07762| 22       | 2,04139068 | 2   | 1152,61394| 4,41     | 144,54  |
| 588| TAVIDHHNY     | 1     | 1          | P39656                   |          | 2,644E7 | 0,006   | 0,07818| 22       | 1,841045515| 2   | 1069,50823| 1,94     | 42,38   |
| 589| HPNSAILHY     | 1     | 1          | A5YKK6                   |          | 5,214E6 | 0,006   | 0,08336| 22       | 2,445285529| 2   | 1164,61650| 0,40     | 75,58   |
| 590| TPYEGQRSY     | 1     | 1          | Q92900                   |          | 7,381E6 | 0,006   | 0,0747 | 21       | 1,731756449| 2   | 1100,50310| 2,15     | 46,88   |
| 591| KTYEVSLEK     | 1     | 1          | Q16531                   |          | 1,976E6 | 0,006   | 0,08118| 21       | 2,380385405| 2   | 1252,68889| -0,58    | 42,70   |
| 592| HPDEKSITY     | 16    | 1          | Q10182                   |          | 2,212E8 | 0,006   | 0,07705| 20       | 4,995794255| 2   | 1202,60686| 1,37     | 69,75   |
| 593| VPVAEIKY      | 1     | 1          | Q6VY07                   |          | 4,822E5 | 0,006   | 0,07791| 19       | 2,539483407| 2   | 1031,61284| -0,74    | 104,08  |
| 594| YPLEDATHIAL   | 1     | 1          | Q9NXN4                   |          | 5,002E6 | 0,006   | 0,07483| 18       | 5,355735184| 2   | 1242,64067| 3,34     | 122,23  |
| 595| SPQPDGVVY     | 1     | 1          | Q9BSV6                   |          | 4,201E7 | 0,006   | 0,07572| 17       | 9,230998564| 2   | 1089,55998| 2,24     | 59,92   |
| 596| KPGSFLYSTF    | 1     | 1          | P83111                   |          | 1,209E7 | 0,006   | 0,08082| 16       | 10,66562013 | 2   | 1274,64568| 3,20     | 107,78  |
| 597| APYRPPDSL     | 1     | 1          | Q9HCD6                   |          | 9,669E6 | 0,008   | 0,0901 | 44       | 0,012161141 | 2   | 1128,60845| 3,20     | 102,21  |
| 598| KITVPASQKL    | 1     | 1          | Q8WV28                   |          | 1,624E7 | 0,008   | 0,08859| 43       | 0,00611542  | 2   | 1084,67339| 0,80     | 57,54   |
| 599| KSNSIIVSPR    | 1     | 1          | P07992                   |          | 0,000E0 | 0,008   | 0,08447| 43       | 0,014032065 | 2   | 1100,64311| 0,76     | 46,47   |
| #  | Sequence     | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area     | q-Value | PEP    | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|----|--------------|--------|------------|--------------------------|-----------|----------|---------|--------|----------|------------|-----|----------|-----------|---------|
| 600| RPILTIITL    | 7      | 1          | P04637                   | 2         | 2,495E6  | 0,008   | 0,0877 | 38       | 0,004348924 | 2   | 1039,68657 | -0,84     | 137,77  |
| 601| YARDETEFY   | 1      | 1          | P18077                   | 3         | 3,544E7  | 0,008   | 0,0853 | 37       | 0,036542247 | 2   | 1193,51531 | 3,63      | 76,33   |
| 602| QTYSTEPNKL  | 1      | 1          | P46779                   | 5         | 5,899E5  | 0,008   | 0,08813| 37       | 0,107695894 | 2   | 1294,63237 | 3,84      | 51,51   |
| 603| GTmTGMLYK   | 3      | 2          | Q5SRD1;O14925           | M3        | 3,429E7  | 0,008   | 0,08554| 36       | 0,064156758 | 2   | 1017,47771 | 3,24      | 58,77   |
| 604| VPLDERIVF   | 15     | 1          | Q96TA1                   | 6         | 6,324E7  | 0,008   | 0,0892 | 36       | 0,110407949 | 2   | 1087,61455 | -0,12     | 123,40  |
| 605| mLDPLEVHL   | 1      | 1          | Q6P2Q9                   | M1        | 2,387E6  | 0,008   | 0,08503| 35       | 0,112337461 | 2   | 1082,55889 | 3,48      | 122,91  |
| 606| IPIGIDKAL   | 2      | 1          | Q13451                   | 3         | 3,594E7  | 0,008   | 0,08815| 34       | 0,02925105   | 2   | 939,58696   | -0,47     | 107,82  |
| 607| SPLKLLTm    | 1      | 1          | P51654                   | M9        | 3,147E6  | 0,008   | 0,08856| 34       | 0,11255322  | 2   | 1005,56828  | 3,32      | 94,95   |
| 608| APAAWLRSA   | 1      | 1          | P24347                   | 3         | 3,432E6  | 0,008   | 0,08837| 34       | 0,095729837 | 2   | 1013,55486  | 2,08      | 82,01   |
| 609| KPAFFAELK   | 2      | 1          | P04083                   | 3         | 3,007E5  | 0,008   | 0,08521| 33       | 0,110801393 | 2   | 1050,59783  | -0,45     | 75,15   |
| 610| DVIRLImQy   | 2      | 1          | Q2TAY7                   | M7        | 8,511E6  | 0,008   | 0,08779| 33       | 0,154466858 | 2   | 1166,62663  | 2,38      | 127,59  |
| 611| VPPTAISHF   | 1      | 1          | Q9NR30                   | 1         | 1,743E7  | 0,008   | 0,08953| 33       | 0,093788721 | 2   | 968,52153   | 1,55      | 82,04   |
| 612| VLFAGQHIAK  | 1      | 1          | P21333                   | 6         | 6,035E6  | 0,008   | 0,08654| 33       | 0,04322424  | 2   | 1083,63518  | 3,86      | 63,08   |
| 613| YLNEKAVSY   | 1      | 1          | Q13492                   | 1         | 1,885E7  | 0,008   | 0,08733| 32       | 0,168408541 | 2   | 1086,54827  | 1,51      | 69,52   |
| 614| VPASFRLQm   | 1      | 1          | Q9BTE3                   | M9        | 2,404E6  | 0,008   | 0,08916| 31       | 0,320796441 | 2   | 1064,55730  | 1,42      | 81,27   |
| 615| LPPPVHVDY   | 1      | 1          | Q13889                   | 3         | 3,862E7  | 0,008   | 0,0869 | 31       | 0,309752433 | 2   | 1036,54924  | 2,89      | 90,10   |
| 616| HVAAPYIAK   | 2      | 1          | Q9H2P0                   | 1         | 1,032E7  | 0,008   | 0,08459| 31       | 0,188976845 | 2   | 969,55205   | 0,40      | 49,33   |
| 617| GLYKAPLSK   | 1      | 1          | Q8NBK4                   | 2         | 2,287E7  | 0,008   | 0,09015| 31       | 0,140274431 | 2   | 976,58599   | 3,43      | 53,41   |
| #  | Sequence     | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area  | q-Value | PEP  | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|----|--------------|--------|------------|--------------------------|----------|-------|---------|------|----------|------------|-----|----------|----------|---------|
| 618| KPSDVMLVHF   | 1      | 1          | Q8WWM7                   | 3,774E6  | 0,008 | 0,08553 | 31   | 0,34709979 | 1172,61638 | 2   | 1172,61638 | 2,63    | 102,06  |
| 619| RVYGGDITTK   | 3      | 1          | Q8WUM4                   | 1,234E8  | 0,008 | 0,08701 | 29   | 0,317584504 | 994,56761 | 2   | 994,56761 | -0,43   | 37,49   |
| 620| APIRPDIVNF   | 1      | 1          | P36578                  | 1,997E7  | 0,008 | 0,0857  | 28   | 0,391280546 | 1141,63701 | 2   | 1141,63701 | 0,46    | 110,33  |
| 621| RPITVSYAF    | 1      | 1          | Q15427                  | 2,512E7  | 0,008 | 0,08513 | 28   | 0,462723653 | 1053,57500 | 2   | 1053,57500 | 2,10    | 98,54   |
| 622| VVLGQFLVLK   | 1      | 1          | O75531                  | 5,837E6  | 0,008 | 0,08775 | 27   | 0,033167785 | 1115,72222 | 2   | 1115,72222 | 3,10    | 135,21  |
| 623| LPWVGKELY    | 1      | 1          | Q09161                  | 9,172E6  | 0,008 | 0,08655 | 27   | 0,68542921  | 1104,61235 | 2   | 1104,61235 | 3,17    | 117,73  |
| 624| LPVLSTDKF    | 1      | 1          | Q7L5N1                  | 4,078E6  | 0,008 | 0,08806 | 26   | 0,590171134 | 1019,57878 | 2   | 1019,57878 | 1,53    | 104,56  |
| 625| RAmAKRTKD    | 1      | 1          | Q68D10                  | 2,960E6  | 0,008 | 0,08548 | 26   | 0,696161014 | 1092,59758 | 2   | 1092,59758 | 3,00    | 35,79   |
| 626| FVELGTQPATQ  | 2      | 1          | P02652                  | 4,743E7  | 0,008 | 0,08915 | 24   | 1,992076261 | 1190,60759 | 2   | 1190,60759 | 1,98    | 97,46   |
| 627| HPAIALREY    | 1      | 1          | P10155                  | 1,638E7  | 0,008 | 0,08456 | 24   | 1,069605999 | 1069,57915 | 2   | 1069,57915 | 0,19    | 64,96   |
| 628| GLYYIHRNK    | 1      | 1          | P50750                  | 3,677E4  | 0,008 | 0,08684 | 24   | 1,465505753 | 1163,63335 | 2   | 1163,63335 | 1,14    | 37,55   |
| 629| NWRPRFKY     | 3      | 1          | Q9UP95                  | 1,403E5  | 0,008 | 0,08653 | 23   | 1,496052894 | 1166,62346 | 2   | 1166,62346 | 1,41    | 134,78  |
| 630| YWGEISSQY    | 1      | 1          | P14735                  | 4,012E7  | 0,008 | 0,08557 | 22   | 2,374462626 | 1286,61052 | 2   | 1286,61052 | 4,13    | 134,74  |
| 631| RQIPYTMmK    | 1      | 1          | Q00325                  | 1,011E7  | 0,008 | 0,08531 | 21   | 3,338428799 | 1183,59941 | 2   | 1183,59941 | 2,66    | 51,41   |
| 632| MPLGTJKALPSm | 1      | 1          | Q9UMZ2                  | 0,000E0  | 0,008 | 0,08958 | 20   | 4,120099194 | 1258,65569 | 2   | 1258,65569 | 1,76    | 90,77   |
| 633| SFmDPASALY   | 1      | 1          | P28070                  | 4,625E6  | 0,008 | 0,08808 | 20   | 1,804149429 | 1117,49040 | 2   | 1117,49040 | 2,97    | 120,98  |
| 634| VPEEGGATHVY  | 1      | 1          | Q9NQ31                  | 6,594E7  | 0,008 | 0,08878 | 13   | 15,90668631 | 1158,54766 | 2   | 1158,54766 | 4,34    | 58,61   |
| 635| AGQNDPLK     | 1      | 1          | P27816                  | 1,226E7  | 0,009 | 0,1009  | 55   | 0,001007809 | 842,43706 | 2   | 842,43706  | 0,42    | 33,12   |
| #    | Sequence        | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area     | q-Value | PEP    | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|------|-----------------|-------|------------|--------------------------|-----------|----------|---------|--------|----------|------------|-----|----------|----------|---------|
| 636  | SVAQLLSK        | 1     | 1          | P29375                   |           | 1,506E7  | 0,009   | 0,09882| 49       | 0,001870189 | 2   | 958,59551 | 2,40     | 99,54   |
| 637  | RPGGLGSSSL      | 16    | 1          | P08729                   |           | 1,003E9  | 0,009   | 0,09208| 45       | 0,014625555 | 2   | 930,49993 | -0,48    | 53,50   |
| 638  | VQVTKASY        | 1     | 1          | P35221                   |           | 4,696E6  | 0,009   | 0,1083 | 45       | 0,007183141 | 2   | 994,56041 | 3,63     | 53,42   |
| 639  | ATAVAVPLVGK     | 1     | 1          | Q98UN8                   |           | 1,985E5  | 0,009   | 0,1039 | 44       | 0,003464094 | 2   | 954,59776 | -0,56    | 91,38   |
| 640  | HPHQNLIA TY     | 1     | 1          | Q2TAY7                   |           | 1,476E7  | 0,009   | 0,09831| 43       | 0,019818203 | 2   | 1193,61199 | 4,85     | 59,46   |
| 641  | QPYTDGVRm       | 1     | 1          | P14923                   | M9        | 4,804E6  | 0,009   | 0,09737| 43       | 0,016220925 | 2   | 1082,49468 | 1,03     | 48,27   |
| 642  | SVSNVITK        | 1     | 1          | P42566                   |           | 2,379E5  | 0,009   | 0,09182| 42       | 0,013964926 | 2   | 946,55675 | -0,07    | 56,35   |
| 643  | VSFPIGIYK       | 1     | 1          | Q8TCA0                   |           | 2,642E7  | 0,009   | 0,09874| 41       | 0,012961866 | 2   | 1023,58989 | 2,45     | 113,38  |
| 644  | HPTDITSLDQY     | 1     | 1          | P14625                   |           | 6,828E6  | 0,009   | 0,1079 | 41       | 0,028831968 | 2   | 1289,60454 | 2,86     | 93,92   |
| 645  | DAIRLAVSY       | 4     | 2          | Q9UBK7;Q9UNT1            |           | 3,642E5  | 0,009   | 0,09789| 40       | 0,035552321 | 2   | 1007,55168 | -0,38    | 115,46  |
| 646  | YADPVN AHY      | 1     | 1          | O95758                   |           | 3,356E6  | 0,009   | 0,1041 | 39       | 0,033420684 | 2   | 1049,47063 | 1,84     | 70,37   |
| 647  | AVLKAVQQY       | 1     | 2          | Q9P0M2;O43687            |           | 6,483E6  | 0,009   | 0,09303| 39       | 0,029102584 | 2   | 1019,59200 | 1,72     | 68,80   |
| 648  | ASINRIYG       | 1     | 3          | P36873;P62140;P62136     |           | 3,751E7  | 0,009   | 0,104  | 39       | 0,025843477 | 2   | 1040,55400 | 1,55     | 97,95   |
| 649  | SIIRLLEV        | 1     | 1          | P62136                   |           | 2,540E7  | 0,009   | 0,1087 | 38       | 0,025514966 | 2   | 999,62193 | 2,17     | 132,72  |
| 650  | KPFD AFTDL      | 1     | 1          | P04004                   |           | 1,123E7  | 0,009   | 0,1079 | 38       | 0,05806641 | 2   | 1053,52825 | 2,90     | 121,32  |
| 651  | NAESGRGQVm      | 1     | 1          | P24001                   | M10       | 2,133E5  | 0,009   | 0,1005 | 38       | 0,038015704 | 2   | 1064,48235 | 3,15     | 23,85   |
| 652  | TVRPPAVK        | 1     | 1          | P12111                   |           | 5,642E7  | 0,009   | 0,09413| 38       | 0,007880168 | 2   | 966,61156 | 2,10     | 47,19   |
| 653  | VPDPNVIKL       | 1     | 2          | Q9UMR2;Q9NUU7            |           | 1,854E7  | 0,009   | 0,09142| 37       | 0,022603113 | 2   | 994,59502 | 1,82     | 101,42  |
| #  | Sequence       | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area   | q-Value | PEP   | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|----|----------------|--------|------------|--------------------------|-----------|--------|---------|-------|----------|------------|-----|----------|----------|----------|
| 654 | ALAFHLISQK     | 1      | 1          | P42566                   |           | 3,229E6| 0,009   | 0,1041| 37       | 0,030956144| 2   | 1127,66081| 3,20     | 86,96    |
| 655 | TNFEDRNAF      | 1      | 2          | Q96F07;Q7L576            |           | 1,955E7| 0,009   | 0,0964| 36       | 0,042405465| 2   | 1113,49968| 3,30     | 73,75    |
| 656 | ATFGTQVVEK     | 1      | 1          | P01024                   |           | 2,833E6| 0,009   | 0,1011| 36       | 0,091556294| 2   | 1079,57280| -0,37    | 65,15    |
| 657 | KVGCSGANK      | 1      | 1          | P10599                   |           | 1,651E7| 0,009   | 0,1068| 36       | 0,101198937| 2   | 1036,54399| 1,69     | 30,77    |
| 658 | KVYGPGVAK      | 1      | 1          | P21333                   |           | 2,060E7| 0,009   | 0,09128| 35       | 0,060223708| 2   | 918,53972 | -1,14    | 31,85    |
| 659 | KIEQLLGF       | 5      | 1          | Q96DE5                   |           | 1,794E7| 0,009   | 0,09243| 35       | 0,114912951| 2   | 1044,60820| -0,63    | 129,60   |
| 660 | TPLDRVTEF      | 1      | 1          | Q9UFW8                   |           | 5,783E6| 0,009   | 0,1022| 34       | 0,199055784| 2   | 1077,56011| 2,37     | 102,63   |
| 661 | SVmRLTISY      | 4      | 1          | Q16665                   | M3        | 1,021E7| 0,009   | 0,1015| 34       | 0,151416209| 2   | 1085,56584| -0,14    | 86,41    |
| 662 | AAMLDTVVKF     | 1      | 1          | O00487                   |           | 2,886E6| 0,009   | 0,1042| 33       | 0,150639938| 2   | 1094,59490| 3,09     | 110,76   |
| 663 | IPAPTDLKF      | 1      | 1          | P02751                   |           | 2,202E6| 0,009   | 0,09637| 33       | 0,09713942 | 2   | 1001,56780| 1,13     | 110,25   |
| 664 | EAQPIVTKY      | 1      | 1          | Q1KMD3                   |           | 2,935E7| 0,009   | 0,104  | 33       | 0,228824197| 2   | 1048,56780| 0,41     | 65,52    |
| 665 | IIAEVKAQY      | 6      | 11         | P05787;P13647;Q95678;P08729;P02538;P04259;P48668;P35908;Q5XKE5;P04264;Q9NSB2 | 7,970E7  | 0,009   | 0,09339| 32     | 0,161722369| 2   | 1034,58745| -0,64    | 77,00    |
| 666 | APYRTOSSASL    | 1      | 1          | Q96PK6                   |           | 8,817E6| 0,009   | 0,1085| 32       | 0,300182799| 2   | 1180,60100| 4,48     | 52,53    |
| 667 | RTNWPNTGK      | 1      | 1          | Q6NUQ1                   |           | 3,732E7| 0,009   | 0,09493| 32       | 0,235649653| 2   | 1073,55058| 1,75     | 33,46    |
| 668 | SPTKLDVTL      | 5      | 1          | P27816                   |           | 8,363E5| 0,009   | 0,1032| 32       | 0,183072274| 2   | 973,55614 | -0,35    | 91,20    |
| 669 | RTIAPIGN      | 2       | 1          | Q99459                   |           | 3,603E7| 0,009   | 0,1075| 32       | 0,024507957| 2   | 996,63567 | 4,35     | 63,56    |
| 670 | RPGFQQTSH      | 1      | 1          | Q13443                   |           | 4,645E6| 0,009   | 0,103  | 32       | 0,263285037| 2   | 1057,51763| 0,21     | 28,71    |
| 671 | AVL5WKLAK      | 1      | 1          | Q7Z3B0                   |           | 1,405E7| 0,009   | 0,09464| 31       | 0,083071582| 2   | 1015,63036| 0,42     | 81,06    |
| #  | Sequence       | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area     | q-Value | PEP    | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|----|----------------|-------|------------|--------------------------|-----------|----------|---------|--------|----------|------------|-----|----------|----------|---------|
| 672| APPRPGSSF      | 2     | 1          | Q86XP3                   |           | 2,757E8  | 0,009   | 0,09599| 31       | 0,196959894 | 2   | 915,47161| 3,57     | 52,60   |
| 673| APKLFPVAF      | 1     | 1          | Q9UDX3                   |           | 3,133E6  | 0,009   | 0,102  | 31       | 0,123277878 | 2   | 989,58519| 3,30     | 129,93  |
| 674| SPmSADRVVAF    | 1     | 2          | P10589;P24468            | M3        | 1,759E7  | 0,009   | 0,09553| 31       | 0,317778367 | 2   | 1195,57878| 0,94     | 81,85   |
| 675| IIFDPLLLY      | 2     | 1          | Q9UPQ8                   |           | 4,884E6  | 0,009   | 0,09122| 31       | 0,105371287 | 2   | 1149,67107| 3,80     | 132,19  |
| 676| LPDLNHSQVY     | 1     | 1          | Q92900                   |           | 1,399E7  | 0,009   | 0,1007 | 31       | 0,324674216 | 2   | 1185,59453| 3,91     | 90,76   |
| 677| EPAQRKIlm      | 6     | 1          | Q87B72                   | M9        | 1,292E6  | 0,009   | 0,101  | 31       | 0,243518274 | 2   | 1101,60893| 0,34     | 133,30  |
| 678| AVFGPDGTLLAK   | 1     | 1          | Q9NQR4                   |           | 5,918E6  | 0,009   | 0,09131| 31       | 0,267570038 | 2   | 1188,66606| 3,11     | 106,13  |
| 679| ImLPFRFTY      | 1     | 1          | Q96CS3                   | M2        | 1,855E6  | 0,009   | 0,09254| 30       | 0,506565371 | 2   | 1203,62724| 3,42     | 140,66  |
| 680| ASLVGQTSPK     | 1     | 1          | Q9Y2X3                   |           | 6,437E6  | 0,009   | 0,09353| 30       | 0,416843811 | 2   | 987,54601| -0,99    | 46,01   |
| 681| IPIALSRGDIL    | 1     | 1          | P26196                   |           | 4,066E6  | 0,009   | 0,09326| 29       | 0,094144701 | 2   | 1167,71196| 1,98     | 121,95  |
| 682| YFIDSTNLKTHF   | 1     | 1          | O00488                   |           | 1,353E7  | 0,009   | 0,1047 | 29       | 0,547770826 | 3   | 1485,73944| 1,45     | 106,73  |
| 683| RPTDKPLRL      | 5     | 3          | P68104;Q05639;Q5VTE0     |           | 4,974E7  | 0,009   | 0,1049 | 28       | 0,107952255 | 2   | 1095,66313| -0,21    | 40,17   |
| 684| LPLPAPHAQY     | 1     | 1          | P42694                   |           | 4,823E6  | 0,009   | 0,0902 | 28       | 0,392387801 | 2   | 1106,60222| 2,60     | 89,59   |
| 685| KLALEGALQK     | 1     | 5          | Q14533;Q43790;A6NCN2;P7838 S;P78386 |           | 4,794E6  | 0,009   | 0,09966| 28       | 0,366763295 | 2   | 1199,70244| 2,47     | 71,68   |
