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

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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 10^6 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-γ ELISPOT

IFN-γ 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-γ antibody (clone 1-D1K, Mabtech, Nacka Strand, Sweden). Phytohaemagglutinin-L (PHA-L) (for pool I stimulated cells) or Staphyloccocus 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-γ was detected using biotinylated anti-IFN-γ 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℃/ 1900 rpm). Serum was collected and centrifuged twice before freezing aliquots at -80℃ 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, Carrightwohill, 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 chromatograpy 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

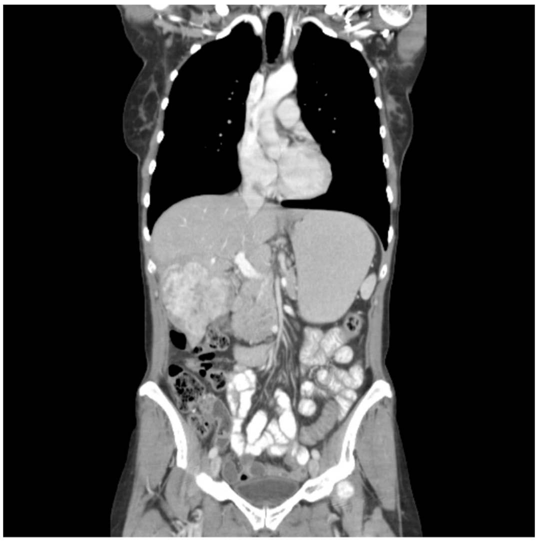
Sample	CD3	CD4	CD8	CD25	FOX P3	granzyme B	CD45	HLA DR	HLA DQ
L06/10	1.5	0.1	0.8	0.5	0.2	0.0	1.4	6.2	5.0
L03/11	3.3	0.2	0.6	2.4	0.2	0.0	6.1	5.6	7.9
L04/12	2.0	1.4	0.2	2.6	0.5	0.1	0.9	7.5	10.4
P03/13	4.8	1.4	0.2	3.8	-	0.1	0.3	35.5	29.5

Supplementary Figure 1-15: Selected Radiological Imaging Results

Selected Images: computed tomography (CT) / magnetic resonance imaging (MRI)/ 18Fluordeoxyglucose 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)

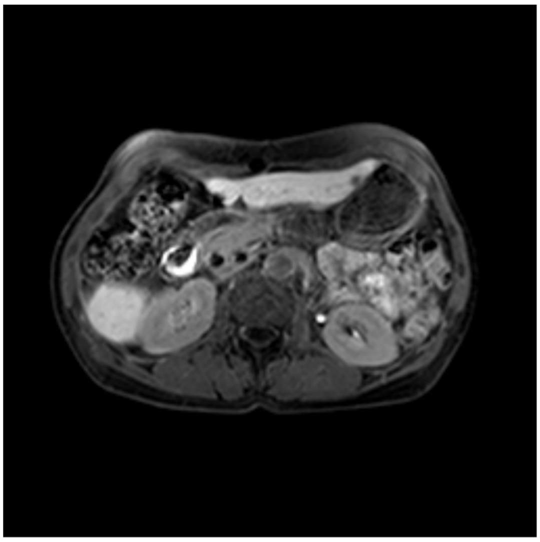
liver transversal (CT June/2010)

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

liver coronal (CT November /2010)

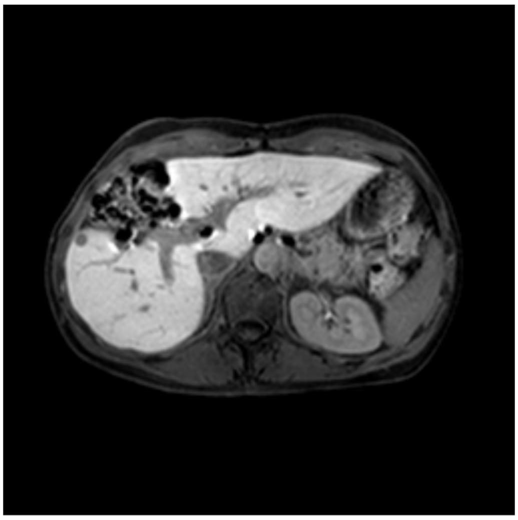
liver transversal (CT November/2010)

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



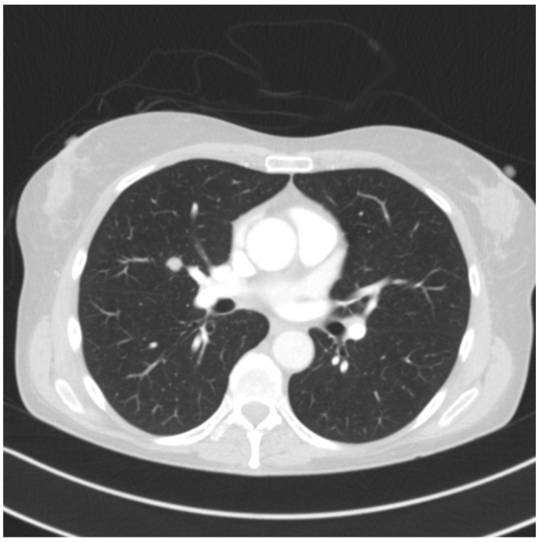
liver (segment 5) transversal (MRI February/2011)

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)

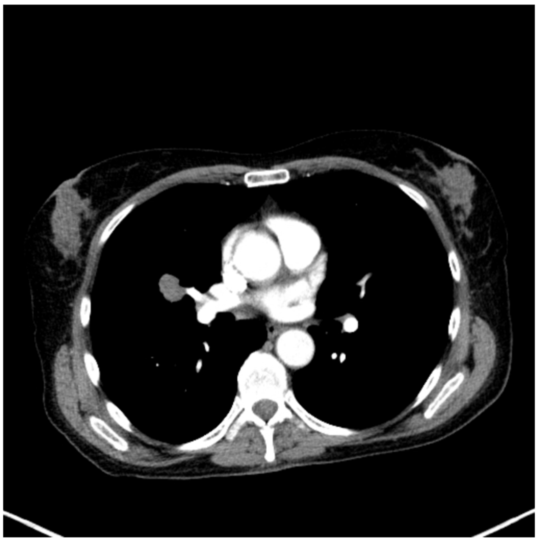
Supplementary Figure 10



lung transversal (CT September/2012)

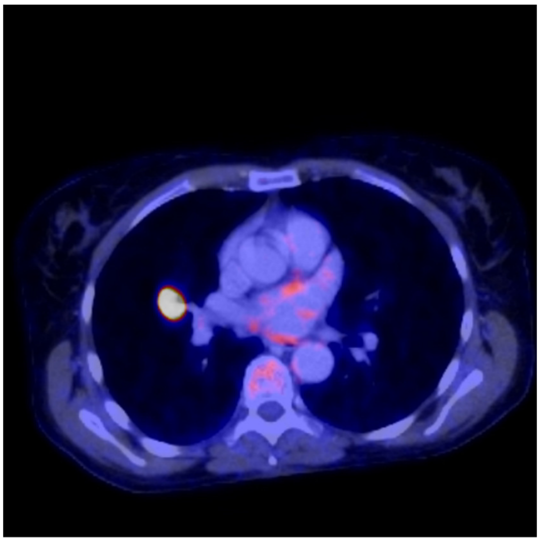
P03/13 (pulmonal metastasis) CT /^{18}FDG PET CT scan before surgery
(Supplementary Figure 11 (left)/ 12 (right))

lung transversal (CT March/2013)



lung transversal (CT March/2013)

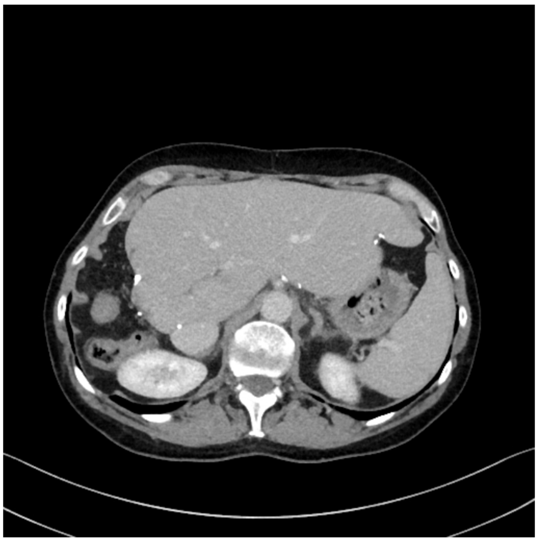
Supplementary Figure 13



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 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).

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	PTPN11	SMARCB1	ADH1C	CYP2E1	JAG2	PHLPP2
BCL2L1	PTEN	SMO	ADRB1	CYP2J2	KCNH2	PRAM1
BRAF	SMAD2	SOX2	ADRB2	CYP3A4	KCNJ11	PTCH2
CARD11	STK11	WT1	AHR	DDR2	LRP1B	PTPRD
CASP8	TSC1	SRSF2	AKT2	DICER1	MAP2K2	RAF1
CBL	TSC2	TET2	ALDH1A1	DLL1	GSTP1	RGL1
CCND1	TGFBR2	ATM	ALOX5	DLL3	IGF1R	RGL2
CCNE1	TP53	BAP1	ARAF	DOT1L	IKBKE	PIK3CG
CDKN2A	VHL	BRCA1	ARFRP1	DPYD	IRS2	PKHD1
CDKN2B	SMAD4	BRCA2	ATR	DRD2	KDR	PRKDC
CEBPA	TNFAIP3	MDM2	AURKA	EPHA3	LRP6	PTGS2
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	ERRFI1	INHBA	PLCG1
GNAQ	CTNNB1	KMT2D	CD38	FANCA	MDM4	PMS2
EGFR	ERG	MED1	CD79A	FLT1	MRE11A	PTGIS
ERBB2	FBXW7	IRF6	CD79B	G6PD	MS4A1	SCN5A
GNA11	EZH2	NRXN3	CDH2	DLL4	MTHFR	SLCO1B1
KRAS	FOXL2	PIK3AP1	CDH5	EPHA7	MYB	SMAD3
JAK3	GATA1	RIPK4	CDH20	EPHB4	MYCN	SOX10
KIT	DNMT3A	RASA1	CDK6	ERCC2	NR1I2	TNKS
MAP2K1	IDH1	RIMBP2	CDKN2C	FGFR1	NTRK1	TNKS2
MAP2K4	IDH2	RIMS2	CHEK2	FGFR4	MTOR	VDR
HRAS	KDM6A	RXFP3	COMT	FLT4	MYCL1	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	NT5C2	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	CDK8	GUCY1A2	MUC1	STAT3
NF1	MYC		CHEK1	HMGCR	MUTYH	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 **NM_001282386.1** **c.394C>T:p.Arg132Cys**	missense variant	+ (28.6%)	+ (19.8%)	+ (18.9%)	+ (26.3%)	Oncogene(19)	chromatin modification(19)	metabolism (hypermethylation), HIF1α stabilization(20)	cell fate(19) angiogenesis(20)
PBRM1 **NM_018313.4** **c.2128C>T:p.Arg710***	stop gain	+ (19.9%)	+ (13.3%)	+ (10.2%)	+ (18.3%)	TSG(19)	chromatin modification(19)	chromatin SWI/SNF complex(21)	cell fate(19)
KMT2C **NM_170606.2** **c.12545A>G:p.Asp4182Gly**	missense variant	+ (11.6%)	+ (8.1%)	+ (10.6%)	+ (15.3%)	TSG(19)	chromatin modification(19)	chromatin histone methyltransferase(21)	Cell Fate(19)
PTGS2 **NM_000963.3** **c.G304T:p.V102L**	missense variant	+ (14.4%)	-	-	+ (10.6%)	probably oncogene	prostaglandine synthesis	N/A	angiogenesis(22)
NOTCH2 **NM_024408.3** **c.3416T>G:p.Leu1139Arg**	missense variant	-	+ (9.8%)	-	-	TSG(23)	notch-signaling(21, 24)	NOTCH(19, 25, 26)	cell fate(19)
PIK3R1 **NM_181523.2** **c.1453G>T:p.Glu485***	stop gain	-	+ (10%)	-	-	TSG(27)	PI3K-signaling(28, 29)	PI3K(19, 30)	cell survival(19)
PTPN11 **NM_002834.3** **c.1492C>T:p.Arg498Trp**	missense variant	-	-	-	+ (18.1%)	oncogene(19, 31) TSG(32)	RAS/MAPK sig. (31, 33) PI3K pathway(34-36)	RAS(19, 21)	cell Survival(19, 37, 38)

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 **NM_000963** **c.G304T:p.V102L**	nonsyn. SNV	+	-	-	probable oncogene	prostaglandine synthesis	angiogenesis(22)	n.a.
IDH1 **NM_005896** **c.C394T:p.R132C**	nonsyn. SNV	+	-	+	oncogene(19)	chromatin modification	cell fate(19) angiogenesis(20)	metabolism (hypermethylation), HIF-1α stabilized(20)
PBRM1 **NM_018313** **c.C2128T:p.R710X**	stopgain SNV	+	-	-	TSG(19)	chromatin modification(19)	cell fate(19)	chromatin SWI/SNF complex(21)
KMT2C **NM_170606** **c.A12545G:p.D4182G**	nonsyn. SNV	+	+	-	TSG(19)	chromatin modification(19)	cell fate(19)	chromatin histone methyltransferase(21)
KDM6B **NM_001080424.1** **c.740C>T:p.Pro247Leu**	nonsyn. SNV	-	+	-	probable TSG(39, 40)	chromatin modification(41)	cell fate(41)	histone demethylase(41)

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; $^{\pm}$ variant excluded for peptide prediction.

							WES				WTS		deep sequencing				
							tumor		normal		tumor		tumor		normal		Ref. Seq. *variant type* [**AA alteration**]
#	#chr	start	end	gene	ref.	obs.	allele freq.	depth	allele freq.	depth	freq.	depth	freq.	depth	freq.	depth	
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.]$^{\pm}$

							WES				WTS		deep sequencing				
							tumor		normal		tumor		tumor		normal		Ref. Seq. *variant type* [**AA alteration**]
#	#chr	start	end	gene	ref.	obs.	allelle freq.	depth	allele freq.	depth	freq.	depth	freq.	depth	freq.	depth	
																	[b] NM_001267809.1 *DV* [n.d.][±]
2	chr1	186648199	186648199	*PTGS2*	C	A	0.16	125	0.00	22	0.00	32	0.11	1679	0.00	815	NM_000963.3 *MV* [**V102L**]
3	chr2	179989221	179989221	*SESTD1*	T	A	0.22	161	0.00	99	0.16	44	0.23	3842	0.00	2402	NM_178123.4 *MV* [**E346V**]
4	chr2	209113113	209113113	*IDH1*	G	A	0.23	229	0.00	33	0.10	622	0.27	2027	0.00	1257	NM_001282386.1; NM_001282387.1; NM_005896.3 *MV* [**R132C**]
5	chr3	52643768	52643768	*PBRM1*	G	A	0.18	146	0.00	55	0.10	31	0.15	936	0.00	641	NM_018313.4 *SG* [**R710***][±]
6	chr4	24578282	24578282	*DHX15*	G	C	0.14	177	0.00	45	0.10	194	0.13	784	0.00	602	NM_001358.2 *MV* [**R31G**]
7	chr5	176011599	176011599	*CDHR2*	G	A	0.06	105	0.00	31	0.00	53	0.06	2044	0.00	1598	NM_001171976.1; NM_017675.4 *MV* [**V773I**]
8	chr6	155581528	155581528	*TFB1M*[a], *CLDN20*[b], *TIAM2*[c]	C	T	0.16	160	0.00	115	0.00	36	0.17	1024	0.00	759	[a] NM_016020.3 *MV* [**V225M**] [b] NM_001001346.3 *UV* [n.d.][±] [c] NM_012454.3; [c] NM_001010927.2 *DV* [n.d.][±]
9	chr7	5662641	5662641	*RNF216*	G	T	0.14	118	0.00	109	0.00	45	0.09	376	0.00	271	NM_207111.3; NM_207116.2 *MV* [**N817K**]

							WES				WTS		deep sequencing				
							tumor		normal		tumor		tumor		normal		Ref. Seq. *variant type* [**AA alteration**]
#	#chr	start	end	gene	ref.	obs.	allelle freq.	depth	allele freq.	depth	freq.	depth	freq.	depth	freq.	depth	
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***]$^{\pm}$
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	[a] NM_022143.4 *MV* [**E294D**] [b] SND1 [b] NM_014390.2 *IV* [n.d.]$^{\pm}$
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.]$^{\pm}$

							WES				WTS		deep sequencing				
							tumor		normal		tumor		tumor		normal		Ref. Seq. *variant type* [**AA alteration**]
#	#chr	start	end	gene	ref.	obs.	allelle freq.	depth	allele freq.	depth	freq.	depth	freq.	depth	freq.	depth	
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 *MV* [**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 *SG* [**R122***]$^{\pm}$
20	chr17	74005271	74005271	*EVPL*[a], *CDK3*[b]	C	A	0.23	26	0.00	28	n/a	0	0.32	3560	0.00	2705	[a] NM_001988.2 *SG* [**E1339***]$^{\pm}$ [b] NM_001258.2 *DV* [n.d.]$^{\pm}$
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 *MV* [**Q472K**]
22	chrX	21674105	21674105	*KLHL34*[a], *CNKSR2*[b]	C	T	0.22	89	0.00	65	n/a	0	0.32	981	0.00	652	[a] NM_153270.1 *MV* [**R601H**] [b] NM_014927.3; [b] NM_001168647.1 *DV* [n.d.]$^{\pm}$
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 *MV* [**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 *SV* [n.d.]$^{\pm}$
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 *MV* [**I739T**] NM_001171163.1 *DV* [n.d.]$^{\pm}$

