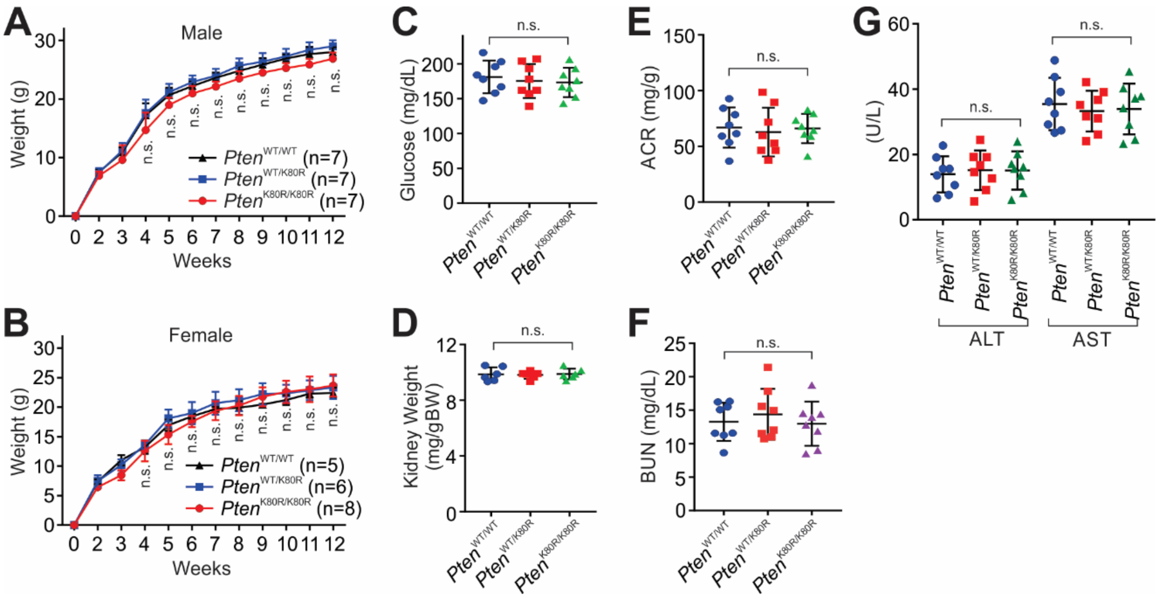
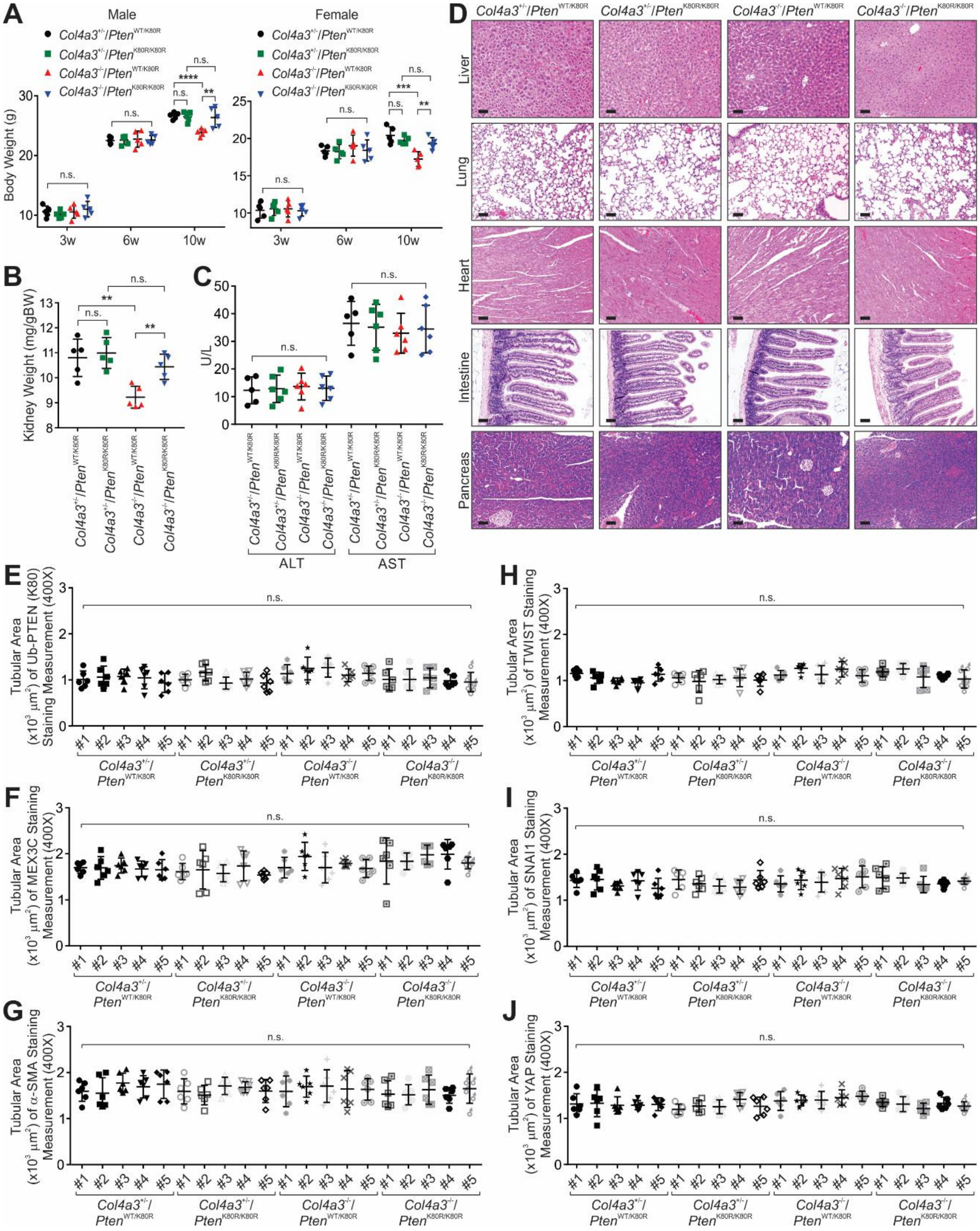
Supplemental Information