| 686| KILGPOQNTIK    | 1     | 1          | Q07666                   |           | 4,024E6  | 0,009   | 0,09455| 28       | 0,16489812  | 2   | 1168,70537| 0,41     | 47,80   |
| 687| DPWIGKLLY      | 1     | 1          | P21673                   |           | 4,419E6  | 0,009   | 0,09605| 28       | 0,539464174 | 2   | 1104,61284| 3,61     | 144,33  |
| 688| AVYENAREK      | 1     | 1          | Q75QN2                   |           | 6,130E6  | 0,009   | 0,09812| 28       | 0,697570625 | 2   | 1079,55254| 4,17     | 27,49   |
| 689| YRYPTGESY      | 1     | 1          | Q16875                   |           | 3,147E6  | 0,009   | 0,1046 | 28       | 0,37093169  | 2   | 1135,50517| -0,26    | 67,68   |
| #  | Sequence     | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area    | q-Value | PEP    | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|----|--------------|--------|------------|--------------------------|-----------|---------|---------|--------|----------|------------|-----|----------|----------|---------|
| 690| APLSKkmY     | 2      | 3          | P23528;Q9Y281;P60981     | M7        | 3,923E7 | 0,009  | 0,1051 | 27       | 0,426031643 | 2   | 1066,59636 | -0,20    | 42,89   |
| 691| LYEVSQLKD    | 2      | 1          | Q96KP4                   |           | 7,445E6 | 0,009  | 0,09877| 27       | 0,71102198  | 2   | 1094,57244 | -0,38    | 81,89   |
| 692| RVFQDVAQK    | 1      | 2          | Q9UPQ3;Q96P47            |           | 7,805E6 | 0,009  | 0,1072 | 27       | 0,646405484 | 2   | 1090,60137 | 0,87     | 44,19   |
| 693| RVAPEEHPVLL  | 1      | 3          | P60709;P63261;A5A3E0     |           | 3,808E6 | 0,009  | 0,09793| 27       | 0,48736079  | 2   | 1259,71343 | 2,16     | 75,33   |
| 694| KLLDDPSKQK   | 1      | 2          | Q6STE5;Q92925            |           | 1,498E7 | 0,009  | 0,102  | 27       | 0,617038216 | 2   | 1171,67204 | 3,31     | 35,19   |
| 695| ATIRPWSTF    | 1      | 1          | Q9UJ14                   |           | 4,936E6 | 0,009  | 0,1078 | 27       | 0,64166519  | 2   | 1078,57134 | 3,05     | 105,02  |
| 696| SLEPPFLK     | 1      | 1          | Q5GLZ8                   |           | 1,065E7 | 0,009  | 0,09358| 27       | 0,382631632 | 2   | 1142,68559 | 3,12     | 128,77  |
| 697| ILDPHVVLL    | 3      | 1          | Q99567                   |           | 1,519E7 | 0,009  | 0,1086 | 26       | 0,182235304 | 2   | 1018,63164 | 2,01     | 130,15  |
| 698| LPNEGRNDY    | 1      | 1          | Q96JJ3                   |           | 2,254E6 | 0,009  | 0,1086 | 26       | 0,635008595 | 2   | 1077,49626 | 0,24     | 49,57   |
| 699| LPQHPDVEm    | 1      | 1          | Q7Z7E8                   | M9        | 8,125E6 | 0,009  | 0,09177| 26       | 0,855577708 | 2   | 1081,49980 | 1,37     | 58,02   |
| 700| LPSDVPLHF    | 1      | 1          | A0AUZ9                   |           | 2,073E6 | 0,009  | 0,09902| 26       | 0,46155859  | 2   | 1024,54741 | 1,13     | 118,79  |
| 701| AVLPRAFTY    | 1      | 1          | P08F94                   |           | 8,273E7 | 0,009  | 0,1034 | 25       | 0,552460496 | 2   | 1037,58049 | 2,52     | 102,63  |
| 702| VLSPADTNVKA  | 1      | 1          | P69905                   |           | 7,428E5 | 0,009  | 0,1037 | 25       | 0,905485785 | 2   | 1242,70586 | 0,46     | 48,04   |
| 703| RLYDLPAKR    | 1      | 1          | Q8NF91                   |           | 2,488E6 | 0,009  | 0,1049 | 24       | 0,564725794 | 2   | 1131,66582 | 2,18     | 50,69   |
| 704| IQFNPPLSEK   | 3      | 1          | Q8NB78                   |           | 2,641E7 | 0,009  | 0,09647| 23       | 1,661570503 | 2   | 1172,63323 | 1,85     | 92,45   |
| 705| KLAEVITK     | 1      | 1          | Q8IVL0                   |           | 6,071E6 | 0,009  | 0,102  | 23       | 0,480856775 | 2   | 1064,63750 | 2,29     | 62,35   |
| 706| RGNPLVVRF    | 1      | 1          | Q96CX6                   |           | 1,535E7 | 0,009  | 0,1072 | 23       | 1,07201198  | 2   | 1057,62859 | 1,90     | 79,81   |
| 707| mVTEIRLKY    | 2      | 1          | Q15393                   | M1        | 8,777E6 | 0,009  | 0,1    | 23       | 1,337482316 | 2   | 1168,64372 | 3,61     | 74,61   |
| #   | Sequence         | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area         | q-Value | PEP     | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|------------------|--------|------------|--------------------------|-----------|--------------|---------|---------|----------|------------|-----|----------|----------|---------|
| 708 | KVVTHNLLYY      | 1      | 1          | Q96EK5                   |           | 1,106E7      | 0,009   | 0,09884 | 22       | 2,858548245 | 2   | 1200,60881 | 3,36     | 60,31   |
| 709 | LPISPKLEEF       | 1      | 1          | Q9Y6I7                   |           | 1,799E6      | 0,009   | 0,09058 | 21       | 0,947488464 | 2   | 1156,70207 | 3,80     | 142,27  |
| 710 | TPVLEPTKVT       | 1      | 1          | Q9ULD2                   |           | 1,777E6      | 0,009   | 0,09708 | 21       | 2,662191079 | 2   | 1231,69524 | 1,56     | 107,44  |
| 711 | YPSRAVITTm       | 1      | 1          | Q06136                   |           | 4,286E6      | 0,009   | 0,1044  | 21       | 3,346039359 | 2   | 1154,58867 | 1,04     | 65,29   |
| 712 | RTALNLFFK        | 1      | 1          | P53621                   |           | 1,360E7      | 0,009   | 0,09479 | 20       | 0,750842692 | 2   | 1109,64934 | 2,43     | 101,26  |
| 713 | KPFNPLLGETY      | 1      | 2          | Q98XW6;Q9H1P3            |           | 9,109E6      | 0,009   | 0,09973 | 20       | 3,773348219 | 2   | 1278,67632 | 2,66     | 111,50  |
| 714 | NPYHNEPGF        | 1      | 1          | Q9H832                   |           | 1,958E7      | 0,009   | 0,09386 | 20       | 1,590339302 | 2   | 1074,46721 | 3,02     | 63,21   |
| 715 | VLREIAEETY       | 1      | 1          | Q00341                   |           | 2,780E6      | 0,009   | 0,09838 | 20       | 4,178328936 | 2   | 1121,58696 | 2,85     | 84,89   |
| 716 | VPYRIFPY         | 1      | 1          | Q14739                   |           | 0,000E0      | 0,009   | 0,1006  | 20       | 2,741878268 | 2   | 1054,57439 | 2,22     | 114,33  |
| 717 | AVQKAIPmYK       | 1      | 1          | P36543                   | M8        | 2,721E6      | 0,009   | 0,09066 | 19       | 3,524780283 | 2   | 1164,64641 | 1,56     | 48,12   |
| 718 | KmDDLNLHY        | 2      | 1          | Q8NCJ5                   | M2        | 1,693E7      | 0,009   | 0,1012  | 18       | 4,838275131 | 2   | 1164,53899 | 3,06     | 68,91   |
| 719 | FPEQIAEKL        | 1      | 1          | Q9Y546                   |           | 1,301E7      | 0,009   | 0,09534 | 18       | 8,274691951 | 2   | 1074,58403 | 0,92     | 97,60   |
| 720 | RPDEKAImTY       | 1      | 2          | P12814;O43707            | M8        | 9,240E6      | 0,009   | 0,09282 | 18       | 7,651174169 | 2   | 1239,60576 | 1,54     | 50,80   |
| 721 | TPVDLNKHLY       | 1      | 1          | O00443                   |           | 2,318E6      | 0,009   | 0,1027  | 18       | 7,416956152 | 2   | 1199,64372 | 1,49     | 75,23   |
| 722 | FVYPGNPLRH       | 1      | 1          | Q96EK7                   |           | 6,650E6      | 0,009   | 0,105   | 15       | 10,58379722 | 2   | 1199,63432 | 1,90     | 82,48   |
| 723 | KPFEOVKGITL      | 1      | 1          | P33121                   |           | 8,764E6      | 0,009   | 0,1001  | 14       | 6,480233488 | 2   | 1259,74040 | 3,61     | 88,45   |
| 724 | DEVVQIFDKEG       | 1      | 1          | P30085                   |           | 3,013E6      | 0,009   | 0,09647 | 13       | 17,02261391 | 2   | 1278,62590 | 3,61     | 110,71  |
| 725 | HPYSQALIQY       | 1      | 1          | Q7K285                   |           | 6,497E6      | 0,009   | 0,09544 | 13       | 26,61227385 | 2   | 1219,61467 | 3,33     | 90,73   |
| #   | Sequence          | PSMs | Proteins | Protein Group Accessions | Mod. (ox) | Area   | q-Value | PEP   | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|-------------------|------|----------|--------------------------|-----------|--------|---------|-------|----------|------------|-----|----------|----------|----------|
| 726 | LFYDKLQY         | 1    | 1        | Q9NQT8                   |           | 2,508E6| 0,009   | 0,1048| 12       | 22,76265003| 2   | 1188,63323| 2,75     | 124,45   |
| 727 | YYNGKIHAY        | 1    | 1        | O75643                   |           | 1,665E6| 0,009   | 0,1002| 12       | 21,91548481| 2   | 1128,54949| 1,96     | 50,74    |
| 728 | RPPIGAEV         | 20   | 1        | Q07820                   |           | 1,155E9| 0,01    | 0,1089| 42       | 0,017288978| 2   | 935,53063| -0,35    | 64,52    |
| 729 | APYKSDFLKAL      | 1    | 1        | Q9NZD2                   |           | 2,962E6| 0,01    | 0,1091| 24       | 0,868713204| 2   | 1252,69792| 3,41     | 98,11    |
| 730 | APSKTSIm         | 1    | 1        | Q9H334                   | Mod. (ox) | 2,560E7| 0,011   | 0,1123| 43       | 0,010711633| 2   | 963,51995| 2,02     | 54,40    |
| 731 | SIFAGQNDPLK      | 1    | 1        | P27816                   |           | 1,121E7| 0,011   | 0,1095| 42       | 0,035985569| 2   | 1189,62688| 4,76     | 90,96    |
| 732 | VPVIISRAL        | 1    | 1        | Q14919                   |           | 1,940E6| 0,011   | 0,1123| 38       | 0,005079908| 2   | 967,63072| 0,82     | 102,81   |
| 733 | GLNKTIGY         | 1    | 1        | Q8TE76                   |           | 4,065E7| 0,011   | 0,1097| 38       | 0,078534264| 2   | 979,52342| 2,73     | 62,10    |
| 734 | GQYNPDLNK        | 1    | 1        | O14672                   |           | 8,336E7| 0,011   | 0,1099| 36       | 0,112493749| 2   | 990,50359| 3,27     | 54,37    |
| 735 | RTGPPMGSRF       | 1    | 1        | Q15056                   |           | 3,530E7| 0,011   | 0,111 | 35       | 0,134892438| 2   | 1105,55620| -0,90    | 49,80    |
| 736 | LPSNDSSKF        | 1    | 1        | P17480                   |           | 1,489E7| 0,011   | 0,11  | 34       | 0,176356119| 2   | 994,48711| 3,08     | 54,85    |
| 737 | SPAGAGTLHAL      | 1    | 1        | Q8TEV9                   |           | 3,547E6| 0,011   | 0,1106| 34       | 0,123166996| 2   | 994,53331| 1,65     | 69,58    |
| 738 | FPLQPGKATF       | 1    | 1        | Q96Q05                   |           | 5,029E6| 0,011   | 0,1119| 34       | 0,125940738| 2   | 1204,67681| 3,55     | 112,79   |
| 739 | mAVYLSAGVIS      | 1    | 1        | Q9H300                   | Mod. (ox) | 1,288E5| 0,011   | 0,1116| 34       | 0,167752023| 2   | 1126,57744| -3,45    | 91,94    |
| 740 | GSYNKVLAK        | 7    | 1        | P48556                   |           | 1,565E8| 0,011   | 0,111 | 30       | 0,27658857 | 2   | 1126,62541| -0,13    | 56,30    |
| 741 | IVDGNHRLTL       | 1    | 3        | C9H254;C01082;C015020    |           | 1,019E7| 0,011   | 0,1104| 27       | 0,4652518   | 2   | 1137,63738| -0,14    | 67,33    |
| 742 | VPRIDPYGF        | 1    | 1        | Q5TC63                   |           | 3,134E6| 0,011   | 0,1119| 26       | 0,806383827 | 2   | 1063,55864| 1,40     | 110,74   |
| 743 | NPWDNKAVY        | 4    | 1        | Q86TM6                   |           | 3,657E5| 0,011   | 0,1096| 25       | 1,183430493| 2   | 1106,52629| -0,25    | 88,23    |
| #   | Sequence     | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area  | q-Value | PEP  | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT  [min] |
|-----|--------------|--------|------------|--------------------------|-----------|-------|---------|------|----------|------------|-----|----------|----------|----------|
| 744 | KmAEVIGSKL   | 1      | 1          | Q9NU22                   | M2        | 2,207E6 | 0,011   | 0,1124| 24       | 1,166840672 | 2   | 1091,61394| 0,88     | 50,82    |
| 745 | ILRDGITAGK   | 3      | 1          | O00478;O00481;P78410     | 2,044E6   | 0,011   | 0,1094  | 21   | 2,186118611 | 2   | 1043,62444| 3,46     | 48,56    |
| 746 | GNYEKVFYEY  | 3      | 1          | Q92624                   | 1,489E7   | 0,011   | 0,1101  | 20   | 3,379800607 | 2   | 1148,52800| 1,84     | 92,32    |
| 747 | DPADPHKVKY   | 1      | 1          | Q92985                   | 3,910E6   | 0,011   | 0,1099  | 17   | 6,984602561 | 2   | 1041,50066| 0,61     | 46,46    |
| 748 | RTYYPVYR    | 1      | 1          | Q99569                   | 2,372E6   | 0,011   | 0,1116  | 16   | 13,20384811 | 2   | 1204,61516| 3,50     | 56,79    |
| 749 | RPYAPINANAI  | 1      | 1          | O94776                   | 1,333E7   | 0,012   | 0,1126  | 52   | 0,001676763 | 2   | 1199,65679| 3,00     | 84,43    |
| 750 | APVGGHILSY  | 4      | 1          | Q99569                   | 2,271E5   | 0,012   | 0,1187  | 46   | 0,009365775 | 2   | 1013,54082| -0,66    | 85,36    |
| 751 | RAAQSLLNK   | 3      | 2          | Q9UMR2;Q9NUU7            | 9,742E6   | 0,012   | 0,1144  | 41   | 0,017972408 | 2   | 1000,59422| 4,37     | 36,04    |
| 752 | RTNKEIAK    | 1      | 1          | P27216                   | 1,938E6   | 0,012   | 0,113   | 41   | 0,009276191 | 2   | 1185,72978| -1,40    | 41,69    |
| 753 | LPIGDVATQY  | 2      | 1          | Q99832                   | 7,773E5   | 0,012   | 0,1135  | 41   | 0,047140997 | 2   | 1076,56194| -0,33    | 123,95   |
| 754 | GLATQAFHY   | 1      | 1          | O15027                   | 9,261E6   | 0,012   | 0,1185  | 35   | 0,119625837 | 2   | 1007,49870| 4,14     | 88,06    |
| 755 | KSTDVAKTF   | 1      | 1          | P13796                   | 1,525E7   | 0,012   | 0,1172  | 34   | 0,110720838 | 2   | 996,53789 | 1,81     | 41,19    |
| 756 | RLFEHPLYR   | 1      | 1          | Q8IXL6                   | 2,552E7   | 0,012   | 0,1184  | 34   | 0,131615524 | 3   | 1230,67517| 0,76     | 66,69    |
| 757 | QVGLAIRSK   | 4      | 1          | P52895;Q04828;P42330;P17516 | 9,379E6   | 0,012   | 0,1176  | 33   | 0,072025762 | 2   | 971,60155 | 1,91     | 47,48    |
| 758 | ATNASVFKY   | 3      | 1          | Q7Z687;Q75044;P0JJ0      | 1,005E7   | 0,012   | 0,1143  | 33   | 0,208709847 | 2   | 1000,51262| 2,77     | 72,79    |
| 759 | IPASVEHGRVY | 1      | 1          | Q9H2F3                   | 3,028E6   | 0,012   | 0,1135  | 32   | 0,187440712 | 2   | 1227,65044| 1,91     | 57,93    |
| 760 | SPVSKGILQY  | 1      | 1          | P23921                   | 1,117E7   | 0,012   | 0,1154  | 32   | 0,196299845 | 2   | 1091,61235| 2,55     | 85,37    |
| 761 | LPVDIRQYL   | 1      | 1          | P52630                   | 2,208E6   | 0,012   | 0,1165  | 31   | 0,173658065 | 2   | 1116,64519| 3,56     | 135,75   |
| #    | Sequence   | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area     | q-Value | PEP   | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|------|------------|--------|------------|--------------------------|-----------|----------|---------|-------|----------|------------|-----|----------|----------|---------|
| 762  | MPAETIKEL  | 6      | 1          | Q9H694                   |           | 2,931E7  | 0,012   | 0,1161| 31       | 0,319361457 | 2   | 1031,54350| -0,69    | 84,18   |
| 763  | KQIEHTLNEK | 1      | 2          | P22694;P17612            |           | 7,717E5  | 0,012   | 0,115 | 31       | 0,325956478 | 2   | 1239,67485| 4,54     | 26,80   |
| 764  | I PTRVVTNY | 7      | 1          | P21980                   |           | 7,505E7  | 0,012   | 0,116 | 28       | 0,488184358 | 2   | 1062,59368| -0,54    | 72,69   |
| 765  | VPVGKTTY   | 1      | 1          | P08582                   |           | 3,267E6  | 0,012   | 0,1143| 28       | 0,632111518 | 2   | 993,52464 | -0,53    | 50,32   |
| 766  | RAQHLIGF   | 1      | 1          | P22314                   |           | 6,971E7  | 0,012   | 0,1139| 26       | 0,506321695 | 2   | 1038,58745| 2,96     | 79,06   |
| 767  | NPVENIRF   | 1      | 1          | Q8WUJ0                   |           | 2,502E6  | 0,012   | 0,114 | 25       | 0,965009429 | 2   | 1101,60857| 3,08     | 118,24  |
| 768  | SYYVKVLK   | 3      | 9          | Q99879;O60814;P57053;Q93079;Q5QNW6;P62807;P58876;Q99880;Q99877 |           | 4,973E7  | 0,012   | 0,114 | 23       | 0,915714001 | 2   | 1098,65703| 1,14     | 71,67   |
| 769  | LPLTHFELY | 1      | 1          | P43686                   |           | 1,287E7  | 0,012   | 0,1186| 22       | 2,99178564  | 2   | 1132,60808| 3,82     | 126,67  |
| 770  | mTHNLLNY   | 3      | 2          | Q92769;Q13547            | M1        | 2,219E7  | 0,012   | 0,119 | 21       | 3,880029078 | 2   | 1134,56291| 1,48     | 97,97   |
| 771  | RILNHVLQH  | 1      | 1          | P21964                   |           | 1,105E6  | 0,012   | 0,1148| 18       | 4,046621001 | 2   | 1129,66191| 2,65     | 51,00   |
| 772  | KTIHLTLKV  | 1      | 1          | O15205                   |           | 2,700E6  | 0,012   | 0,1172| 18       | 0,510605277 | 2   | 1052,68242| -0,25    | 64,24   |
| 773  | RIFQEPTPK  | 1      | 1          | P31350                   |           | 2,012E6  | 0,012   | 0,1186| 15       | 12,66514847 | 2   | 1244,66643| 2,42     | 58,41   |
| 774  | VIGTVTSK   | 2      | 1          | P01008                   |           | 6,886E5  | 0,013   | 0,1193| 44       | 0,010259035 | 2   | 861,50389 | -0,18    | 40,49   |
| 775  | KLLPSVVLK  | 2      | 1          | Q99075                   |           | 2,007E5  | 0,013   | 0,1216| 44       | 0,000680657 | 2   | 996,68114 | -0,49    | 81,40   |
| 776  | IVAGSLITK  | 2      | 1          | O75400                   |           | 3,893E5  | 0,013   | 0,1241| 43       | 0,005249936 | 2   | 901,57121 | -0,58    | 73,61   |
| 777  | SPKVTLVL   | 1      | 1          | P05107                   |           | 3,161E5  | 0,013   | 0,1254| 43       | 0,012811767 | 2   | 1048,60393| 0,17     | 92,74   |
| 778  | TPLEKLSL   | 1      | 2          | Q15014;Q9UBU8            |           | 6,864E6  | 0,013   | 0,1214| 42       | 0,016219349 | 2   | 1086,60710| 2,70     | 101,09  |
| 779  | IAQFLPLL   | 1      | 1          | Q98XW9                   |           | 2,092E7  | 0,013   | 0,1224| 41       | 0,000822391 | 2   | 979,65776 | 2,74     | 130,83  |
| #   | Sequence   | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area     | q-Value | PEP       | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|------------|--------|------------|--------------------------|-----------|----------|---------|-----------|----------|------------|-----|----------|----------|---------|
| 780 | IPARFAGVLL | 4      | 1          | P04275                   |           | 4,939E5  | 0,013   | 0,1229    | 40       | 0,012395004 | 2   | 1056,65618 | -0,30   | 122,53  |
| 781 | APWDRVVDL  | 1      | 1          | O00116                   |           | 2,504E7  | 0,013   | 0,12       | 37       | 0,063227011  | 2   | 1070,56536 | 2,22    | 126,52  |