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	MSYLLTSR	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
			netMHCpan 2.4	101 nM	B*07:05	
			netMHC 3.0	110 nM	B*35:01	
			netMHCpan 2.4	115 nM	B*35:01	
9	YLVDLHLH	8	netMHCpan 2.4	310 nM	A*29:01	*LRRC4*
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	PIIIGCHAY	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	TIHWRGQTR	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	57%	B*07:02	*TEP1*
37	PLPPVRPVFK	10	netMHC 3.0	193 nM	A*03:01	*RNF216*
			SYFPEITHI	67%	A*03:01	
38	QPIFNLTVSA	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	SHATFKAMAY	10	netMHCpan 2.4	328 nM	A*29:01	*IL2RA*
40	TPPKHIPGVV	10	SYFPEITHI	60%	B*07:02	*EBF3*
41	VMAEMSGVHK	10	netMHC 3.0	31 nM	A*03:01	*CCT8L2*
			netMHCpan 2.4	79 nM	A*03:01	
42	VPKPEVDMGV	10	SYFPEITHI	57%	B*07:02	*TFB1M*
43	VPNKERPMGT	10	SYFPEITHI	57%	B*07:02	*FGFBP3*
44	IIGCHAYGDQY	11	netMHCpan 2.4	225 nM	A*29:01	*IDH1*
45	ISHATFKAMAY	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	KPEVDMGVVHF	11	netMHC 3.0	341 nM	B*07:02	*TFB1M*
			netMHC 3.0	248 nM	B*35:01	
47	MSYLLTSRSHL	11	netMHCpan 2.4	169 nM	C15:05	*PTGS2*
48	NMVAFFLGCSF	11	netMHCpan 2.4	131 nM	B*35:01	*C14orf159*
49	RPVFKNFPLNM	11	netMHC 3.0	16 nM	B*07:02	*RNF216*
			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	EISHATFKAMAY	12	netMHC 3.0	93 nM	B*35:01	*IL2RA*
54	EVDMGVVHFTPL	12	netMHC 3.0	483 nM	B*35:01	*TFB1M*
55	IPFLRNAIMSYL	12	netMHC 3.0	53 nM	B*07:02	*PTGS2*
56	ISHATFKAMAYK	12	netMHC 3.0	21 nM	A*03:01	*IL2RA*
57	KAALVPNKERPM	12	netMHC 3.0	426 nM	B*07:02	*FGFBP3*
58	PPEISHATFKAM	12	netMHC 3.0	223 nM	B*35:01	*IL2RA*
			netMHC 3.0	303 nM	B*07:02	

#	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	GYDLDLDH	8	SYFPEITHI*	54%	C*04:01	*KLHL34*
5	HPHSHWAQ	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	KAALVPNK	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	mer	Method	Score	HLA	Gene
			netMHCpan 2.8	175 nM	A*03:01	
10	QPIFNLTV	8	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	8	SYFPEITHI*	59%	C*04:01	*LRRC4*
12	VPNKERPM	8	netMHCpan 2.8	22 nM	B*35:01	*FGFBP3*
			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	
13	YLVDLHLH	8	netMHCpan 2.8	267 nM	A*29:01	*LRRC4*
14	AIRVQTPPK	9	netMHCpan 2.8	103 nM	A*03:01	*EBF3*
			netMHC 3.4	107 nM	A*03:01	
			SYFPEITHI*	68%	A*03:01	
15	DPPEISHAT	9	SYFPEITHI*	52%	B*07:02	*IL2RA*
16	DVEDLVELK	9	SYFPEITHI*	74%	A*03:01	*SESTD1*
17	EQLKNMVAF	9	netMHCpan 2.8	316 nM	C*04:01	*C14orf159*
18	EVDMGVVHF	9	SYFPEITHI*	61%	C*04:01	*TFB1M*
19	GDVEDLVEL	9	SYFPEITHI*	54%	B*35:01	*SESTD1*
20	GYDLDLDHW	9	SYFPEITHI*	61%	C*04:01	*KLHL34*
21	HPHSHWAQQ	9	netMHC 3.4	354 nM	B*35:01	*TEP1*
22	HWEDIGCAL	9	SYFPEITHI*	57%	B*35:01	*KLHL34*
23	IMSYLLTSR	9	netMHC 3.4	414 nM	A*03:01	*PTGS2*
			netMHCpan 2.8	497 nM	A*03:01	
24	ISHATFKAM	9	netMHCpan 2.8	477 nM	C*04:01	*IL2RA*
25	KEDLTWEDF	9	SYFPEITHI*	58%	C*04:01	*DUOX1*
26	KPEVDMGVV	9	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	KPIIIGCHA	9	SYFPEITHI*	55%	B*07:02	*IDH1*
28	MGVVHFTPL	9	netMHCpan 2.8	385 nM	C*04:01	*TFB1M*
29	NLPDHPHSH	9	SYFPEITHI*	61%	A*03:01	*TEP1*
30	PIIIGCHAY	9	netMHCpan 2.8	134 nM	A*29:01	*IDH1*
			SYFPEITHI*	52%	A*03:01	
31	PLRYLVDLH	9	SYFPEITHI*	58%	A*03:01	*LRRC4*
32	PPEISHATF	9	SYFPEITHI*	71%	B*35:01	*IL2RA*
			SYFPEITHI*	52%	B*07:02	
33	PPKHIPGVV	9	SYFPEITHI*	52%	B*07:02	*EBF3*
34	QYSEQLKNM	9	SYFPEITHI*	56%	C*04:01	*C14orf159*
35	RKAALVPNK	9	SYFPEITHI*	52%	A*03:01	*FGFBP3*
36	RPVFKNFPL	9	netMHCpan 2.8	6 Nm	C*15:02	*RNF216*
			netMHC 3.4	9 nM	B*07:02	
			netMHCpan 2.8	213 nM	C*04:01	

#	Peptide	mer	Method	Score	HLA	Gene
			netMHC 3.4	429 nM	B*35:01	
			SYFPEITHI*	75%	B*35:01	
			SYFPEITHI*	67%	C*04:01	
37	RVQTPPKHI	9	SYFPEITHI*	52%	A*03:01	*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		SYFPEITHI*	55%	B*07:02	*EBF3*
42	VFKNFPLNM	9	SYFPEITHI*	53%	C*04:01	*RNF216*
43	YLVDLHLHH	9	netMHCpan 2.8	178 nM	A*29:01	*LRRC4*
			SYFPEITHI*	61%	A*03:01	
44	AGDVEDLVEL	10	SYFPEITHI*	56%	C*04:01	*SESTD1*
45	AIMSYLLTSR	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	DYETQPIFNL	10	SYFPEITHI*	51%	C*04:01	*CDHR2*
48	EISHATFKAM	10	netMHCpan 2.8	486 nM	C*04:01	*IL2RA*
49	FLRNAIMSYL	10	netMHCpan 2.8	310 nM	C*15:05	*PTGS2*
50	GYDLDLDHWE	10	SYFPEITHI*	54%	C*04:01	*KLHL34*
51	HAIRVQTPPK	10	netMHC 3.4	422 nM	A*03:01	*EBF3*
52	HPHSHWAQQY	10	netMHCpan 2.8	11 nM	C*04:01	*TEP1*
			netMHC 3.4	37nM	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	LPDHPHSHWA	10	SYFPEITHI*	57%	B*07:02	*TEP1*
55	PLPPVRPVFK	10	SYFPEITHI*	71%	A*03:01	*RNF216*
56	PPVRPVFKNF	10	SYFPEITHI*	77%	B*35:01	*RNF216*
			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	RLACSGDDLR	10	SYFPEITHI*	52%	A*03:01	*DCAF8L1*
59	RVQTPPKHIP	10	SYFPEITHI*	52%	A*03:01	*EBF3*
60	SHATFKAMAY	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	SYLLTSRSHL	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	VPKPEVDMGV	10	SYFPEITHI*	57%	B*07:02	*TFB1M*
67	VPNKERPMGT	10	SYFPEITHI*	57%	B*07:02	*FGFBP3*
68	DVMAEMSGVHK	11	SYFPEITHI*	69%	A*03:01	*CCT8L2*
69	IIGCHAYGDQY	11	netMHCpan 2.8	163 nM	A*29:01	*IDH1*
70	ISHATFKAMAY	11	netMHCpan 2.8	79 nM	C*04:01	*IL2RA*
			netMHCpan 2.8	80 nM	A*29:01	
			netMHC 3.4	133 nM	B*35:01	
71	KPEVDMGVVHF	11	SYFPEITHI*	67%	B*07:02	*TFB1M*
72	LPPVRPVFKNF	11	SYFPEITHI*	57%	B*07:02	*RNF216*
73	MSYLLTSRSHL	11	netMHCpan 2.8	229 nM	B*07:05	*PTGS2*
74	NMVAFFLGCSF	11	netMHCpan 2.8	268 nM	C*04:01	*C14orf159*
			netMHC 3.4	447 nM	B*35:01	
75	PPEISHATFKA	11	SYFPEITHI*	57%	B*07:02	*IL2RA*
76	PPKHIPGVVEV	11	SYFPEITHI*	63%	B*07:02	*EBF3*
77	RPVFKNFPLNM	11	netMHC 3.4	25 nM	B*07:02	*RNF216*
			netMHCpan 2.8	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	
78	TPLRYLVDLHL	11	netMHCpan 2.8	275 nM	C*15:05	*LRRC4*
			netMHCpan 2.8	449 nM	B*35:01	
			SYFPEITHI*	73%	B*07:02	
79	VAKGTARRRAM	11	netMHCpan 2.8	337 nM	C*15:05	*SNAPIN*
			netMHCpan 2.8	344 nM	B*35:01	
			netMHC 3.4	430 nM	B*35:01	
80	VDMGVVHFTPL	11	SYFPEITHI *	53%	B*07:02	*TFB1M*
81	VPKPEVDMGVV	11	netMHCpan 2.8	401 nM	C*15:05	*TFB1M*
			netMHCpan 2.8	595 nM	B*35:01	
			SYFPEITHI*	60%	B*07:02	
82	YSEQLKNMVAF	11	netMHC 3.4	172 nM	B*35:01	*C14orf159*
			netMHCpan 2.8	309 nM	C*04:01	
83	DVSLDYETQPIF	12	netMHC 3.4	414 nM	B*35:01	*CDHR2*
84	EISHATFKAMAY	12	netMHC 3.4	91 nM	B*35:01	*IL2RA*
85	HPHSHWAQQYPS	12	netMHC 3.4	89 nM	B*35:01	*TEP1*
86	IIIGCHAYGDQY	12	netMHC 3.4	398 nM	B*35:01	*IDH1*
87	IPFLRNAIMSYL	12	netMHC 3.4	72 nM	B*07:02	*PTGS2*
88	ISHATFKAMAYK	12	netMHC 3.4	52 nM	A*03:01	*IL2RA*
89	PPVRPVFKNFPL	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	WVKPIIIGCHAY	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.	WES				Ref. Seq. *variant type* [**AA alteration**]
							tumor		normal		
							allele freq.	depth	allele freq.	depth	
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**]

							WES				Ref. Seq. *variant type* [**AA alteration**]
							tumor		normal		
#	#chr	start	end	gene	ref.	obs.	allele freq.	depth	allele freq.	depth	
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.]$^{\pm}$
12	chr17	3101176	3101176	*OR1A2*	C	T	0.15	108	0.00	158	NM_012352.1 *SG* [**R122***]$^{\pm}$
13	chr17	7750165	7750165	*KDM6B*	C	T	0.08	65	0.00	71	NM_001080424.1 *MV* [**P247L**]

							WES				
							tumor		normal		Ref. Seq. *variant type* [**AA alteration**]
#	#chr	start	end	gene	ref.	obs.	allele freq.	depth	allele freq.	depth	
14	chr19	43920102	43920102	*TEX101*	A	T	0.11	45	0.00	46	NM_031451.4 *MV* [**I29F**] NM_001130011.1 *MV* [**I11F**]
15	chr22	17072027	17072027	*CCT8L2*	G	T	0.07	68	0.00	86	NM_014406.4 *MV* [**Q472K**]
16	chrX	21674105	21674105	*KLHL34*[a], *CNKSR2*[b]	C	T	0.17	63	0.00	65	[a] NM_153270.1 *MV* [**R601H**] [b] NM_014927.3; [b] NM_001168647.1 *DV* [n.d.]±
17	chrX	91873547	91873547	*PCDH11X*	G	A	0.06	271	0.00	393	NM_032968.4 *MV* [**A1218T**] NM_001168360.1 *MV* [**A1210T**] NM_001168362.1 *MV* [**A1181T**] NM_001168363.1 *MV* [**A1200T**] 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	DPQFGDVF	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	FVWQPGPL	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	KTPDDFSY	8	netMHCpan 2.4	331 nM	A*29:01	*MAP1B*
6	LPDHPHSH	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
			netMHCpan 2.4	113 nM	B*35:01	
			netMHCpan 2.4	115 nM	B*07:05	
			netMHC 3.0	140 nM	B*35:01	
8	VFWNSSKY	8	netMHCpan 2.4	27 nM	A*29:01	*AGPAT6*
			netMHC 3.0	321 nM	B*35:01	
9	ALLNAGDVE	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	EFVWQPGPL	9	netMHC 3.0	201 nM	B*35:01	*MDN1*
14	EQLKNMVAF	9	netMHCpan 2.4	153 nM	B*35:01	*C14orf159*
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	PPGLPLLPP	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	SPPPIQVST	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	CTPGTAPPPK	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	GLSGYKGSSH	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
			netMHCpan 2.4	28 nM	B*35:01	
30	KTPDDFSYAY	10	netMHCpan 2.4	80 nM	A*29:01	*MAP1B*
31	LPDHPHSHWA	10	SYFPEITHI	57%	B*07:02	*TEP1*
32	QPGPLTQAAT	10	netMHC 3.0	262 nM	B*35:01	*MDN1*
			SYFPEITHI	67%	B*07:02	
33	SHATFKAMAY	10	netMHCpan 2.4	328 nM	A*29:01	*IL2RA*
34	SPPPIQVSTL	10	netMHCpan 2.4	82 nM	B*07:02	*PCDH11X*
			netMHC 3.0	199 nM	B*07:02	
			netMHCpan 2.4	227 nM	B*07:05	
			SYFPEITHI	73%	B*07:02	
35	TPRIQHLLFL	10	netMHCpan 2.4	23 nM	B*07:02	*TEX101*
			netMHC 3.0	24 nM	B*07:02	
			netMHCpan 2.4	75 nM	B*07:05	
			SYFPEITHI	83%	B*07:02	
36	VMAEMSGVHK	10	netMHC 3.0	31 nM	A*03:01	*CCT8L2*
			netMHCpan 2.4	79 nM	A*03:01	
37	DVFWNSSKYGM	11	netMHCpan 2.4	132 nM	B*35:01	*AGPAT6*
			netMHC 3.0	342 nM	B*35:01	
38	ISHATFKAMAY	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	
39	NMVAFFLGCSF	11	netMHCpan 2.4	131 nM	B*35:01	*C14orf159*
40	QPGPLTQAATM	11	netMHCpan 2.4	70 nM	B*35:01	*MDN1*
			netMHCpan 2.4	149 nM	B*07:02	
			netMHC 3.0	436 nM	B*07:02	
41	TPRIQHLLFLL	11	netMHC 3.0	55 nM	B*07:02	*TEX101*
			netMHCpan 2.4	58 nM	B*07:02	
			netMHCpan 2.4	177 nM	B*07:05	
42	VSTLHHSPPLV	11	netMHCpan 2.4	247 nM	C*15:05	*PCDH11X*
43	YSEQLKNMVAF	11	netMHC 3.0	86 nM	B*35:01	*C14orf159*
			netMHCpan 2.4	230 nM	B*35:01	
44	EISHATFKAMAY	12	netMHC 3.0	93 nM	B*35:01	*IL2RA*
45	FVWQPGPLTQAA	12	netMHC 3.0	157 nM	B*35:01	*MDN1*
46	ISHATFKAMAYK	12	netMHC 3.0	21 nM	A*03:01	*IL2RA*
47	KTPDDFSYAYQK	12	netMHC 3.0	332 nM	A*03:01	*MAP1B*
48	LPPGLPLLPPPL	12	netMHC 3.0	164 nM	B*35:01	*KDM6B*
			netMHC 3.0	397 nM	B*07:02	
49	PPEISHATFKAM	12	netMHC 3.0	223 nM	B*35:01	*IL2RA*
			netMHC 3.0	303 nM	B*07:02	
50	TPRIQHLLFLLV	12	netMHC 3.0	122 nM	B*07:02	*TEX101*
51	VPGEFVWQPGPL	12	netMHC 3.0	83 nM	B*35:01	*MDN1*
				309 nM	B*07:02	
52	YSEQLKNMVAFF	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	GYDLDLDH	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
			netMHC 3.4	67 nM	B*35:01	
			netMHC 3.4	228 nM	B*07:02	
9	PPIQVSTL	8	netMHC 3.4	487 nM	B*35:01	*PDCDHX11*
10	VFWNSSKY	8	netMHCpan 2.8	16 nM	A*29:01	*AGPAT6*
11	DPPEISHAT	9	SYFPEITHI*	52%	B*07:02	*IL2RA*
12	DVEDLVELK	9	SYFPEITHI*	74%	A*03:01	*SESTD1*
13	DVFWNSSKY	9	netMHC 3.4	18 nM	B*35:01	*AGPAT6*
			netMHCpan 2.8	27 nM	C*04:01	
			netMHCpan 2.8	59 nM	A*29:01	
			SYFPEITHI*	55%	A*03:01	
14	EFVWQPGPL	9	SYFPEITHI*	56%	C*04:01	*MDN1*
15	EQLKNMVAF	9	netMHCpan 2.8	316 nM	C*04:01	*C14orf159*
16	GDVEDLVEL	9	SYFPEITHI*	54%	B*35:01	*SESTD1*
17	GPLTQAATM	9	netMHCpan 2.8	122 nM	C*15:05	*MDN1*
			netMHCpan 2.8	133 nM	B*35:01	
			netMHC 3.4	191 nM	B*07:02	
			netMHCpan 2.8	254 nM	C*04:01	
			netMHC 3.4	312 nM	B*35:01	
			SYFPEITHI*	68%	B*35:01	
			SYFPEITHI*	52%	B*07:02	
18	GYDLDLDHW	9	SYFPEITHI*	61%	C*04:01	*KLHL34*
19	HPHSHWAQQ	9	SYFPEITHI*	354 nM	B*35:01	*TEP1*
20	HWEDIGCAL	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	NLPDHPHSH	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*
			SYFPEITHI*	52%	B*07:02	
27	PPGLPLLPP	9	SYFPEITHI*	52%	B*07:02	*KDM6B*
28	PPPIQVSTL	9	SYFPEITHI*	75%	B*35:01	*PCDH11X*
			SYFPEITHI*	64%	B*07:02	
29	QPGPLTQAA	9	netMHCpan 2.8	206 nM	C*15:05	*MDN1*
			netMHC 3.4	284 nM	B*35:01	
			SYFPEITHI*	61%	B*07:02	
30	QYSEQLKNM	9	SYFPEITHI*	56%	C*04:01	*C14orf159*
31	RIQHLLFLL	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*
			netMHCpan 2.8	5 nM	C*04:01	
			SYFPEITHI*	82%	B*35:01	
34	TPRIQHLLF	9	netMHC 3.4	53 nM	B*07:02	*TEX101*
			netMHCpan 2.8	96 nM	B*35:01	