Supplemental Figures and Figure legends

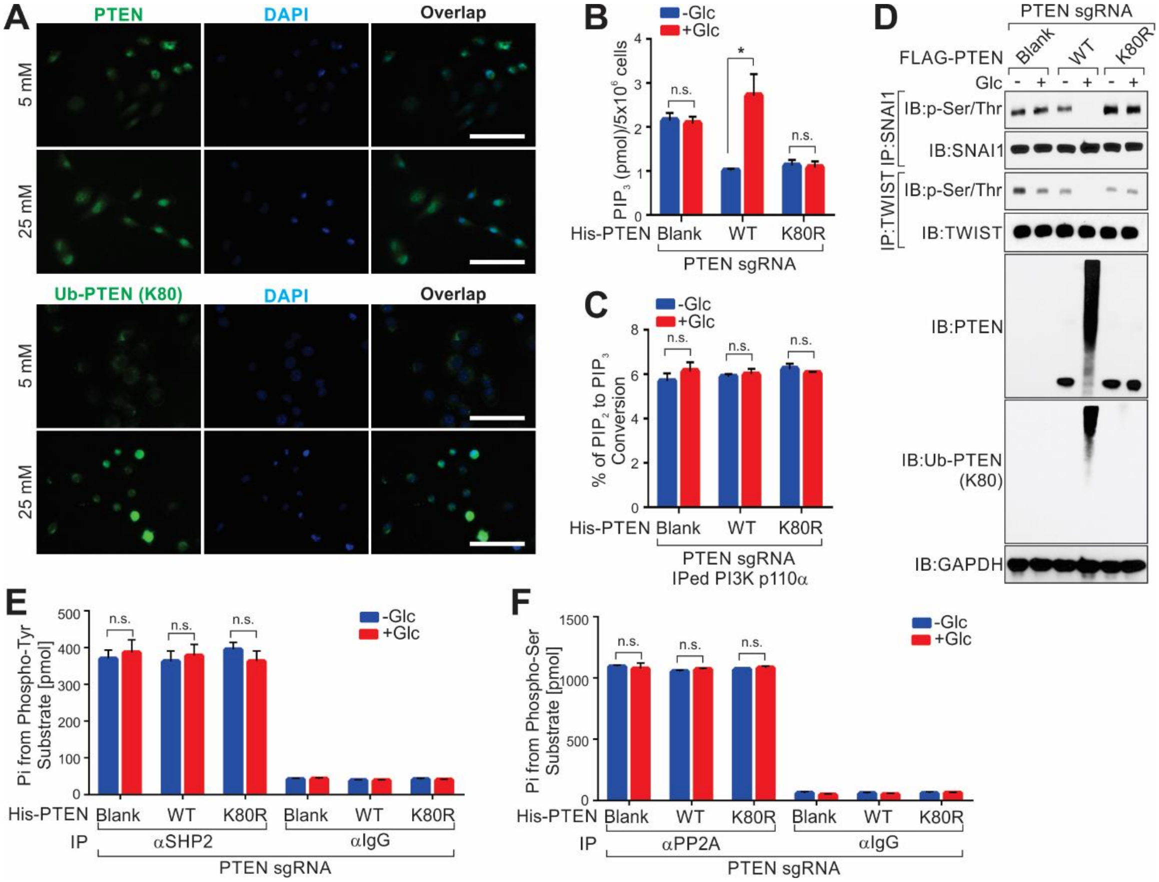


Supplemental Figure 1. Characterization of phenotype of *Pten*$^{K80R/K80R}$ animals.

(A) Body weight of male *Pten*$^{WT/WT}$, *Pten*$^{WT/K80R}$, *Pten*$^{K80R/K80R}$ animals (n=7, 7, 7). **(B)** Body weight of female *Pten*$^{WT/WT}$, *Pten*$^{WT/K80R}$, *Pten*$^{K80R/K80R}$ animals (n=5, 6, 8). **(C-G)** Blood glucose level (n=8, 8, 8) (C)**,** kidney weight was normalized by body weight (n=6, 6, 6) (D), urinary albumin to creatinine ratio (ACR) (n=8, 8, 8) (E), blood urea nitrogen (BUN) (n=8, 8, 8) (F) or serum alanine transaminase (ALT) and aspartate aminotransferase (AST) level (n=8, 8, 8) of male and female *Pten*$^{WT/WT}$, *Pten*$^{WT/K80R}$, *Pten*$^{K80R/K80R}$ animals. All error bars, SD, n.s., p>0.05, one-way ANOVA.