| 782 | SPLNTGKAL  | 3      | 1          | P12111                   |           | 1,561E5  | 0,013   | 0,1206    | 36       | 0,102797113 | 2   | 900,51457  | -0,42   | 56,56   |
| 783 | RSLGSSPVK  | 1      | 1          | Q9HCM1                   |           | 1,605E7  | 0,013   | 0,1211    | 36       | 0,111273502 | 2   | 930,53728  | 0,57    | 30,44   |
| 784 | FVQmmTAK   | 2      | 1          | P62158                   | M4; M5    | 1,594E5  | 0,013   | 0,1233    | 35       | 0,077000161 | 2   | 987,46330  | -0,56   | 33,48   |
| 785 | SPDKIPWSAL | 2      | 1          | Q14204                   |           | 2,096E5  | 0,013   | 0,1256    | 35       | 0,104617416 | 2   | 1113,59343 | -0,46   | 120,26  |
| 786 | APAAWLRSA  | 1      | 1          | P24347                   |           | 6,086E6  | 0,013   | 0,1254    | 35       | 0,06374468  | 2   | 942,51756  | 2,05    | 79,48   |
| 787 | LPEPVVARF  | 1      | 1          | Q8IUX7                   |           | 7,106E6  | 0,013   | 0,1216    | 35       | 0,033806102 | 2   | 1027,59551 | 1,90    | 103,23  |
| 788 | LPASVHPQL  | 1      | 1          | Q9H0K1                   |           | 1,152E7  | 0,013   | 0,1255    | 35       | 0,089943539 | 2   | 961,54766  | 1,12    | 78,02   |
| 789 | QLVSNLIF   | 1      | 1          | O95622                   |           | 6,339E5  | 0,013   | 0,1251    | 35       | 0,074407492 | 2   | 1032,60832 | -0,51   | 132,56  |
| 790 | LPRTDYSF   | 1      | 1          | P20036                   |           | 2,530E5  | 0,013   | 0,1208    | 35       | 0,136416999 | 2   | 998,49364  | -0,56   | 88,60   |
| 791 | RPLTPESL   | 1      | 1          | P46379                   |           | 1,195E7  | 0,013   | 0,1221    | 34       | 0,111784126 | 2   | 999,54607  | -0,91   | 68,51   |
| 792 | RPLVVKTSL  | 1      | 1          | P78345                   |           | 7,787E6  | 0,013   | 0,1236    | 34       | 0,03142059  | 2   | 1012,65245 | 1,05    | 62,65   |
| 793 | KPPVGTWLGL | 1      | 1          | O75995                   |           | 4,460E6  | 0,013   | 0,1194    | 33       | 0,062275204 | 2   | 1067,62798 | 2,93    | 120,69  |
| 794 | RIGKVNQK   | 3      | 1          | P51665                   |           | 3,153E5  | 0,013   | 0,1213    | 32       | 0,104637518 | 2   | 999,60533  | -0,51   | 21,65   |
| 795 | GVSGIFmKY  | 4      | 1          | Q96RQ1                   | M7        | 1,958E5  | 0,013   | 0,1198    | 32       | 0,282102056 | 2   | 1017,50688 | -0,53   | 88,51   |
| 796 | PILYNDILY  | 4      | 1          | Q5VW36                   |           | 2,049E6  | 0,013   | 0,125     | 31       | 0,233135337 | 2   | 1123,60332 | -0,08   | 155,08  |
| 797 | GTLSGWILSK | 4      | 1          | P27824                   |           | 2,046E7  | 0,013   | 0,1246    | 31       | 0,293579913 | 2   | 1061,59905  | 0,02    | 114,66  |
| #   | Sequence   | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area   | q-Value | PEP   | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|------------|--------|------------|--------------------------|-----------|--------|---------|-------|----------|------------|-----|-----------|----------|---------|
| 798 | KTGEVLDTK  | 1      | 1          | Q92520                   |           | 5,535E6| 0,013   | 0,1241| 30       | 0,291351584| 2   | 990,54711| 0,46     | 30,67   |
| 799 | SPISQKIIY  | 1      | 1          | P08603                   |           | 1,278E7| 0,013   | 0,1196| 30       | 0,244828637| 2   | 1048,60539| 1,57     | 84,32   |
| 800 | RPPPFSEKF  | 1      | 1          | Q8TDJ6                   |           | 5,831E6| 0,013   | 0,1232| 29       | 0,476012446| 2   | 1104,58354| -0,15    | 67,92   |
| 801 | EAIRISPTF  | 1      | 1          | O15294                   |           | 2,654E7| 0,013   | 0,1226| 28       | 0,655014595| 2   | 1033,57024| 2,43     | 102,97  |
| 802 | QSLIPKFL   | 4      | 1          | Q9ULK4                   |           | 5,980E7| 0,013   | 0,1246| 27       | 0,184832678| 2   | 1058,66069| -0,19    | 144,73  |
| 803 | ALIRQLKQ   | 1      | 1          | Q7Z6K1                   |           | 4,191E7| 0,013   | 0,1251| 26       | 0,137079878| 2   | 969,62297| 2,63     | 62,75   |
| 804 | AVFPKPVEK  | 1      | 1          | Q6PFW1                   |           | 2,222E7| 0,013   | 0,1208| 26       | 0,585814647| 2   | 1161,66753| 0,69     | 81,29   |
| 805 | TPIEGmLSH  | 1      | 1          | Q9UQ80                   | M6        | 2,797E6| 0,013   | 0,1205| 26       | 0,769279856| 2   | 1000,48003| 3,17     | 60,00   |
| 806 | KFDGAVFL   | 1      | 1          | O14974                   |           | 3,524E5| 0,013   | 0,1245| 26       | 1,045809726| 2   | 1011,51415| -0,48    | 120,76  |
| 807 | FAYDGKDYI  | 4      | 11         | P30462;P18463;Q95365;P30475;Q29836;Q31612;P30504;Q95604;Q29865;Q8TNN7;P30505;P13747 | 1,446E7| 0,013 | 0,1222 | 26   | 0,828665044 | 2   | 1091,50664| 2,02     | 101,96  |
| 808 | KLYGKPIRV  | 1      | 1          | Q15427                   |           | 3,287E6| 0,013   | 0,1248| 26       | 0,087878647| 2   | 1073,68303| 0,01     | 46,11   |
| 809 | NLLPSLRY   | 1      | 1          | Q709C8                   |           | 2,345E5| 0,013   | 0,1212| 25       | 0,899530345| 2   | 1138,62541| -0,11    | 119,97  |
| 810 | SWNNHSYLY  | 4      | 1          | P38435                   |           | 4,782E5| 0,013   | 0,1256| 24       | 0,631909198| 2   | 1183,51641| -0,25    | 86,88   |
| 811 | YPKYQTQTF  | 1      | 1          | Q96FX8                   |           | 4,793E6| 0,013   | 0,1243| 23       | 2,010506189| 2   | 1146,58660| 3,13     | 83,52   |
| 812 | PSRILLWK   | 4      | 1          | Q98RK3                   |           | 7,920E7| 0,013   | 0,1217| 23       | 0,486716253| 2   | 1012,62950| -0,75    | 104,37  |
| 813 | FPILMGITY  | 1      | 1          | P29371                   |           | 3,486E5| 0,013   | 0,1206| 23       | 1,366597757| 2   | 1167,65203| 3,21     | 120,25  |
| 814 | LLHDFSFSY  | 1      | 1          | Q98SJ2                   |           | 2,088E7| 0,013   | 0,1244| 22       | 1,958580677| 2   | 1137,57085| 1,83     | 70,61   |
| #  | Sequence         | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area    | q-Value | PEP   | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|----|------------------|--------|------------|--------------------------|-----------|---------|---------|-------|----------|-----------|-----|----------|----------|----------|
| 815| RPKKPGQSF        | 1      | 1          | O15042                   |           | 6,400E6 | 0,013   | 0,1251| 22       | 0,967371085 | 2   | 1044,59892 | 3,81     | 24,94    |
| 816| KLNNRQLNY        | 2      | 1          | Q12792                   |           | 1,107E8 | 0,013   | 0,1236| 21       | 2,320452454 | 2   | 1162,63262 | -0,13    | 40,50    |
| 817| SVDHVRVTK        | 1      | 1          | P20929                   |           | 9,089E6 | 0,013   | 0,1242| 21       | 1,654130449 | 2   | 1040,58940 | 4,46     | 26,71    |
| 818| RVHAYIISY        | 1      | 1          | Q9NZN4                   |           | 0,000E0 | 0,013   | 0,1237| 20       | 1,988133386 | 2   | 1121,61284 | 2,34     | 79,83    |
| 819| DAFKSGIVQY       | 1      | 1          | Q9NZ08                   |           | 1,166E7 | 0,013   | 0,1207| 20       | 3,669067241 | 2   | 1127,57561 | 2,14     | 98,19    |
| 820| KLCGYVIFR        | 1      | 1          | Q14739                   |           | 5,775E5 | 0,013   | 0,1217| 20       | 2,540274625 | 2   | 1098,61455 | 1,51     | 112,05   |
| 821| SLYHKLREK        | 1      | 1          | Q15392                   |           | 1,210E7 | 0,013   | 0,1245| 20       | 2,032180042 | 2   | 1173,67607 | 1,85     | 29,83    |
| 822| APWQRSTm         | 1      | 1          | P57764                   | M9        | 1,150E6 | 0,013   | 0,1225| 19       | 4,14366889  | 2   | 1121,50932 | 4,32     | 52,58    |
| 823| KFTNFNLFY        | 2      | 1          | P28039                   |           | 3,083E6 | 0,013   | 0,1244| 16       | 12,51296959 | 2   | 1193,60393 | 4,13     | 130,29   |
| 824| QTYVGI TEK       | 1      | 1          | O75643                   |           | 1,735E8 | 0,013   | 0,1222| 12       | 16,59645498 | 2   | 1038,54973 | 2,98     | 60,83    |
| 825| T W N P L K H Y    | 1      | 1          | Q9H4A6                   |           | 1,717E7 | 0,013   | 0,1225| 12       | 20,42079629 | 2   | 1171,62895 | 2,62     | 102,83   |
| 826| I G N G V V I H L  | 1      | 2          | Q8N142;P30520            |           | 5,506E6 | 0,014   | 0,1294| 49       | 0,01467941  | 2   | 921,55351 | 2,00     | 100,33   |
| 827| R L S P P L R P R  | 1      | 1          | O75882                   |           | 1,311E8 | 0,014   | 0,1301| 40       | 0,002028535 | 3   | 1204,76749 | 3,10     | 59,89    |
| 828| SIRQAGGIGK       | 1      | 5          | Q9NAQ3;C4ACMC7;A8K0Z3;Q6VEQ5;A8MWX3 | 1,163E7 | 0,014   | 0,1293| 38     | 0,038607149 | 2   | 986,57640 | 2,22     | 30,90    |
| 829| SVAEHPLSR        | 1      | 1          | O60287                   |           | 3,678E6 | 0,014   | 0,1263| 36       | 0,092185751 | 2   | 995,52367 | -3,26    | 34,53    |
| 830| AQNEPLTQK        | 1      | 1          | O95104                   |           | 2,676E6 | 0,014   | 0,1269| 33       | 0,153229878 | 2   | 1028,53667 | -0,46    | 32,61    |
| 831| V M A P R T L L   | 2      | 8          | P04222;P30504;Q29963;P30508;P30510;Q29960;Q9TNN7;P30505;P30443;P04439;P13746;P16188;P10314;P30455;P30459 | 2,771E5 | 0,014   | 0,1304| 33     | 0,055294476 | 2   | 1013,61705 | -0,60    | 109,42   |

| #  | Sequence         | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area    | q-Value | PEP   | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
| # | Sequence   | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area   | q-Value | PEP    | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|---|------------|--------|------------|--------------------------|-----------|--------|---------|--------|----------|-----------|-----|----------|----------|---------|
| 832 | SPFSYKNVL  | 1      | 1          | P05556                   |           | 1,269E7| 0,014   | 0,1282 | 32       | 0,208962298 | 2   | 1054,55962 | 2,67     | 99,86   |
| 833 | HPIHQGITEI | 1      | 1          | Q9H410                   |           | 5,925E6| 0,014   | 0,1269 | 29       | 0,416650645 | 2   | 1144,61431 | 2,91     | 60,05   |
| 834 | GTYGFWYPK  | 1      | 1          | Q8N6M3                   |           | 2,441E6| 0,014   | 0,1258 | 29       | 0,453454542 | 2   | 1118,53288 | 2,06     | 109,79  |
| 835 | KLYLPTGPR  | 1      | 1          | P38936                   |           | 9,951E6| 0,014   | 0,1275 | 29       | 0,279398397 | 2   | 1044,62114 | 1,01     | 64,28   |
| 836 | KLPNTVLGK  | 1      | 1          | Q9H4M9                   |           | 6,525E6| 0,014   | 0,1289 | 28       | 0,154911758 | 2   | 969,61266  | 3,57     | 53,84   |
| 837 | KVISSNTSLK | 1      | 1          | Q8IY18                   |           | 3,424E6| 0,014   | 0,1262 | 28       | 0,300903488 | 2   | 1076,63323 | 2,03     | 34,92   |
| 838 | KVETFSGKVYK| 2      | 1          | P62081                   |           | 1,216E5| 0,014   | 0,1287 | 27       | 0,80052366  | 2   | 1157,61992 | -0,19    | 52,28   |
| 839 | FPIDKPPSF  | 1      | 1          | P51805                   |           | 8,475E6| 0,014   | 0,1257 | 27       | 1,00771713  | 2   | 1047,55327 | 2,16     | 109,63  |
| 840 | YTRPTPVQK  | 3      | 2          | O00571; O15523           |           | 8,010E7| 0,014   | 0,1322 | 27       | 0,737385055 | 2   | 1089,60515 | 0,00     | 33,14   |
| 841 | ADKQLSFEF | 1      | 1          | P06702                   |           | 2,183E6| 0,014   | 0,1287 | 26       | 0,817224265 | 2   | 1213,57781 | 3,47     | 106,62  |
| 842 | LVSESSDLPK | 1      | 1          | P05787                   |           | 4,021E6| 0,014   | 0,1301 | 25       | 1,30522768  | 2   | 1173,63811 | 1,63     | 76,43   |
| 843 | ALSYVVKK   | 1      | 1          | O95714                   |           | 4,588E6| 0,014   | 0,1276 | 24       | 0,420500375 | 2   | 994,59276  | -0,43    | 48,91   |
| 844 | APWKPTWPA  | 4      | 1          | O95084                   |           | 8,904E7| 0,014   | 0,132  | 24       | 1,106392022 | 2   | 1053,55327 | 1,51     | 102,81  |
| 845 | RLEKSRVK   | 1      | 1          | P10586                   |           | 3,692E6| 0,014   | 0,1306 | 23       | 0,757321974 | 2   | 1144,68047 | 0,63     | 19,77   |
| 846 | YVIQFFEF   | 1      | 2          | Q8TB72; Q14671           |           | 3,577E6| 0,014   | 0,1288 | 22       | 2,820315215 | 2   | 1220,63994 | 4,00     | 142,07  |
| 847 | NPYPGDVTKF | 1      | 1          | QST6F2                   |           | 2,154E6| 0,014   | 0,1278 | 22       | 3,01512749  | 2   | 1137,56243 | 4,29     | 88,34   |
| 848 | KPINVRVTm  | 1      | 2          | P35241; P15311           | M10       | 8,361E6| 0,014   | 0,1298 | 19       | 3,611981318 | 2   | 1174,65984 | -1,26    | 48,76   |
| 849 | FLGISTFSQY | 1      | 1          | P07327                   |           | 2,766E5| 0,014   | 0,1283 | 18       | 6,361290485 | 2   | 1162,57756 | -0,32    | 112,14  |
| #   | Sequence     | # PSMs | # Proteins | Protein Group Accessions                      | Mod. (ox) | Area     | q-Value | PEP    | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|--------------|--------|------------|------------------------------------------------|-----------|----------|---------|--------|----------|------------|-----|----------|----------|---------|
| 850 | KPYAFDRVF    | 1      | 1          | P33176                                           |           | 4,852E6  | 0,014   | 0,1265 | 17       | 6,518041425 | 2   | 1142,60124 | 1,66    | 90,53   |
| 851 | KmLRDLYY     | 1      | 1          | P42356                                           | M2        | 2,257E6  | 0,014   | 0,129  | 16       | 12,4910163 | 2   | 1218,61858 | -0,15   | 68,59   |
| 852 | YFPRVGELEY   | 1      | 1          | O15050                                           |           | 3,879E6  | 0,014   | 0,1262 | 14       | 17,26994065 | 2   | 1272,63066 | 3,70    | 117,19  |
| 853 | YFRDQKDGY    | 1      | 2          | Q99613;B5ME19                                    |           | 1,933E6  | 0,014   | 0,1272 | 14       | 12,57725703 | 2   | 1191,54643 | 2,93    | 47,24   |
| 854 | IMRIALGGLL   | 1      | 1          | P04278                                           |           | 5,874E5  | 0,015   | 0,1343 | 43       | 0,006029019 | 2   | 1056,65581 | -3,84   | 122,36  |
| 855 | IQTAVRLLL    | 1      | 14         | Q99879;P06899;O60814;P57053;Q93079;P23527;Q5QNW6;P62807;Q16778;P58876;Q99880;Q99877;P33778;Q96A08 | 1,675E5  | 0,015   | 0,1374  | 42     | 0,003688546 | 2   | 1026,66631 | -0,71   | 117,41  |
| 856 | KPLGIKTAL    | 1      | 1          | Q63HN8                                           |           | 5,849E7  | 0,015   | 0,133  | 40       | 0,00545726 | 2   | 940,62029  | 1,33    | 62,25   |
| 857 | LPSQVSRVV    | 1      | 1          | P35606                                           |           | 1,420E6  | 0,015   | 0,1341 | 39       | 0,025469153 | 2   | 984,58763  | 3,99    | 74,58   |
| 858 | RPVPFASEm    | 1      | 1          | Q16828                                           | M9        | 4,726E6  | 0,015   | 0,1372 | 39       | 0,051044613 | 2   | 1049,50957 | 1,01    | 66,48   |
| 859 | LPPPPHVPL    | 1      | 1          | Q98Q83                                           |           | 2,776E7  | 0,015   | 0,1357 | 39       | 0,009917964 | 2   | 966,57976  | 2,69    | 98,98   |
| 860 | GAYGEPRVK    | 1      | 1          | Q15392                                           |           | 8,516E4  | 0,015   | 0,1341 | 38       | 0,058771438 | 2   | 976,52056  | -0,56   | 34,89   |
| 861 | YPTISLHAL    | 1      | 1          | P54105                                           |           | 8,843E6  | 0,015   | 0,1326 | 37       | 0,037237637 | 2   | 1014,56346 | 1,56    | 112,20  |
| 862 | PKNLPFPQNL   | 3      | 1          | P59047                                           |           | 3,486E5  | 0,015   | 0,1328 | 37       | 0,048702647 | 2   | 1167,65227 | 0,13    | 120,32  |
| 863 | KVNTGLmTSK   | 1      | 1          | Q8N3C7                                           | M7        | 3,481E6  | 0,015   | 0,1351 | 36       | 0,10522345 | 2   | 1094,58916 | 1,54    | 28,63   |
| 864 | ALASVVIHK    | 1      | 1          | Q6PIW4                                           |           | 2,062E6  | 0,015   | 0,1374 | 33       | 0,03254362 | 2   | 937,58379  | 0,87    | 58,06   |
| 865 | TPIKDGILY    | 1      | 1          | Q7L591                                           |           | 3,533E7  | 0,015   | 0,133  | 33       | 0,104656809 | 2   | 1019,58000 | 2,74    | 92,08   |
| 866 | VFDIHVIDF    | 3      | 1          | O95302                                           |           | 1,284E5  | 0,015   | 0,1345 | 32       | 0,264625086 | 2   | 1104,57219 | -0,25   | 158,29  |
| #  | Sequence     | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area  | q-Value | PEP  | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|----|--------------|--------|------------|--------------------------|-----------|-------|---------|------|----------|------------|-----|----------|----------|---------|
| 867 | NPHEVPQPAY   | 1      | 1          | Q9GZT9                   |           | 1,895E7 | 0,015   | 0,1368 | 29       | 0,313526888 | 2   | 1054,49639 | 1,07     | 49,55   |
| 868 | LPILLNERL    | 1      | 1          | Q8NF50                   |           | 1,397E6 | 0,015   | 0,1361 | 29       | 0,06693238  | 2   | 1080,67986 | 2,08     | 122,14  |
| 869 | KAIENKVLFL   | 1      | 1          | P10644                   |           | 1,179E7 | 0,015   | 0,1346 | 28       | 0,183090984 | 2   | 1061,63701 | 1,51     | 69,57   |
| 870 | RAAPFSLEY    | 1      | 1          | Q15181                   |           | 3,999E7 | 0,015   | 0,1337 | 28       | 0,556703401 | 2   | 1053,53960 | 3,03     | 100,08  |
| 871 | ALIDYENSNK   | 1      | 1          | Q95X3                    |           | 3,797E6 | 0,015   | 0,1353 | 26       | 1,028142013 | 2   | 1166,57158 | 2,36     | 71,21   |
| 872 | QLYSKFLLK    | 1      | 1          | P04114                   |           | 4,043E6 | 0,015   | 0,134  | 24       | 0,336472582 | 2   | 1139,68559 | 2,85     | 88,64   |
| 873 | AILSKFLYY    | 1      | 1          | Q387T1                   |           | 1,630E6 | 0,015   | 0,1374 | 24       | 1,146710565 | 2   | 1117,63176 | 2,26     | 128,06  |
| 874 | HPARLTIEAY   | 1      | 1          | Q03001                   |           | 4,010E6 | 0,015   | 0,1363 | 23       | 1,198837242 | 2   | 1170,62981 | 2,72     | 69,48   |
| 875 | LFPFDEHERY   | 1      | 1          | O43292                   |           | 4,749E7 | 0,015   | 0,1328 | 20       | 3,38468903  | 3   | 1403,66150 | 1,75     | 83,56   |