#	Peptide	mer	Method	Score	HLA	Gene
			netMHCpan 2.8	215 nM	C*15:05	
			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	
35	TPSCTPGTA	9	netMHCpan 2.8	55 nM	B*07:02	*MUC5B*
			netMHC 3.4	185 nM	C*15:05	
36	AGDVEDLVEL	10	SYFPEITHI*	56%	C*04:01	*SESTD1*
37	CTPGTAPPPK	10	SYFPEITHI*	65%	A*03:01	*MUC5B*
38	DPPEISHATF	10	netMHCpan 2.8	201 nM	C*04:01	*IL2RA*
			SYFPEITHI*	77%	B*35:01	
			SYFPEITHI*	57%	B*07:02	
39	EISHATFKAM	10	netMHCpan 2.8	486 nM	C*04:01	*IL2RA*
40	FLLVLGASLL	10	SYFPEITHI*	54%	B*35:01	*TEX101*
41	GYDLDLDHWE	10	SYFPEITHI*	54%	C*04:01	*KLHL34*
42	HPHSHWAQQY	10	netMHCpan 2.8	11 nM	C*04:01	*TEP1*
			netMHC 3.4	37 nM	B*35:01	
			SYFPEITHI*	85%	B*35:01	
43	KTPDDFSYAY	10	netMHCpan 2.8	83 nM	A*29:01	*MAP1B*
44	KYDPQFGDVF	10	SYFPEITHI*	79%	C*04:01	*AGPAT6*
45	LFLLVLGASL	10	SYFPEITHI*	54%	C*04:01	*TEX101*
46	LPDHPHSHWA	10	SYFPEITHI*	57%	B*07:02	*TEP1*
47	QPGPLTQAAT	10	SYFPEITHI*	67%	B*07:02	*MDN1*
48	RIQHLLFLLV	10	SYFPEITHI*	52%	A*03:01	*TEX101*
49	SHATFKAMAY	10	netMHCpan 2.8	479 nM	A*29:01	*IL2RA*
50	SPPPIQVSTL	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	TPRIQHLLFL	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	netMHC 3.4	42 nM	A*03:01	*CCT8L2*
			netMHCpan 2.8	72 nM	A*03:01	
54	DVFWNSSKYGM	11	netMHC 3.4	123 nM	B*35:01	*AGPAT6*
			netMHCpan 2.8	211 nM	C*04:01	
55	DVMAEMSGVHK	11	SYFPEITHI*	69%	A*03:01	*CCT8L2*
56	FGDVFWNSSKY	11	netMHC 3.4	258 nM	B*35:01	*AGPAT6*
57	HSPPPIQVSTL	11	netMHCpan 2.8	483 nM	B*07:05	*PCDH11X*
58	ISHATFKAMAY	11	netMHCpan 2.8	79 nM	C*04:01	*IL2RA*

#	Peptide	mer	Method	Score	HLA	Gene
			netMHCpan 2.8	80 nM	A*29:01	
			netMHC 3.4	133 nM	B*35:01	
59	NMVAFFLGCSF	11	netMHCpan 2.8	268 nM	C*04:01	*C14orf159*
			netMHC 3.4	447 nM	B*35:01	
			netMHCpan 2.8	550 nM	A*29:01	
60	PPEISHATFKA	11	SYFPEITHI*	57%	B*07:02	*IL2RA*
61	PPGLPLLPPPL	11	netMHC 3.4	77 nM	B*07:02	*KDM6B*
			SYFPEITHI*	263 nM	B*07:02	
62	QPGPLTQAATM	11	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	TPRIQHLLFLL	11	netMHC 3.4	32 nM	B*07:02	*TEX101*
			netMHCpan 2.8	55 nM	B*35:01	
			netMHCpan 2.8	67 nM	C*15:05	
			SYFPEITHI*	73%	B*07:02	
64	YSEQLKNMVAF	11	netMHC 3.4	172 nM	B*35:01	*C14orf159*
			netMHCpan 2.8	309 nM	C*04:01	
65	EISHATFKAMAY	12	netMHC 3.4	91 nM	B*35:01	*IL2RA*
66	FVWQPGPLTQAA	12	netMHC 3.4	397 nM	B*35:01	*MDN1*
67	HPHSHWAQQYPS	12	netMHC 3.4	89 nM	B*35:01	*TEP1*
68	ISHATFKAMAYK	12	netMHC 3.4	52 nM	A*03:01	*IL2RA*
69	LPPGLPLLPPPL	12	netMHC 3.4	111 nM	B*07:02	*KDM6B*
			netMHC 3.4	192 nM	B*35:01	
70	TPRIQHLLFLLV	12	netMHC 3.4	83 nM	B*07:02	*TEX101*
71	VPGEFVWQPGPL	12	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.

							WES				WTS		
							tumor		normal		tumor		Ref. Seq. *variant type* [**AA alteration**]
#	#chr	start	end	gene	ref.	obs.	allele freq.	depth	allele freq.	depth	freq.	depth	
1	chr1	186277277	186277277	*PRG4* [a], *TPR* [b]	G	A	0.06	89	0.00	217	0.00	1.00	[a] NM_005807.3 *MV* [**G809E**]± [a] NM_001127708.1 *MV* [**G768E**]± [a] NM_001127709.1 *MV* [**G716E**]±

							WES				WTS		
							tumor		normal		tumor		Ref. Seq. *variant type* [**AA alteration**]
#	#chr	start	end	gene	ref.	obs.	allelle freq.	depth	allele freq.	depth	freq.	depth	
													[a] NM_001127710.1 *MV* [**G675E**]$^{\pm}$ [b] NM_003292.2 *DV* [n.d.]$^{\pm}$
2	chr2	25358435	25358435	*EFR3B*	C	T	0.08	85	0.00	130	n/a	0.00	NM_014971.1 *SG* [**R471***]$^{\pm}$
3	chr2	179989221	179989221	*SESTD1*	T	A	0.11	80	0.00	99	0.56	32.00	NM_178123.4 *MV* [**E346V**]
4	chr2	209113113	209113113	*IDH1*	G	A	0.17	36	0.00	33	0.42	237.00	NM_001282386.1; NM_001282387.1; NM_005896.3 *MV* [**R132C**]
5	chr5	58289248	58289248	*PDE4D*	C	A	0.07	54	0.00	48	0.20	5.00	NM_001104631.1 *MV* [**M322I**]$^{\pm}$ NM_001197223.1 *MV* [**M31I**]$^{\pm}$ NM_001197221.1 *MV* [**M20I**]$^{\pm}$ NM_001197222.1 *MV* [**M98I**]$^{\pm}$ NM_001197220.1 *MV* [**M192I**]$^{\pm}$ NM_001197219.1 MV [**M200I**]$^{\pm}$ NM_006203.4 *MV* [**M186I**]$^{\pm}$ NM_001197218.1 *MV* [**M258I**]$^{\pm}$

							WES				WTS		
							tumor		normal		tumor		Ref. Seq. *variant type* [**AA alteration**]
#	#chr	start	end	gene	ref.	obs.	allelle freq.	depth	allele freq.	depth	freq.	depth	
													NM_001165899.1 *MV* [**M261I**]$^{\pm}$
6	chr7	99313514	99313514	*CYP3A7-CYP3AP1, CYP3A7*	G	T	0.06	114	0.00	111	0.15	20.00	NM_001256497.2; NM_000765.4 *SG* [**Y179***]$^{\pm}$
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* [**P32S**]
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**] NM_001286473.1 *DV* [n.d.]$^{\pm}$
11	chr17	3101176	3101176	*OR1A2*	C	T	0.14	111	0.00	158	n/a	0.00	NM_012352.1 *SG* [**R122***]$^{\pm}$
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	EQLKNMVAF	9	netMHCpan 2.4	153 nM	B*35:01	*C14orf159*
6	KPIIIGCHA	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	PPEISHATF	9	netMHC 3.0	238 nM	B*35:01	*IL2RA*
			SYFPEITHI	52%	B*07:02	
10	DPPEISHATF	10	netMHC 3.0	20 nM	B*35:01	*IL2RA*
			netMHCpan 2.4	239 nM	B*35:01	
			SYFPEITHI	57%	B*07:02	
11	EISHATFKAM	10	netMHC 3.0	256 nM	B*35:01	*IL2RA*
			netMHCpan 2.4	274 nM	B*35:01	
12	KLFSELPLVK	10	netMHCpan 2.4	18 nM	A*03:01	*MRPS33*
			netMHC 3.0	31 nM	A*03:01	
			SYFPEITHI	74%	A*03:01	
13	KPIIIGCHAY	10	netMHCpan 2.4	19 nM	B*35:01	*IDH1*
			netMHC 3.0	24 nM	B*35:01	
14	LPLVKKKETY	10	netMHC 3.0	75 nM	B*35:01	*MRPS33*
			netMHCpan 2.4	120 nM	B*35:01	
15	NPCHEALAAQ	10	netMHC 3.0	402 nM	B*35:01	*DCD*
16	SHATFKAMAY	10	netMHCpan 2.4	328 nM	A*29:01	*IL2RA*
17	VMAEMSGVHK	10	netMHC 3.0	31 nM	A*03:01	*CCT8L2*
			netMHCpan 2.4	79 nM	A*03:01	
18	IIGCHAYGDQY	11	netMHCpan 2.4	225 nM	A*29:01	*IDH1*
19	ISHATFKAMAY	11	netMHC 3.0	102 nM	A*29:01	*IL2RA*
			netMHCpan 2.4	209 nM	A*03:01	
			netMHCpan 2.4	247 nM	B*35:01	
20	KLFSELPLVKK	11	netMHC 3.0	7 nM	A*03:01	*MRPS33*
			netMHCpan 2.4	23 nM	A*03:01	
21	NMVAFFLGCSF	11	netMHCpan 2.4	131 nM	B*35:01	*C14orf159*
22	YSEQLKNMVAF	11	netMHC 3.0	86 nM	B*35:01	*C14orf159*
			netMHCpan 2.4	230 nM	B*35:01	
23	APGSGNPCHEAL	12	netMHC 3.0	30 nM	B*07:02	*DCD*
24	EISHATFKAMAY	12	netMHC 3.0	93 nM	B*35:01	*IL2RA*
25	ISHATFKAMAYK	12	netMHC 3.0	21 nM	A*03:01	*IL2RA*
26	KLFSELPLVKKK	12	netMHC 3.0	11 nM	A*03:01	*MRPS33*
27	PPEISHATFKAM	12	netMHC 3.0	223 nM	B*35:01	*IL2RA*
			netMHC 3.0	303 nM	B*07:02	
28	VVKLFSELPLVK	12	netMHC 3.0	382 nM	A*03:01	*MRPS33*
29	WVKPIIIGCHAY	12	netMHC 3.0	37 nM	B*35:01	*IDH1*
30	YSEQLKNMVAFF	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	LFSELPLV	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	ISHATFKAM	9	netMHCpan 2.8	477 nM	C*04:01	*IL2RA*
10	KLFSELPLV	9	SYFPEITHI*	58%	A*03:01	*MRPS33*
11	KPIIIGCHA	9	SYFPEITHI*	55%	B*07:02	*IDH1*
12	NPCHEALAA	9	netMHC 3.4	412 nM	B*35:01	*DCD*
			SYFPEITHI*	58%	B*07:02	
13	PIIIGCHAY	9	netMHCpan 2.8	134 nM	A*29:01	*IDH1*

			SYFPEITHI*	52%	A*03:01	
14	PLVKKKETY	9	SYFPEITHI*	55%	A*03:01	*MRPS33*
15	PPEISHATF	9	SYFPEITHI*	71%	B*35:01	*IL2RA*
16	QYSEQLKNM	9	SYFPEITHI*	56%	C*04:01	*C14orf159*
17	AGDVEDLVEL	10	SYFPEITHI*	56%	C*04:01	*SESTD1*
18	DPPEISHATF	10	netMHCpan 2.8	201 nM	C*04:01	*IL2RA*
			SYFPEITHI*	77%	B*35:01	
			SYFPEITHI*	57%	B*07:02	
19	EISHATFKAM	10	netMHCpan 2.8	486 nM	C*04:01	*IL2RA*
20	KLFSELPLVK	10	netMHCpan 2.8	13 nM	A*03:01	*MRPS33*
			netMHC 3.4	18 nM	A*03:01	
			SYFPEITHI*	87%	A*03:01	
21	KPIIGCHAY	10	netMHCpan 2.8	31 nM	C*04:01	*IDH1*
			netMHC 3.4	34 nM	B*35:01	
			SYFPEITHI*	81%	B*35:01	
22	LLPLVKKKETY	10	netMHC 3.4	148 nM	B*35:01	*MRPS33*
			netMHCpan 2.8	277 nM	C*04:01	
			SYFPEITHI*	88%	B*35:01	
23	SHATFKAMAY	10	netMHCpan 2.8	479 nM	A*29:01	*IL2RA*
24	VEDLVELKSL	10	SYFPEITHI*	62%	C*04:01	*SESTD1*
25	VMAEMSGVHK	10	netMHCpan 2.8	72 nM	A*03:01	*CCT8L2*
26	DVMAEMSGVHK	11	SYFPEITHI*	69%	A*03:01	*CCT8L2*
27	IIGCHAYGDQY	11	netMHCpan 2.8	163 nM	A*29:01	*IDH1*
28	ISHATFKAMAY	11	netMHCpan 2.8	79 nM	C*04:01	*IL2RA*
			netMHCpan 2.8	80 nM	A*29:01	
			netMHC 3.4	133 nM	B*35:01	
29	KLFSELPLVKK	11	netMHCpan 2.8	14 nM	A*03:01	*MRPS33*
			netMHC 3.4	109 nM	A*03:01	
			SYFPEITHI*	88%	A*03:01	
30	NMVAFFLGCSF	11	netMHCpan 2.8	268 nM	C*04:01	*C14orf159*
			netMHC 3.4	447 nM	B*35:01	
31	PPEISHATFKA	11	SYFPEITHI*	57%	B*07:02	*IL2RA*
32	YSEQLKNMVAF	11	netMHC 3.4	172 nM	B*35:01	*C14orf159*
			netMHCpan 2.8	309 nM	C*04:01	
33	APGSGNPCHEAL	12	netMHC 3.4	22 nM	B*07:02	*DCD*
34	EISHATFKAMAY	12	netMHC 3.4	91 nM	B*35:01	*IL2RA*
35	IIIGCHAYGDQY	12	netMHC 3.4	398 nM	B*35:01	*IDH1*
36	ISHATFKAMAYK	12	netMHC 3.4	52 nM	A*03:01	*IL2RA*
37	KLFSELPLVKKK	12	netMHC 3.4	22 nM	A*03:01	*MRPS33*
38	VVKLFSELPLVK	12	netMHC 3.4	218 nM	A*03:01	*MRPS33*
39	WVKPIIIGCHAY	12	netMHC 3.4	43 nM	B*35:01	*IDH1*

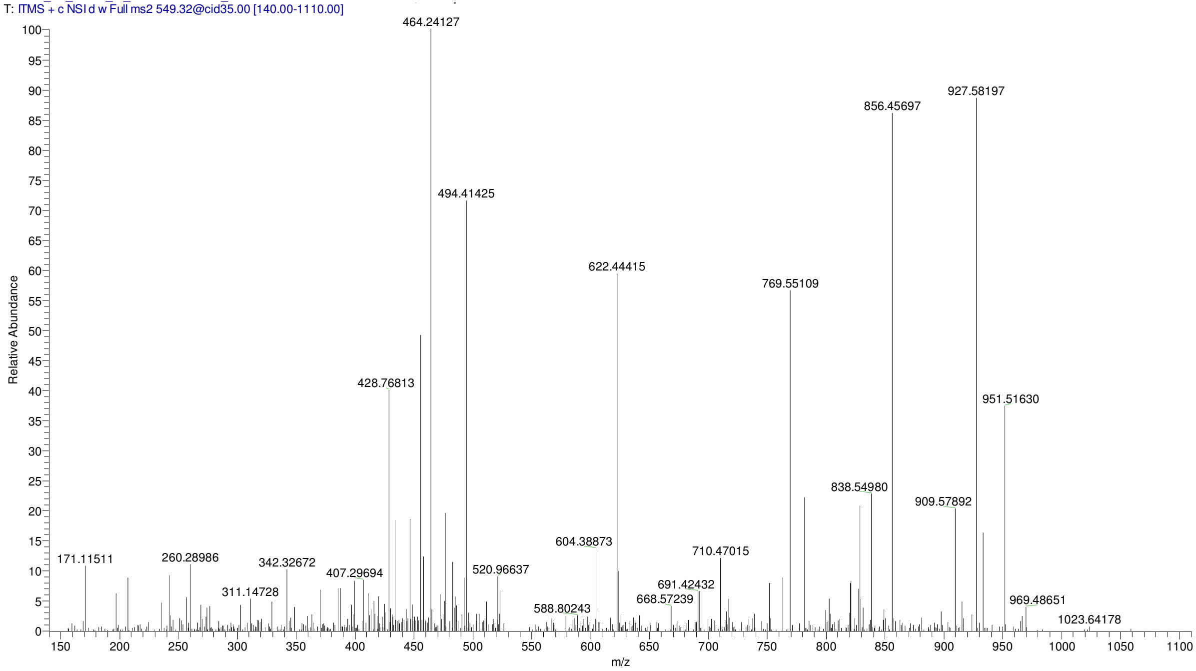
Supplementary Figure 16-21: Comparison mass spectra of immunopetidome (L06/10) and respective synthetic peptides

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).