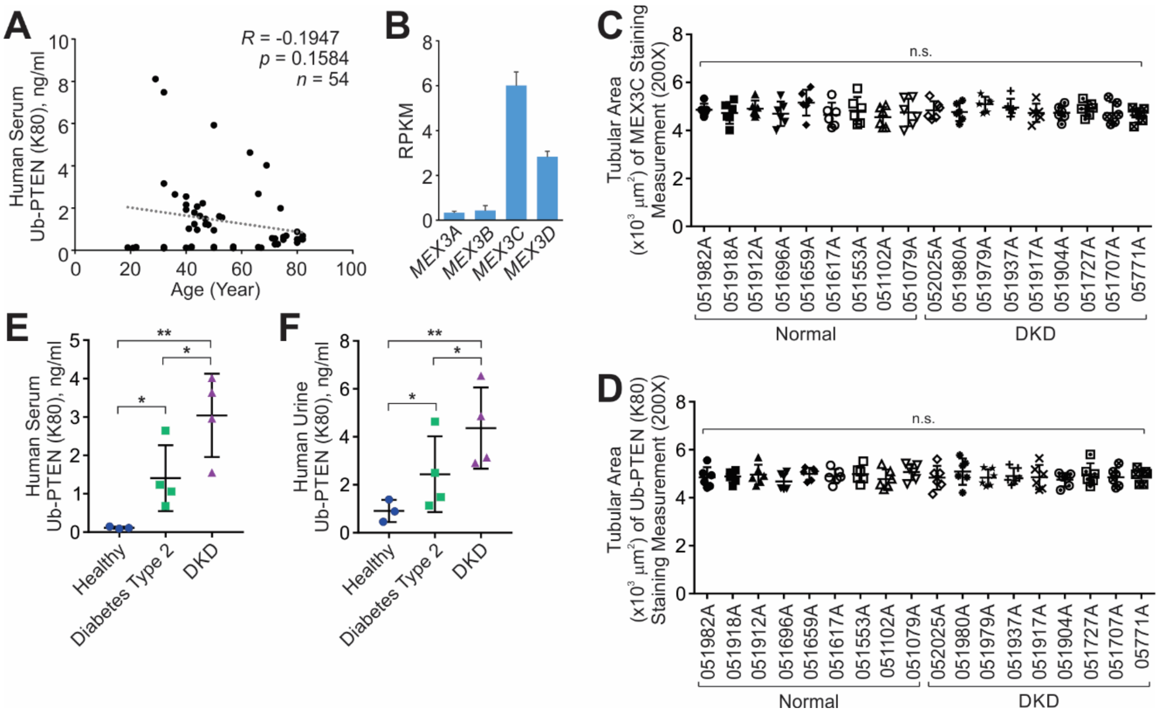


Supplemental Figure 2. Characterization of phenotype of *Col4a3/Pten K80R* animals. (A) Body weight of male (left) and female (right) *Col4a3/Pten K80R* animals (n=5, 5, 5, 5). **(B, C)** Normalized kidney weight (n=5, 5, 5, 5) (B) or serum ALT and AST levels (n=5, 5, 5, 5) of *Col4a3*$^{+/-}$/*Pten*$^{\mathrm{WT/K80R}}$, *Col4a3*$^{+/-}$/*Pten*$^{\mathrm{K80R/K80R}}$, *Col4a3*$^{-/-}$/*Pten*$^{\mathrm{WT/K80R}}$ and *Col4a3*$^{-/-}$/*Pten*$^{\mathrm{K80R/K80R}}$ animals. **(D)** H&E staining of liver, lung, heart, intestine and pancreas of *Col4a3*$^{+/-}$/*Pten*$^{\mathrm{WT/K80R}}$, *Col4a3*$^{+/-}$/*Pten*$^{\mathrm{K80R/K80R}}$, *Col4a3*$^{-/-}$/*Pten*$^{\mathrm{WT/K80R}}$ or *Col4a3*$^{-/-}$/*Pten*$^{\mathrm{K80R/K80R}}$ animals (male and female). Scale bar: 100 µm. **(E-J)** Tubule area of measurement of Ub-Pten (K80) (E), MEX3C (F), α-SMA (G), TWIST (H), SNAIl (I) and YAP (J) staining intensity per tubule of *Col4a3*$^{+/-}$/*Pten*$^{\mathrm{WT/K80R}}$, *Col4a3*$^{+/-}$/*Pten*$^{\mathrm{K80R/K80R}}$, *Col4a3*$^{-/-}$/*Pten*$^{\mathrm{WT/K80R}}$ or *Col4a3*$^{-/-}$/*Pten*$^{\mathrm{K80R/K80R}}$ kidneys. 6 independent area for each animal is shown. Error bars, SD, n=6 independent fields per animal per experimental condition. All error bars, SD, n.s., $p > 0.05$, *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$, and ****$p < 0.0001$, one-way ANOVA.



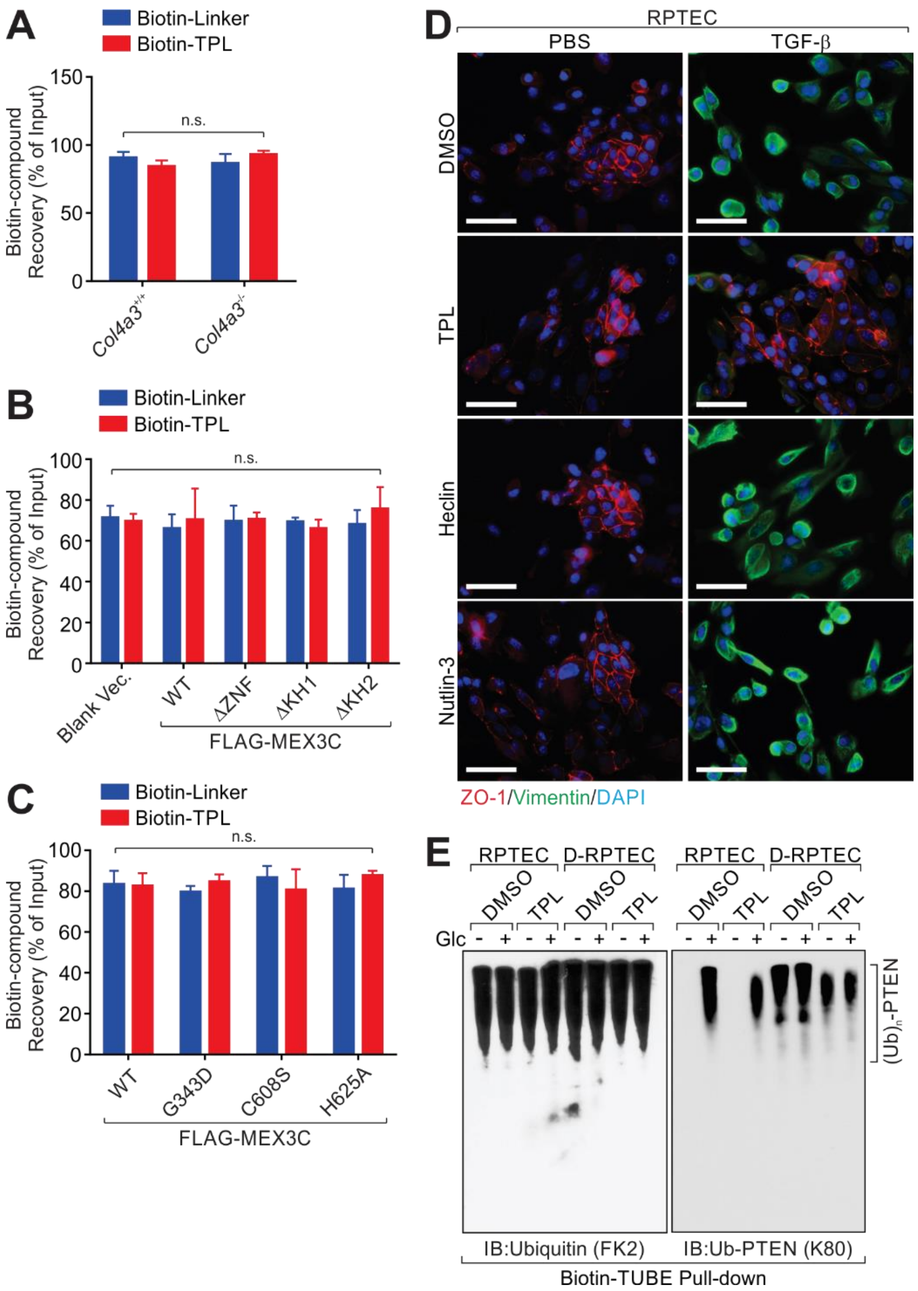
Supplemental Figure 3. PTEN$^{K27\text{-}polyUb}$ is required for growth factor-induced EMT.