| 876 | SSIQHSSVPSI  | 1      | 1          | Q9H4D0                   |           | 2,429E6 | 0,015   | 0,1357 | 20       | 3,256394794 | 2   | 1240,65703 | 3,06     | 106,73  |
| 877 | VLLEYHIAY    | 1      | 1          | P51114                   |           | 2,059E6 | 0,015   | 0,1372 | 20       | 3,748378267 | 2   | 1120,60613 | 2,13     | 115,47  |
| 878 | mLPLDLREL    | 1      | 1          | Q9NPC4                   |           | 9,976E6 | 0,015   | 0,1326 | 20       | 4,773040531 | 2   | 1115,61077 | -1,98    | 98,90   |
| 879 | YYVFTNELK    | 1      | 1          | P50591                   |           | 2,663E6 | 0,015   | 0,1359 | 18       | 6,495024692 | 2   | 1176,59636 | 2,37     | 97,06   |
| 880 | RIRDLAQLK    | 1      | 1          | P42226                   |           | 4,277E6 | 0,015   | 0,1333 | 17       | 1,778060173 | 2   | 1112,69341 | 3,14     | 54,93   |
| 881 | SLAEILLKK    | 1      | 2          | Q95373;Q15397            |           | 2,461E7 | 0,015   | 0,1348 | 16       | 1,182087709 | 2   | 1014,65807 | 2,22     | 94,62   |
| 882 | LPHLADLV5Y   | 2      | 1          | P11473                   |           | 2,295E5 | 0,015   | 0,1353 | 16       | 8,003247889 | 2   | 1127,60893 | -0,56    | 132,86  |
| 883 | VLKVTKAAGTK  | 1      | 1          | P62280                   |           | 1,782E6 | 0,015   | 0,1362 | 16       | 0,617552269 | 2   | 1115,71929 | 4,08     | 27,62   |
| 884 | YYDPKHVIF    | 1      | 1          | Q9NUQ8                   |           | 2,871E6 | 0,015   | 0,136  | 16       | 11,23511102 | 2   | 1181,60149 | 2,11     | 92,47   |
| #    | Sequence      | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area     | q-Value | PEP    | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|------|---------------|--------|------------|--------------------------|-----------|----------|---------|--------|----------|------------|-----|----------|----------|---------|
| 885  | LPNSIASRF     | 1      | 1          | Q9ULT0                   |           | 5,311E6  | 0,015   | 0,1346 | 15       | 10,67495814 | 2   | 1004,55492 | 2,51     | 87,06   |
| 886  | RVAPSLKSQR    | 1      | 1          | P49257                   |           | 8,092E5  | 0,015   | 0,1356 | 13       | 7,258487198  | 2   | 1141,67876 | -1,15    | 28,47   |
| 887  | NPHFGSHRY     | 1      | 1          | Q08211                   |           | 3,288E6  | 0,015   | 0,1341 | 12       | 17,58503544  | 2   | 1114,51824 | 0,46     | 30,15   |
| 888  | RPAEPPFQAL    | 1      | 1          | A6NC56                   |           | 7,484E6  | 0,016   | 0,1383 | 45       | 0,007540431  | 2   | 1125,60857 | 3,01     | 91,97   |
| 889  | RILGPGLNK     | 1      | 1          | P62906                   |           | 1,114E7  | 0,016   | 0,1375 | 38       | 0,007787472  | 2   | 967,60484  | 0,07     | 51,08   |
| 890  | FPVPKPIDY     | 1      | 1          | Q98VS4                   |           | 8,244E6  | 0,016   | 0,1403 | 37       | 0,072778889  | 2   | 1075,58513 | 2,63     | 106,91  |
| 891  | VVGAVVFQK     | 1      | 1          | Q12907                   |           | 4,324E6  | 0,016   | 0,1383 | 31       | 0,081209271  | 2   | 946,57305  | 1,02     | 77,60   |
| 892  | VLYENPNLK     | 1      | 1          | Q14204                   |           | 1,120E7  | 0,016   | 0,1376 | 31       | 0,297956519  | 2   | 1089,59722 | 3,02     | 71,44   |
| 893  | LPAQDIKAL     | 1      | 1          | P00751                   |           | 1,796E6  | 0,016   | 0,138  | 30       | 0,131357875  | 2   | 968,57878  | 1,26     | 83,92   |
| 894  | AVAHALTEK     | 1      | 1          | P49368                   |           | 8,950E6  | 0,016   | 0,1401 | 30       | 0,249328709  | 2   | 939,52513  | -0,76    | 30,09   |
| 895  | SSVPGVRL     | 1      | 1          | P08670                   |           | 5,371E7  | 0,016   | 0,1383 | 30       | 0,227109557  | 2   | 927,56365  | 1,51     | 97,04   |
| 896  | KPVKPHSSF     | 1      | 1          | Q9Y520                   |           | 6,297E6  | 0,016   | 0,1404 | 29       | 0,181902655  | 2   | 1026,57756 | 4,32     | 25,92   |
| 897  | YASGRTTGIVm   | 1      | 3          | P60709;P63261;Q562R1     | M11       | 4,942E6  | 0,016   | 0,138  | 29       | 0,419593514  | 2   | 1171,58135 | 3,17     | 54,97   |
| 898  | LPGTAPKLLY    | 1      | 4          | P01700;P01701;P01702;P06887 |      | 9,968E6  | 0,016   | 0,1379 | 28       | 0,171606315  | 2   | 1185,72783 | 3,04     | 117,42  |
| 899  | FYDDKVSAL     | 2      | 1          | Q68C22                   |           | 2,240E5  | 0,016   | 0,1401 | 27       | 0,738546346  | 2   | 1057,52043 | 0,32     | 95,07   |
| 900  | LPGFPFKEL     | 1      | 1          | Q7Z449                   |           | 4,230E6  | 0,016   | 0,1419 | 25       | 0,627440466  | 2   | 1047,58928 | 1,79     | 129,13  |
| 901  | APLDLSKIKL    | 1      | 1          | Q75369                   |           | 4,135E6  | 0,016   | 0,1399 | 25       | 0,223649808  | 2   | 1097,69609 | 2,88     | 112,62  |
| 902  | LPHQPLATY     | 1      | 1          | Q16633                   |           | 4,381E7  | 0,016   | 0,1378 | 24       | 1,116805048  | 2   | 1039,55998 | 2,74     | 76,90   |
| #   | Sequence      | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area   | q-Value | PEP  | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|---------------|--------|------------|--------------------------|-----------|--------|---------|------|----------|------------|-----|----------|----------|---------|
| 903 | YFHHQDGYRY    | 1      | 1          | Q92802                   |           | 2,660E7| 0,016   | 0,1412| 22       | 1,189385627 | 3   | 1385,60566| 2,52     | 47,40   |
| 904 | SPQQVDFRSLV   | 1      | 1          | Q15746                   |           | 2,369E6| 0,016   | 0,1392| 21       | 3,539476289 | 2   | 1275,67266| 2,68     | 110,21  |
| 905 | KSLGHGLINK    | 1      | 1          | Q8Ni36                   |           | 2,918E6| 0,016   | 0,1423| 21       | 0,864330678 | 2   | 1066,63725| 0,43     | 34,50   |
| 906 | VPVPPLPEY     | 1      | 1          | P24539                   | 2         | 6,114E7| 0,016   | 0,1412| 20       | 2,738803344 | 2   | 1010,55864| 2,86     | 128,71  |
| 907 | FPVVRDFLY     | 1      | 1          | P12111                   | 3         | 4,067E6| 0,016   | 0,1401| 18       | 4,184800631 | 2   | 1155,62432| 3,95     | 133,59  |
| 908 | GLNKEFRY      | 1      | 1          | QSVWQ0                   |           | 6,487E6| 0,016   | 0,1415| 18       | 5,073283434 | 2   | 1113,57219| 3,07     | 59,26   |
| 909 | QPINLIFRY     | 3      | 1          | P62304                   |           | 1,529E7| 0,016   | 0,1386| 17       | 2,634876514 | 2   | 1163,66045| 2,80     | 125,94  |
| 910 | KLREPNFLK     | 1      | 1          | Q92545                   |           | 6,949E6| 0,016   | 0,1387| 17       | 3,356240169 | 2   | 1245,73686| 4,35     | 62,06   |
| 911 | VYNHFLLY      | 1      | 1          | Q7X285                   |           | 9,711E4| 0,016   | 0,1412| 15       | 14,65000341 | 2   | 1231,61577| 0,93     | 126,98  |
| 912 | RPWLEGRIKHL   | 1      | 1          | Q9U110                   |           | 6,881E6| 0,016   | 0,1378| 13       | 16,05576355 | 2   | 1264,69621| 4,15     | 61,18   |
| 913 | HIYDTKLGTDK   | 1      | 1          | Q99439                   |           | 6,942E5| 0,016   | 0,138  | 12       | 29,03034742 | 2   | 1290,67241| 2,73     | 51,24   |
| 914 | RPADSMNLVL    | 1      | 1          | Q9BTL4                   |           | 2,181E5| 0,017   | 0,1447| 44       | 0,014440355 | 2   | 1115,58769| -0,11    | 111,86  |
| 915 | HASDRIIAL     | 1      | 1          | P29401                   |           | 2,086E7| 0,017   | 0,1451| 43       | 0,09164209  | 2   | 995,56517 | 1,88     | 71,11   |
| 916 | IPTKQTQTF     | 1      | 3          | P54652;P11142;P17066     |           | 1,325E8| 0,017   | 0,1475| 39       | 0,048306514 | 2   | 1063,58098| 2,55     | 54,30   |
| 917 | KLISEEDLLRK   | 1      | 1          | P01106                   |           | 1,204E7| 0,017   | 0,149  | 38       | 0,032074547 | 3   | 1343,79544| 4,53     | 74,76   |
| 918 | AVASFPKQGE    | 1      | 1          | P14406                   |           | 5,458E4| 0,017   | 0,1462| 33       | 0,186928138 | 2   | 1104,60442| -0,38    | 38,44   |
| 919 | MPRVQTQKY     | 1      | 1          | O94979                   |           | 4,295E6| 0,017   | 0,1479| 33       | 0,233904301 | 2   | 1150,57280| 4,70     | 60,37   |
| 920 | RVKLPSSKK     | 1      | 1          | P62917                   |           | 2,420E5| 0,017   | 0,145  | 33       | 0,034480945 | 2   | 1099,69426| -0,36    | 24,08   |
| #  | Sequence       | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area    | q-Value | PEP   | IonScore | Exp. Value | Ch. | MH+ [Da] | ∆M [ppm] | RT [min] |
|----|----------------|--------|------------|--------------------------|-----------|---------|---------|-------|----------|------------|-----|---------|----------|---------|
| 921| TmVGKFTTY     | 1      | 1          | Q16850                   | M2        | 7,247E6 | 0,017   | 0,1443| 28       | 0,428300524 | 2   | 1063,51421| 1,23     | 69,81 |
| 922| APLHSVGYTL    | 1      | 1          | Q968D6                   |           | 4,801E6 | 0,017   | 0,1439| 28       | 0,680894059 | 2   | 1158,61821| 2,44     | 85,40 |
| 923| PSLSHNLLVD    | 1      | 1          | Q9ULA0                   |           | 4,006E7 | 0,017   | 0,1428| 27       | 0,829366401 | 2   | 1094,58623| 1,95     | 92,88 |
| 924| FFGDVVLRF     | 1      | 1          | Q9H6E4                   |           | 8,240E4 | 0,017   | 0,1427| 25       | 0,82469269  | 2   | 1099,59245| -1,00    | 158,23 |
| 925| GIKNFTDVI     | 3      | 1          | P0DI81                   |           | 1,933E5 | 0,017   | 0,1453| 24       | 1,71304503  | 2   | 1203,60527| 0,65     | 127,58 |
| 926| GLWHmKTYK     | 1      | 1          | Q9ULC4                   | M5        | 2,308E6 | 0,017   | 0,1486| 22       | 2,535922955 | 2   | 1179,59844| 0,40     | 42,10 |
| 927| RLKGPLLNKF    | 1      | 1          | P01024                   |           | 7,746E6 | 0,017   | 0,1468| 21       | 0,35352479  | 2   | 1185,74687| 0,15     | 67,61 |
| 928| LPYQGHNSF     | 1      | 1          | Q7Z4G4                   |           | 3,754E6 | 0,017   | 0,1446| 21       | 3,013073129  | 2   | 1062,50261| 2,14     | 70,80 |
| 929| SINDKIEI      | 1      | 2          | Q12772;P36956            |           | 1,898E5 | 0,017   | 0,147  | 20       | 2,914039269 | 2   | 1044,59307| -0,51    | 110,69 |
| 930| DVYNHFLLY     | 3      | 1          | Q7X285                   |           | 3,412E5 | 0,017   | 0,1427| 20       | 3,343526231  | 2   | 1183,57817| -0,07    | 145,92 |
| 931| KPHSGFHVA      | 1     | 1          | Q8IYU8                   |           | 1,906E7 | 0,017   | 0,1436| 20       | 3,982727654  | 2   | 1126,58000| 0,64     | 57,59 |
| 932| PRAWKETNm     | 1      | 1          | O76024                   | M9        | 0,000E0 | 0,017   | 0,149  | 19       | 5,317554884  | 2   | 1148,55620| 3,86     | 61,99 |
| 933| EVQPLHPDK     | 1      | 1          | P48067                   |           | 3,051E8 | 0,017   | 0,1476| 19       | 6,051813347  | 2   | 1062,56011| 2,09     | 44,67 |
| 934| GQYSGSQQLK    | 1      | 1          | Q96N67                   |           | 4,833E6 | 0,017   | 0,1448| 18       | 7,816862351  | 2   | 1177,62334| 1,81     | 69,53 |
| 935| HLFDHVNVR     | 1      | 1          | Q9UM54                   |           | 1,190E6 | 0,017   | 0,144  | 17       | 7,698719642  | 2   | 1136,59587| -0,10    | 64,73 |
| 936| SFVDPGERLY    | 1      | 1          | P16333                   |           | 3,786E6 | 0,017   | 0,1461| 17       | 8,549063166  | 2   | 1182,58086| 1,56     | 104,12 |
| 937| NPVDWKEKY     | 1      | 1          | O00469                   |           | 8,283E6 | 0,017   | 0,1488| 17       | 8,929738636  | 2   | 1178,58354| -0,46    | 65,47 |
| 938| LIYVAGGLTK    | 1      | 1          | Q6TL4                    |           | 1,011E7 | 0,017   | 0,1431| 13       | 4,527831994  | 2   | 1034,62749| 2,89     | 91,14 |
| #   | Sequence       | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area     | q-Value | PEP     | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|----------------|--------|------------|--------------------------|-----------|----------|--------|--------|----------|-----------|-----|----------|--------|---------|
| 939 | RSVQEALRF     | 1      | 1          | P50053                   |           | 1,034E6  | 0,017  | 0,1485 | 12       | 17,87474954 | 2   | 1105,61601 | 4,24   | 74,34   |
| 940 | LTGPvmPVR     | 1      | 1          | P26373                   | M6        | 2,064E7  | 0,018  | 0,1495 | 46       | 0.007104761  | 2   | 985,55266 | 2,72   | 60,53   |
| 941 | SLFPKALQR     | 1      | 1          | O43306                   |           | 2,223E7  | 0,018  | 0,1519 | 37       | 0.021479479  | 2   | 1059,63335 | 2,22   | 77,85   |
| 942 | DAADIRFVY     | 1      | 1          | P01033                   |           | 2,510E7  | 0,018  | 0,1527 | 37       | 0.072958221  | 2   | 1069,53386 | 2,37   | 117,67  |
| 943 | YADVGGKQF     | 1      | 1          | P51571                   |           | 7,490E6  | 0,018  | 0,1522 | 35       | 0.107653028  | 2   | 984,47905 | 0,50   | 65,41   |
| 944 | LGSNERLEF     | 1      | 1          | Q08188                   |           | 1,980E5  | 0,018  | 0,1527 | 33       | 0.221716493  | 2   | 1064,53691 | -0,22  | 88,11   |
| 945 | AANKVVLQLK    | 1      | 1          | Q9NX08                   |           | 2,361E6  | 0,018  | 0,1499 | 32       | 0.043580994  | 2   | 1083,69048 | 1,81   | 58,35   |
| 946 | ILYGPPGTGK    | 1      | 1          | P62191                   |           | 1,128E5  | 0,018  | 0,1502 | 31       | 0.388234853  | 2   | 1002,56182 | -0,09  | 75,30   |
| 947 | KGNLEVLLF     | 2      | 4          | Q9H254;Q01082;P11277;O15020 |           | 6,339E5  | 0,018  | 0,15    | 31       | 0.177262417  | 2   | 1032,60832 | -0,52  | 132,43  |
| 948 | RPPPSPSGTI    | 1      | 1          | Q9Y2G0                   |           | 3,636E7  | 0,018  | 0,1524 | 30       | 0.308428566  | 2   | 1008,54961 | 2,27   | 53,66   |
| 949 | KLPSEPLSR     | 1      | 1          | Q14714                   |           | 1,592E6  | 0,018  | 0,1523 | 29       | 0.369837432  | 2   | 1113,62590 | -0,36  | 49,50   |
| 950 | APIAKVGVL     | 1      | 1          | Q9UHB6                   |           | 6,324E7  | 0,018  | 0,1552 | 29       | 0.058216769  | 2   | 867,56713 | 0,98   | 84,55   |
| 951 | NAARDFVNY     | 1      | 1          | Q08211                   |           | 2,651E7  | 0,018  | 0,1529 | 28       | 0.399689483  | 2   | 1069,50945 | 3,06   | 76,32   |
| 952 | GVmDRGYSY     | 1      | 1          | P28074                   | M3        | 3,373E4  | 0,018  | 0,1523 | 28       | 0.335648271  | 2   | 1063,45122 | -0,13  | 55,95   |
| 953 | AVTARGDGYGTF  | 1      | 1          | Q9NQ94                   |           | 6,870E6  | 0,018  | 0,1555 | 26       | 0.670449441  | 2   | 1214,58354 | 2,85   | 72,43   |
| 954 | VLN1KEPLY     | 4      | 1          | O00468                   |           | 2,394E5  | 0,018  | 0,1534 | 26       | 0.651837602  | 2   | 1088,63469 | -0,34  | 117,04  |
| 955 | AVYGmLNLT PK  | 1      | 1          | O43776                   | M5        | 3,850E6  | 0,018  | 0,1514 | 26       | 0.862429483  | 2   | 1222,65349 | 2,79   | 92,10   |
| 956 | LPQHPDVEM     | 1      | 1          | Q7Z7E8                   |           | 8,597E6  | 0,018  | 0,1551 | 25       | 1.258055503  | 2   | 1065,50603 | 2,46   | 77,83   |
| #  | Sequence       | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area       | q-Value | PEP  | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|----|----------------|--------|------------|--------------------------|-----------|------------|---------|------|----------|------------|-----|----------|----------|---------|
| 957 | AVQRTLEK      | 1      | 1          | P14209                   |           | 2,364E6    | 0,018   | 0,1525 | 25       | 0,691075657 | 2   | 1057,63664 | 0,16     | 43,72   |
| 958 | ILDQKINEV     | 1      | 1          | P11926                   |           | 4,684E5    | 0,018   | 0,1503 | 23       | 1,528408644 | 2   | 1071,60430 | -0,19    | 81,89   |
| 959 | KTAEDAKDFF    | 1      | 1          | Q99471                   |           | 4,584E6    | 0,018   | 0,1518 | 23       | 1,641597736 | 2   | 1171,56670 | 3,12     | 72,73   |
| 960 | LPPENILSAY    | 2      | 1          | P02743                   |           | 1,781E7    | 0,018   | 0,154  | 23       | 2,031871993 | 2   | 1116,59770 | 3,68     | 133,06  |
| 961 | TPAEVSHRF     | 1      | 1          | Q3T8J9                   |           | 2,262E6    | 0,018   | 0,1524 | 22       | 1,421496058 | 2   | 1043,52861 | 1,63     | 44,86   |
| 962 | LLDIQSSGRAK   | 1      | 2          | Q99613;B5ME19            |           | 2,766E7    | 0,018   | 0,1547 | 22       | 2,204904491 | 2   | 1187,67986 | 4,66     | 55,81   |
| 963 | AVREEVEVLK    | 1      | 3          | O75157;Q15714;Q9Y3Q8     |           | 5,063E6    | 0,018   | 0,152  | 22       | 1,977716177 | 2   | 1171,67156 | 2,88     | 60,65   |
| 964 | KLSTLYK       | 1      | 1          | O14980                   |           | 5,833E6    | 0,018   | 0,1535 | 20       | 0,257484187 | 2   | 1078,68877 | 1,55     | 81,51   |
| 965 | SFGLALIY      | 1      | 2          | P10644;P31321            |           | 3,666E7    | 0,018   | 0,1528 | 18       | 4,519589646 | 2   | 1012,53777 | 2,72     | 157,66  |
| 966 | YIYDGEVLSK    | 1      | 1          | Q9Y2D2                   |           | 5,211E6    | 0,018   | 0,153  | 17       | 7,587039955 | 2   | 1186,60173 | 2,25     | 91,08   |
| 967 | VVLEKAmHK     | 1      | 1          | Q8WYP3                   | M7        | 4,333E5    | 0,018   | 0,1492 | 17       | 4,898983856 | 2   | 1070,60661 | 3,62     | 26,58   |
| 968 | GYLHDFLKY     | 2      | 1          | Q15014                   |           | 5,922E7    | 0,018   | 0,1541 | 16       | 8,5571565   | 2   | 1155,58696 | 3,13     | 107,66  |
| 969 | RVLDFDVKRK    | 1      | 1          | Q726Z7                   |           | 2,496E6    | 0,018   | 0,1554 | 15       | 3,816310707 | 2   | 1275,75884 | 4,38     | 52,35   |
| 970 | NPPEFLHETY    | 1      | 1          | P5S287                   |           | 4,531E6    | 0,018   | 0,154  | 12       | 20,51009545 | 2   | 1246,57842 | 3,61     | 95,90   |
| 971 | RCGKTDDLLY    | 1      | 1          | Q9UL11                   |           | 3,412E5    | 0,019   | 0,1561 | 41       | 0,026753374 | 2   | 1183,57878 | 0,97     | 145,98  |
| 972 | VPVDSKWLGHFY  | 1      | 1          | P09327                   |           | 1,176E7    | 0,019   | 0,1567 | 36       | 0,138868427 | 3   | 1447,73975 | 1,96     | 113,99  |
| 973 | LPPHVFEAL     | 1      | 1          | Q9H4Z3                   |           | 4,005E6    | 0,019   | 0,1586 | 35       | 0,054257982 | 2   | 1024,58721 | 4,45     | 120,94  |