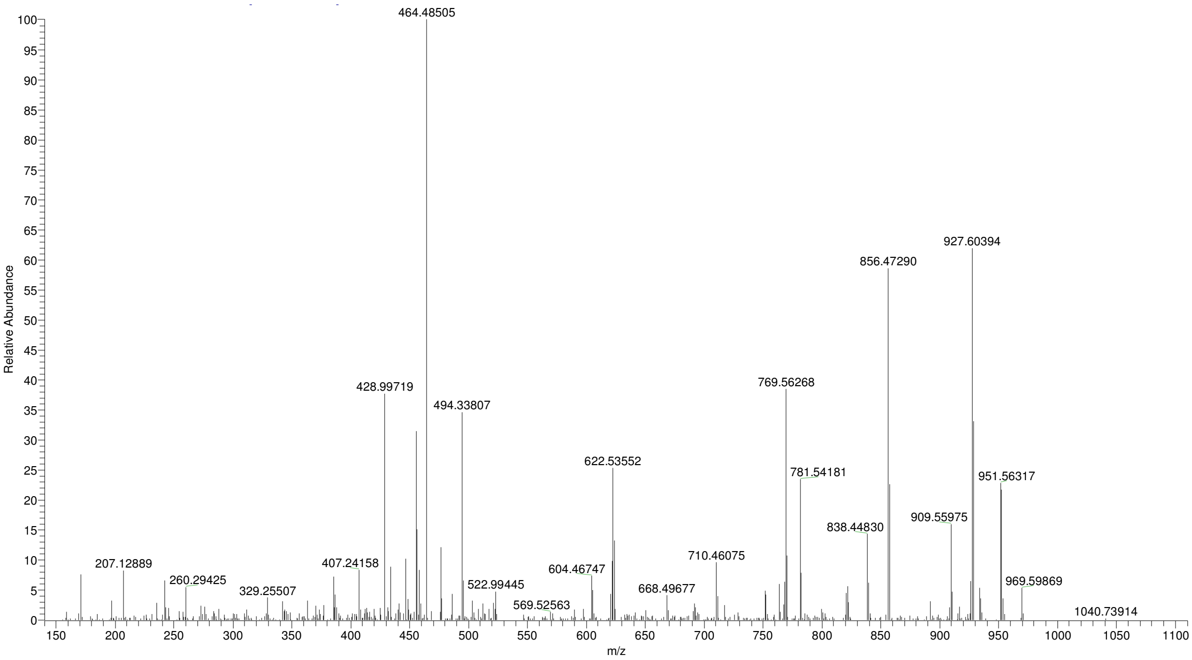
Supplementary Figure 16 (RGS-5 peptide immunopeptidome: autologous tumor mass spectrum)

G| L| A| S| F| K| S| F| L| K (Tumor L06/10)

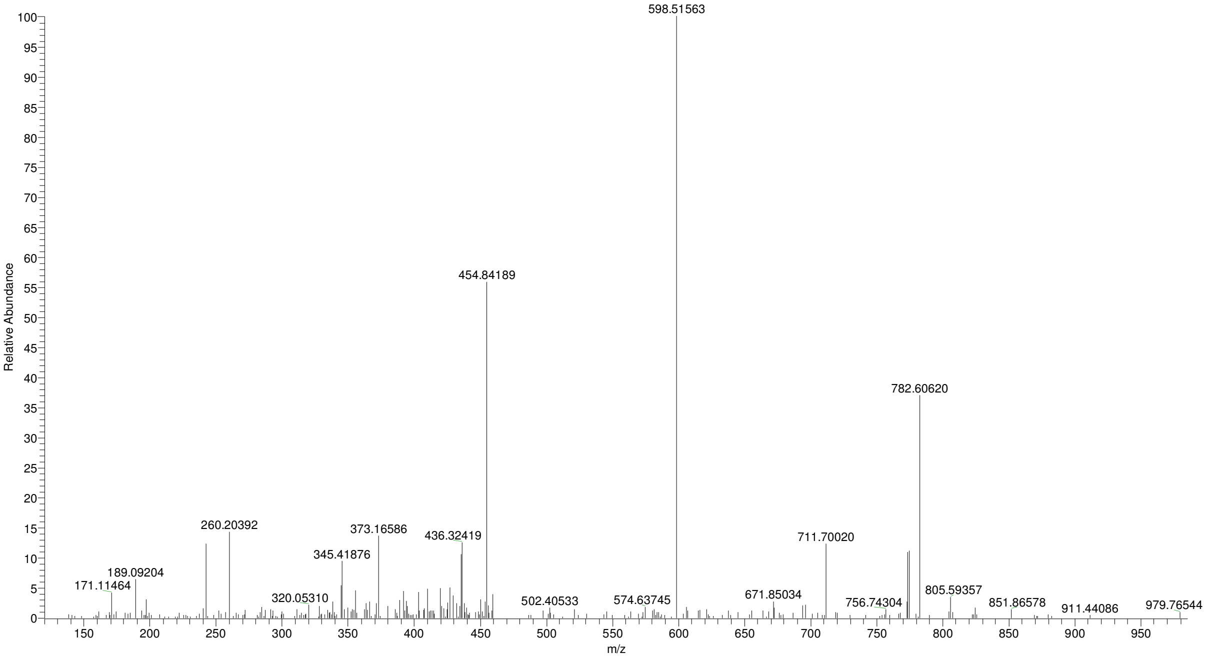


Supplementary Figure 17 (RGS-5 synthetic peptide mass spectrum)

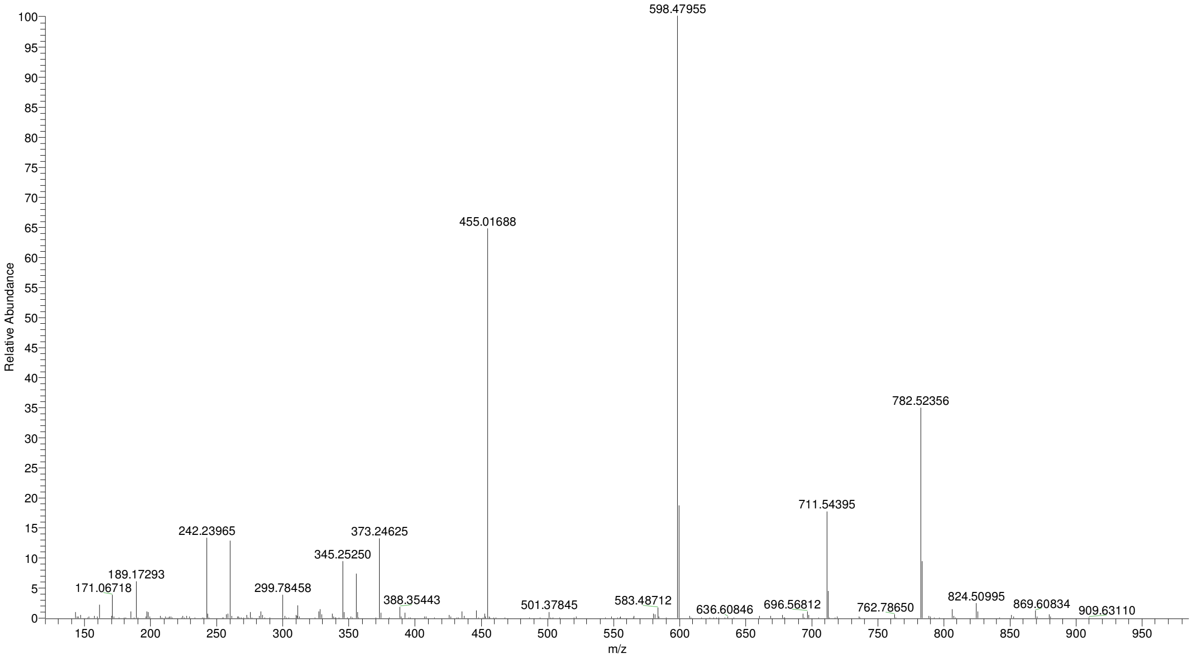
G| L| A| S| F| K| S| F| L| K (synthetic peptide)



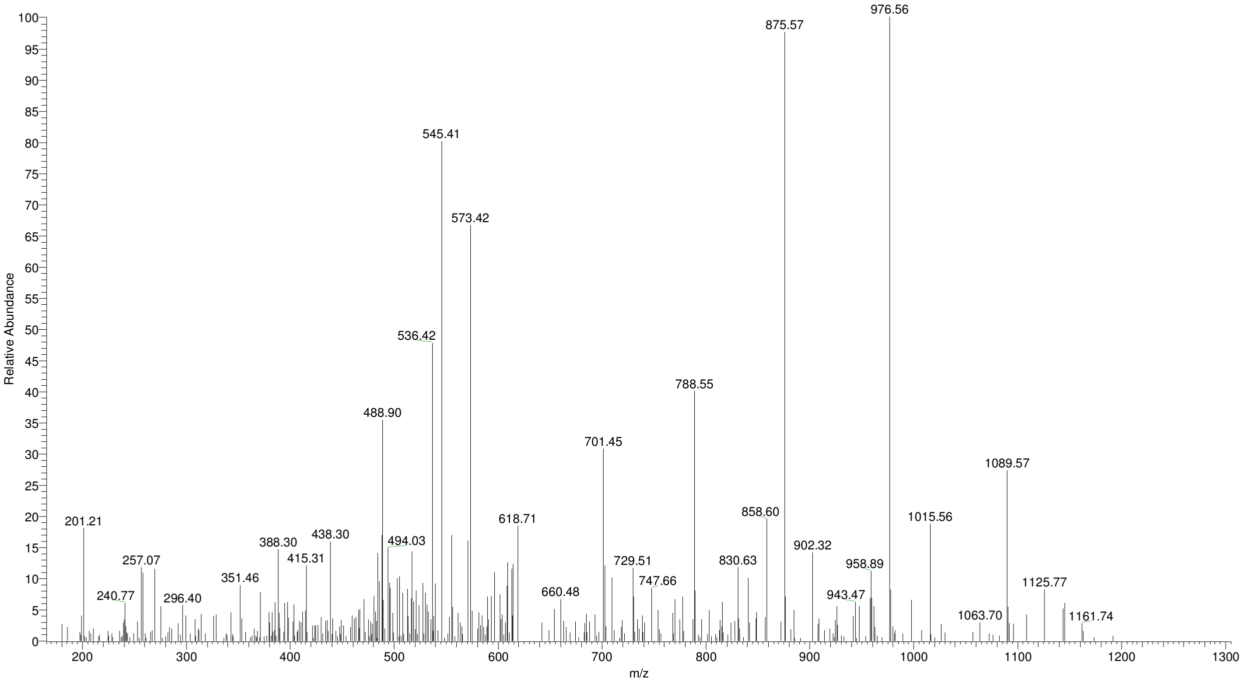
Supplementary Figure 18 (ADFP-3 immunopeptidome: autologous tumor mass spectrum)


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

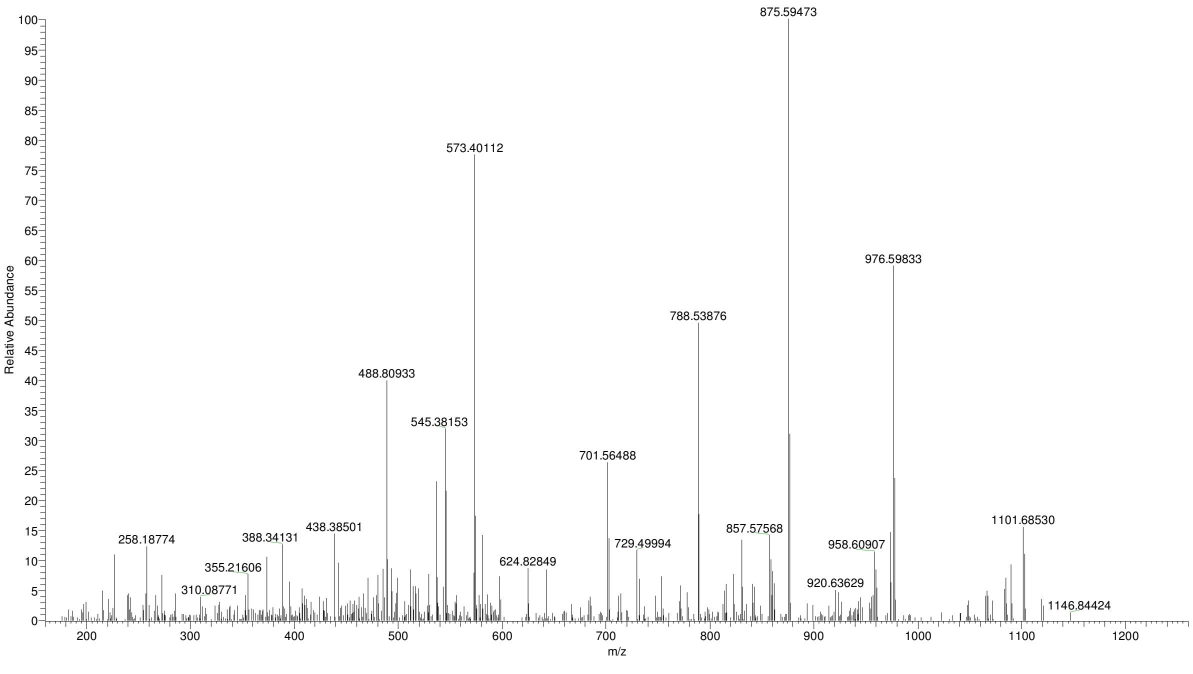
Supplementary Figure 19 (ADFP-3 synthetic peptide mass spectrum)


T| S| A| L| P| I| I| Q|K (synthetic peptide)

Supplementary Figure 20 (ADFP-2) immunopeptidome: autologous tumor mass spectrum)


S| L| L| T| S| S| K| G| Q| L| Q| K (Tumor L06/10)

Supplementary Figure 21 (ADFP-2) synthetic peptide mass spectrum)


S| L| L| T| S| S| K| G| Q| L| Q| K (synthetic peptide)

Supplementary Table 17: L06/10 Immunopeptidome (tumor tissue)

#	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	0,000132642	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	IYADLSLKY	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	TPAGVVNKY	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	IPNEIIHAL	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	0,0009627	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	O43707		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	YSLKVLLSY	68	1	P50416		2,247E7	0	0,001692	60	0,000282864	2	1085,62419	0,05	129,62
19	APAARFNNSQF	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	TAADIFKQY	1	1	Q8N3U4		1,643E7	0	0,007845	59	0,000406553	2	1056,53887	2,65	96,58
22	ALLDGSNVVFK	34	1	O15212		9,182E7	0	0,006907	59	0,000396864	2	1162,64604	-0,57	117,94
23	APISLHVSY	1	1	Q9BZZ2		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	Q5TAA0		1,192E8	0	0,02003	58	0,00056772	2	1013,52983	-0,41	98,98
28	RPAPPPISGGGY	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	VLQAADILLYK	4	1	Q9UGM6		1,259E7	0	0,002853	57	0,000188188	2	1246,74443	3,07	123,89
32	SVSDQFYRY	53	1	P55010		1,097E8	0	0,005652	57	0,000690279	2	1164,53740	4,61	88,10
33	AVAIKAMAK	3	2	P63241;Q6IS14		4,872E7	0	0,01599	57	0,000284904	2	902,54949	0,26	40,59
34	SVAQVVLSR	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	RISVAAASK	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	SVFNHAIRH	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	Q9BZJ0		2,914E7	0	0,00154	52	0,003055891	2	1204,59966	-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	KLLNYAPLEK	6	1	P62875		1,114E8	0	0,008789	52	0,001205105	2	1188,69817	-0,47	75,48
51	DPDVGNFHY	1	1	O15379		1,055E7	0	0,01068	52	0,001373676	2	1063,45146	3,27	95,16
52	NVTQVRAFY	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		1,161E9	0	0,007001	52	0,001113642	2	1138,66167	-0,25	100,77
55	IMLPGVLRY	22	1	O60832		1,644E7	0	0,009831	52	0,001167049	2	1061,62041	2,60	124,05
56	SSITASLRF	35	9	P68363;Q9H853;A6NHL2;Q71U36;Q9BQE3;P68366;Q13748;Q6PEY2;Q9NY65		7,721E7	0	0,01526	51	0,002099281	2	981,53600	-0,42	101,47
57	ILmEHIHKL	81	1	P84098	M3	1,170E6	0	0,02045	51	0,001361965	2	1149,64482	-0,09	47,71
58	YFDPANGKF	38	1	P13639		7,807E7	0	0,02192	51	0,002201027	2	1058,49358	-0,60	97,82
59	NVADLHEKY	20	1	P28074		1,523E8	0	0,01262	51	0,004208725	2	1088,54180	4,28	53,51
60	FLLPIVVRY	41	1	Q8TF05		9,009E6	0	0,004628	50	0,000499782	2	1119,69243	-0,08	151,59
61	RPVPPEVAQQY	1	1	Q6P1N0		6,629E6	0	0,01064	50	0,00274834	2	1283,67742	2,42	72,03
62	DPLGGSAAIHLY	1	1	P07333		3,570E6	0	0,002838	50	0,003544963	2	1213,62358	1,95	119,62
63	VSYSHIQSK	1	1	P27816		1,519E7	0	0,01693	50	0,004061982	2	1048,54375	1,48	31,99
64	YPNVNIHNF	76	1	Q01082		2,188E8	0	0,004369	50	0,003534404	2	1117,54265	0,10	96,38
65	VLAPEGSVANK	1	1	Q13283		1,737E7	0	0,02275	50	0,003128748	2	1084,60271	2,72	53,66
66	NPVEDKDAVAF	16	3	P13688;P31997;P40199		9,131E7	0	0,01202	49	0,004944626	2	1204,58403	-0,40	88,21
67	ImLPGVLRY	36	1	O60832	M2	9,943E7	0	0,002583	49	0,00226304	2	1077,61601	3,20	118,80
68	AFIHISTAY	30	1	Q96K12		9,232E7	0	0,01317	49	0,005465851	2	1022,53032	-0,25	102,28
69	DAARLQAAY	1	1	Q01082		4,846E7	0	0,02443	49	0,005510418	2	978,50017	-0,20	68,25
70	LPSEIEVKY	23	1	Q9UJX3		5,808E7	0	0,005831	49	0,004344253	2	1077,58281	0,11	97,72
71	VVYPWTQRF	66	5	P68871;P02042;P02100;P69891;P69892		9,710E7	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	PSLRILAIGTR	15	1	Q6P1M3		2,543E6	0	0,025	48	0,000588776	2	1196,75090	2,90	104,70
74	RVQEAVESmVK	2	1	Q96C01	M9	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	YEVSQLKD	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	0,00719722	2	1162,57817	0,22	112,17
80	ILMEHIHKL	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	0,0199	48	0,006033006	2	1169,62004	3,34	83,75
84	RLFVGSIPK	20	2	O60506;O43390		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	QTYGQQLQK	1	1	P20591		1,473E7	0	0,02011	47	0,007976071	2	1093,56499	1,20	42,43
87	HVIDVKFLY	106	1	Q16531		7,529E7	0	0,004834	47	0,006327291	2	1133,63518	-0,19	111,15
88	HPNYPYSDEY	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