(A) Immunofluorescence staining using antibodies targeting indicated antibodies in HK-2 cells subjected with glucose starvation followed by 5 or 25 mM glucose overnight. Scale bar: 100 µm. **(B-D)** Measurement of total cellular PIP$_3$ (B), measurement of kinase activity of immunoprecipitated PI3K (C) or immunoblotting using indicated antibodies (D) from in PTEN sgRNA-harboring HK2 cells transfected with indicated vectors followed by glucose starvation and stimulation (5 mM or 25 mM, 1 h). **(E, F)** Measurement of phosphatase activity of immunoprecipitated SHP2 (E) and PP2A (F) from PTEN sgRNA-harboring HK2 cells transfected with indicated vectors followed by glucose starvation and stimulation (5mM or 25mM, 1 hr), using p-Tyr (E) or p-Ser (F) as substrates respectively. All error bars, S.E.M n.s., *p*>0.05, **p*< 0.05, Student's t-test.



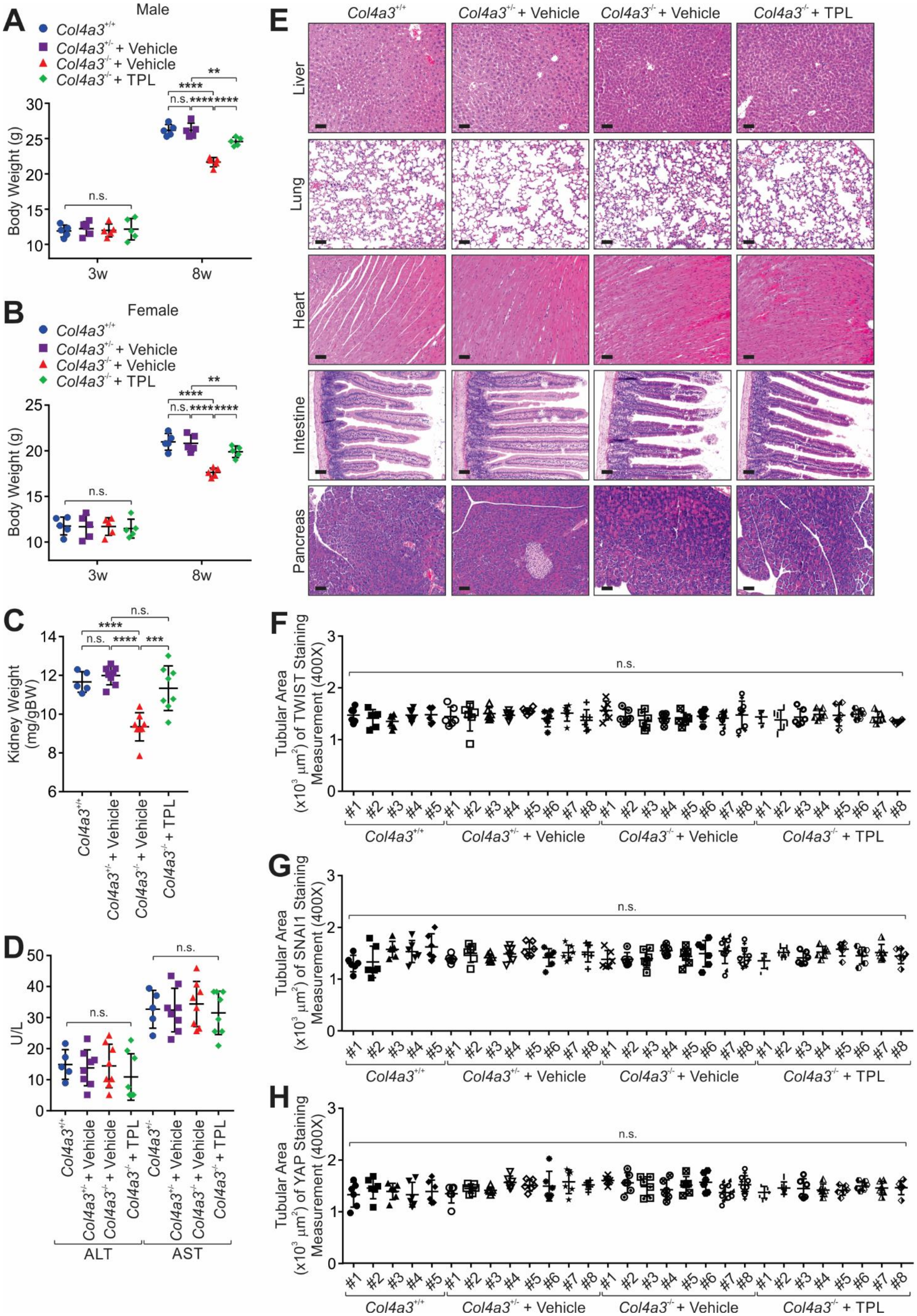
Supplemental Figure 4. Characterization of serum PTEN$^{\text{K27-polyUb}}$ in diabetic kidney disease.

(A) Pearson's correlation of serum PTEN$^{\text{K27-polyUb}}$ with age of all donors (n=54 serum, Pearson chi-square test). **(B)** The expression of MEX family members in kidney tissues; data extracted from RNA-seq - The Human Protein Atlas, Error bars, S.E.M. **(C, D)** Tubule area of measurement of MEX3C (C) and Ub-PTEN (K80) (D) staining intensity per tubule. 6 independent area for each patient is shown. Error bars, SD, n=6 independent field per donor per experimental condition. (n.s., $p>0.05$, one-way ANOVA). (**E, F**) Measurement of Ub-PTEN (K80) in serum (E) or urine (F) of healthy donors (n = 3), type 2 diabetic patients (n = 4), or DKD patients (n = 4). Error bars, SD, n = 3, 4, 4 respectively, one-way ANOVA, n.s. $p>0.05$, *$p<0.05$, **$p<0.01$, ***$p<0.001$, ****$p<0.0001$.