| 974 | KIAAFVLEGK    | 4      | 1          | O43493                   |           | 2,338E5    | 0,019   | 0,1559 | 34       | 0,021672567 | 2   | 1117,69805 | 0,02     | 93,71   |
|   | Sequence | PSMs | Proteins | Protein Group Accessions | Mod. (ox) | Area | q-Value | PEP | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|---|----------|------|----------|--------------------------|-----------|------|---------|-----|----------|------------|-----|----------|-----------|---------|
| 975 | KVYNIQIRY | 1    | 1        | Q13094                   |           | 3,113E7 | 0,019   | 0,1592 | 32       | 0,106807046 | 2   | 1196,68059 | 1,63      | 78,82  |
| 976 | NAIKESDY  | 1    | 1        | O75530                   |           | 4,574E6 | 0,019   | 0,1592 | 27       | 0,426255935 | 2   | 1102,50749 | 2,12      | 62,58  |
| 977 | PVLPRLDPE | 1    | 1        | Q9NRY2                   |           | 1,940E7 | 0,019   | 0,1575 | 27       | 0,620159398 | 2   | 1035,58623 | 2,75      | 96,87  |
| 978 | FIHVQTLS  | 1    | 1        | Q9NVM4                   |           | 8,734E6 | 0,019   | 0,1561 | 24       | 0,790236295 | 2   | 1041,57414 | 1,30      | 104,58 |
| 979 | SPAGSIHEL | 1    | 1        | O43776                   |           | 1,095E7 | 0,019   | 0,1581 | 23       | 2,201224774 | 2   | 1009,53472 | 3,35      | 83,31  |
| 980 | RPVEEIVTF | 1    | 1        | P34949                   |           | 1,147E7 | 0,019   | 0,1591 | 22       | 2,419975519 | 2   | 1089,59709 | 2,89      | 103,11 |
| 981 | RPTGEIQY  | 1    | 1        | P04114                   |           | 8,065E6 | 0,019   | 0,1569 | 22       | 3,169581179 | 2   | 1092,53557 | 3,22      | 54,73  |
| 982 | RPKLPEDPL | 1    | 1        | P49327                   |           | 4,310E6 | 0,019   | 0,1567 | 19       | 1,916268394 | 2   | 1177,69927 | 4,47      | 88,18  |
| 983 | AFROPSLFY | 1    | 1        | Q99683                   |           | 9,871E6 | 0,019   | 0,1558 | 18       | 5,567080336 | 2   | 1128,58586 | 1,92      | 106,74 |
| 984 | ATYETKESK | 1    | 2        | P23528;Q9Y281            |           | 7,577E5 | 0,019   | 0,1582 | 16       | 7,543063307 | 2   | 1056,52129 | 0,45      | 19,95  |
| 985 | RWLIPLLEGK| 1    | 1        | Q6JQN1                   |           | 1,052E6 | 0,019   | 0,1571 | 15       | 2,197441777 | 2   | 1224,75176 | 4,40      | 138,19 |
| 986 | KVLDKLLLY | 1    | 1        | Q98XP5                   |           | 6,706E6 | 0,019   | 0,1574 | 15       | 0,740242014 | 2   | 1104,70549 | 2,48      | 107,72 |
| 987 | ISFDKRAAAL| 1    | 1        | Q6NWY9                   |           | 7,190E5 | 0,02    | 0,1597 | 45       | 0,008451575 | 2   | 1091,62029 | -0,50     | 75,83  |
| 988 | RAAEELAFP | 1    | 1        | P33076                   |           | 2,410E5 | 0,02    | 0,1597 | 35       | 0,151920433 | 2   | 1090,55596 | 2,88      | 114,66 |
| 989 | GTYRDANIK | 1    | 1        | Q96PU8                   |           | 3,571E7 | 0,02    | 0,1602 | 26       | 1,038766376 | 2   | 1037,54094 | 3,34      | 31,02  |
| 990 | GVPFTIAR  | 6    | 1        | P12111                   |           | 9,061E5 | 0,021   | 0,1646 | 54       | 0,001079898 | 2   | 931,53563 | -0,43     | 90,21  |
| 991 | APAQRAQSL | 1    | 1        | Q63Y3                    |           | 2,455E7 | 0,021   | 0,1639 | 41       | 0,020340288 | 2   | 941,51671 | 0,38      | 34,61  |
| 992 | TPISRLVAL | 1    | 1        | Q9H765                   |           | 7,632E6 | 0,021   | 0,163  | 40       | 0,012649285 | 2   | 969,61070 | 1,56      | 107,36 |
| #    | Sequence       | # PSMs | # Proteins | Protein Group Accessions       | Area     | q-Value | PEP     | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|------|----------------|--------|------------|-------------------------------|----------|---------|---------|----------|------------|-----|----------|----------|---------|
| 993  | GVSGLFMKY      | 2      | 1          | Q96RQ1                        | 1,299E5  | 0,021   | 0,1659 | 38       | 0,077035307 | 2   | 1001,51268 | 0,17    | 103,17  |
| 994  | KVFDAKPSAK     | 1      | 1          | Q8WVV9                        | 5,883E6  | 0,021   | 0,1606 | 35       | 0,079905991 | 2   | 1090,62749 | 1,75    | 30,78   |
| 995  | SVAKTILK       | 2      | 2          | Q9H859;Q7L9L4                 | 9,475E6  | 0,021   | 0,165  | 35       | 0,021343252 | 2   | 859,56114  | -0,03   | 40,53   |
| 996  | SPSPNYQKY      | 1      | 1          | Q12778                        | 1,905E6  | 0,021   | 0,1608 | 34       | 0,129084425 | 2   | 1083,51164 | 1,00    | 48,09   |
| 997  | IKVQGILSY      | 4      | 1          | Q6NXT6                        | 7,881E5  | 0,021   | 0,1638 | 34       | 0,05277271  | 2   | 1020,60851 | -0,33   | 102,94  |
| 998  | AVSAVVHEY      | 1      | 1          | P35610                        | 1,506E7  | 0,021   | 0,1662 | 33       | 0,26164468  | 2   | 974,49846  | 4,37    | 63,45   |
| 999  | NVVKLGEQY      | 1      | 1          | Q92785                        | 4,420E6  | 0,021   | 0,1637 | 30       | 0,291971516 | 2   | 1162,65044 | 3,22    | 100,52  |
| 1000 | ALHOUYQK       | 3      | 3          | P01859;P01857;P01861          | 3,116E6  | 0,021   | 0,1651 | 27       | 0,76367192  | 2   | 1111,56511 | 0,70    | 20,21   |
| 1001 | KTLFPLIEAK     | 1      | 1          | P13010                        | 1,588E6  | 0,021   | 0,1646 | 26       | 0,195908879 | 2   | 1159,71037 | 1,55    | 98,40   |
| 1002 | FPNRNVFQEF     | 1      | 1          | P35579                        | 1,384E7  | 0,021   | 0,1663 | 26       | 0,990712122 | 2   | 1282,66240 | 3,48    | 118,97  |
| 1003 | RPPVQIEEL      | 1      | 1          | Q8IU18                        | 1,336E6  | 0,021   | 0,1647 | 25       | 0,682269132 | 2   | 1080,60564 | 0,74    | 90,00   |
| 1004 | HAIRLLLEY      | 3      | 3          | P09488;P03013;P46439          | 1,059E5  | 0,021   | 0,167  | 25       | 0,647019666 | 2   | 1127,65666 | -0,47   | 103,51  |
| 1005 | EPPLIVSY       | 1      | 1          | Q7L513                        | 2,024E5  | 0,021   | 0,1671 | 25       | 1,498411204 | 2   | 1104,57219 | -0,24   | 131,41  |
| 1006 | VPASFRLMQM     | 1      | 1          | Q98TE3                        | 2,818E6  | 0,021   | 0,1611 | 24       | 1,42633921  | 2   | 1048,56255 | 1,60    | 101,78  |
| 1007 | KVSDYILQH      | 1      | 1          | Q7S129                        | 5,525E6  | 0,021   | 0,1664 | 24       | 1,758294347 | 2   | 1102,59233 | 2,88    | 72,68   |
| 1008 | KTIQVPQQK      | 1      | 1          | Q9BY77                        | 1,593E6  | 0,021   | 0,1629 | 22       | 1,034485442 | 2   | 1069,64141 | 4,62    | 35,09   |
| 1009 | KVVEQGFLYK     | 1      | 1          | P31150                        | 2,068E7  | 0,021   | 0,1664 | 19       | 5,437602525 | 2   | 1155,64250 | 1,40    | 60,95   |
| 1010 | LRLPALRlmNA    | 1      | 1          | P13056                        | M9       | 0,000E0 | 0,1606 | 18       | 1,805660046 | 2   | 1283,76079 | -0,72   | 161,86  |
| #   | Sequence       | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area     | q-Value | PEP  | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|----------------|--------|------------|--------------------------|-----------|----------|---------|------|----------|------------|-----|----------|----------|---------|
| 1011| RPPFPQQI       | 1      | 1          | Q9HBZ2                   |           | 4,540E6  | 0,021   | 0,164| 18       | 2,88991555 | 2   | 1039,57109| 2,60     | 78,23   |
| 1012| MENVHGHITIK    | 1      | 1          | Q92887                   |           | 8,586E6  | 0,021   | 0,1614| 15       | 15,0062021 | 2   | 1278,66374| 1,07     | 85,98   |
| 1013| QPNGGASVIHAY   | 1      | 1          | Q6PC85                   |           | 5,023E6  | 0,022   | 0,1677| 31       | 0,259576108 | 2   | 1213,59612| 0,05     | 68,15   |
| 1014| IPLRHGGGLSL    | 1      | 2          | Q99611;P49903            |           | 4,401E6  | 0,023   | 0,1698| 42       | 0,005519872 | 2   | 1062,64311| 1,15     | 75,69   |
| 1015| TPTVIAVHY      | 1      | 1          | P01024                   |           | 0,000E0  | 0,023   | 0,1734| 41       | 0,036168505 | 2   | 1000,54588| -0,35    | 91,68   |
| 1016| VPVAKTAEL      | 1      | 1          | P49790                   |           | 3,356E7  | 0,023   | 0,171  | 38       | 0,031624391 | 2   | 927,55242 | 1,51     | 62,43   |
| 1017| RPGWLTVSLS     | 3      | 1          | Q15392                   |           | 2,737E7  | 0,023   | 0,17   | 38       | 0,031818305 | 2   | 1028,59111| 2,26     | 121,83  |
| 1018| DASKVTVF       | 3      | 1          | O75083                   |           | 9,694E5  | 0,023   | 0,1735| 37       | 0,062531523 | 2   | 965,53008 | -0,20    | 107,31  |
| 1019| GPPRLLLPL      | 3      | 1          | P09564                   |           | 2,531E7  | 0,023   | 0,1721| 35       | 0,00254143 | 2   | 1088,72380| 4,33     | 146,38  |
| 1020| ATAPVSAALKL    | 1      | 1          | Q9NQ94                   |           | 1,880E6  | 0,023   | 0,1715| 32       | 0,163746982 | 2   | 1056,60820| 3,18     | 60,68   |
| 1021| SVNGKVLSDK     | 3      | 3          | P69849;Q15155;Q5JPE7     |           | 3,531E8  | 0,023   | 0,1701| 32       | 0,081932482 | 2   | 931,55644 | -0,76    | 29,97   |
| 1022| AIFPSPmLY      | 1      | 1          | O95340                   | M7        | 6,735E6  | 0,023   | 0,1726| 31       | 0,298563048 | 2   | 1054,52898| 1,09     | 140,22  |
| 1023| RPSAAGINL      | 2      | 1          | Q08211                   |           | 3,415E5  | 0,023   | 0,1712| 31       | 0,195789979 | 2   | 898,51042 | -0,13    | 68,79   |
| 1024| RLFTDVLHL      | 1      | 1          | O14682                   |           | 1,018E7  | 0,023   | 0,1695| 28       | 0,278838232 | 2   | 1113,64348| 1,73     | 109,59  |
| 1025| SLPTVIMRNK     | 1      | 1          | Q12802                   |           | 3,346E6  | 0,023   | 0,1717| 28       | 0,420297999 | 2   | 1158,66887| 2,13     | 69,25   |
| 1026| RPSPPVQSV      | 1      | 1          | Q5VV67                   |           | 9,598E6  | 0,023   | 0,1691| 27       | 0,43713771  | 2   | 966,53923 | 2,57     | 52,78   |
| 1027| SFPKADEm       | 1      | 1          | O75369                   | M9        | 6,123E6  | 0,023   | 0,1741| 26       | 0,71403027  | 2   | 1053,49492| 2,60     | 73,69   |
| 1028| RTFTWLVGK      | 1      | 1          | O00159                   |           | 2,734E7  | 0,023   | 0,1728| 26       | 0,277846856 | 2   | 1107,63396| 2,68     | 90,90   |
| #   | Sequence        | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area    | q-Value | PEP   | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|----------------|--------|------------|--------------------------|-----------|---------|---------|-------|----------|------------|-----|----------|----------|---------|
| 1029| IWDPDAVKI       | 1      | 1          | Q14195                   |           | 0,000E0 | 0,023   | 0,1743| 24       | 0,656735847| 2   | 1056,57390| 1,34     | 113,33  |
| 1030| VVFVIDPGFAK     | 1      | 1          | O43143                   |           | 1,270E6 | 0,023   | 0,1712| 24       | 0,886283216| 2   | 1191,68083| 2,97     | 128,05  |
| 1031| NFYLVPLHY       | 3      | 1          | P39210                   |           | 8,992E4 | 0,023   | 0,1687| 23       | 1,498093163| 2   | 1165,60320| -0,75    | 139,61  |
| 1032| RPPAQGTVT       | 1      | 1          | Q68DI1                   |           | 6,391E6 | 0,023   | 0,1726| 23       | 1,7013817 | 2   | 1073,57585| 1,85     | 66,79   |
| 1033| KVRGDIVVQK      | 1      | 1          | P35749                   |           | 1,221E7 | 0,023   | 0,174  | 23       | 1,009522834| 2   | 1028,6126 | 0,10     | 18,16   |
| 1034| QTNPTYLAK       | 1      | 1          | P46940                   |           | 2,580E6 | 0,023   | 0,1704| 21       | 3,965908927| 2   | 1035,54753| 0,55     | 49,97   |
| 1035| KIDDTIRYL       | 1      | 1          | Q6UXN9                   |           | 7,322E6 | 0,023   | 0,1721| 20       | 2,880070284| 2   | 1136,63506| 3,53     | 90,51   |
| 1036| TAYGSTVSK       | 1      | 1          | P04114                   |           | 4,219E7 | 0,023   | 0,1686| 20       | 3,563627618| 2   | 913,46330 | 0,81     | 32,14   |
| 1037| RPQAPALHL       | 1      | 1          | Q99988                   |           | 5,210E6 | 0,023   | 0,1679| 20       | 2,748591061| 2   | 1002,58379| -0,58    | 68,02   |
| 1038| LPEDRALYY       | 1      | 1          | Q99558                   |           | 2,324E6 | 0,023   | 0,1728| 19       | 4,602065713| 2   | 1139,57756| 3,84     | 91,24   |
| 1039| RLYSVTTTK       | 1      | 1          | P23467                   |           | 2,683E6 | 0,023   | 0,1721| 19       | 2,025274731| 2   | 1167,67339| 0,13     | 57,35   |
| 1040| RVRDVFEAK       | 1      | 1          | P12268                   |           | 1,467E7 | 0,023   | 0,1691| 19       | 3,319579765| 2   | 1119,63042| 3,07     | 57,35   |
| 1041| SPYLPREGDPVL    | 2      | 1          | P49754                   |           | 2,545E7 | 0,023   | 0,1721| 15       | 10,84865889| 2   | 1213,66155| 3,25     | 100,28  |
| 1042| AILDKTTNK       | 1      | 2          | P29558;Q15434            |           | 2,371E7 | 0,024   | 0,175 | 41       | 0,022166844| 2   | 1003,57915| 0,86     | 33,12   |
| 1043| MLMLPLLILL     | 1      | 1          | A6NNS52                  |           | 4,504E5 | 0,024   | 0,1767| 40       | 0,011174977| 2   | 1056,65618| 0,14     | 122,41  |
| 1044| RVmKALVNR       | 1      | 1          | Q08945                   | M3        | 7,536E6 | 0,024   | 0,1778| 32       | 0,101466646| 2   | 1102,65557| 3,75     | 26,75   |
| 1045| IYKGGTSR       | 2      | 1          | P06396                   |           | 1,119E8 | 0,024   | 0,1762| 28       | 0,294875913| 2   | 994,56951 | 1,47     | 31,22   |
| 1046| RIFQKFLQR       | 2      | 1          | Q12965                   |           | 4,582E7 | 0,024   | 0,1756| 28       | 0,182075898| 3   | 1235,73841| 0,98     | 69,76   |
| #    | Sequence       | # PSMs | # Proteins | Protein Group Accessions  | Mod. (ox) | Area  | q-Value | PEP   | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|------|----------------|--------|------------|---------------------------|----------|-------|---------|-------|----------|------------|-----|----------|----------|---------|
| 1047 | GLNVSSISRK    | 1      | 1          | P82979                    |          | 1,847E6 | 0,024   | 0,1744| 27       | 0,574810356 | 2   | 1060,61150| 0,49     | 50,22   |
| 1048 | CDPVIERPR     | 1      | 1          | Q6P522                    |          | 2,073E6 | 0,024   | 0,177 | 24       | 1,240900763 | 2   | 1240,65752| -0,37    | 106,80  |
| 1049 | IPLPLVKSL     | 1      | 1          | Q9H0A0                    |          | 3,965E6 | 0,024   | 0,1776| 22       | 0,068561205 | 2   | 979,65801| 2,99     | 122,69  |
| 1050 | RPSQFPHSL     | 1      | 1          | Q96RT8                    |          | 2,634E6 | 0,024   | 0,1746| 22       | 1,953256111 | 2   | 1068,55962| 1,01     | 57,19   |
| 1051 | NLLRAFYEL     | 1      | 1          | Q9NRD5                    |          | 2,499E5 | 0,024   | 0,1774| 18       | 4,285641298 | 2   | 1138,62517| -0,34    | 119,87  |
| 1052 | NYLHDFLKY     | 2      | 1          | Q9UBU8                    |          | 1,347E7 | 0,024   | 0,1743| 18       | 6,27712661 | 2   | 1212,60942| 3,81     | 109,88  |
| 1053 | RTSLPWQGL     | 1      | 2          | Q8N752;P48729             |          | 4,440E6 | 0,024   | 0,1785| 18       | 4,017907898 | 2   | 1057,58269| 3,53     | 109,14  |
| 1054 | HLLETPLVVK     | 1      | 1          | Q8WYP5                    |          | 2,229E6 | 0,024   | 0,1785| 18       | 1,007387739 | 2   | 1148,70574| 1,67     | 90,01   |
| 1055 | KLLEPVLLLGK   | 1      | 1          | P62249                    |          | 4,789E7 | 0,024   | 0,1746| 18       | 0,214645745 | 2   | 1222,81645| 2,50     | 113,56  |
| 1056 | HLKEDLNLNR    | 1      | 1          | Q76003                    |          | 3,971E6 | 0,024   | 0,1767| 18       | 3,907990137 | 2   | 1137,63713| -0,35    | 50,11   |
| 1057 | KDLIRFKP      | 3      | 1          | Q86YR7                    |          | 2,832E6 | 0,024   | 0,1759| 17       | 2,141682692 | 2   | 1016,62456| -0,61    | 69,96   |
| 1058 | RPAEVEGGMqM   | 1      | 1          | P33316                    | M8       | 6,377E6 | 0,025   | 0,1804| 42       | 0,032176136 | 2   | 1073,54424| 3,13     | 54,91   |
| 1059 | HPQPTQVQF     | 1      | 1          | P51610                    |          | 1,796E7 | 0,025   | 0,1804| 41       | 0,023269786 | 2   | 1081,54497| 2,24     | 69,12   |
| 1060 | KTWTVDADKTLK  | 1      | 1          | P13010                    |          | 4,823E6 | 0,025   | 0,1798| 29       | 0,211792809 | 3   | 1389,80994| -0,11    | 66,18   |
| 1061 | RLLDQIVEK     | 1      | 1          | Q96AE4                    |          | 3,707E6 | 0,025   | 0,181 | 28       | 0,325461205 | 2   | 1113,66594| 2,92     | 79,11   |
| 1062 | HAVSPIAKY     | 1      | 1          | Q8NDF8                    |          | 4,252E6 | 0,025   | 0,1798| 27       | 0,35462469  | 2   | 985,54875| 2,21     | 48,41   |
| 1063 | RLGSTVATGK    | 1      | 1          | Q96X96                    |          | 1,806E6 | 0,025   | 0,1794| 26       | 0,601173706 | 2   | 989,57463| 0,77     | 29,63   |
| 1064 | ASYENVRAK     | 1      | 1          | P15153                    |          | 3,859E6 | 0,025   | 0,1793| 26       | 0,887401593 | 2   | 1037,53801| 0,52     | 29,79   |
| #  | Sequence       | PSMs | Proteins                                                                 | Protein Group Accessions                                                                 | Mod. (ox) | Area    | q-Value | PEP   | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|----|----------------|------|--------------------------------------------------------------------------|------------------------------------------------------------------------------------------|-----------|---------|---------|-------|----------|------------|-----|-----------|----------|---------|
| 1065 | GSHSMRYFYT    | 1    | 35                                                                       | P01891;P10316;P13746;P18462;P30450;P30453;P30456;P30457;P01889;P30461;P30462;P30464;P30685;Q95365;P30475;P30480;P30481;P30484;P30485;P30486;P18464;P30490;P30491;P30492;P30493;P30495;P18465;P10319;Q29990;Q29836;P30498;Q31610;Q29718;P04222;Q95604 | 2,171E7   | 2,171E7 | 0,025   | 0,18  | 21       | 1,654935802 | 2   | 1248,54766 | 0,81     | 66,17   |
| 1066 | KLYEEGSNK     | 1    | 1 P25788                                                                |                                                                                          | 2,902E6   | 2,902E6 | 0,025   | 0,1802 | 19       | 4,984903277 | 2   | 1067,54167 | 4,56     | 27,12   |