#	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	1197,60112	3,19	105,12
91	KLKKTETQEK	26	3	P63313;O14604;P62328		6,074E6	0	0,005257	46	0,003613992	2	1232,72075	-0,15	21,06
92	TPALIALRY	3	4	P52895;Q04828;P42330;P17516		1,439E7	0	0,009127	46	0,003059072	2	1017,61211	2,88	110,18
93	FPDKPITQY	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	RTLSDYNIQK	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	QVDPLSALKY	1	1	Q9UL63		4,122E6	0	0,01913	45	0,011251222	2	1133,62395	3,36	116,21
100	RSDTPLIYK	4	1	P41252		5,146E7	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	NAFKEITTm	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	2	1149,59355	-0,30	123,74
109	VFNEKGWNY	12	1	P43490		5,202E7	0	0,01057	44	0,012404932	2	1156,54570	3,01	90,33
110	AIITTHLQY	24	1	Q96B45		1,337E8	0	0,02876	44	0,021324574	2	1059,58306	-0,27	92,51
111	QIFVKTLTGK	25	4	P62987;P62979;P0CG47;P0CG48		2,430E8	0	0,01116	44	0,003614351	2	1134,68779	-0,33	68,26
112	AQYSPQQLAGK	1	1	Q01581		2,378E7	0	0,01099	44	0,022471835	2	1190,62139	4,14	61,86
113	ISNPIPIKV	1	1	Q92614		8,240E6	0	0,02065	44	0,002202774	2	980,61553	1,62	102,29
114	GPGSRISSSSF	37	1	P05787		5,348E8	0	0,02765	44	0,01520025	2	1081,52703	-0,26	58,68
115	TVSDAILRY	1	1	Q9Y5W9		5,589E7	0	0,01036	43	0,013926929	2	1037,56462	1,93	96,09
116	TPLEEAIKF	1	1	Q9BXJ9		5,689E6	0	0,01895	43	0,01453644	2	1047,57463	2,38	113,39
117	VIYNEQMASK	1	1	Q9H8H3		5,683E6	0	0,01225	43	0,022564524	2	1182,58464	1,91	58,12
118	IVSSLRLAY	26	1	Q9NP61		1,123E8	0	0,01895	43	0,00669272	2	1021,60399	-0,10	99,93
119	RTQNVLGEK	1	1	P23396		2,070E7	0	0,02252	43	0,018507177	2	1044,57891	-0,74	29,96
120	VFLPIHITY	10	1	Q99788		2,204E7	0	0,0244	43	0,0137483	2	1102,62883	-0,67	139,98
121	FIDASRLVY	43	2	P35221;P26232		1,009E8	0	0,00229	43	0,018261169	2	1083,58269	-0,62	119,06
122	AFTDLHLRY	16	1	P04114		7,399E7	0	0,01742	43	0,016694992	2	1135,59197	2,17	95,86
123	VTFPEFLRY	13	1	Q8NCH0		3,031E7	0	0,01765	43	0,017258717	2	1171,61443	-0,20	138,94
124	RSPDFASSFK	1	1	Q99828		2,574E7	0	0,01341	43	0,019529788	2	1141,56218	-1,33	64,48
125	RIFAPNHVVAK	1	1	Q02543		1,284E7	0	0,004994	43	0,006177735	2	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		9,344E6	0	0,02165	42	0,003205486	2	1204,72344	2,73	115,71
127	KIWADIPAPK	1	1	P49419		5,583E6	0	0,02787	42	0,007563925	2	1138,66435	2,09	84,50
128	TIFTARLYY	28	2	Q8IUX4;Q9NRW3		4,705E7	0	0,01886	42	0,025030325	2	1147,61846	3,32	116,40
129	DPFKDIILY	52	1	Q7L1Q6		2,049E6	0	0,02284	42	0,017848762	2	1123,60356	0,12	155,32
130	SPVFTSRSAAF	1	1	P08729		3,089E7	0	0,007637	42	0,019794711	2	1169,59844	2,94	86,28
131	FPSIYDVKY	32	1	Q9UFF9		4,996E7	0	0,01364	42	0,027078793	2	1131,57524	2,77	117,86
132	FPEEDKKTY	2	1	O95298		3,439E7	0	0,0126	42	0,023134765	2	1156,55193	-0,17	47,99
133	RTNEVVAIK	1	1	Q7L7X3		9,998E6	0	0,02441	42	0,019896508	2	1029,60747	2,23	40,83
134	QLYWSHPRK	11	1	P62273		1,070E8	0	0,008521	41	0,037871535	2	1214,64311	0,15	38,25
135	YWNASDLRY	1	1	P20929		3,416E7	0	0,005677	41	0,019650264	2	1187,55107	2,57	102,43
136	AIAQAESLRYK	1	1	P23396		3,612E6	0	0,01073	41	0,020932698	2	1249,69426	3,44	58,38
137	SPIDVVEKY	9	1	Q53G59		5,121E7	0	0,01455	41	0,028466101	2	1049,55364	2,14	97,37
138	HGYENPTYK	1	1	Q06481		1,110E7	0	0,02756	41	0,023313427	2	1108,50810	2,07	34,88
139	SPVNSSKQPSY	1	1	P05496		1,024E7	0	0,007354	41	0,031226593	2	1193,58025	0,44	44,59
140	AFDLTEQRY	1	1	Q86UE8		2,897E6	0	0,01551	41	0,03008209	2	1142,54924	1,35	92,69
141	VLFEHAVGY	1	1	O00567		4,124E7	0	0,02315	41	0,042488455	2	1034,53362	2,92	99,24
142	EVYAGSHQY	1	1	Q9H3P7		5,659E7	0	0,01348	41	0,018649422	2	1053,46391	0,29	49,75
143	RQTGIVLNR	1	1	Q13435		8,758E6	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	VLYDRVLKY	27	1	Q9UHB9		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	AVIEDTWHY	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	STVSRFFLY	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	VVQDGITLITK	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	0,048484619	2	1037,49004	0,18	65,72
157	ALAEYVIYR	3	1	Q9H2K2		2,032E7	0	0,01252	39	0,037000539	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	YPSRVFVGDTF	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	Q9Y3Z3		6,697E7	0	0,01041	38	0,061055908	2	1091,51567	0,01	107,47
162	RQIPYTmmK	2	1	Q00325	M7; M8	2,550E7	0	0,02618	38	0,066184118	2	1199,59392	2,28	41,05
163	YVYEYPSRY	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;Q9BVA1;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	M5	7,125E7	0	0,02859	37	0,089903234	2	1063,52715	2,83	54,13
169	AVYGGFKSK	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;P0C0S8;Q6FI13;Q8IUE6;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	M3	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	Q9BRK3		7,094E8	0	0,01212	36	0,009930018	2	1196,75127	-0,15	104,80
175	FPSPILKVQY	1	1	Q15291		2,193E6	0	0,01929	36	0,048369603	2	1191,68083	3,00	117,69
176	KWTDLALQY	20	1	Q9BS18		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	YVHDDGRVSY	1	1	O60234		1,427E7	0	0,01072	36	0,07011458	2	1210,54961	0,71	49,43
179	RLSPSPTSQR	1	1	P02545		1,174E8	0	0,00835	36	0,0850875	2	1128,61406	1,79	30,47
180	KPFDQTTISL	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	KVFDGIPPPY	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;A8K0Z3;Q6VEQ5;A8MWX3		4,112E6	0	0,00587	35	0,05164459	2	1218,71135	1,67	98,23
184	YYIFIPSKF	17	1	Q9H0S4		2,052E7	0	0,01219	35	0,108864775	2	1177,63298	3,19	135,72
185	SVYQIKVHR	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	AVYSHVIQKL	1	1	P20132		1,442E7	0	0,02426	35	0,065922643	2	1157,67156	3,29	73,68
188	AYWNASDLRY	1	1	P20929		6,166E6	0	0,01094	34	0,124954264	2	1258,58953	3,48	106,99
189	LPIPVDAKVGY	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	APFQGDQRSL	4	1	Q00978		3,776E7	0	0,01676	34	0,175535943	2	1118,56011	1,03	67,29
192	SFEQFHLFY	2	1	P16885		9,649E6	0	0,005867	34	0,149673556	2	1217,56706	3,66	139,67
193	YPFHKQPPTY	2	1	Q9BU23		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	NFDKLSFLY	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	IPFDPKFITY	15	1	Q8N7H5		5,652E7	0	0,02085	33	0,191398254	2	1240,66631	4,05	134,55
197	IPIYADKDVF	1	1	Q15181		3,655E6	0	0,02755	33	0,191522904	2	1180,62688	1,67	111,39
198	KVLDKIVHY	1	2	Q2NKQ1;O75897		1,017E7	0	0,02058	32	0,128171203	2	1114,66191	-0,03	68,38
199	RTYLPSQVSR	1	1	P35606		1,214E7	0	0,01861	32	0,185857085	2	1206,66460	4,66	55,41
200	VPESSLAGHSF	1	1	P55854		2,297E7	0	0,01183	32	0,228972554	2	1130,54949	1,57	78,39
201	FPDPAGKLNQF	1	2	Q9BT22;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	mPRVQTQQY	1	1	O94979	M1	1,211E6	0	0,02783	31	0,268295697	2	1166,56255	0,21	45,70
205	RWNPLPLSY	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	APSLFHLNTL	1	1	Q96QB1		1,304E7	0	0,02853	30	0,239164958	2	1112,61272	2,52	122,18
211	FFPSIYDVKY	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	Mod. (ox)	Area	q-Value	PEP	IonScore	Exp. Value	Ch.	MH+ [Da]	ΔM [ppm]	RT [min]
214	RLFNAIIHR	1	1	Q15149		2,958E6	0	0,02424	29	0,131336786	2	1139,68401	3,80	69,27
215	IPYHSEVPVSL	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	0,173222511	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	LPYNQQHLY	1	1	Q9Y5Q0		1,875E7	0	0,01551	27	0,811488986	2	1175,58647	1,77	78,99
221	YVYPKYLKY	1	1	Q9BZ29		3,808E7	0	0,01146	27	0,588791578	2	1236,66948	2,56	83,81
222	RFDHVITNm	2	1	P02746	M9	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
224	IPIERLYVTY	5	1	P49588		1,242E7	0	0,00724	26	0,459335087	2	1266,71294	2,89	116,44
225	MPAVKAIIYQY	2	1	P37268		6,500E6	0	0,02423	26	0,893462026	2	1296,70439	1,77	112,31
226	FYSEVHPHY	5	1	Q9BRR6		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	TPLSQAIIHQY	1	1	Q9NQS7		7,076E6	0	0,01135	24	1,253531607	2	1270,68218	2,47	98,70
231	VVYSGLENIKK	1	1	Q9HBL8		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	KLIKDGLIIRK	2	1	P84098		3,958E7	0	0,01687	23	0,015706089	2	1296,87639	2,89	56,96
233	YPDRImNTF	11	5	Q13885;Q9BVA1;P68371;P07437;Q13509	M6	8,527E7	0	0,02364	23	1,842428776	2	1172,54228	1,51	85,71
234	LPDEIYHVY	2	1	Q9BV86		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	Q96J88		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	VPHSIINGY	16	2	Q8NHW5;P05388		6,221E5	0,001	0,03406	51	0,003034349	2	999,52501	-0,82	80,21
239	KTLDHVLTH	1	1	Q9BTW9		9,545E6	0,001	0,03648	51	0,002680802	2	1063,58989	0,37	42,62
240	KIGDFGLTK	3	2	O60674;P23458		3,521E5	0,001	0,03591	51	0,002047457	2	978,56145	-0,47	70,69
241	AVAAVAARR	1	1	Q14697		3,428E6	0,001	0,03909	50	0,001681852	2	884,54436	2,08	28,87
242	GLASFKSFLK	3	1	O15539		5,876E7	0,001	0,02945	49	0,00228778	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	STNNWVLIK	1	1	O14617		6,576E6	0,001	0,04381	47	0,006628142	2	1074,59636	1,95	96,18
245	APPPPAHAL	2	1	Q96RK1		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	YPVDLGDKF	1	1	P52434		1,207E7	0,001	0,03676	44	0,014925366	2	1053,52837	3,02	105,06
249	SVNLKVSPK	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	SIIDVYHKY	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	0,03098	42	0,016101296	2	1035,57390	1,70	107,62
255	AVmGAYVLLK	2	1	Q9BY50	M3	5,271E6	0,001	0,03823	42	0,011600163	2	1080,61162	-0,57	92,04
256	VKKAALVIQQ	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	O94952		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	0,022722218	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	TSFDKFYKY	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	KIKEHVRSK	1	1	O15205		2,794E6	0,001	0,0304	36	0,015033313	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	MTHNLLLNY	10	2	Q92769;Q13547		2,588E5	0,001	0,03841	35	0,132655477	2	1118,56609	-0,21	103,52
277	SWIQNVDTKY	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	RVFVVGVGmTK	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	0,16415525	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	Q969T4;P51965;Q96LR5		3,085E8	0,001	0,02904	34	0,090006128	2	1223,68559	2,65	99,61
287	FPEHIFPAL	1	1	P61160		0,000E0	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	RQTATQLLK	1	1	P62424		2,079E7	0,001	0,03672	33	0,112606448	2	1058,63213	0,39	41,09
290	HISPNAIFK	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	IPQKFIVDY	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	Q9UBB9		5,532E7	0,001	0,04185	32	0,283655881	2	1177,59892	2,45	58,85
295	LSQNRVAEF	1	1	P48556		4,070E6	0,001	0,03737	32	0,293138169	2	1063,55559	2,31	66,57
296	VVYTSHLQLK	1	7	P0DJD0;P49792;P0DJD1;A6NKT7;Q7Z3J3;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	SLLHLGALY	11	1	O00767		4,640E7	0,001	0,03025	31	0,229909111	2	986,56975	2,82	123,98
299	ASFDKAKLK	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	KVTEGSFVYK	3	1	P50395		4,554E7	0,001	0,03561	30	0,322492676	2	1157,62444	3,71	55,32
302	SVLDSFLKY	2	1	Q96JI7		3,129E7	0,001	0,0299	30	0,321919233	2	1071,57536	3,03	139,76
303	YAIDNPLHY	14	1	A5YKK6		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	0,267447782	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	MAVDDFNLKY	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	IPVNEKDTLTY	1	1	O75446		8,063E6	0,001	0,03807	27	0,736658151	2	1292,67656	2,52	83,64
314	RPSLPLPHF	1	1	Q9BV38		1,579E7	0,001	0,04251	27	0,241955924	2	1063,60613	1,27	101,03
315	FPPYHVGQTF	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	ALDTKIGRYK	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	SPLPTAETPKPL	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	2	1285,57268	-0,22	84,13
323	SVYDSVLQK	1	1	Q8NF91		2,498E7	0,001	0,03056	26	0,780149096	2	1038,54802	1,34	81,65
324	LPFPPGDRVTF	3	1	Q6H8Q1		4,090E6	0,001	0,03408	26	1,149104555	2	1245,66741	3,78	123,29
325	RTAHVILRY	2	1	Q9UKV5		3,285E7	0,001	0,04213	26	0,665239401	2	1128,66460	0,82	49,21
326	SFIDVDDERWHY	1	1	O14929		1,748E7	0,001	0,03913	25	0,70273335	3	1581,70017	2,07	116,16
327	LPIENDTYKY	1	1	O00186		2,575E6	0,001	0,04033	25	1,377926824	2	1255,62602	4,38	87,48
328	FGGRNPFDTF	1	1	P25685		7,455E6	0,001	0,03878	25	0,818853749	2	1157,53679	-0,61	113,62
329	RPPYYTPNQL	1	1	Q13310		2,863E6	0,001	0,04376	24	1,365276701	2	1248,64031	2,51	82,79
330	RLLEYTPTAR	1	1	P49841		2,839E6	0,001	0,03221	24	1,045581756	2	1219,67986	0,38	67,81
331	KLGGVIKEK	1	1	Q9Y2X3		1,775E7	0,001	0,03548	24	0,329621937	2	971,62462	-0,24	30,13
332	YLLPHILVY	11	1	Q13535		1,066E7	0,001	0,03106	24	0,826284528	2	1130,66081	-0,04	144,49
333	TPYPAILHEY	1	1	Q9P2H3		6,138E6	0,001	0,04016	24	1,920807075	2	1203,60820	3,10	105,43
334	KTYHALSNLPK	1	1	O00231		2,016E6	0,001	0,04255	23	1,62925834	2	1271,71221	1,20	45,98
335	LHLGYLPNQL	9	1	Q92499		3,982E7	0,001	0,0313	23	1,251850787	2	1167,65239	0,25	120,05
336	LPEEHARFY	1	2	Q05513;P41743		2,391E6	0,001	0,03175	23	2,067840932	2	1161,57207	2,84	68,88
337	YPFDGPGNTLAH	1	1	P09237		5,898E6	0,001	0,03604	21	1,956176473	2	1288,59831	2,01	96,12
338	KYFDEHYEY	5	1	P33552		5,629E7	0,001	0,03619	20	1,412222504	2	1293,54228	0,03	75,99
339	VVYQYWNTK	1	1	Q8N766		3,824E6	0,001	0,03529	19	5,538911648	2	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	O43913		2,031E6	0,001	0,03577	15	10,50499673	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	IVAGTLTNK	1	1	O75251		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	KLYDIDVAK	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	P08670		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	ATGDMSGLLK	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;Q96LR5		2,635E5	0,002	0,04934	45	0,002440742	2	1141,71904	-0,09	126,46
354	KLYEEPLSK	1	1	Q13535		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	RVGTVIGSNK	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	RSVDVTNTTF	1	1	O14579		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	RPSQNNTIGL	1	1	Q9H0H0		3,362E6	0,002	0,04768	40	0,026425514	2	1099,58733	1,67	59,14
363	SVYRTPVVNLK	1	1	P20929		4,952E6	0,002	0,05211	40	0,014748922	2	1275,74590	3,06	72,45
364	SFFDLNPKY	1	2	Q9BQL6;Q96AC1		3,745E6	0,002	0,05677	40	0,041335109	2	1130,55596	3,75	123,27
365	FPANNIVKF	4	1	P43307		4,298E5	0,002	0,05523	39	0,036599739	2	1049,57756	-0,31	108,36
366	SSYGGTLRY	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	GVIGQDGLLFK	1	1	Q9NQT5		5,442E6	0,002	0,05631	39	0,036282501	2	1146,65373	1,69	115,46