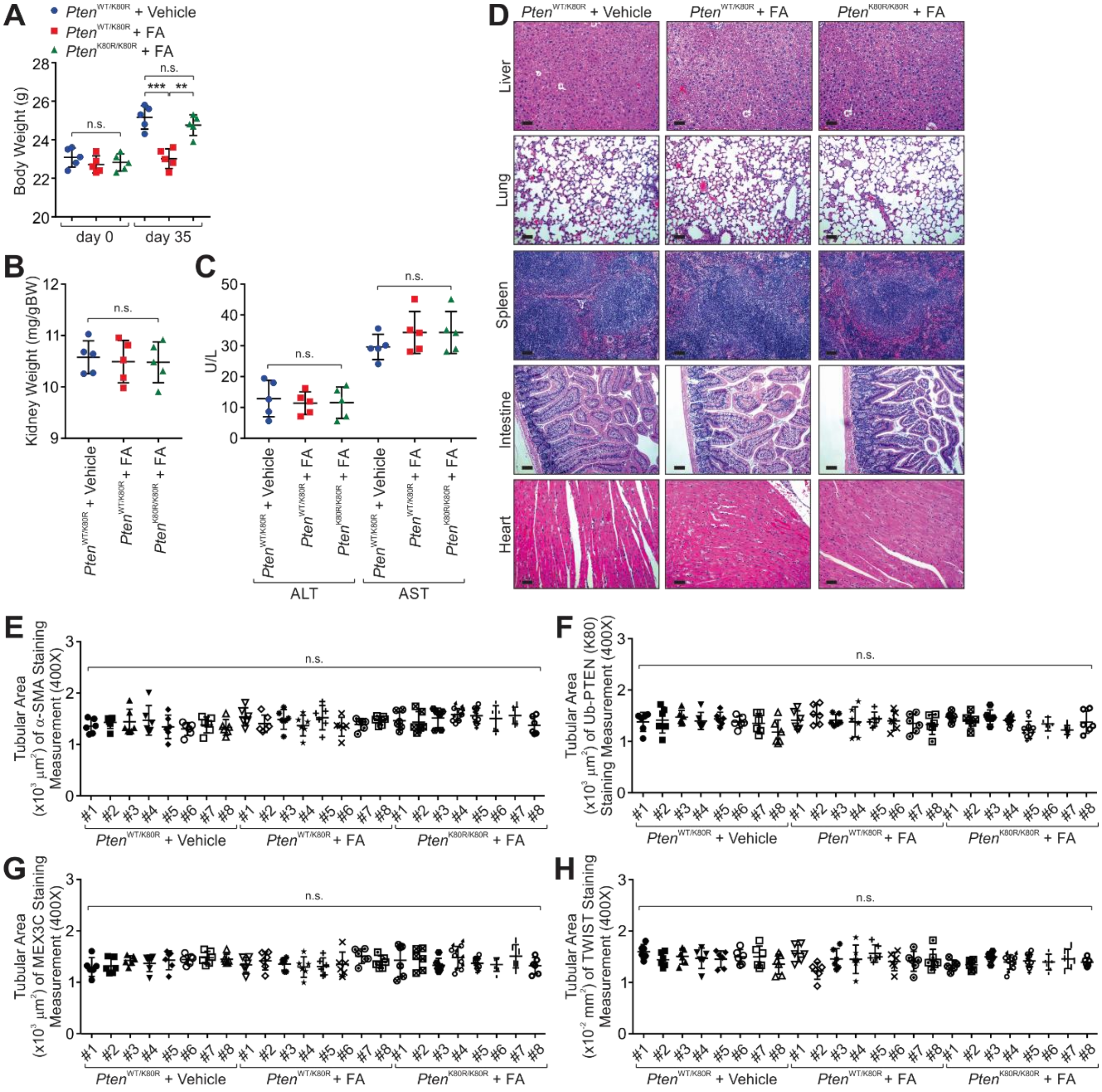
Supplemental Figure 5. Screen and characterization of MEX3C inhibitor.

(A-C) Recovery percentile of Biotin-Linker or Biotin-TPL from streptavidin pulldown using *Col4a3*$^{+/+}$ or *Col4a3*$^{-/-}$ kidney (A), 293T cells expressing indicated expression constructs (B), or recombinant proteins as indicated (C). (**D**) Immunofluorescence labeling using indicated antibodies of RPTEC cells treated with PBS or TGF-β followed by indicated treatment for 72 hr. Scale bar: 50 µm. (**E**) Immunoblotting detection using indicated antibodies in RPTEC or D-RPTEC cells treated with DMSO or TPL (1 µM, 2h), with glucose 5 or 25 mM for 1 h. All error bars, SD, n.s. $p>0.05$, one-way ANOVA.



Supplemental Figure 6. Triptolide reduces *Col4a3* KO-dependent kidney fibrosis.

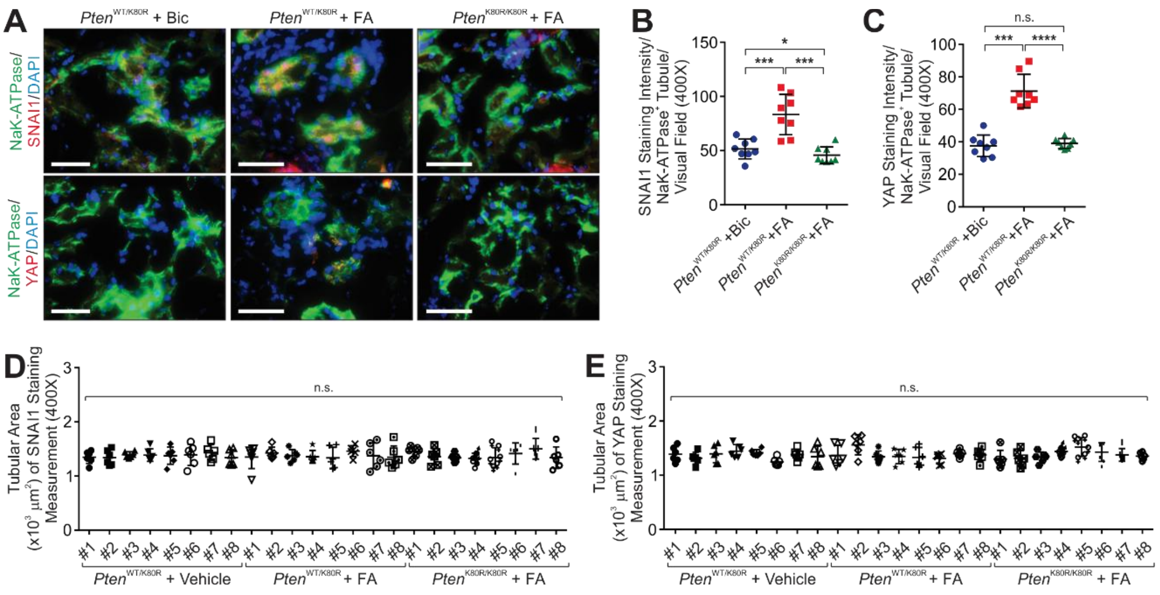
(A, B) Body weight of male (A) and female (B) *Col4a3*$^{+/+}$, *Col4a3*$^{+/-}$ + Vehicle, *Col4a3*$^{-/-}$ + Vehicle, and *Col4a3*$^{-/-}$ +TPL animals (n=5, 5, 5, 5 animals). **(C-E)** Normalized kidney weight (n=8, 8, 8) (C), serum ALT and AST levels (n=5, 8, 8, 8) (D), or H&E staining of liver, lung, heart, intestine and pancreas (E) of *Col4a3*$^{+/+}$, *Col4a3*$^{+/+}$, *Col4a3*$^{+/-}$ + vehicle, *Col4a3*$^{-/-}$ + vehicle, or *Col4a3*$^{-/-}$ + TPL animals. Scale bar: 100 µm. **(F-H)** Tubule area of measurement of TWIST (F), SNAI1 (G) and YAP (H) staining intensity per tubule of *Col4a3*$^{+/+}$, *Col4a3*$^{+/-}$ + vehicle, *Col4a3*$^{-/-}$ + vehicle, or *Col4a3*$^{-/-}$ + TPL kidneys. 6 independent area for each animal is shown, n=5, 8, 8, 8 animals 6 independent fields per animal per experimental condition. All error bars, SD, n.s., $p>0.05$, *$p< 0.05$, **$p< 0.01$, ***$p<0.001$, and ****$p< 0.0001$, one-way ANOVA.