| 1067 | KTLDEILQEK    | 1    | 2 Q9UQ88;P21127                                                         |                                                                                          | 1,761E6   | 1,761E6 | 0,025   | 0,1797 | 18       | 4,691148849 | 2   | 1216,68328 | 4,01     | 83,27   |
| 1068 | IPTDVKIVY     | 1    | 1 Q6P179                                                                |                                                                                          | 1,561E6   | 1,561E6 | 0,026   | 0,18  | 29       | 0,115877627 | 2   | 1160,69646 | 3,34     | 132,66  |
| 1069 | AmHGVFLYH     | 1    | 1 Q99707                                                                |                                                                                          | 3,210E6   | 3,210E6 | 0,026   | 0,1816 | 27       | 0,497858594 | 2   | 1090,51396 | 0,06     | 65,96   |
| 1070 | KQLTSHPWK     | 1    | 1 Q6ZNB7                                                                |                                                                                          | 2,188E6   | 2,188E6 | 0,026   | 0,1824 | 21       | 1,934068266 | 2   | 1124,62065 | -0,43    | 34,47   |
| 1071 | ATAVHAYRY     | 1    | 1 QST1M5                                                                |                                                                                          | 9,223E5   | 9,223E5 | 0,026   | 0,1828 | 20       | 3,364793988 | 2   | 1051,53374 | 1,68     | 41,85   |
| 1072 | KTYGVSSFILK   | 1    | 1 Q9Y490                                                                |                                                                                          | 2,445E6   | 2,445E6 | 0,026   | 0,1814 | 15       | 9,574639308 | 2   | 1288,73442 | 3,41     | 107,71  |
| 1073 | APRTQFSGL     | 1    | 1 O00754                                                                |                                                                                          | 1,293E7   | 1,293E7 | 0,027   | 0,183  | 19       | 3,731828805 | 2   | 1073,57524 | 1,28     | 75,56   |
| 1074 | LmLPEKLRPLY   | 1    | 1 Q95563                                                                |                                                                                          | 8,688E6   | 8,688E6 | 0,027   | 0,1833 | 15       | 6,428149927 | 3   | 1388,79920 | 1,52     | 106,42  |
| 1075 | RPOSGANGL     | 1    | 1 Q8WVX3                                                                |                                                                                          | 1,075E7   | 1,075E7 | 0,028   | 0,1854 | 59       | 0,000244416 | 2   | 899,47118 | 1,98     | 31,19   |
| 1076 | APAPAPARSL    | 1    | 1 Q6QNY0                                                                |                                                                                          | 5,827E6   | 5,827E6 | 0,028   | 0,1852 | 43       | 0,009076864 | 2   | 950,54582 | 4,18     | 53,52   |
| 1077 | HNADQPLRV     | 1    | 2 Q99613;B5ME19                                                         |                                                                                          | 1,449E7   | 1,449E7 | 0,028   | 0,1846 | 40       | 0,03881997 | 2   | 1049,55083 | 2,02     | 44,29   |
| 1078 | VPPPCHRPL     | 1    | 1 Q9YS20                                                                |                                                                                          | 1,834E7   | 1,834E7 | 0,028   | 0,1862 | 35       | 0,031577939 | 2   | 1009,59349 | -0,71    | 48,98   |
| 1079 | HPISDHEATL    | 1    | 39 P30447;P05534;P30443;P04439;P13746;P16188;P30455;Q09160             |                                                                                          | 1,110E8   | 1,110E8 | 0,028   | 0,1859 | 32       | 0,244491794 | 2   | 1119,54534 | 2,13     | 48,51   |
| #  | Sequence      | PSMs | Proteins                | Protein Group Accessions                                                                 | Mod. (ox) | Area  | q-Value | PEP   | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|----|---------------|------|-------------------------|------------------------------------------------------------------------------------------|-----------|-------|---------|-------|----------|------------|-----|----------|----------|---------|
| 1080 | MPNVKVAVF    | 2    | 1                       | Q13838;P01889;P30460;P30461;P30462;P30464;P30466;P30989;P18463;Q93656;P30475;Q04826;P30479;P30480;P30483;P30484;P30485;P30486;P30487;P30488;P30492;P30495;P30499;P31610;Q29718;P01893;P13747;P30511 | 1,229E7   | 0,028 | 0,1849 | 30    | 0,257658691 | 2 | 1004,56236 | 2,54 | 106,33 |
| 1081 | AFSAEPLLIY   | 2    | 1                       | Q81YK4                                                                                   | 1,885E6   | 0,028 | 0,1867 | 28    | 0,455625587 | 2 | 1123,60344 | 0,01 | 155,87 |
| 1082 | RKLHmRR      | 1    | 1                       | Q9H9H4;M6                                                                                | 3,328E5   | 0,028 | 0,185  | 28    | 0,241536292 | 2 | 1083,63103 | -0,61 | 34,85  |
| 1083 | KPAKTQKTSL   | 1    | 1                       | O15539                                                                                   | 1,623E6   | 0,028 | 0,1836 | 27    | 0,307569686 | 2 | 1101,66301 | 0,30 | 20,10  |
| 1084 | GTLNQPLTK    | 1    | 1                       | Q15650                                                                                   | 1,118E7   | 0,028 | 0,184  | 26    | 0,861300218 | 2 | 971,55559  | 3,63 | 52,35  |
| 1085 | KVLOQIGSAK   | 1    | 1                       | Q9UGM6                                                                                   | 4,165E6   | 0,028 | 0,1839 | 26    | 0,336289824 | 2 | 943,59349  | -0,05 | 41,63  |
| 1086 | QDLSQIAQ     | 1    | 1                       | Q5EBL4                                                                                   | 2,952E7   | 0,028 | 0,1842 | 25    | 1,344055539 | 2 | 1015,54259 | 0,69 | 47,65  |
| 1087 | TVEEGORLK    | 1    | 3                       | Q8N4C8;Q9UKE5;Q95819                                                                 | 5,830E6   | 0,028 | 0,1864 | 23    | 2,044274319 | 2 | 1059,57854 | -0,77 | 29,15  |
| 1088 | SPWKPTL      | 1    | 1                       | Q81Y47                                                                                   | 1,163E7   | 0,028 | 0,1846 | 23    | 2,844855045 | 2 | 1088,57878 | 1,14 | 104,28 |
| 1089 | SVIEQILHY    | 1    | 1                       | Q15386                                                                                   | 5,077E4   | 0,028 | 0,1839 | 23    | 2,674792998 | 2 | 1101,59368 | -0,21 | 136,11 |
| 1090 | LPAPPTQNM    | 1    | 2                       | Q15532;Q75177                                                                            | 2,522E7   | 0,028 | 0,1838 | 22    | 2,711023014 | 2 | 968,49108  | 4,18 | 88,06  |
| 1091 | A1YGRKFK     | 2    | 1                       | Q2M385                                                                                   | 3,328E5   | 0,028 | 0,1857 | 21    | 1,071475871 | 2 | 1083,63140 | 0,38 | 35,03  |
| 1092 | NPISGLGGTKY  | 1    | 1                       | Q14192                                                                                   | 3,089E6   | 0,028 | 0,1848 | 21    | 3,278469301 | 2 | 1106,58537 | 1,16 | 78,72  |
| 1093 | RPSGKGIVEF   | 1    | 1                       | Q15233                                                                                   | 7,557E7   | 0,028 | 0,1839 | 18    | 5,592474203 | 2 | 1089,61040 | 4,79 | 63,39  |
| #    | Sequence       | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area     | q-Value  | PEP | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|------|----------------|--------|------------|--------------------------|-----------|----------|----------|-----|----------|------------|-----|----------|----------|--------|
| 1094 | QTLQRSWAY     | 1      | 1          | Q9Y6J8                   |           | 4,400E6  | 0,028    | 0,186| 15       | 9,976788282 | 2   | 1152,58281 | 2,73    | 78,41  |
| 1095 | KCPEDRTSEE    | 1      | 1          | Q98U70                   |           | 1,403E5  | 0,028    | 0,1859| 12       | 9,937860702 | 2   | 1193,51091 | 0,47    | 77,56  |
| 1096 | LPTENVDKM     | 1      | 1          | Q9Y4C2                   |           | 2,842E6  | 0,028    | 0,1842| 12       | 27,59496213  | 2   | 1046,52031 | 1,51    | 68,23  |
| 1097 | SPFCCRARLSL   | 1      | 1          | Q13370                   |           | 5,679E5  | 0,03     | 0,188 | 41       | 0,03464147   | 2   | 1149,61540 | -3,81   | 108,31 |
| 1098 | RPAAPGQTPL    | 1      | 1          | Q12796                   |           | 9,302E6  | 0,03     | 0,1886| 40       | 0,02434219   | 2   | 1007,56725 | 3,91    | 55,64  |
| 1099 | ATITKVLQK     | 1      | 1          | Q98YK8                   |           | 3,680E6  | 0,03     | 0,1873| 38       | 0,005910094  | 2   | 1001,63408 | -1,32   | 48,82  |
| 1100 | APWGGVAKTL    | 2      | 1          | Q8NCC3                   |           | 7,752E6  | 0,03     | 0,1876| 35       | 0,047416985  | 2   | 999,56420 | 1,95    | 91,77  |
| 1101 | YPNGVVHY      | 1      | 1          | Q96JC1                   |           | 6,697E6  | 0,03     | 0,1879| 27       | 0,905216109  | 2   | 1047,52910 | 3,13    | 82,75  |
| 1102 | YIFKERESF     | 1      | 1          | Q8N9N2                   |           | 2,989E6  | 0,03     | 0,1879| 23       | 2,420483745  | 2   | 1218,61894 | 2,92    | 76,94  |
| 1103 | RPAQVSQPF     | 1      | 1          | Q9Y520                   |           | 1,766E7  | 0,03     | 0,1879| 21       | 2,311904934  | 2   | 1029,54949 | 1,78    | 62,81  |
| 1104 | mPAETIKEL     | 1      | 1          | Q9H694                   | M1         | 6,748E6  | 0,031    | 0,1905| 39       | 0,042557247  | 2   | 1047,54167 | 2,42    | 69,08  |
| 1105 | SLNQAVVSK     | 1      | 1          | P61201                   |           | 1,402E7  | 0,031    | 0,1906| 39       | 0,04131839   | 2   | 945,53502 | -1,47   | 45,83  |
| 1106 | ATWKNAVRH     | 1      | 3          | O15409;Q9H334;Q8IVH2     |           | 2,497E6  | 0,031    | 0,1906| 32       | 0,198117226  | 2   | 1082,58769 | 2,09    | 30,94  |
| 1107 | LPVDKAQEL     | 1      | 1          | Q8TEK9                   |           | 5,113E6  | 0,031    | 0,1909| 30       | 0,220223484  | 2   | 1012,56993 | 2,51    | 72,98  |
| 1108 | RVYSQITVQK    | 1      | 1          | Q12929                   |           | 9,918E5  | 0,031    | 0,1906| 21       | 1,832420743  | 2   | 1221,69487 | -0,13   | 48,79  |
| 1109 | SSFSGLLRK     | 1      | 1          | Q5VY09                   |           | 1,530E7  | 0,031    | 0,1904| 18       | 3,640346111  | 2   | 994,56804 | -0,01   | 65,52  |
| 1110 | AVHLKTLKK     | 1      | 1          | Q12796                   |           | 1,194E6  | 0,031    | 0,1901| 15       | 0,477734129  | 2   | 1022,67394 | 1,78    | 54,70  |
| 1111 | RDVKQmLLK     | 1      | 1          | Q9H074                   | M6         | 2,943E6  | 0,031    | 0,1903| 13       | 9,115635273  | 2   | 1146,66741 | 0,87    | 58,16  |
| #   | Sequence       | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area | q-Value | PEP | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|----------------|--------|------------|--------------------------|-----------|------|---------|-----|----------|-----------|-----|----------|----------|---------|
| 1112| YVYPLQLKY      | 1      | 1          | Q5JSL3                   |           | 1,823E7 | 0,031   | 0,1902 | 13       | 18,08277536 | 2   | 1186,65337 | 2,26     | 115,84  |
| 1113| RPPGASQSL      | 1      | 1          | Q15477                   |           | 1,363E6 | 0,032   | 0,1932 | 26       | 0,95675329  | 2   | 1009,54271 | 0,14     | 50,32   |
| 1114| IPARIVTNY      | 2      | 1          | P00488                   |           | 2,252E7 | 0,032   | 0,1933 | 25       | 0,826950292 | 2   | 1046,59953 | 0,18     | 78,85   |
| 1115| KQYDEALNK      | 1      | 1          | P78527                   |           | 2,451E6 | 0,032   | 0,1921 | 15       | 14,28810457 | 2   | 1108,56584 | 2,25     | 34,65   |
| 1116| KVFVGRFK       | 1      | 3          | Q13310;P11940;P0CB38     |           | 4,733E6 | 0,032   | 0,1925 | 15       | 1,837056556 | 2   | 980,60466   | 0,62     | 43,29   |
| 1117| APIDRVGQTI     | 1      | 1          | P52272                   |           | 5,932E6 | 0,033   | 0,1971 | 30       | 0,293207274 | 2   | 1069,60283 | 2,56     | 77,41   |
| 1118| RPYAGAVQKF     | 1      | 1          | P49842                   |           | 8,485E6 | 0,033   | 0,1965 | 29       | 0,295264194 | 2   | 1136,62517 | 3,54     | 52,70   |
| 1119| FPMTHGNTGF     | 1      | 1          | Q15366                   |           | 4,870E6 | 0,033   | 0,1971 | 27       | 0,474114545 | 2   | 1108,49101 | 2,64     | 85,26   |
| 1120| RVAPEEHPVL     | 3      | 3          | P60709;P63261;AS3A0      |           | 9,987E7 | 0,033   | 0,1943 | 26       | 0,766540973 | 2   | 1146,63042 | 3,29     | 56,92   |
| 1121| GLDPSQRPK      | 1      | 1          | Q8WVB6                   |           | 4,903E6 | 0,033   | 0,1969 | 26       | 0,589873133 | 2   | 997,54418  | 1,61     | 34,12   |
| 1122| MPVPGHDVEAY    | 1      | 1          | Q9P0T7                   |           | 4,921E6 | 0,033   | 0,1945 | 25       | 0,79684543  | 2   | 1214,55425 | 2,60     | 83,85   |
| 1123| SPFFSPIHL      | 1      | 1          | Q8IVT2                   |           | 1,501E6 | 0,033   | 0,1949 | 24       | 1,729375486 | 2   | 1044,55498 | 3,49     | 132,37  |
| 1124| RLTPVFGL       | 1      | 1          | Q16850                   |           | 1,995E7 | 0,033   | 0,1939 | 22       | 0,962174998 | 2   | 1018,60338 | -1,04    | 64,84   |
| 1125| FLEKAAQTYY     | 1      | 1          | Q6IQ26                   |           | 3,106E5 | 0,033   | 0,1957 | 16       | 11,27495497 | 2   | 1162,57793 | 0,01     | 112,11  |
| 1126| QPNPVEQRY      | 1      | 1          | Q13496                   |           | 2,456E6 | 0,033   | 0,1947 | 15       | 14,27231451 | 2   | 1130,56316 | 3,74     | 54,79   |
| 1127| ALYKLGFNK      | 2      | 1          | P11215                   |           | 3,197E6 | 0,033   | 0,1961 | 13       | 9,049829327  | 2   | 1086,63616 | 1,37     | 101,52  |
| 1128| SVLRLSVSY      | 2      | 2          | P35869;A9YTQ3            |           | 1,240E5 | 0,034   | 0,1986 | 43       | 0,011312067 | 2   | 1023,58257 | -0,77    | 103,28  |
| 1129| RPWDPAVGVL     | 1      | 1          | Q9P2N6                   |           | 6,403E6 | 0,034   | 0,1982 | 39       | 0,025128269 | 2   | 1109,61284 | 2,32     | 116,16  |
| #   | Sequence     | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area       | q-Value | PEP       | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|--------------|--------|------------|--------------------------|-----------|------------|---------|-----------|----------|------------|-----|----------|----------|---------|
| 1130| APEEHPVL     | 2      | 3          | P60709;P63261;A5A3E0     |           | 3,996E8    | 0,034   | 0,1982   | 38       | 0,112743854 | 2   | 891,45683| -0,30    | 57,81   |
| 1131| RVDDHLMGK    | 1      | 1          | O95232                   |           | 1,664E6    | 0,034   | 0,1983   | 35       | 0,110802984 | 2   | 1086,53728| 1,07     | 28,19   |
| 1132| SAVDVHINM    | 1      | 1          | P46379                   |           | 2,871E5    | 0,034   | 0,1993   | 34       | 0,13069798  | 2   | 985,47392| -3,31    | 94,33   |
| 1133| GPLDKWRL     | 2      | 1          | P27635                   |           | 7,986E7    | 0,034   | 0,1997   | 29       | 0,245426335 | 2   | 1055,59953| -0,16    | 96,24   |
| 1134| RIHGVFKK     | 1      | 1          | P62899                   |           | 2,010E6    | 0,034   | 0,1986   | 25       | 0,500658309 | 2   | 1041,63164| -0,02    | 28,38   |
| 1135| TPGGTRIIY    | 1      | 3          | Q13541;Q13542;O60516     |           | 3,142E7    | 0,034   | 0,1982   | 23       | 1,953802058 | 2   | 977,54271| 1,25     | 70,83   |
| 1136| RAAEHTLLH    | 1      | 1          | Q98YK8                   |           | 1,279E6    | 0,034   | 0,1986   | 22       | 2,203824657 | 2   | 1047,57085| 1,34     | 30,41   |
| 1137| RTFGHLLRY    | 1      | 1          | Q13200                   |           | 1,531E7    | 0,034   | 0,198   | 18       | 4,912363863 | 2   | 1162,64885| 0,71     | 67,14   |
| 1138| QVVVLmLVKEC  | 1      | 1          | Q8W274                   |           | 2,364E5    | 0,034   | 0,1987   | 18       | 6,522384705 | 2   | 1177,62871| -2,79    | 140,23  |
| 1139| RTDVHIRVF    | 1      | 1          | Q13454                   |           | 2,859E6    | 0,034   | 0,1983   | 15       | 8,494266264 | 2   | 1142,64141| -1,35    | 68,70   |
| 1140| TREDPNLVPsi  | 5      | 1          | P10606                   |           | 2,098E6    | 0,035   | 0,2006   | 29       | 0,45606433  | 2   | 1240,65764| 3,54     | 107,04  |
| 1141| HPDAPmSQVY   | 1      | 2          | Q15014;Q9UBU8            |           | 2,167E7    | 0,035   | 0,201    | 21       | 1,518910721 | 2   | 1160,50823| 3,53     | 56,86   |
| 1142| KLKSTESELK   | 1      | 1          | Q92878                   |           | 1,354E6    | 0,035   | 0,2007   | 16       | 3,982826978 | 2   | 1162,67290| 4,36     | 26,48   |
| 1143| APARLFAL     | 3      | 1          | P31431                   |           | 3,894E5    | 0,036   | 0,2017   | 43       | 0,011354297 | 2   | 858,51940| -0,30    | 102,76  |
| 1144| GLTTPPIVK    | 1      | 2          | Q86V97;Q8WVZ9            |           | 9,430E6    | 0,036   | 0,2033   | 41       | 0,00180298  | 2   | 968,65416| 3,95     | 63,69   |
| 1145| RIAKLNVEK    | 1      | 1          | Q9H4A5;Q9H4A6            |           | 4,633E6    | 0,036   | 0,2059   | 37       | 0,02378097  | 2   | 1070,66948| 1,28     | 30,75   |
| 1146| VPLPPPGRSL   | 1      | 2          | Q6IQ26;Q6ZUT9            |           | 2,404E7    | 0,036   | 0,2028   | 33       | 0,067333851 | 2   | 1032,62114| 1,01     | 82,42   |
| 1147| KINNWIVQL    | 1      | 2          | P22415;Q15853            |           | 4,067E6    | 0,036   | 0,2016   | 33       | 0,066183063 | 2   | 1127,66094| 3,31     | 123,38  |
| #   | Sequence      | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area   | q-Value | PEP | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|---------------|-------|------------|--------------------------|-----------|--------|---------|-----|----------|------------|-----|----------|----------|---------|
| 1148| RPPIGSISSM    | 1     | 1          | Q9BJY9                   |           | 3,748E6| 0.036   | 0.2013 | 32       | 0.234197053 | 2   | 1044,55181 | 1,06     | 78.94   |