369	GLTDVILYH	1	1	O60506		2,762E7	0,002	0,05449	39	0,058447508	2	1030,56035	3,44	120,38
370	RTAVPSFLTK	5	1	Q96QD9		4,409E7	0,002	0,04858	38	0,026839336	2	1119,65532	2,86	73,78
371	STFNQVVLK	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	RVAPAHGLFLK	1	1	Q8N0Z8		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		9,078E6	0,002	0,0439	36	0,009372159	2	1103,69585	2,05	86,08
377	RPELVRPAL	11	3	P52895;Q04828;P42330		1,106E6	0,002	0,04623	35	0,017288068	2	1050,64128	-0,59	67,85
378	LPHAPGVQm	1	2	Q92769;Q13547	M9	1,189E7	0,002	0,05424	35	0,142213884	2	965,49083	3,59	62,48
379	RPPSITSQTSL	1	1	Q9NYB9		4,046E6	0,002	0,04625	35	0,139693612	2	1186,64531	2,22	71,70
380	DVIRLIMQY	14	1	Q2TAY7		5,191E5	0,002	0,05145	35	0,084681899	2	1150,62883	-0,10	158,08
381	RSNPYYIVK	1	1	Q9UQE7		4,599E6	0,002	0,04813	35	0,092999026	2	1139,62505	3,73	54,92
382	GVADKILKK	3	1	Q13287		2,104E5	0,002	0,05708	34	0,032810746	2	971,62444	-0,43	43,69
383	RPYEPINSI	3	1	Q8WUA4		4,020E7	0,002	0,04425	34	0,189992643	2	1088,57305	-0,44	79,38
384	KVFQEPLFY	10	1	P07711		2,685E5	0,002	0,04876	34	0,139374498	2	1170,61907	-0,29	117,36
385	LPPPVFQmL	1	1	Q15388	M8	2,689E7	0,002	0,04938	34	0,140694657	2	1057,57854	3,23	136,59
386	TPVDDRVDY	1	1	P20929		1,251E7	0,002	0,04483	34	0,163108241	2	1079,50163	1,12	68,11
387	GVYSFQFNK	2	1	Q15434		1,681E5	0,002	0,04983	33	0,182672514	2	1089,53606	-0,31	94,43
388	IFIEDAIKY	6	1	O14791		6,782E6	0,002	0,0483	33	0,137288765	2	1111,60283	-0,54	127,57
389	NPVNYGRPY	1	1	Q9UJK0		1,795E6	0,002	0,05617	33	0,189404277	2	1079,53069	3,52	63,41
390	DPIGGHIHSY	1	1	B0I1T2		1,552E7	0,002	0,04501	33	0,166108068	2	1095,52532	3,20	62,16
391	DYDPLVVKL	1	1	Q96A65		9,581E6	0,002	0,05383	32	0,159517277	2	1061,59172	3,71	130,22
392	AVLTKQLLH	1	1	Q14094		8,672E6	0,002	0,05354	32	0,034846951	2	1022,63487	-0,84	64,60
393	QSFDKEWVAK	1	1	P13073		9,829E6	0,002	0,04617	32	0,26830297	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	RIIEETLALK	1	1	O15144		1,736E7	0,002	0,04425	32	0,089725401	2	1185,72368	2,93	82,61
395	APAPIHNQF	16	1	Q15011		2,304E8	0,002	0,05239	32	0,173974943	2	994,51189	1,36	62,94
396	APEEHPVLL	7	3	P60709;P63261;A5A3E0		1,782E6	0,002	0,0537	32	0,382228623	2	1004,54094	-0,23	83,52
397	HPVPQPLQSF	8	1	Q9Y5Q3		2,368E5	0,002	0,04969	31	0,255128686	2	1149,60491	-0,22	94,87
398	NPYSGDLTKF	2	1	Q14157		1,513E7	0,002	0,05109	31	0,265942785	2	1141,55254	0,08	95,84
399	RQNVQVFEF	5	3	P52895;Q04828;P42330		2,320E5	0,002	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	0,002	0,05771	31	0,137402967	2	1163,49870	4,15	53,54
401	KVADMALHY	13	1	P50990		1,086E8	0,002	0,04983	31	0,433220222	2	1047,52873	-0,47	69,76
402	YPVEIHEYL	2	1	Q13901		2,253E7	0,002	0,0551	31	0,380355256	2	1162,58196	3,47	110,17
403	LPYTVVIHY	1	1	Q9NZ08		7,379E6	0,002	0,05192	30	0,316832566	2	1104,61138	2,31	113,99
404	GTmTGmLYK	3	2	Q5SRD1;O14925	M3; M6	4,482E7	0,002	0,04518	30	0,233171671	2	1033,47026	0,90	43,67
405	ATGSWDSFLK	3	3	P62879;P62873;P16520		2,540E7	0,002	0,04695	30	0,359021291	2	1111,54399	1,88	111,18
406	QLYKEQLAK	3	1	P35579		8,672E7	0,002	0,05263	30	0,23843724	2	1120,63689	0,68	45,91
407	VVYVGGILTK	4	1	Q16880		2,039E5	0,002	0,04932	30	0,076524711	2	1048,64006	-0,08	99,66
408	KPYNPIIGETF	2	2	Q9BXB5;Q9BXB4		1,478E7	0,002	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	GPGVAFRAPSI	1	1	P08727		6,094E6	0,002	0,04876	30	0,237301645	2	1071,59807	3,22	99,91
411	KLNITPTKK	1	1	Q7KZ85		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	Q7Z3Z3		1,337E6	0,002	0,05585	29	0,366042537	2	1101,60918	0,02	133,06
415	LPDKWQHDL	1	1	Q86V81		7,849E6	0,002	0,0479	29	0,430287522	2	1151,58684	2,09	77,11
416	RPPIGSISSm	1	1	Q9BQY9	M10	9,219E6	0,002	0,04693	29	0,756445315	2	1060,54704	1,35	60,77
417	LAVASFPKKQE	1	1	P14406		4,869E6	0,002	0,05613	29	0,348302216	2	1217,69267	3,09	60,12
418	RTFPFSLQY	2	1	O75159		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	VIHEKGFYY	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	EAIKILKGEY	1	1	Q92499		1,674E7	0,002	0,04862	27	0,330112297	2	1163,67082	3,20	79,07
426	YLPKEQYLY	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]	ΔM [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	Q8IWD5		1,370E5	0,002	0,05026	26	0,337242824	2	1263,74211	0,09	81,72
429	AVADKVHLmYK	1	1	Q14258	M9	2,335E6	0,002	0,04532	25	1,302408873	2	1290,69390	4,93	53,85
430	RVLLPTGNQR	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	AILDTAHQY	1	1	Q5VSG8		1,610E7	0,002	0,05194	25	1,17168781	2	1031,51738	1,67	76,88
433	YRDIPELQGF	1	1	Q86V21		9,997E6	0,002	0,05723	25	1,246783116	2	1237,62432	2,51	116,18
434	AIALALREK	1	1	P42285		0,000E0	0,002	0,05359	24	0,410988894	2	984,62419	4,16	63,68
435	LFDHAVSKF	1	1	O60488		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	NPAENFRVL	12	1	P13010		7,976E7	0,002	0,04825	24	1,631126674	2	1059,55828	0,05	92,78
438	STYPRPHEY	3	1	Q9UBR2		9,151E7	0,002	0,05506	22	1,67267086	2	1149,53435	1,73	43,49
439	YLWHIPLTY	7	1	Q6P179		1,314E7	0,002	0,04729	22	3,258811029	2	1205,63591	0,45	146,80
440	RPIEDDQEVY	1	1	O15117		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	YPDEYHGEY	2	1	Q15417		3,054E7	0,002	0,05302	21	0,445771467	2	1172,45622	2,66	70,57
443	FPDRImNTF	1	2	P04350;Q9BUF5	M6	6,150E6	0,002	0,04875	21	2,681430011	2	1156,54924	3,13	97,02
444	EVNKFQmAY	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	FPDPNVKYVF	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	KPITTGGVTY	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	LPLPDPLKY	1	1	Q9NV79		6,814E6	0,003	0,05854	43	0,00768533	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	RIYNGIGVSR	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	1020,60857	-0,27	102,79
468	KVAPAPAVVKK	1	1	P62424		1,662E6	0,003	0,06074	38	0,00192799	2	1107,72490	-0,01	30,18
469	AIIDHIFASK	1	1	Q8TAS1		3,082E7	0,003	0,06275	38	0,042080603	2	1114,62859	2,71	96,76
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	RLFPPLRQR	2	1	Q8NBM4		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	Q9BUJ2		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	NPYHVVILF	12	1	Q86X29		1,337E6	0,003	0,05923	31	0,20822437	2	1101,60906	-0,10	133,42
479	SPVIHPPVSY	1	1	Q15904		1,133E7	0,003	0,05908	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	ATAASSSSLEKS	1	7	P60709;P63261;Q6S8J3;P62736; P68032;P63267;P68133		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	M5	4,958E7	0,003	0,05841	29	0,217085602	2	1248,54582	-0,67	68,63
484	PYNHQHEY	1	1	O95864		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	O95782;O94973		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	1094,56609	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;Q9UKE5;O95819		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]
				P30685;Q95365;P30475;P30480;P30481;P30484;P30485;P30486;P18464;P30490;P30491;P30492;P30493;P30495;P18465;P10319;Q29940;Q29836;P30498;Q31610;Q29718;P04222;Q95604										
499	QPWEEIKTSY	1	1	P49961		2,219E7	0,003	0,05851	19	5,356432155	2	1280,61821	1,90	97,04
500	AIYKTPPGIQK	1	1	Q6W2J9		3,507E6	0,003	0,06011	14	6,974571967	2	1215,71355	3,22	57,03
501	KLYEMILKR	1	1	P56559		2,279E6	0,003	0,06502	13	4,208955831	2	1193,71184	3,61	75,14
502	LPVAKDVSY	1	1	Q16851		1,120E7	0,004	0,06737	51	0,002500008	2	991,54827	2,37	75,28
503	AVYSHVIQK	1	1	P20132		7,615E6	0,004	0,06582	45	0,006010713	2	1044,58489	1,15	46,62
504	AVMGAYVLLK	7	1	Q9BY50		2,152E5	0,004	0,06684	45	0,004535268	2	1064,61699	-0,31	110,94
505	KVFERAVQY	1	1	Q14690		1,416E7	0,004	0,06579	44	0,010623969	2	1139,62615	4,68	59,46
506	FNSHVHVEY	1	1	O43150		6,976E6	0,004	0,06559	41	0,021086881	2	1131,52397	1,92	60,94
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		7,852E7	0,004	0,06751	31	0,331847305	2	1059,52873	2,73	63,23
509	KVLDAIIQEK	1	1	Q9NTJ3		4,504E6	0,004	0,06717	28	0,282357002	2	1156,69621	2,21	77,96
510	SVYSPSGPVNR	1	1	Q9NS56		9,128E6	0,004	0,06658	24	1,60363642	2	1162,58476	-0,33	57,90
511	LPWNITVHF	1	1	Q9H1Y0		1,151E6	0,004	0,06624	17	5,792315053	2	1126,60613	1,50	142,65
512	MYDAAKLLY	2	1	Q00610		2,882E6	0,005	0,07097	51	0,0033832	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	GPGSRISSSSFS	1	1	P05787		6,983E6	0,005	0,07183	49	0,004808194	2	1168,56340	3,48	58,73
515	VQSNARLLY	1	1	P35869		0,000E0	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	RLGDSQLVK	2	1	Q16531		3,226E7	0,005	0,07311	34	0,126265355	2	1015,58843	-1,08	47,68
520	FVQmMTAK	4	1	P62158	M4	1,241E7	0,005	0,06856	34	0,119074389	2	971,46941	0,48	50,16
521	SAEEGYRTY	1	1	Q96QU6		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	M5	9,862E6	0,005	0,07136	29	0,139823354	2	1209,70708	3,83	61,89
527	RVLPYPFTH	1	1	Q9BVJ6		1,656E5	0,005	0,07038	29	0,417008928	2	1129,61455	-0,68	87,78
528	SIGQVFLLK	1	1	Q9Y3B3		5,543E6	0,005	0,07042	29	0,145597538	2	1004,61504	1,09	114,13
529	RPAFFAERL	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]
				P30685;Q95365;P30475;P30480;P30481;P30484;P30485;P30486;P18464;P30490;P30491;P30492;P30493;P30495;P18465;P10319;Q29940;Q29836;P30498;Q31610;Q29718;P04222;Q95604										
531	LPDLRPWTSL	1	1	Q03519		9,802E6	0,005	0,06837	24	0,885910454	2	1197,66692	3,53	139,59
532	AVVNKVPLTGK	1	1	Q8WUH6		1,140E6	0,005	0,07262	23	0,396039557	2	1125,70293	3,42	54,94
533	YPAYLGARL	1	1	P38606		3,961E6	0,005	0,07293	21	1,12914272	2	1023,56352	1,27	97,93
534	FVYEPKEQK	1	1	Q16666		5,393E6	0,005	0,07171	18	6,984296097	2	1167,60576	1,09	49,03
535	RVFPYSVFY	1	1	O15118		1,369E7	0,005	0,07251	15	15,67709849	2	1177,60832	3,60	129,53
536	LPIESNPHSF	1	1	Q8N3C0		3,679E6	0,005	0,06959	14	13,45054736	2	1140,57146	2,65	83,81
537	LPHDPDLSY	1	1	Q9P217		1,568E7	0,005	0,07029	13	16,30150036	2	1056,50237	2,54	84,34
538	TPTGIKVVm	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	0,0782	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	APVKPGPAL	1	1	Q9UBP4		3,294E7	0,006	0,07485	47	0,002359449	2	849,52098	1,96	56,89
543	GVMDRGYSY	5	1	P28074		2,079E5	0,006	0,08226	46	0,005115166	2	1047,45635	-0,09	76,08
544	ALSDLALHF	1	1	P50991		5,216E6	0,006	0,07914	43	0,013002105	2	986,53246	1,88	132,60
545	SIFKQPVTK	1	2	Q9UBB5;O95983		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	Q6DKI1		2,771E5	0,006	0,07597	40	0,011934721	2	1024,61882	-0,20	77,68
547	IFDGNVAHI	1	1	P46939		1,545E7	0,006	0,07331	39	0,035940534	2	985,51262	2,46	97,02
548	KPYQGSAGF	1	1	P22670		5,193E6	0,006	0,08349	39	0,041281812	2	954,47081	2,95	51,86
549	KPAGPPGILAL	6	1	P35579		2,315E8	0,006	0,07752	38	0,010443302	2	1033,63970	-0,79	107,70
550	LPQDVILKF	1	1	Q96GQ7		1,352E7	0,006	0,07944	37	0,037962682	2	1072,64287	2,53	126,97
551	IVAKHTSAL	1	2	Q9Y490;Q9Y4G6		2,335E7	0,006	0,07693	36	0,034146846	2	939,56352	1,38	32,23
552	LPSPFLRAL	1	1	O95456		2,905E6	0,006	0,07751	36	0,012340137	2	1013,61595	1,65	121,94
553	SPEETRAAL	1	1	P78549		4,989E6	0,006	0,07887	35	0,142698022	2	973,49498	0,03	49,47
554	KLHDETLTY	1	2	Q9NZI7;Q12800		8,592E6	0,006	0,07475	35	0,154816792	2	1119,57195	3,44	57,70
555	NVYEVVNPK	1	1	Q86YQ8		4,281E6	0,006	0,08337	33	0,261764263	2	1061,56218	-0,41	68,59
556	ATYHGSFSTK	4	1	P12111		2,910E5	0,006	0,08344	33	0,167805873	2	1098,52068	-0,72	34,53
557	GLEAIQRTPK	1	1	P61769		3,315E6	0,006	0,08177	33	0,1095344	2	1112,64409	1,62	50,72
558	AVAIKAmAK	2	2	P63241;Q6IS14	M7	5,703E7	0,006	0,08008	32	0,100937808	2	918,54442	0,28	40,70
559	FPPREIVTY	3	1	Q13409		5,285E6	0,006	0,07443	32	0,203678393	2	1121,60198	2,64	97,70
560	IVDGNAKMTL	1	1	O43707		2,644E6	0,006	0,0818	31	0,328041542	2	1061,56938	3,17	77,14
561	HINGRVLYY	8	1	Q13751		3,698E7	0,006	0,07623	31	0,315587855	2	1134,60515	-0,28	63,64
562	YPSETTVKY	2	1	P11047		7,272E7	0,006	0,07876	31	0,279107855	2	1087,53179	1,06	66,01
563	RTFGQGTKL	1	1	P01593		6,951E6	0,006	0,08185	29	0,28761357	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	DIYKRFLF	1	1	Q5H8A3		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	RVWDVESGSLK	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	NPLQKDPQY	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	SLAERSSLLQK	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	HPNSAIILHY	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	KTYEVSLREK	1	1	Q16531		1,976E6	0,006	0,08118	21	2,380385405	2	1252,68889	-0,58	42,70
592	HPDEKSIITY	16	1	Q01082		2,212E8	0,006	0,07705	20	4,995794255	2	1202,60686	1,37	69,75
593	VPVAEIKIY	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	SPQPDGKVVY	1	1	Q9BSV6		4,201E7	0,006	0,07572	17	9,230998564	2	1089,55998	2,24	59,92
596	KPGSQFLYSTF	1	1	P83111		1,209E7	0,006	0,08082	16	10,66562013	2	1274,64568	3,20	107,78
597	APYRPPDISL	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		2,495E6	0,008	0,0877	38	0,004348924	2	1039,68657	-0,84	137,77
601	YARDETEFY	1	1	P18077		3,544E7	0,008	0,0853	37	0,036542247	2	1193,51531	3,63	76,33
602	QTYSTEPNNLK	1	1	P46779		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		6,324E7	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		3,594E7	0,008	0,08815	34	0,02925105	2	939,58696	-0,47	107,82
607	SPLKLLTSm	1	1	P51654	M9	3,147E6	0,008	0,08856	34	0,112555322	2	1005,56828	3,32	94,95
608	APAAWLRSAA	1	1	P24347		3,432E6	0,008	0,08837	34	0,095729837	2	1013,55486	2,08	82,01
609	KPAFFAEKL	2	1	P04083		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		1,743E7	0,008	0,08953	33	0,093788721	2	968,52153	1,55	82,04
612	VLFAGQHIAK	1	1	P21333		6,035E6	0,008	0,08654	33	0,04322424	2	1083,63518	3,86	63,08
613	YLNEKAVSY	1	1	Q13492		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		3,862E7	0,008	0,0869	31	0,309752433	2	1036,54924	2,89	90,10
616	HVAAPYIAK	1	1	Q9H2P0		1,032E7	0,008	0,08459	31	0,188976845	2	969,55205	0,40	49,33
617	GLYKAPLSK	1	1	Q8NBM4		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	2	1172,61638	2,63	102,06
619	RVYGGLTTK	3	1	Q8WUM4		1,234E8	0,008	0,08701	29	0,317584504	2	994,56761	-0,43	37,49
620	APIRPDIVNF	1	1	P36578		1,997E7	0,008	0,0857	28	0,391280546	2	1141,63701	0,46	110,33
621	RPITVSYAF	1	1	Q15427		2,512E7	0,008	0,08513	28	0,462723653	2	1053,57500	2,10	98,54
622	VVLGQFLVLK	1	1	O75531		5,837E6	0,008	0,08775	27	0,033167785	2	1115,72222	3,10	135,21
623	LPWVGKELY	1	1	Q09161		9,172E6	0,008	0,08655	27	0,68542921	2	1104,61235	3,17	117,73