Supplemental Figure 7. Genetic inhibition of PTEN$^{K27\text{-}polyUb}$ reduces FA-induced kidney injury.

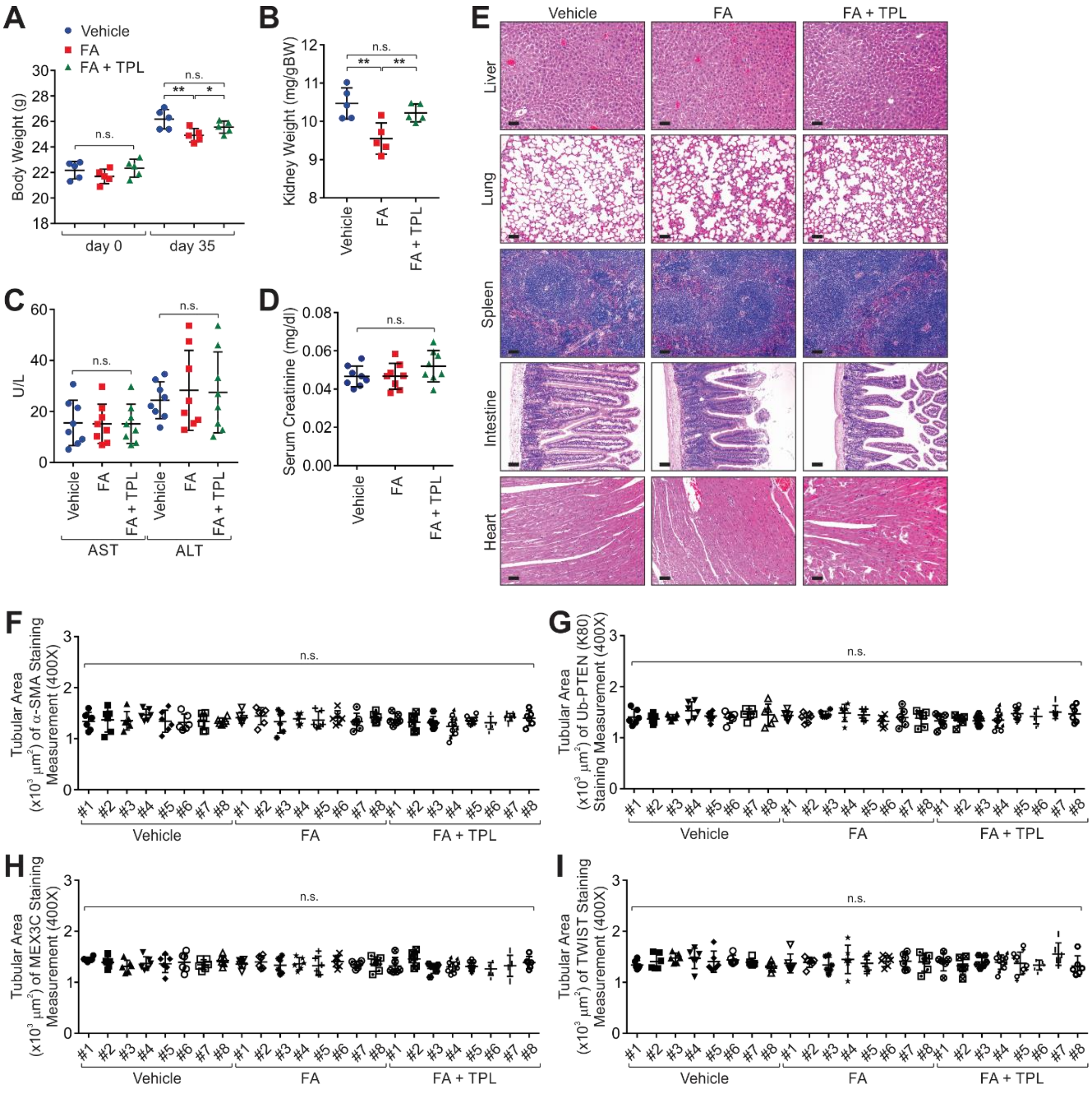
(A) Body weight of animals of *Pten*$^{WT/K80R}$ with biocarbonate (Bic), *Pten*$^{K80R/K80R}$ with FA, and *Pten*$^{K80R/K80R}$ with FA injection (n=5, 5, 5 animals). **(B-D)** Normalized kidney weight (B) serum ALT and AST levels (C), and H&E staining of liver, lung, spleen, intestine and heart (D) of *Pten*$^{WT/K80R}$ + vehicle, *Pten*$^{WT/K80R}$ + FA, or *Pten*$^{K80R/K80R}$ + FA animals (n=5 animals per group). Scale bar: 100 μm. **(E-H)** Tubule area of measurement of α-SMA (E), Ub-PTEN (K80) (F), MEX3C (G), TWIST (H) staining intensity per tubule of *Pten*$^{WT/K80R}$

+ vehicle, *Pten*$^{WT/K80R}$ + FA, or *Pten*$^{K80R/K80R}$ + FA kidneys. 6 independent area for each animal is shown, n=8 animals and 6 independent fields per experimental condition. All error bars, SD, n.s., p>0.05, *p< 0.05, **p< 0.01, ***p<0.001, and ****p< 0.0001, one-way ANOVA.



Supplemental Figure 8. PTEN K80R inhibit expression of EMT regulators upon FA-induced injury.