| 1149| RQAVPLFSK     | 1     | 1          | Q9BZ5                    |           | 9,553E6| 0.036   | 0.204  | 30       | 0.173151611 | 2   | 1045,62041 | 4,85     | 63.58   |
| 1150| GTPLLVIAK     | 1     | 1          | P56559                   |           | 5,968E6| 0.036   | 0.2077 | 28       | 0.114281418 | 2   | 1025,63860 | 3,11     | 94.45   |
| 1151| FPVEIKSFY     | 2     | 1          | O43776                   |           | 1,228E7| 0.036   | 0.2067 | 28       | 0.698608999 | 2   | 1129,59526 | 2,13     | 123.82  |
| 1152| AVLQSPGLSGK   | 1     | 1          | Q13045                   |           | 3,984E6| 0.036   | 0.2032 | 27       | 0.563211545 | 2   | 1056,60527 | 0,41     | 67.44   |
| 1153| RPPFTYATL     | 1     | 2          | O15409;Q9BZ51            |           | 4,237E6| 0.036   | 0.2054 | 24       | 1,024040382 | 2   | 1065,57475 | 1,84     | 100.24  |
| 1154| LPDERTISL     | 1     | 1          | Q05048                   |           | 1,515E5| 0.036   | 0.2066 | 22       | 2,13361549  | 2   | 1043,57329 | 0,08     | 100.65  |
| 1155| VLNAALREK     | 1     | 1          | Q8TAP8                   |           | 1,681E6| 0.036   | 0.2067 | 22       | 1,0704056   | 2   | 1013,61223 | 1,94     | 44.23   |
| 1156| MVTEIRLKY     | 1     | 1          | Q15393                   |           | 1,191E5| 0.036   | 0.2065 | 22       | 1,381835971 | 2   | 1152,64458 | -0.01    | 83.00   |
| 1157| GSHSmRYFF     | 1     | 7          | P01892;P30443;P04439;P10314;P30455;P30459;Q09160 | M5 | 2,341E7| 0.036   | 0.2057 | 22       | 1,204368411 | 2   | 1147,50273 | 3,27     | 69.44   |
| 1158| ALYGVVNVKK    | 1     | 1          | Q94952                   |           | 1,223E6| 0.036   | 0.2081 | 20       | 0,933192579 | 2   | 1090,66631 | 3,99     | 63.77   |
| 1159| TIADLEHY      | 1     | 1          | P15924                   |           | 3,061E7| 0.036   | 0.2045 | 20       | 4,695481711 | 2   | 1074,54924 | 2,43     | 113.50  |
| 1160| EVFPLAmNY     | 1     | 3          | P24385;P30281;P30279     | M7 | 4,179E6| 0.036   | 0.2016 | 19       | 3,153024371 | 2   | 1099,51506 | 1,96     | 129.72  |
| 1161| APFKFDmEL     | 1     | 1          | P28482                   | M7 | 4,613E6| 0.036   | 0.2036 | 17       | 6,702304995 | 2   | 1113,52983 | 1,13     | 108.66  |
| 1162| QLMKALLKH     | 1     | 1          | Q98RR0                   |           | 1,169E6| 0.036   | 0.205  | 15       | 1,362217142 | 2   | 1081,65349 | -1,49    | 39.43   |
| 1163| VGIYPAQNY     | 1     | 1          | Q8NDV1                   |           | 4,733E7| 0.036   | 0.2021 | 14       | 14,37027194 | 2   | 1137,59831 | 3,87     | 119.19  |
| 1164| RLYPTPRVR     | 1     | 1          | Q9NXW2                   |           | 2,316E7| 0.036   | 0.2025 | 13       | 9,743141347 | 2   | 1157,69304 | 2,43     | 47.13   |
| 1165| YYDNDKDL      | 1     | 1          | Q8IY63                   |           | 7,062E6| 0.036   | 0.203  | 12       | 16,29727826 | 2   | 1001,46092 | 3,45     | 63.06   |
| #   | Sequence       | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area   | q-Value | PEP   | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|----------------|-------|-----------|--------------------------|----------|--------|---------|-------|----------|------------|-----|----------|----------|---------|
| 1166| LASRPLL        | 1     | 1         | Q9P2B2                   |          | 1,029E7| 0,037   | 0,2111| 42       | 0,002402118| 2   | 882,57842| 1,42     | 94,43   |
| 1167| KPTHFTVNA      | 1     | 1         | P21333                   |          | 6,041E6| 0,037   | 0,2137| 40       | 0,022378111| 2   | 1014,53807| 1,31     | 41,28   |
| 1168| ASVKVLEL       | 1     | 1         | O14979                   |          | 3,984E5| 0,037   | 0,2102| 35       | 0,099225335| 2   | 973,55614| -0,36    | 105,41  |
| 1169| TPKKGNLNY      | 1     | 1         | Q13439                   |          | 1,406E7| 0,037   | 0,2102| 34       | 0,129828833| 2   | 1012,51268| 2,81     | 60,97   |
| 1170| GVLGTVVHGIK    | 1     | 1         | Q9Y6C9                   |          | 1,319E7| 0,037   | 0,2145| 29       | 0,155253198| 2   | 966,57665| 3,63     | 56,22   |
| 1171| ALPEKVKNK      | 1     | 1         | Q4LE39                   |          | 5,723E6| 0,037   | 0,2108| 29       | 0,168357081| 2   | 997,60448| 0,37     | 40,54   |
| 1172| IYDKFIAQL      | 1     | 1         | Q6P1K2                   |          | 5,041E6| 0,037   | 0,2123| 26       | 0,55604141  | 2   | 1110,62212| 2,44     | 119,58  |
| 1173| SPFYPGKTBY     | 1     | 1         | P49790                   |          | 1,315E7| 0,037   | 0,2113| 26       | 1,256527109| 2   | 1160,56401| 1,50     | 79,77   |
| 1174| VLGQLVLK       | 1     | 1         | O75531                   |          | 3,007E6| 0,037   | 0,2127| 26       | 0,056421844| 2   | 1016,65221| 1,85     | 121,52  |
| 1175| RIRDQLSAVASK   | 1     | 1         | Q9P000                   |          | 7,312E6| 0,037   | 0,2099| 24       | 0,70296185  | 3   | 1343,77933| 2,89     | 53,90   |
| 1176| VYSDLHAFY      | 2     | 1         | Q5VSG8                   |          | 1,665E5| 0,037   | 0,2084| 24       | 1,231821161| 2   | 1114,52031| -0,08    | 109,52  |
| 1177| RSAQPLPLKI     | 1     | 1         | Q9UKV3                   |          | 5,422E6| 0,037   | 0,2087| 22       | 0,255454267| 2   | 1122,69963| 0,20     | 78,49   |
| 1178| LQRANLLSY      | 1     | 1         | Q15742                   |          | 7,633E6| 0,037   | 0,2105| 22       | 1,776199042| 2   | 1077,60710| 1,81     | 93,97   |
| 1179| LPSSEVVKF      | 1     | 1         | Q96CG3                   |          | 5,588E6| 0,037   | 0,2098| 20       | 3,336119607| 2   | 1005,56273| 1,15     | 93,05   |
| 1180| ILFPLRFTL      | 1     | 1         | O43156                   |          | 3,833E5| 0,037   | 0,2137| 20       | 0,600870051| 2   | 1119,69255| 0,02     | 151,65  |
| 1181| ALWGGTQPLLK    | 1     | 1         | Q8WY98                   |          | 3,499E6| 0,037   | 0,2088| 20       | 1,888092032| 2   | 1183,68791| 3,79     | 110,66  |
| 1182| SIFEPAGGKEK    | 1     | 1         | P5S265                   |          | 1,865E6| 0,037   | 0,2085| 18       | 6,997125852| 2   | 1162,61101| 0,58     | 50,30   |
| 1183| TAAETHYTY      | 1     | 1         | P22415                   |          | 1,464E7| 0,037   | 0,2135| 17       | 4,498659974| 2   | 1056,46550| 2,11     | 50,88   |
| #   | Sequence         | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area     | q-Value | PEP     | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|------------------|--------|------------|--------------------------|-----------|----------|---------|---------|----------|-----------|-----|----------|----------|---------|
| 1184| GYMEEYLY        | 1      | 1          | Q9NX31                   |           | 2,170E6  | 0,037   | 0,2135  | 17       | 2,287728744 | 2   | 1101,46355 | 3,44     | 76,05   |
| 1185| LNLPYFLRY       | 1      | 1          | Q5T457                   |           | 9,998E4  | 0,037   | 0,2089  | 16       | 4,912894628 | 2   | 1198,66142 | -0,42    | 146,11  |
| 1186| LRTALIFGGF      | 1      | 1          | Q8N5G0                   |           | 4,253E5  | 0,037   | 0,2103  | 16       | 4,032950983 | 2   | 1094,63677 | 0,93     | 136,27  |
| 1187| SLTSSKGQLQK     | 1      | 1          | Q99541                   |           | 3,348E4  | 0,037   | 0,211   | 15       | 5,422150946 | 2   | 1289,74309 | 0,54     | 48,97   |
| 1188| FPRDPEIEm       | 1      | 1          | P19320                   | M9        | 5,261E6  | 0,037   | 0,2124  | 12       | 16,56812889 | 2   | 1149,52788 | 2,89     | 76,71   |
| 1189| YLWHIPLSY       | 1      | 1          | Q9UIQ6                   |           | 2,164E6  | 0,037   | 0,2138  | 12       | 28,45870011 | 2   | 1191,62456 | 4,06     | 140,74  |
| 1190| RPIRQILYL       | 1      | 1          | Q9UBQ5                   |           | 2,633E7  | 0,037   | 0,2106  | 11       | 5,258345169 | 2   | 1171,73503 | 3,42     | 91,00   |
| 1191| mPVPGHDEAY      | 1      | 1          | Q9P0T7                   | M1        | 0,000E0  | 0,038   | 0,2181  | 33       | 0,099302409 | 2   | 1230,54473 | -1,04    | 67,66   |
| 1192| APWKKGLIAV      | 1      | 1          | P16284                   |           | 3,695E6  | 0,038   | 0,215   | 31       | 0,030546666 | 2   | 1082,67388 | 1,60     | 82,37   |
| 1193| LYDPVISKL       | 1      | 1          | Q96E28                   |           | 6,652E4  | 0,038   | 0,2194  | 31       | 0,173978149 | 2   | 1047,60808 | -0,41    | 111,11  |
| 1194| MVPRLAVL        | 1      | 1          | Q63HM2                   |           | 8,681E4  | 0,038   | 0,2165  | 30       | 0,128161163 | 2   | 999,60112 | -0,89    | 97,61   |
| 1195| MLVQALKSGDW     | 1      | 1          | Q9NU22                   |           | 7,258E5  | 0,038   | 0,217   | 28       | 0,802946079 | 2   | 1247,64556 | 0,17     | 114,01  |
| 1196| SPIPDSEKJ       | 1      | 1          | Q6ZRH7                   |           | 1,056E7  | 0,038   | 0,2152  | 26       | 1,163834145 | 2   | 1035,49822 | -1,10    | 64,85   |
| 1197| KLLDAYLLY       | 1      | 1          | P61803                   |           | 2,448E5  | 0,038   | 0,2183  | 24       | 0,633775724 | 2   | 1111,63921 | -0,53    | 140,15  |
| 1198| VVMRDPASK       | 1      | 1          | P22626                   |           | 3,719E7  | 0,038   | 0,2193  | 23       | 2,584763033 | 2   | 1002,54503 | 4,88     | 35,68   |
| 1199| KSTAISLFY       | 1      | 1          | P13639                   |           | 1,912E7  | 0,038   | 0,2156  | 23       | 2,117614111 | 2   | 1029,56365 | 2,03     | 107,25  |
| 1200| RIFEPPPPK       | 1      | 1          | O43143                   |           | 3,374E7  | 0,038   | 0,216   | 23       | 0,890401791 | 2   | 1080,62493 | 4,46     | 56,58   |
| 1201| RPKFGYEGLSL     | 1      | 2          | Q93062;Q6ZRY4            |           | 7,473E6  | 0,038   | 0,2167  | 22       | 2,298206228 | 2   | 1153,60417 | 3,55     | 62,16   |
| #   | Sequence                      | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area     | q-Value | PEP   | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|------------------------------|--------|------------|--------------------------|-----------|----------|---------|-------|----------|------------|-----|----------|----------|---------|
| 1202| mPSRPSTTPF                   | 1      | 1          | P27816                   | M1        | 1,406E6  | 0,038   | 0,2178| 20       | 3,214804356 | 2   | 1136,5395 | -1,03    | 64,58   |
| 1203| ATIPNARQF                    | 1      | 1          | P42285                   |           | 8,182E6  | 0,038   | 0,2189| 20       | 2,695968931 | 2   | 1017,5515 | 3,84    | 72,23   |
| 1204| KTVPVEAVTSK                  | 1      | 1          | Q14247                   |           | 3,223E6  | 0,038   | 0,2155| 18       | 3,715248177 | 2   | 1158,6748 | 1,67    | 44,27   |
| 1205| SQYPNQPTRF                   | 1      | 1          | P24468                   |           | 8,895E5  | 0,038   | 0,2174| 14       | 14,49980706 | 2   | 1237,5963 | 0,26    | 66,05   |
| 1206| GVLKIQVHY                    | 1      | 1          | P52907                   |           | 8,049E6  | 0,038   | 0,2184| 11       | 7,808214468 | 2   | 1056,62163 | 1,47    | 81,66   |
| 1207| AVDORGLYK                    | 1      | 2          | P67812;P0C7V7            |           | 2,619E6  | 0,039   | 0,2205| 23       | 1,973870501 | 2   | 1036,54241 | 0,17    | 45,40   |
| 1208| RPWHPAVVF                    | 1      | 1          | Q96G91                   |           | 7,737E6  | 0,039   | 0,2198| 20       | 3,03005227 | 2   | 1108,60723 | 1,91    | 90,23   |
| 1209| PQNSDYLLAL                   | 1      | 1          | Q99523                   |           | 8,362E5  | 0,04    | 0,2225| 36       | 0,10252293 | 2   | 1133,58769 | 3,48    | 145,96  |
| 1210| KPPPPAQEF                    | 1      | 1          | Q86X10                   |           | 0,000E0  | 0,04    | 0,2232| 34       | 0,130137494 | 2   | 1010,53526 | 4,61    | 55,90   |
| 1211| GVDVTGHLY                    | 1      | 1          | Q99436                   |           | 5,668E6  | 0,04    | 0,2216| 28       | 0,630558789 | 2   | 1057,53349 | 2,06    | 92,34   |
| 1212| KPIPLPRF                     | 1      | 1          | Q8WV28                   |           | 1,494E7  | 0,04    | 0,2211| 24       | 0,045953964 | 2   | 967,61046 | 1,71    | 85,84   |
| 1213| HPIQTQAGY                    | 1      | 1          | Q71RC2                   |           | 1,251E7  | 0,04    | 0,2212| 24       | 1,43319694 | 2   | 1085,53801 | 0,52    | 47,57   |
| 1214| ALLDSQFSY                    | 2      | 1          | O15372                   |           | 5,926E7  | 0,04    | 0,2224| 22       | 2,334540043 | 2   | 1043,50383 | -0,57   | 140,86  |
| 1215| KGNSPLLQK                    | 1      | 1          | Q9H118                   |           | 1,366E7  | 0,041   | 0,2273| 44       | 0,009630444 | 2   | 984,58385 | 0,15    | 31,70   |
| 1216| SSSPRNLGF                    | 1      | 1          | Q9U8F8                   |           | 3,192E6  | 0,041   | 0,2254| 43       | 0,021999072 | 2   | 964,48509 | 0,40    | 67,99   |
| 1217| RPYPSPGAVL                   | 1      | 1          | O60828                   |           | 6,222E4  | 0,041   | 0,2258| 34       | 0,108628554 | 2   | 1056,58342 | -0,26   | 83,96   |
| 1218| LPTENVDKm                    | 1      | 1          | Q9Y4C2                   | M9        | 2,550E6  | 0,041   | 0,2265| 33       | 0,210018972 | 2   | 1062,51494 | 1,22    | 50,91   |
| 1219| LATRLAPIYK                   | 1      | 1          | Q8NFU7                   |           | 7,963E5  | 0,041   | 0,2273| 25       | 0,266175674 | 2   | 1145,70561 | 1,28    | 86,03   |
| #   | Sequence       | # PSMs | # Proteins | Protein Group Accessions                  | Mod. (ox) | Area    | q-Value | PEP   | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|----------------|--------|------------|------------------------------------------|-----------|---------|---------|-------|----------|------------|-----|----------|----------|---------|
| 1220 | RSDELTRHF      | 1      | 3          | O95600;Q99612;P57682                      | 1,136E7   | 0,041   | 0,2282  | 25    | 1,296726923 | 1160,58330   | 2   | 2,20     | 44,65    |
| 1221 | MRYVASYLL      | 1      | 1          | P05387                                    | 1,378E5   | 0,041   | 0,2255  | 25    | 1,431442971 | 1115,59184   | 2   | 0,03     | 114,02   |
| 1222 | RALDLLAGFY     | 2      | 1          | Q96RY7                                    | 2,499E5   | 0,041   | 0,2284  | 24    | 1,276485302 | 1138,62529   | 2   | -0,25    | 120,02   |
| 1223 | RPQSAISSF      | 1      | 1          | QSVT06                                    | 1,523E6   | 0,041   | 0,2274  | 20    | 4,620912924 | 992,51506    | 2   | -0,96    | 64,57    |
| 1224 | KLHEETLTY      | 1      | 1          | Q9NZI6                                    | 9,460E6   | 0,041   | 0,2245  | 19    | 6,775183671 | 1133,58440   | 2   | 0,58     | 57,25    |
| 1225 | RSSTYEVRL      | 1      | 1          | P05161                                    | 1,996E7   | 0,041   | 0,2262  | 18    | 5,51522276  | 1110,59343   | 2   | 2,88     | 58,92    |
| 1226 | ISKYIILQ       | 1      | 6          | P0CH99;A8MUZ8;P0C100;Q6ZN79;A8MWA4;A8MV51 | 4,460E6   | 0,041   | 0,2284  | 18    | 1,845082288 | 1064,63750   | 2   | 2,30     | 117,48   |
| 1227 | DPNPNFEKF      | 1      | 1          | Q9H8H3                                    | 4,648E6   | 0,041   | 0,2247  | 17    | 7,185129009 | 1107,51433   | 2   | 3,37     | 91,70    |
| 1228 | IPVFLEKL       | 1      | 1          | Q14669                                    | 2,962E6   | 0,042   | 0,2298  | 23    | 0,600171712 | 958,59972    | 2   | 2,59     | 125,71   |
| 1229 | GVNVRIAVSK     | 1      | 1          | Q8IV08                                    | 2,584E6   | 0,042   | 0,2293  | 20    | 1,298726592 | 1042,63835   | 2   | 1,48     | 57,32    |
| 1230 | RYPDLELKY      | 1      | 1          | O7S290                                    | 3,385E6   | 0,042   | 0,2288  | 13    | 21,00328502 | 1196,63237   | 2   | 1,12     | 92,78    |
| 1231 | MLLRLNALL      | 1      | 1          | O60287                                    | 4,939E5   | 0,043   | 0,2334  | 38    | 0,020713174 | 1056,65605   | 2   | -3,60    | 122,26   |
| 1232 | SSNSYAIKK      | 1      | 1          | P46782                                    | 9,632E6   | 0,043   | 0,2318  | 33    | 0,193040565 | 997,53594    | 2   | 4,64     | 27,38    |
| 1233 | SLNKQIAQK      | 1      | 1          | Q567U6                                    | 3,553E6   | 0,043   | 0,2328  | 32    | 0,201887217 | 1029,60588   | 2   | 0,70     | 28,53    |
| 1234 | VAFKKTFSY      | 1      | 1          | Q99382                                    | 5,779E6   | 0,043   | 0,232  | 31    | 0,336496783 | 1090,59624   | 2   | 2,79     | 68,92    |
| 1235 | ALKNTSDFVYL    | 1      | 1          | Q12959                                    | 0,000E0   | 0,043   | 0,2324 | 24    | 1,718653877 | 1270,66692   | 2   | -0,71    | 139,26   |
| 1236 | GVSSIFYH       | 1      | 1          | P33076                                    | 0,000E0   | 0,043   | 0,233  | 23    | 1,740128025 | 1022,53343   | 2   | 2,79     | 109,27   |
| 1237 | MPSHPDRAY      | 1      | 1          | O75888                                    | 1,462E6   | 0,043   | 0,2317 | 23    | 1,058935648 | 1073,48479   | 2   | 1,36     | 40,99    |
| #    | Sequence       | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area  | q-Value | PEP   | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|------|----------------|--------|-----------|--------------------------|-----------|-------|---------|-------|----------|------------|-----|----------|----------|---------|
| 1238 | RPDDRSQGAll   | 1      | 1         | Q04637                   |           | 2,000E7 | 0,043   | 0,2327| 23       | 1,623094856 | 2   | 1227,64715 | 2,78    | 53,91   |
| 1239 | SIWDETLYK     | 1      | 2         | Q7L523;Q5VZM2            |           | 7,805E4 | 0,043   | 0,233 | 21       | 3,127284487 | 2   | 1154,57341 | 0,49    | 121,92  |
| 1240 | GTQPGPLK      | 1      | 1         | Q8GU2                    |           | 2,791E8 | 0,043   | 0,2304| 21       | 0,750989602  | 2   | 1038,63323 | 2,47    | 41,35   |
| 1241 | GTDELRLLY     | 1      | 1         | Q9Y4W2                   |           | 1,435E7 | 0,043   | 0,2318| 21       | 3,382216383  | 2   | 1079,57622 | 2,80    | 115,35  |
| 1242 | KQYDFTYR      | 1      | 1         | Q9Y3Q3                   |           | 3,102E6 | 0,043   | 0,231 | 20       | 3,796522524  | 2   | 1207,57512 | 0,74    | 57,17   |
| 1243 | GLYEPFLNK     | 1      | 1         | Q9UJA5                   |           | 3,613E6 | 0,043   | 0,2309| 20       | 3,880530713  | 2   | 1080,57536 | 2,69    | 105,89  |