624	LPVLSTDKF	1	1	Q7L5N1		4,078E6	0,008	0,08806	26	0,590171134	2	1019,57878	1,53	104,56
625	RAmAKRTKD	1	1	Q68D10	M3	2,960E6	0,008	0,08548	26	0,696161014	2	1092,59758	3,00	35,79
626	FVELGTQPATQ	2	1	P02652		4,743E7	0,008	0,08915	24	1,992076261	2	1190,60759	1,98	97,46
627	HPAIALREY	1	1	P10155		1,638E7	0,008	0,08456	24	1,069605999	2	1069,57915	0,19	64,96
628	GLYYIHRNK	1	1	P50750		3,677E4	0,008	0,08684	24	1,465505753	2	1163,63335	1,14	37,55
629	NWRPRFKY	3	1	Q9UP95		1,403E5	0,008	0,08653	23	1,496052894	2	1166,62346	1,41	134,78
630	YWGEIISQQY	1	1	P14735		4,012E7	0,008	0,08557	22	2,374462626	2	1286,61052	4,13	134,74
631	RQIPYTMmK	1	1	Q00325	M8	1,011E7	0,008	0,08531	21	3,338428799	2	1183,59941	2,66	51,41
632	MPLPGTKALPSm	1	1	Q9UMZ2	M12	0,000E0	0,008	0,08958	20	4,120099194	2	1258,65569	1,76	90,77
633	SFmDPASALY	1	1	P28070	M3	4,625E6	0,008	0,08808	20	1,804149429	2	1117,49040	2,97	120,98
634	VPEEGGATHVY	1	1	Q9NQ31		6,594E7	0,008	0,08878	13	15,90668631	2	1158,54766	4,34	58,61
635	AGQNDPLK	1	1	P27816		1,226E7	0,009	0,1009	55	0,001007809	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	SVAQLLLSK	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	VVQTVKASY	1	1	P35221		4,696E6	0,009	0,1083	45	0,007183141	2	994,56041	3,63	53,42
639	ATVAVPLVGK	1	1	Q9BUN8		1,985E5	0,009	0,1039	44	0,003464094	2	954,59776	-0,56	91,38
640	HPHQNLIATY	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	SVSNVVITK	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	YADPVNAHY	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	1019,59020	1,72	68,80
648	ASINRIYGF	1	3	P36873;P62140;P62136		3,751E7	0,009	0,104	39	0,025843477	2	1040,55400	1,55	97,95
649	SIIGRLLEV	1	1	P62136		2,540E7	0,009	0,1087	38	0,025514966	2	999,62193	2,17	132,72
650	KPFDAFTDL	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	TVRPPVAVK	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	0,09064	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	KVGEFSGANK	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	KPIEQLLGF	5	1	Q96DE5		1,794E7	0,009	0,09243	35	0,114912951	2	1044,60820	-0,63	129,60
660	TPLDRVTEF	1	1	Q9UFW8		5,878E6	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	AAMLDTVVFK	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;O95678;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	APYRTQSSASL	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	RTIAPIIGR	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	AVLSWKLAK	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	IIFDRPLLY	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	EPAQRKIIm	6	1	Q8TB72	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	IPIALSGRDIL	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	KLAELEGALQK	1	5	Q14533;O43790;A6NCN2;P78385;P78386		4,794E6	0,009	0,09966	28	0,366763295	2	1199,70244	2,47	71,68
686	KILGPQGNTIK	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	APLKSKmIY	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	Q9UI14		4,936E6	0,009	0,1078	27	0,64166519	2	1078,57134	3,05	105,22
696	SVLEPPLFLK	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	VLSPADKTNVKA	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	KLAEYVITK	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	KVYTHNLYY	1	1	Q96EK5		1,106E7	0,009	0,09884	22	2,858548245	2	1200,60881	3,36	60,31
709	LPIPSKLLEF	1	1	Q9Y6I7		1,799E6	0,009	0,09058	21	0,947488464	2	1156,70207	3,80	142,27
710	TPVLEPTKVTF	1	1	Q9ULD2		1,777E6	0,009	0,09708	21	2,662191079	2	1231,69524	1,56	107,44
711	YPSRAVITTm	1	1	Q06136	M10	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	Q9BXW6;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	1,590333902	2	1074,46721	3,02	63,21
715	VLREIAEEY	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	KPFEQVKGITL	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	Q7KZ85		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	LFYDVKLQY	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	RPPPIGAEV	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	APSKTSLIm	1	1	Q9H334	M9	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	GLNNKTIGY	1	1	Q8TE76		4,065E7	0,011	0,1097	38	0,078534264	2	979,52342	2,73	62,10
734	GQYGNPLNK	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	FPLQPGKVATF	1	1	Q96Q05		5,029E6	0,011	0,1119	34	0,125940738	2	1204,67681	3,55	112,79
739	mAVYLSAGVIS	1	1	Q9H300	M1	1,288E5	0,011	0,1116	34	0,167752023	2	1126,57744	-3,45	91,94
740	GSYNKVFLAK	7	1	P48556		1,565E8	0,011	0,111	30	0,27658857	2	1126,62541	-0,13	56,30
741	IVDGNHRLTL	1	3	Q9H254;Q01082;O15020		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	1	3	O00478;O00481;P78410		2,044E6	0,011	0,1094	21	2,186118611	2	1043,62444	3,46	48,56
746	GNYEKVFEY	3	1	Q92624		1,489E7	0,011	0,1101	20	3,379800607	2	1148,52800	1,84	92,32
747	DPADPHKVY	1	1	Q92985		3,910E6	0,011	0,1099	17	6,984602561	2	1041,50066	0,61	46,46
748	RTYYSPVYR	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	O00159		2,271E5	0,012	0,1187	46	0,009365775	2	1013,54082	-0,66	85,36
751	RAAQSLLNK	1	2	Q9UMR2;Q9NUU7		9,742E6	0,012	0,1144	41	0,017972408	2	1000,59422	4,37	36,04
752	RTNKEIIAIK	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	0,110720383	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	1	4	P52895;Q04828;P42330;P17516		9,379E6	0,012	0,1176	33	0,072025762	2	971,60155	1,91	47,48
758	ATNASVFKY	1	3	Q7Z6B7;O75044;P0DJJ0		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	IPTRVVTNY	7	1	P21980		7,505E7	0,012	0,116	28	0,488184358	2	1062,59368	-0,54	72,69
765	VPVGEKTTY	1	1	P08582		3,267E6	0,012	0,1143	28	0,632111518	2	993,52464	-0,53	50,32
766	RPAQLHIGF	1	1	P22314		6,971E7	0,012	0,1139	26	0,506321695	2	1038,58745	2,96	79,06
767	NPVENIIRF	1	1	Q8WUJ0		2,502E6	0,012	0,114	25	0,965009429	2	1101,60857	3,08	118,24
768	SVYVYKVLK	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	mTHNLLLNY	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	RIFQEPTEPK	1	1	P31350		2,012E6	0,012	0,1186	15	12,66514847	2	1244,66643	2,42	58,41
774	VIGTVTSGK	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	SPQKVTLYL	1	1	P05107		3,161E5	0,013	0,1254	43	0,012811767	2	1048,60393	0,17	92,74
778	TPLDEKSLAL	1	2	Q15014;Q9UBU8		6,864E6	0,013	0,1214	42	0,016219349	2	1086,60710	2,70	101,09
779	IAINLLPLL	1	1	Q9BXW9		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	0,063744968	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	QLVSNVLIF	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	RPLTSPESL	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	RIGKVGNQK	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	QLSLIPKFL	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	AVFPKPFVEK	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	KFDDGAVFL	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;Q9TNN7;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	NLLPYSLRY	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	YPVKYTQTF	1	1	Q96FX8		4,793E6	0,013	0,1243	23	2,010506189	2	1146,58660	3,13	83,52
812	PSRILLWK	4	1	Q9BRK3		7,920E7	0,013	0,1217	23	0,486716253	2	1012,62950	-0,75	104,37
813	FPLLIMGITY	1	1	P29371		3,486E5	0,013	0,1206	23	1,366597757	2	1167,65203	3,21	120,25
814	LLHDRSFSY	1	1	Q9BSJ2		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	APWQERSTm	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	QTYVGITEK	1	1	O75643		1,735E8	0,013	0,1222	12	16,59645498	2	1038,54973	2,98	60,83
825	TWNPLKLHY	1	1	Q9H4A6		1,717E7	0,013	0,1225	12	20,42079629	2	1171,62895	2,62	102,83
826	IGNGVVIHL	1	2	Q8N142;P30520		5,506E6	0,014	0,1294	49	0,001467941	2	921,55351	2,00	100,33
827	RLLSPPLRPR	1	1	O75882		1,311E8	0,014	0,1301	40	0,002028535	3	1204,76749	3,10	59,89
828	SIRQAGGIGK	1	5	Q9NQA3;C4AMC7;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	VMAPRTLIL	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]
832	SPFSYKNVL	1	1	P05556		1,269E7	0,014	0,1282	32	0,208962298	2	1054,55962	2,67	99,86
833	HPIHQGITEL	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	KVETFSGVYK	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	ADKQLSFEEF	1	1	P06702		2,183E6	0,014	0,1287	26	0,817224265	2	1213,57781	3,47	106,62
842	LVSESSDVLPK	1	1	P05787		4,021E6	0,014	0,1301	25	1,305227689	2	1173,63811	1,63	76,43
843	ALSSYVVKK	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	RLEEKSRVK	1	1	P10586		3,692E6	0,014	0,1306	23	0,757321974	2	1144,68047	0,63	19,77
846	YVIQKFFEF	1	2	Q8TB72;Q14671		3,577E6	0,014	0,1288	22	2,820315215	2	1220,63994	4,00	142,07
847	NPYPGDVTKF	1	1	Q5T6F2		2,154E6	0,014	0,1278	22	3,01512749	2	1137,56243	4,29	88,34
848	KPINVRVTTm	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	KmLRDTLYY	1	1	P42356	M2	2,257E6	0,014	0,129	16	12,4910163	2	1218,61858	-0,15	68,59
852	YPFRVGELEY	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	Q9BQ83		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	PKNPLFPQNL	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	NPHEVQPAY	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	KAIEKNVLF	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	Q9Y5X3		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	Q3B7T1		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	LPFPDETHERY	1	1	O43292		4,749E7	0,015	0,1328	20	3,38468903	3	1403,66150	1,75	83,56
876	SSIQHSSVVPSI	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	M1	9,976E6	0,015	0,1326	20	4,773040531	2	1115,61077	-1,98	98,90
879	YVYFTNELK	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	O95373;O15397		2,461E7	0,015	0,1348	16	1,182087709	2	1014,65807	2,22	94,62
882	LPHLADLVSY	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	A6NCS6		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	Q9BVS4		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	SSVPGVRLL	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	LPGTAPKLLIY	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	Q68CZ2		2,240E5	0,016	0,1401	27	0,738546346	2	1057,52043	0,32	95,07
900	LPFGPFKEL	1	1	Q7Z449		4,230E6	0,016	0,1419	25	0,627440466	2	1047,58928	1,79	129,13
901	APLDLSKIKL	1	1	O75369		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	SPQQVDFRSVL	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		6,114E7	0,016	0,1412	20	2,738803344	2	1010,55864	2,86	128,71
907	FPVVRDFLY	1	1	P12111		4,067E6	0,016	0,1401	18	4,184800631	2	1155,62432	3,95	133,59
908	GLNKESFRY	1	1	Q5VWQ0		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	KLREPNFTLK	1	1	Q92545		6,949E6	0,016	0,1387	17	3,356240169	2	1245,73686	4,35	62,06
911	VYNHFLLYY	1	1	Q7KZ85		9,711E4	0,016	0,1412	15	14,65000341	2	1231,61577	0,93	126,98
912	RPWLEGRHTL	1	1	Q9UI10		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	RPADSMLNVL	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	0,009164209	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	AVASFPKKQE	1	1	P14406		5,458E4	0,017	0,1462	33	0,186928138	2	1104,60442	-0,38	38,44
919	MPRVQTQQY	1	1	O94979		4,295E6	0,017	0,1479	33	0,233904301	2	1150,57280	4,70	60,37
920	RVKLPSGSKK	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]	ΔM [ppm]	RT [min]
921	TmVGKTFTY	1	1	Q16850	M2	7,247E6	0,017	0,1443	28	0,428300524	2	1063,51421	1,23	69,81
922	APLHSVGYTTL	1	1	Q96BD6		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	GIKNFFTDVY	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	0,353524749	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	SINDKIIEL	1	2	Q12772;P36956		1,898E5	0,017	0,147	20	2,914039269	2	1044,59307	-0,51	110,69
930	DVYNHFLLY	3	1	Q7KZ85		3,412E5	0,017	0,1427	20	3,343526231	2	1183,57817	-0,07	145,92
931	KPHSGFHVAF	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	GQYSGSPQLLK	1	1	Q96N67		4,833E6	0,017	0,1448	18	7,816862351	2	1177,62334	1,81	69,53
935	HLFDHVVNR	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	Q6TFL4		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	KLPSSEPLSR	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	VLNLKEPLY	4	1	O00468		2,394E5	0,018	0,1534	26	0,651837602	2	1088,63469	-0,34	117,04
955	AVYGmLNLTPK	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	AVQRTLLEK	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	KLISTLIYK	1	1	O14980		5,833E6	0,018	0,1535	20	0,257484187	2	1078,68877	1,55	81,51
965	SFGELALIY	1	2	P10644;P31321		3,666E7	0,018	0,1528	18	4,519589646	2	1012,53777	2,72	157,66
966	YIYDGELVSK	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	Q7Z6Z7		2,496E6	0,018	0,1554	15	3,816310707	2	1275,75884	4,38	52,35
970	NPPEFLHETY	1	1	P55287		4,531E6	0,018	0,154	12	20,51009545	2	1246,57842	3,61	95,90
971	RCGKTDDLLY	1	1	Q9ULI1		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	LPVHVFEAL	1	1	Q9H4Z3		4,005E6	0,019	0,1586	35	0,054257982	2	1024,58721	4,45	120,94
974	KIIAFVLEGK	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	NAIKESYDY	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	FPIHVQTSL	1	1	Q9NVM4		8,734E6	0,019	0,1561	24	0,790236295	2	1041,57414	1,30	104,58
979	SPAGSIVHEL	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	RPTGEIEQY	1	1	P04114		8,065E6	0,019	0,1569	22	3,169581179	2	1092,53557	3,22	54,73
982	RPKLPEDPLL	1	1	P49327		4,310E6	0,019	0,1567	19	1,916268394	2	1177,69927	4,47	88,18
983	AFRQPSLFY	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	Q9BXP5		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	RAAESELAFP	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	GVAPFTIAR	6	1	P12111		9,061E5	0,021	0,1646	54	0,001079898	2	931,53563	-0,43	90,21
991	APAQRAQSL	1	1	Q63ZY3		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	Mod. (ox)	Area	q-Value	PEP	IonScore	Exp. Value	Ch.	MH+ [Da]	ΔM [ppm]	RT [min]
993	GVSGIFMKY	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	0,079905591	2	1090,62749	1,75	30,78
995	SVAKTILK	1	2	Q9H8S9;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	NVVKLLGEQY	1	1	Q92785		4,420E6	0,021	0,1637	30	0,291971516	2	1162,65044	3,22	100,52
1000	ALHNHYTQK	1	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	FPNRVVFQEF	2	1	P35579		1,384E7	0,021	0,1663	26	0,990712122	2	1282,66240	3,48	118,97
1003	RPPVQIEEL	1	1	Q8IUI8		1,336E6	0,021	0,1647	25	0,682269132	2	1080,60564	0,74	90,00
1004	HAIRLLLEY	1	3	P09488;Q03013;P46439		1,059E5	0,021	0,167	25	0,647019666	2	1127,65666	-0,47	103,51