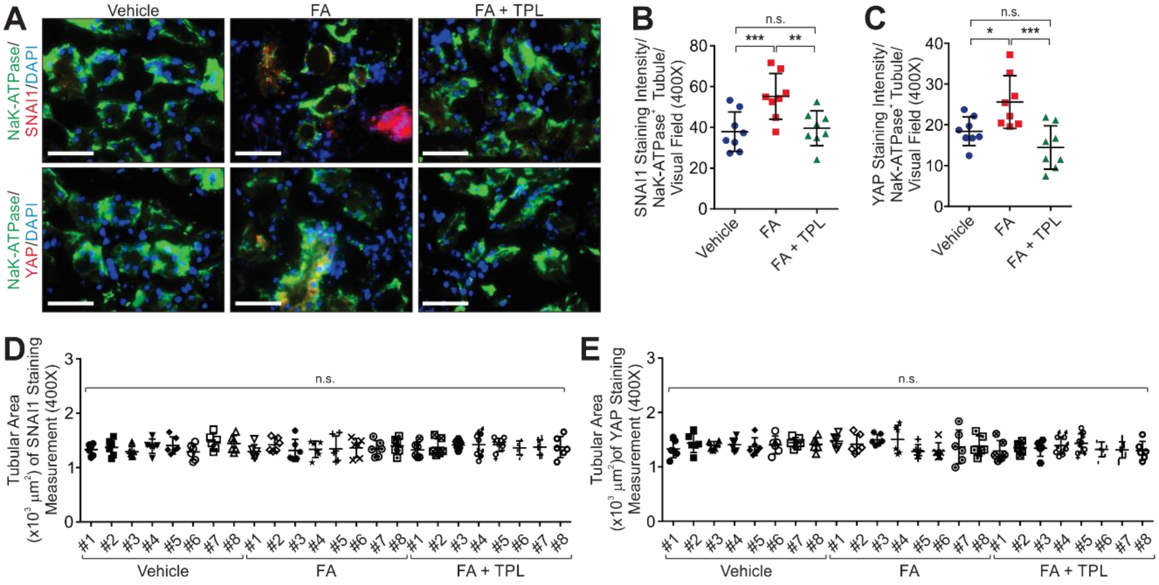
(A) Representative images of immunofluorescence staining using indicated antibodies in *Pten*$^{WT/K80R}$ with biocarbonate (Bic), *Pten*$^{WT/K80R}$ with FA, and *Pten*$^{K80R/K80R}$ with FA injection kidneys. Scale bar: 100 μm. **(B-C)** Statistical analysis of staining intensity of SNAIl (B), and YAP (C) per $Na^{+}K^{+}$-ATPase positive tubule per visual field. Error bars, SD, n=8 animals and 6 independent field per animal is calculated. Error bars, SD, one-way ANOVA. (**D-E**) Tubule area of measurement of SNAIl (D) and YAP (E) staining intensity per tubule of *Pten*$^{WT/K80R}$ + vehicle, *Pten*$^{WT/K80R}$ + FA, or *Pten*$^{K80R/K80R}$ + FA kidneys. 6 independent area for each animal is shown. Error bars, SD, n=8 animals and 6 independent fields per experimental condition (n.s., $p>0.05$, $*p< 0.05$, $**p< 0.01$, $***p<0.001$, and $****p< 0.0001$, one-way ANOVA).



Supplemental Figure 9. PTEN$^{K27\text{-}polyUb}$ promotes FA-induced renal fibrosis.

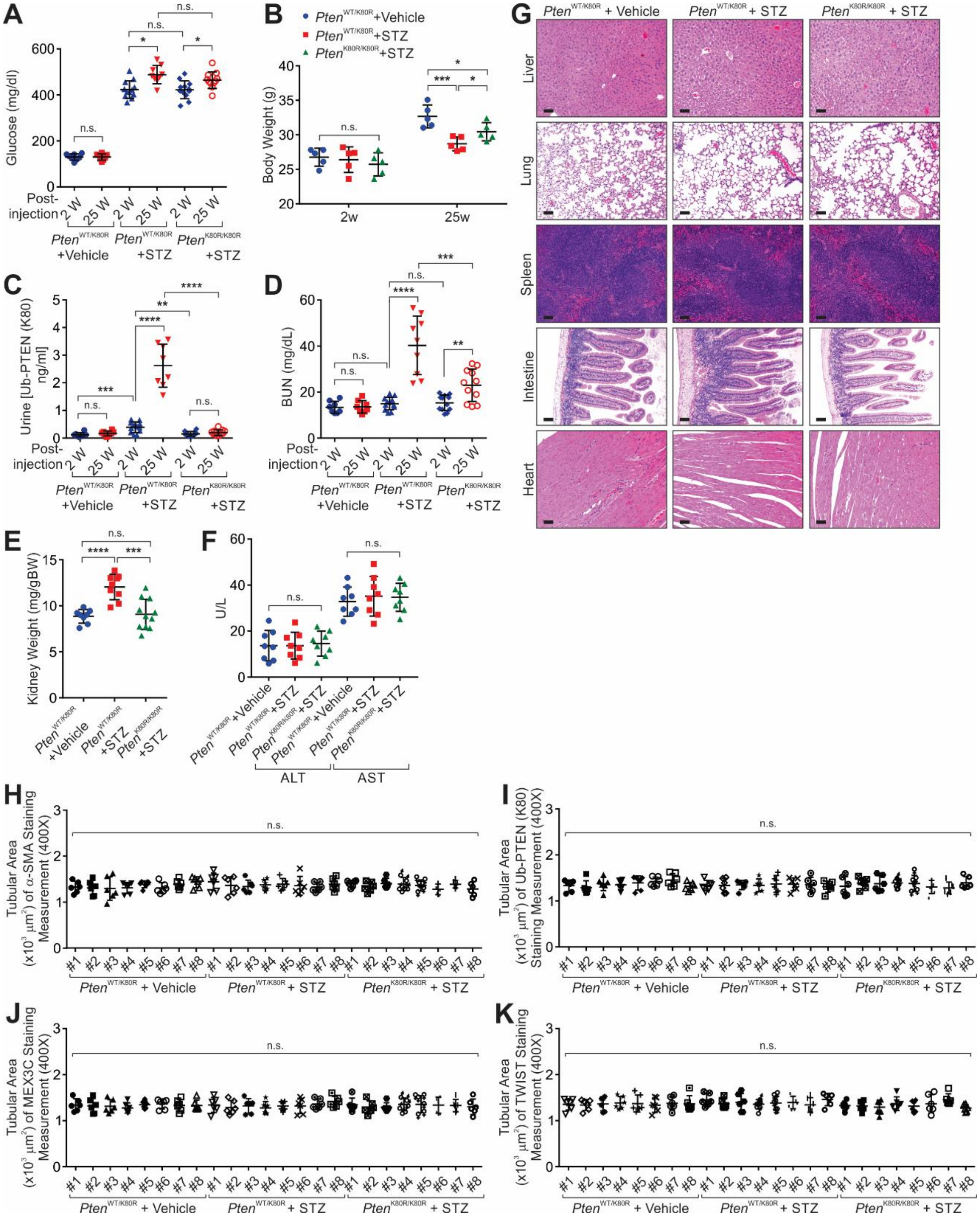
(A) Body weight of C57BL/6J + vehicle, C57BL/6J + FA, or C57BL/6J + FA treated with TPL animals (n=5, 5, 5). **(B-E)** Normalized kidney weight (n=5, 5, 5) (B), serum ALT and AST levels (n=8, 8, 8) (C), serum creatinine level measured by mass spectrometry (n=8, 8,