| 1244 | RPKPPSATS1    | 1      | 1         | Q9UMS4                   |           | 1,378E7 | 0,043   | 0,2334| 19       | 2,363729762  | 2   | 1053,60710 | 1,83    | 44,64   |
| 1245 | HPSLGHQVSY    | 1      | 1         | P17947                   |           | 2,187E6 | 0,043   | 0,2305| 18       | 4,873898444  | 2   | 1124,55071 | 2,09    | 51,92   |
| 1246 | FPWEVPKKLY    | 1      | 1         | P31153                   |           | 3,342E7 | 0,043   | 0,2321| 18       | 3,072962843  | 3   | 1434,81781 | 2,35    | 96,38   |
| 1247 | HPNPGSTHKL    | 1      | 1         | Q93074                   |           | 2,626E6 | 0,043   | 0,233 | 15       | 12,73679009  | 2   | 1072,55425 | 0,74    | 58,06   |
| 1248 | DPVEPHGEm     | 1      | 1         | Q13263                   |           | 4,031E6 | 0,043   | 0,2317| 13       | 6,95698174  | 2   | 1026,41997 | 0,22    | 42,46   |
| 1249 | ALSAAALYL     | 1      | 1         | P56192                   |           | 2,054E6 | 0,043   | 0,2332| 12       | 19,27903481  | 2   | 984,54045 | 0,38    | 137,29  |
| 1250 | RPVQKLIRL     | 1      | 1         | Q5W0V3                   |           | 3,931E6 | 0,043   | 0,2319| 11       | 1,126565481  | 2   | 1122,74919 | 1,93    | 58,09   |
| 1251 | GPWSRSLSAL    | 1      | 1         | P12830                   |           | 2,469E7 | 0,044   | 0,2388| 47       | 0,007574324  | 2   | 1073,57707 | 2,98    | 101,91  |
| 1252 | RVLEKDSVTLK   | 1      | 1         | P08637                   |           | 7,835E6 | 0,044   | 0,236 | 40       | 0,011372429  | 3   | 1287,76334 | 0,15    | 48,23   |
| 1253 | KPPFFFEGL     | 1      | 1         | Q9H8S8                   |           | 5,076E6 | 0,044   | 0,2352| 40       | 0,033885     | 2   | 1081,57610 | 4,02    | 140,72  |
| 1254 | VPGPTGLHY     | 1      | 1         | Q8NF64                   |           | 6,914E6 | 0,044   | 0,2387| 38       | 0,052285419  | 2   | 940,49126 | 2,70    | 77,89   |
| 1255 | RPFEDQTSI     | 1      | 1         | Q9H7B2                   |           | 1,499E7 | 0,044   | 0,2351| 33       | 0,236007698  | 2   | 1092,53411 | 1,87    | 75,55   |
| #   | Sequence     | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area      | q-Value | PEP     | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|--------------|--------|------------|--------------------------|-----------|-----------|---------|---------|----------|-----------|-----|----------|----------|---------|
| 1256 | ASTTHDLRL    | 1      | 1          | Q14032                   |           | 3,637E6   | 0,044   | 0,2366 | 32       | 0,245383315 | 2   | 1013,54051 | 3,00     | 51,18   |
| 1257 | LPSSRIEVL    | 1      | 1          | Q92738                   |           | 1,271E5   | 0,044   | 0,2355 | 30       | 0,230352152 | 2   | 1013,59899 | -0,04    | 104,28  |
| 1258 | APVFRDYVF    | 1      | 1          | Q9NZK5                   |           | 1,342E7   | 0,044   | 0,2338 | 27       | 0,658365029 | 2   | 1113,57671 | 3,51     | 118,16  |
| 1259 | ALSPSLKNK    | 1      | 1          | Q7Z333                   |           | 8,798E6   | 0,044   | 0,2342 | 27       | 0,652455645 | 2   | 957,57689 | 4,27     | 35,81   |
| 1260 | SPFSSRPSL    | 1      | 1          | P41970                   |           | 3,997E6   | 0,044   | 0,2361 | 26       | 1,130593599 | 2   | 1064,53935 | 2,08     | 75,89   |
| 1261 | mPADTNKF     | 1      | 1          | Q9PO12                   | M1        | 2,391E6   | 0,044   | 0,2362 | 26       | 0,88894805  | 2   | 1010,46105 | -0,17    | 45,79   |
| 1262 | AIYGRGIAY    | 1      | 1          | Q8NBP0                   |           | 7,428E6   | 0,044   | 0,2348 | 23       | 0,950723734 | 2   | 983,53307 | 2,18     | 79,79   |
| 1263 | MSPSPVSPKL   | 1      | 1          | Q9UHB7                   |           | 7,941E6   | 0,044   | 0,2368 | 23       | 1,209465302 | 2   | 955,52953 | 1,42     | 82,22   |
| 1264 | mAHAMASKE    | 1      | 1          | P04406                   | M1        | 1,055E5   | 0,044   | 0,2382 | 22       | 1,167001788 | 2   | 920,39610 | -0,44    | 21,60   |
| 1265 | KLTDFGFSNK   | 1      | 1          | Q9NRH2                   |           | 5,178E6   | 0,044   | 0,2352 | 21       | 2,484303726 | 2   | 1156,60344 | 3,19     | 79,40   |
| 1266 | GTSSLFIYK    | 1      | 1          | Q8TAM1                   |           | 1,393E7   | 0,044   | 0,2343 | 20       | 1,83587782  | 2   | 1015,54723 | 1,31     | 92,37   |
| 1267 | QAEKAHAF     | 1      | 1          | Q15149                   |           | 1,346E7   | 0,044   | 0,2355 | 18       | 4,904752235 | 2   | 1030,49541 | 0,12     | 30,67   |
| 1268 | DAIRNLHHEY   | 1      | 2          | Q9BF8;Q9BQD4            |           | 6,790E6   | 0,044   | 0,2387 | 18       | 6,41194746  | 2   | 1138,57793 | 2,36     | 43,96   |
| 1269 | APIVAHLWEY   | 1      | 1          | P50416                   |           | 2,829E6   | 0,044   | 0,2355 | 18       | 5,047078256 | 2   | 1198,62920 | 3,03     | 122,97  |
| 1270 | RLFGISLSY    | 1      | 1          | P51798                   |           | 2,048E6   | 0,044   | 0,2355 | 16       | 6,112522533 | 2   | 1055,59050 | 1,95     | 127,63  |
| 1271 | KPFKLSLGF    | 1      | 1          | P49006                   |           | 4,024E6   | 0,044   | 0,2369 | 14       | 6,319487255 | 2   | 1123,65239 | 1,18     | 100,89  |
| 1272 | APASFGKSF    | 1      | 1          | Q96EY5                   |           | 2,792E7   | 0,045   | 0,2399 | 41       | 0,016625133 | 2   | 911,46324 | 1,15     | 70,03   |
| 1273 | VPQPSGRTL    | 1      | 1          | Q95644                   |           | 2,398E7   | 0,045   | 0,242  | 40       | 0,029676298 | 2   | 954,53935 | 2,73     | 52,77   |
| #   | Sequence         | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area     | q-Value | PEP     | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|-----------------|--------|------------|--------------------------|----------|----------|---------|---------|----------|-----------|-----|----------|----------|----------|
| 1274 | VPQLHLVL       | 1      | 1          | P12111                   |          | 2,238E7  | 0,045   | 0,2403 | 37       | 0,007955831 | 2   | 1017,64769 | 2,08     | 116,99   |
| 1275 | VVDPPVREK      | 1      | 1          | Q9UKV0                   |          | 2,774E7  | 0,045   | 0,2413 | 36       | 0,034770952 | 2   | 1040,60857 | -1,31    | 43,75    |
| 1276 | LLYGHTVTV      | 1      | 1          | Q8TB61                   |          | 1,197E5  | 0,045   | 0,2411 | 35       | 0,175482321 | 2   | 1002,56151 | -0,37    | 75,50    |
| 1277 | SLADQIEK       | 1      | 1          | Q9HC98                   |          | 9,689E4  | 0,045   | 0,2411 | 32       | 0,278772516 | 2   | 1050,54619 | -0,44    | 100,60   |
| 1278 | RVSTEVTLAVK    | 1      | 1          | Q9NTJ5                   |          | 4,597E6  | 0,045   | 0,2407 | 31       | 0,127114779 | 2   | 1202,71355 | 2,64     | 63,01    |
| 1279 | SPEDIKKAY      | 1      | 3          | O75190;Q7Z6W7;Q8NH50     |          | 3,234E7  | 0,045   | 0,2399 | 27       | 0,845765478 | 2   | 1050,54643 | -0,20    | 45,48    |
| 1280 | ALVSTPVRTK     | 1      | 1          | O75376                   |          | 5,277E6  | 0,045   | 0,2418 | 23       | 0,864007045 | 2   | 1071,65203 | -0,09    | 50,00    |
| 1281 | MmNEAPGPINF    | 1      | 2          | P19105;O14950            | M2       | 1,873E5  | 0,045   | 0,24   | 22       | 1,463829581 | 2   | 1236,53923 | 0,32     | 124,61   |
| 1282 | KPFNPLLGETF    | 1      | 1          | P22059                   |          | 4,249E6  | 0,045   | 0,2405 | 20       | 3,881207901 | 2   | 1262,68425 | 4,94     | 125,28   |
| 1283 | QLYDKGLVY      | 1      | 1          | P41252                   |          | 3,156E7  | 0,045   | 0,2418 | 17       | 6,69922801  | 2   | 1098,58513 | 1,93     | 94,39    |
| 1284 | TVDSQTHY       | 1      | 1          | Q9Y3Q3                   |          | 8,583E6  | 0,045   | 0,2418 | 16       | 11,24957343 | 2   | 1063,50945 | 3,73     | 62,14    |
| 1285 | LPLPSHVSL     | 1      | 1          | P09619                   |          | 1,699E6  | 0,046   | 0,2429 | 36       | 0,045293008 | 2   | 962,56944 | 2,56     | 105,04   |
| 1286 | RLYQAGEGR      | 1      | 1          | P20073                   |          | 4,927E5  | 0,046   | 0,2425 | 26       | 0,963308446 | 2   | 1049,55034 | 1,55     | 30,86    |
| 1287 | RPFSPREAL      | 1      | 1          | Q86V48                   |          | 7,415E6  | 0,046   | 0,2429 | 25       | 0,562833546 | 2   | 1072,59404 | 3,90     | 60,76    |
| 1288 | ATFLPSVQK      | 1      | 1          | P26196                   |          | 2,829E7  | 0,046   | 0,2422 | 22       | 1,891604761 | 2   | 990,56389 | 2,01     | 84,46    |
| 1289 | RPSQPTQET      | 1      | 1          | Q9H3M7                   |          | 2,859E6  | 0,047   | 0,2453 | 36       | 0,08649592  | 2   | 1043,51494 | 3,15     | 26,57    |
| 1290 | GTMTGMLYK      | 1      | 2          | Q5SRD1;O14925            |          | 2,778E5  | 0,047   | 0,2436 | 31       | 0,232059076 | 2   | 1001,47942 | -0,08    | 76,20    |
| 1291 | AmNREVSSLK     | 1      | 1          | P35579                   | M2       | 4,480E6  | 0,047   | 0,2455 | 25       | 1,377584139 | 2   | 1150,59050 | 1,70     | 29,87    |
| #   | Sequence       | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area     | q-Value | PEP    | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|-----|----------------|--------|------------|--------------------------|-----------|----------|---------|--------|----------|------------|-----|----------|----------|----------|
| 1292| SPSKmPEI       | 1      | 1          | Q15011                   | M5        | 2,530E6  | 0,047   | 0,2448 | 21       | 3,562657314 | 2   | 904,44402 | -0,53    | 41,60    |
| 1293| KVCNPITKL      | 1      | 1          | P11142                   |           | 6,505E6  | 0,047   | 0,2446 | 17       | 2,65967971  | 2   | 1128,68205 | 0,95     | 98,36    |
| 1294| KSFDEQNPVK     | 1      | 1          | O95425                   |           | 3,152E6  | 0,047   | 0,2454 | 15       | 15,53716143 | 2   | 1191,60210 | 1,36     | 43,69    |
| 1295| YDITNYQSF      | 1      | 1          | P51157                   |           | 8,529E6  | 0,047   | 0,2463 | 14       | 9,02410323  | 2   | 1150,50884 | 3,21     | 94,34    |
| 1296| TAIREEVQYQ     | 1      | 1          | O14910                   |           | 3,986E6  | 0,047   | 0,2446 | 11       | 25,50932076 | 2   | 1142,58733 | 2,85     | 77,73    |
| 1297| RTNEGVIEF      | 1      | 1          | Q13247                   |           | 3,199E7  | 0,048   | 0,2474 | 35       | 0,162786952 | 2   | 1064,54094 | 3,56     | 87,50    |
| 1298| VmQVAIDLQSl    | 1      | 1          | P08047                   | M2        | 6,590E4  | 0,048   | 0,2491 | 26       | 1,088830535 | 2   | 1119,57170 | 0,18     | 105,26   |
| 1299| IILLILIL       | 1      | 1          | QSTF21;P12830            |           | 9,094E5  | 0,048   | 0,2507 | 26       | 0,020035301 | 2   | 923,68999  | -0,45    | 130,02   |
| 1300| APLKLQmEF      | 1      | 1          | Q9Y244                   | M7        | 7,080E6  | 0,048   | 0,2492 | 21       | 2,948270652 | 2   | 1092,58049 | 4,24     | 91,18    |
| 1301| IPFRPSIQF      | 1      | 1          | O00472                   |           | 3,718E6  | 0,048   | 0,2474 | 18       | 4,434498132 | 2   | 1104,62444 | 3,93     | 118,48   |
| 1302| VPFPRILHFF     | 1      | 11         | Q13885;Q9H4B7;Q9BVA1;P04350;P68371;P07437;Q13509;Q9BUF5;Q3ZCM7;A6NNZ2;A6NKZ8 |           | 5,800E6  | 0,048   | 0,2502 | 17       | 7,814597697 | 2   | 1159,64604 | 4,21     | 125,59   |
| 1303| RLVNYQISVK     | 1      | 1          | Q15486                   |           | 8,209E6  | 0,048   | 0,2501 | 16       | 2,855228921 | 2   | 1219,71990 | 3,38     | 72,76    |
| 1304| SIYKPGQTVK     | 1      | 1          | P01023                   |           | 9,387E6  | 0,048   | 0,2498 | 16       | 6,697920812 | 2   | 1120,63762 | 1,34     | 41,07    |
| 1305| AFGWLSSVLFE    | 1      | 1          | P53985                   |           | 2,616E5  | 0,048   | 0,2493 | 14       | 13,43642547 | 2   | 1255,63567 | -0,11    | 109,17   |
| 1306| SRGCLQNEKQ     | 1      | 1          | Q5V7V2                   |           | 3,363E6  | 0,048   | 0,2479 | 13       | 18,31970472 | 2   | 1162,56340 | 0,02     | 114,88   |
| 1307| DANPETHAF      | 1      | 1          | Q99798                   |           | 1,278E7  | 0,048   | 0,2495 | 13       | 8,129322723 | 2   | 1001,43584 | 3,49     | 63,10    |
| 1308| RGLAAPSNL      | 1      | 1          | Q9P210                   |           | 2,940E5  | 0,049   | 0,2539 | 41       | 0,017329677 | 2   | 898,51024  | -0,33    | 68,64    |
| 1309| LPSDTRLVL      | 1      | 1          | P05155                   |           | 3,061E7  | 0,049   | 0,251  | 32       | 0,154050601 | 2   | 1013,60130 | 2,25     | 101,18   |
| #    | Sequence       | # PSMs | # Proteins | Protein Group Accessions | Mod. (ox) | Area     | q-Value | PEP   | IonScore | Exp. Value | Ch. | MH+ [Da] | ΔM [ppm] | RT [min] |
|------|----------------|--------|------------|--------------------------|-----------|----------|---------|-------|----------|------------|-----|----------|----------|---------|
| 1310 | RPPAVTSNGTL    | 1      | 1          | O94868                   |           | 7,26E6   | 0,049   | 0,2516| 31       | 0,255664947| 2   | 1112,60979| 3,49     | 58,65   |
| 1311 | KAGEVFHIHK     | 1      | 1          | Q15233                   |           | 4,96E4   | 0,049   | 0,2527| 29       | 0,316936833| 2   | 1028,58867| -0,12    | 34,39   |
| 1312 | RLYGDSAAK      | 1      | 1          | Q9NWZ8                   |           | 1,42E6   | 0,049   | 0,252  | 27       | 0,606553388| 2   | 980,51482| -1,22    | 29,16   |
| 1313 | KLGGVVSIK      | 1      | 1          | Q9Y4A5                   |           | 5,79E6   | 0,049   | 0,2538| 25       | 0,204715747| 2   | 900,59111| 3,75     | 54,89   |
| 1314 | ANFQPKVVK      | 1      | 2          | Q9UKX2;P13535            |           | 7,51E7   | 0,049   | 0,2539| 24       | 0,348109235| 2   | 1158,70317| 3,25     | 63,15   |
| 1315 | KSIDFLTK       | 1      | 1          | O75844                   |           | 1,19E7   | 0,049   | 0,2527| 23       | 1,012220318| 2   | 1048,60637| 2,48     | 75,51   |
| 1316 | LPDTRSEAY      | 1      | 1          | O60563                   |           | 5,24E6   | 0,049   | 0,2535| 20       | 4,304942334| 2   | 1051,50969| 3,98     | 59,89   |
| 1317 | KPLPLKTAL      | 1      | 1          | P32314                   |           | 9,66E6   | 0,049   | 0,2516| 20       | 0,205131978| 2   | 980,65026| -0,08    | 67,32   |
| 1318 | RTAEYFPTK      | 1      | 1          | QST482                   |           | 1,60E6   | 0,049   | 0,2525| 17       | 6,802219022| 2   | 1112,57402| 0,45     | 50,05   |
Whole transcriptome sequencing (WTS) was performed and expression values of the source transcripts of every epitope of the vaccination cocktail were determined for L06/10 and P03/13 using Cufflinks (47). For sample L06/10 the overall read mapping rate is 91.9% and the concordant pair alignment rate 85.2%. For P03/13 it is 91.7% and 86.5%.

Expression values in the following table are shown in FPKM (Fragments per kilobase of exon per million fragments mapped).

| Peptide   | HLA   | Transcript ID | L06/10 | P03/13 |
|-----------|-------|---------------|--------|--------|
| RGS-5     | A*03  | NM_003617     | 32.23  | 81.06  |
| MMP7-(1)  | A*03  | NM_002423     | 141.39 | 1112.53|
| ADFP-2    | A*03  | NM_001122     | 565.36 | 52.60  |
| ADFP-3    | A*03  | NM_001122     | 565.36 | 52.60  |
| CCND1     | DR    | NM_053056     | 69.69  | 29.62  |
| IGFBP3    | DR    | NM_001013398  | 1.10   | 0.00   |
| MMP7-(2)  | DR    | NM_002423     | 141.39 | 1112.53|
Supplementary Table 19: Epitope Prediction for vaccine peptides

To test whether peptides of the vaccination cocktail show good affinity to the given HLA alleles, epitope prediction methods netMHCpan (15) and netMHCIIpan (48) and SYFPEITHI (16) were used. All of the MHC class I epitopes are binding to A*03:01, class II epitopes are binding to DRB1*0101. Two class II epitopes (IGFBP3, MMP7-(2)) show theoretical affinity to DRB1*1101 as well. IGFBP3 has additional affinity to DRB3*0202.

| Peptide ID | Allele      | Peptide                   | 1-log50k (aff) | Affinity (nM) | SYF |
|------------|-------------|----------------------------|----------------|----------------|-----|
| RGS-5      | A*03:01    | GLASFKSFLK                 | 0.735          | 17.6           | 21  |
| MMP7-(1)   | A*03:01    | SLFPNSPKWTSK               | 0.758          | 13.71          | 16  |
| ADFP-2     | A*03:01    | SLTSSSKGQLQK               | 0.632          | 53.34          | 17  |
| ADFP-3     | A*03:01    | TSALPIIQK                  | 0.473          | 298.04         | 15  |
|            | Core        |                            |                |                |     |
| CCND1      | DRB1*0101  | NPPSMVAAAGSVVAAV            | 0.674          | 22.98          | 16  |
| IGFBP3     | DRB1*0101  | HSKIIIIKKGHAKDSQ           | 0.512          | 109.05         | 25  |
|            | DRB1*1101  | KSIIIIKKGHAKDSQ            | 0.512          | 109.05         | 19  |
|            | DRB3*0202  | IIIIKGHA                   | 0.392          | 345.67         |     |
| MMP7-(2)   | DRB1*0101  | SQDDIKGIQKLYGKRS           | 0.514          | 107.32         | 15  |
|            | DRB1*1101  | IGIQKLYG                  | 0.64           | 31.88          |     |
Supplementary Table 20: Serum IL-10 concentrations during vaccination

Serum IL-10 concentrations during the course of vaccination were detected by an ultra-sensitive SIMOA assay. Before measurement all samples were diluted 1:10 and measured in duplicates; respective mean values are given for each time point. To convert given sample values to the WHO standard concentrations, given analyte concentrations need to be divided by a factor of 0.77.

| Sample [Vaccination time point] | IL-10 [pg·mL⁻¹] |
|--------------------------------|-----------------|
| 1V                             | 1.74            |
| 5V                             | 1.97            |
| 8V                             | 2.22            |
| 10V                            | 1.46            |
| 12V                            | 1.58            |
| 13V                            | 2.81            |
| 15V                            | 2.50            |
| 17V                            | 4.04            |
| 20V                            | 4.55            |
| 21V                            | 2.93            |
| 22V                            | 2.70            |
| 25V                            | 3.64            |
| 28V                            | 2.22            |
| 30V                            | 2.83            |
| 31V                            | 2.23            |
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