1005	EPFHLIVSY	1	1	Q7L513		2,024E5	0,021	0,1671	25	1,498411204	2	1104,57219	-0,24	131,41
1006	VPASFRLQM	1	1	Q9BTE3		2,818E6	0,021	0,1611	24	1,42633921	2	1048,56255	1,60	101,78
1007	KVSDYILQH	1	1	O75129		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	KVVEGSFVYK	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	0,021	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	RPPFPGQQI	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	Q6PCB5		5,023E6	0,022	0,1677	31	0,259576108	2	1213,59612	0,05	68,15
1014	IPLRHGGLSL	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	RPGWLTVSL	3	1	Q15392		2,737E7	0,023	0,17	38	0,031818305	2	1028,59111	2,26	121,83
1018	DASKVVTVF	3	1	O75083		9,694E5	0,023	0,1735	37	0,062531523	2	965,53008	-0,20	107,31
1019	GPPRLLLLPL	3	1	P09564		2,531E7	0,023	0,1721	35	0,00254143	2	1088,72380	4,33	146,38
1020	ATAPVSAAQLK	1	1	Q9NQ94		1,880E6	0,023	0,1715	32	0,163746982	2	1056,60820	3,18	60,68
1021	SVNGKVLSK	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	RLFTDVLLH	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	SPFKADIEm	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	RPPAQGTVTF	1	1	Q68DI1		6,391E6	0,023	0,1726	23	1,7013817	2	1073,57585	1,85	66,79
1033	KVGRDVVQK	1	1	P35749		1,221E7	0,023	0,174	23	1,009522834	2	1028,62126	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	RLYSVTVTTK	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	44,08
1041	SPYLPRGDPVL	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	MLMLPLLLL	1	1	A6NNS2		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	0,10146646	2	1102,65557	3,75	26,75
1045	IIYKGGTSR	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	CDPVIERRPR	1	1	Q6P5Z2		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	HLKEDLNLR	1	1	O76003		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	RPAEVGGmQL	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	KTWTVVDAKTLK	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	Q969X6		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;Q29940;Q29836;P30498;Q31610;Q29718;P04222;Q95604		2,171E7	0,025	0,18	21	1,654935802	2	1248,54766	0,81	66,17
1066	KLYEEGSNK	1	1	P25788		2,902E6	0,025	0,1802	19	4,984903277	2	1067,54167	4,56	27,12
1067	KTLDEILQEK	1	2	Q9UQ88;P21127		1,761E6	0,025	0,1797	18	4,691148849	2	1216,68328	4,01	83,27
1068	IPTDVLKIVY	1	1	Q6P179		1,561E6	0,026	0,182	29	0,115877627	2	1160,69646	3,34	132,66
1069	AmHGVFLYH	1	1	Q99707	M2	3,210E6	0,026	0,1816	27	0,497858594	2	1090,51396	0,06	65,96
1070	KQLTSHPWK	1	1	Q6ZNB7		2,198E6	0,026	0,1824	21	1,934068266	2	1124,62065	-0,43	34,47
1071	ATAVHAYRY	1	1	Q5T1M5		9,223E5	0,026	0,1828	20	3,364793988	2	1051,53374	1,68	41,85
1072	KTYGVSFFLVK	1	1	Q9Y490		2,445E6	0,026	0,1814	15	9,574639308	2	1288,73442	3,41	107,71
1073	APPRTQFSGL	1	1	O00754		1,293E7	0,027	0,183	19	3,731828805	2	1073,57524	1,28	75,56
1074	LmLPEKLRPLY	1	1	O95563	M2	8,688E6	0,027	0,1833	15	6,428149927	3	1388,79920	1,52	106,42
1075	RPQSGANGL	1	1	Q8WVX3		1,075E7	0,028	0,1854	59	0,000244416	2	899,47118	1,98	31,19
1076	APAPAPARSL	1	1	Q6QNY0		5,827E6	0,028	0,1852	43	0,009076864	2	950,54582	4,18	53,52
1077	HNADQPLRV	1	2	Q99613;B5ME19		1,449E7	0,028	0,1846	40	0,03881997	2	1049,55083	2,02	44,29
1078	VPPPPHRPL	1	1	Q9Y520		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	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]
				;P01889;P30460;P30461;P30462;P30464;P30466;P03989;P18463;Q95365;P30475;Q04826;P30479;P30480;P30483;P30484;P30485;P30486;P30487;P30488;P30492;P30493;P30495;P18465;Q29940;Q29836;Q31612;Q31610;Q29718;P01893;P13747;P30511										
1080	MPNVKVAVF	2	1	Q13838		1,229E7	0,028	0,1849	30	0,257658691	2	1004,56236	2,54	106,33
1081	AFSAEPLLIY	2	1	Q8IYK4		1,885E6	0,028	0,1867	28	0,455625587	2	1123,60344	0,01	155,87
1082	RKLAHmRR	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	KVLQIGSAK	1	1	Q9UGM6		4,165E6	0,028	0,1839	26	0,336289824	2	943,59349	-0,05	41,63
1086	QDLLSQIAQ	1	1	Q5EBL4		2,952E7	0,028	0,1842	25	1,344055539	2	1015,54259	0,69	47,65
1087	TVEEGQRLK	1	3	Q8N4C8;Q9UKE5;O95819		5,830E6	0,028	0,1864	23	2,044274319	2	1059,57854	-0,77	29,15
1088	SPWKPPTYL	1	1	Q8IY47		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;O75177		2,522E7	0,028	0,1838	22	2,711023014	2	968,49108	4,18	88,06
1091	AIYGTRKFK	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	3,278463901	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	Q9BU70		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	SPFCRARLSL	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	Q9BYK8		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	YPNGVVVHY	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	Q8TEX9		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	AVHLKTLLK	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	RPPGPASQSL	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;A5A3E0		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	RLTTPVFGK	1	1	Q16850		1,995E7	0,033	0,1939	22	0,962174998	2	1018,60338	-1,04	64,84
1125	FLEKAQTYY	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	ALYKLGFFK	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	M7	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	GPLDKWRAL	2	1	P27635		7,986E7	0,034	0,1997	29	0,245426335	2	1055,59953	-0,16	96,24
1134	RIHGVGFKK	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	Q9BYK8		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	QVVLmLVKEC	1	1	Q8WZ74	M5	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	M6	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	GLLTKPIVK	1	2	Q86V97;Q8WVZ9		9,430E6	0,036	0,2033	41	0,00180298	2	968,65416	3,95	63,69
1145	RIAKNLVEK	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	Q9BQY9		3,748E6	0,036	0,2013	32	0,234197053	2	1044,55181	1,06	78,94
1149	RQAVPLFSK	1	1	Q9BZZ5		9,553E6	0,036	0,204	30	0,173151611	2	1045,62041	4,85	63,58
1150	GTPLLVIANK	1	1	P56559		5,968E6	0,036	0,2077	28	0,114284118	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;Q9BZS1		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	O94952		1,223E6	0,036	0,2081	20	0,933192579	2	1090,66631	3,99	63,77
1159	TIADLELHY	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	Q9BRR0		1,169E6	0,036	0,205	15	1,362217142	2	1081,65349	-1,49	39,43
1163	VGIYPNAQIY	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	YYDNADKL	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	LASRPLLL	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	ASVDKVLEL	1	1	O14979		3,984E5	0,037	0,2102	35	0,099225335	2	973,55614	-0,36	105,41
1169	TPYKGGNLY	1	1	Q13439		1,406E7	0,037	0,2102	34	0,129828833	2	1012,51268	2,81	60,97
1170	GVLGTVVHGK	1	1	Q9Y6C9		1,319E7	0,037	0,2145	29	0,155253198	2	966,57665	3,63	56,22
1171	ALPEKVVNK	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	SPFYPGKTTY	1	1	P49790		1,315E7	0,037	0,2113	26	1,256527109	2	1160,56401	1,50	79,77
1174	VLGQFLVLK	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	SIFEPAKGGEK	1	1	P55265		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	GYMEYYLY	1	1	Q9NX31		2,170E6	0,037	0,2135	17	2,287728744	2	1101,46355	3,44	76,05
1185	LNLPYFLRY	1	1	Q5T4S7		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	SLLTSSKGQLQK	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	mPVPGHDVEAY	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	0,030545666	2	1082,67388	1,60	82,37
1193	LYDPVISKL	1	1	Q96EZ8		6,652E4	0,038	0,2194	31	0,173978149	2	1047,60808	-0,41	111,11
1194	MVPRLTAVL	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	SPIDPSEKY	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	RPFKGYEGSL	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	1136,53935	-1,03	64,58
1203	ATIPNARQF	1	1	P42285		8,182E6	0,038	0,2189	20	2,695968931	2	1017,55156	3,84	72,23
1204	KTVPVEAVTSK	1	1	Q14247		3,223E6	0,038	0,2155	18	3,715248177	2	1158,67485	1,67	44,27
1205	SQYPNQPTRF	1	1	P24468		8,895E5	0,038	0,2174	14	14,49980706	2	1237,59636	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	AVDDRGLYK	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	GVDVTGPHLY	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	HPIQTQAQY	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	Q9H1I8		1,366E7	0,041	0,2273	44	0,009630444	2	984,58385	0,15	31,70
1216	SSSPRNLGF	1	1	Q9UBF8		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	2	1160,58330	2,20	44,65
1221	MRYVASYLL	1	1	P05387		1,378E5	0,041	0,2255	25	1,431442971	2	1115,59184	0,03	114,02
1222	RALDLLAGFY	2	1	Q96RY7		2,499E5	0,041	0,2284	24	1,276485302	2	1138,62529	-0,25	120,02
1223	RPQSAISSF	1	1	Q5VT06		1,523E6	0,041	0,2274	20	4,620912924	2	992,51506	-0,96	64,57
1224	KLHEETLTY	1	1	Q9NZI6		9,460E6	0,041	0,2245	19	6,775183671	2	1133,58440	0,58	57,25
1225	RSSTYEVRL	1	1	P05161		1,996E7	0,041	0,2262	18	5,51522276	2	1110,59343	2,88	58,92
1226	ISKSYIILQ	1	6	P0CH99;A8MUZ8;P0CI00;Q6ZN79;A8MWA4;A8MVS1		4,460E6	0,041	0,2284	18	1,845082288	2	1064,63750	2,30	117,48
1227	DPNPNFEKF	1	1	Q9H8H3		4,648E6	0,041	0,2247	17	7,185129009	2	1107,51433	3,37	91,70
1228	IPVFLEKL	1	1	Q14669		2,962E6	0,042	0,2298	23	0,600171712	2	958,59972	2,59	125,71
1229	GVNVRIAVSK	1	1	Q8IV08		2,584E6	0,042	0,2293	20	1,298726592	2	1042,63835	1,48	57,32
1230	RYPDLELKY	1	1	O75290		3,385E6	0,042	0,2288	13	21,00328502	2	1196,63237	1,12	92,78
1231	MLLRLNALL	1	1	O60287		4,939E5	0,043	0,2334	38	0,020713174	2	1056,65605	-3,60	122,26
1232	SSNSYAIKK	1	1	P46782		9,632E6	0,043	0,2318	33	0,193040565	2	997,53594	4,64	27,38
1233	SLNKQIAQK	1	1	Q567U6		3,553E6	0,043	0,2328	32	0,201887217	2	1029,60588	0,70	28,53
1234	VAFKKTFSY	1	1	Q99832		5,779E6	0,043	0,232	31	0,336496783	2	1090,59624	2,79	68,92
1235	ALKNTSDFVYL	1	1	Q12959		0,000E0	0,043	0,2324	24	1,718653877	2	1270,66692	-0,71	139,26
1236	GVSSIFIYH	1	1	P33076		0,000E0	0,043	0,233	23	1,740128025	2	1022,53343	2,79	109,27
1237	MPSHPDRAY	1	1	O75888		1,462E6	0,043	0,2317	23	1,058935648	2	1073,48479	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	RPDDRSQGAII	1	1	Q04637		2,000E7	0,043	0,2327	23	1,623094856	2	1227,64751	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	GTQPGPLLKK	1	1	Q86UX2		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	KQYDSFTYR	1	1	Q9Y3Q3		3,102E6	0,043	0,231	20	3,796522524	2	1207,57512	0,74	57,17
1243	GLYEFPLNK	1	1	Q9UJA5		3,613E6	0,043	0,2309	20	3,880530713	2	1080,57536	2,69	105,89
1244	RPKPPSATSI	1	1	Q9UMS4		1,378E7	0,043	0,2334	19	2,363727962	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	FPWEVPKKLKY	1	1	P31153		3,342E7	0,043	0,2321	18	3,072962843	3	1434,81781	2,35	96,38
1247	HPNPGSITHL	1	1	Q93074		2,626E6	0,043	0,233	15	12,73679009	2	1072,55425	0,74	58,06
1248	DPVEPHGEm	1	1	Q13263	M9	4,031E6	0,043	0,2317	13	6,95698174	2	1026,41997	0,22	42,46
1249	ALSAALYYL	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	KPFPFFEGL	1	1	Q9HB58		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	RPFEDQTSL	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	SPFSSRSPSL	1	1	P41970		3,997E6	0,044	0,2361	26	1,130593599	2	1064,53935	2,08	75,89
1261	mPADTNKAF	1	1	Q9P0I2	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	MPSPVSPKL	1	1	Q9UHB7		7,941E6	0,044	0,2368	23	1,209465302	2	955,52953	1,42	82,22
1264	mAHMASKE	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	QAEEKAHAF	1	1	Q15149		1,346E7	0,044	0,2355	18	4,904752235	2	1030,49541	0,12	30,67
1268	DAIRNLHHY	1	2	Q9BWF3;Q9BQ04		6,790E6	0,044	0,2387	18	6,411194746	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	0,235	16	6,112522533	2	1055,59050	1,95	127,63
1271	KPFKLSGLSF	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	O95644		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	VPQHLVLVL	1	1	P12111		2,238E7	0,045	0,2403	37	0,007955831	2	1017,64769	2,08	116,99
1275	VVDPVVREK	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	SLADFQIEK	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;Q8NHS0		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	TVIDSQTHY	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	ATFPLSVQK	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	KVCNPIITKL	1	1	P11142		6,505E6	0,047	0,2446	17	2,65967971	2	1128,68205	0,95	98,36
1294	KSFDEQNVPK	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	TAIREVYQY	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	VmQVADLQSI	1	1	P08047	M2	6,590E4	0,048	0,2491	26	1,088830535	2	1119,57170	0,18	105,26
1299	IILLILIL	1	1	Q5TF21;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	VPFPRLHFF	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	Q5VVJ2		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	Q9P2L0		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		7,262E6	0,049	0,2516	31	0,255664947	2	1112,60979	3,49	58,65
1311	KAGEVFIHK	1	1	Q15233		4,962E4	0,049	0,2527	29	0,316936833	2	1028,58867	-0,12	34,39
1312	RLYGDSAAK	1	1	Q9NWZ8		1,424E6	0,049	0,252	27	0,606553388	2	980,51482	-1,22	29,16
1313	KLGGVVSIK	1	1	Q9Y4A5		5,794E6	0,049	0,2538	25	0,204715747	2	900,59111	3,75	54,89
1314	ANFQKPKVVK	1	2	Q9UKX2;P13535		7,513E7	0,049	0,2539	24	0,348109235	2	1158,70317	3,25	63,15
1315	KSIDFPLTK	1	1	O75844		1,192E7	0,049	0,2527	23	1,012220318	2	1048,60637	2,48	75,51
1316	LPDTRSEAY	1	1	O60563		5,240E6	0,049	0,2535	20	4,304942334	2	1051,50969	3,98	59,89
1317	KPLPLKTAL	1	1	P32314		9,663E6	0,049	0,2516	20	0,205131978	2	980,65026	-0,08	67,32
1318	RTAEYFPTK	1	1	Q5T4B2		1,601E6	0,049	0,2525	17	6,802219022	2	1112,57402	0,45	50,05

Supplementary Table 18: Expression of source transcripts of vaccine peptides

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	
		SLFPNSPKWT			16
		PNSPKWTSK			17
ADFP-2	A*03:01	**SLLTSSKGQLQK**	0.632	53.34	
		SLLTSSKGQL			17
		TSSKGQLQK			18
ADFP-3	A*03:01	**TSALPIIQK**	0.473	298.04	15
		Core			
CCND1	DRB1*0101	**NPPSMVAAGSVVAAV**			16
		MVAAGSVVA	0.674	22.98	
IGFBP3		**HSKIIIIKKGHAKDSQ**			
	DRB1*0101	HSKIIIIKKGHAKDS			25
		SKIIIIKKGHAKDSQ			19
		IIIIKKGHA	0.512	109.05	
	DRB1*1101	IIIIKKGHA	0.788	7.65	
	DRB3*0202	IIIIKKGHA	0.392	345.67	
MMP7-(2)		**SQDDIKGIQKLYGKRS**			
		QDDIKGIQKLYGKRS			15
	DRB1*0101	IQKLYGKRS	0.514	107.32	
	DRB1*1101	IKGIQKLYG	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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