8) (D) and H&E staining of liver, lung, spleen, intestine and heart (E) of vehicle, FA, or FA with TPL treatment animals. Scale bar: 100 µm. **(F-I)** Tubule area of measurement of α-SMA (F), Ub-PTEN (K80) (G), MEX3C (H), TWIST (I) staining intensity per tubule of kidneys. 6 independent area for each animal is shown, n=8 animals and 6 independent fields per experimental condition. All error bars, SD, n.s., $p>0.05$, $*p< 0.05$, $**p< 0.01$, $***p<0.001$, and $****p< 0.0001$, one-way ANOVA.



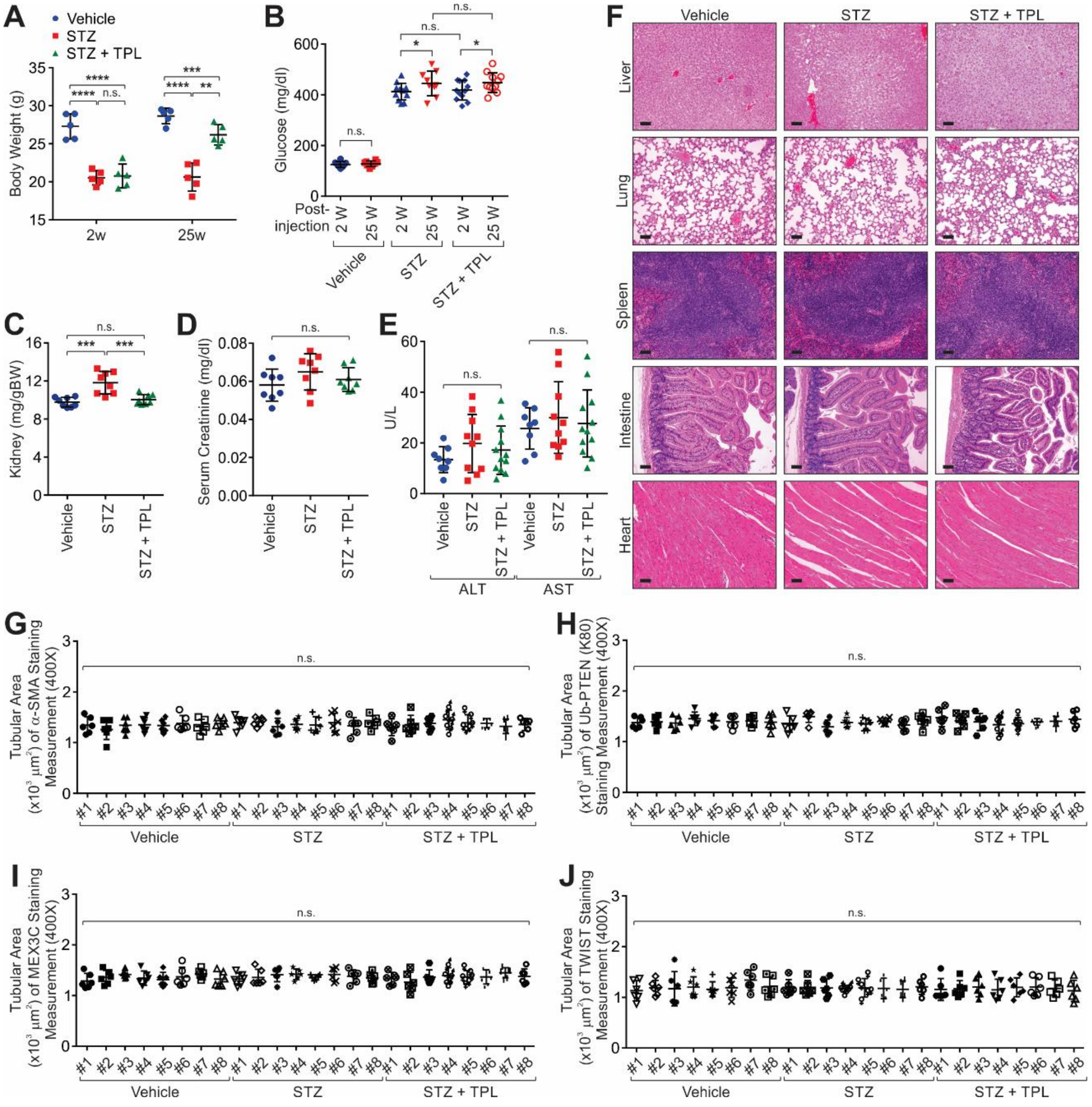
Supplemental Figure 10. PTEN K80R inhibits FA-induced renal fibrosis.

(A) Representative images of immunofluorescence staining using indicated antibodies in vehicle, FA and FA + TPL kidneys. Scale bar:100 µm. **(B-C)** Statistical analysis of staining intensity of SNAIl (B), and YAP (C) per $Na^{+}K^{+}$-ATPase positive tubule per visual field. Error bars, SD, n=8 animals and 6 independent field per animal is calculated (one-way ANOVA). (**D-E**) Tubule area of measurement of SNAIl (D) and YAP (E) staining intensity per tubule of vehicle, FA and FA + TPL kidneys. 6 independent area for each animal is shown. Error bars, SD, n=8 animals and 6 independent fields per experimental condition ($n.s., p > 0.05$, $*p < 0.05$, $**p < 0.01$, $***p < 0.001$, and $****p < 0.0001$, one-way ANOVA).



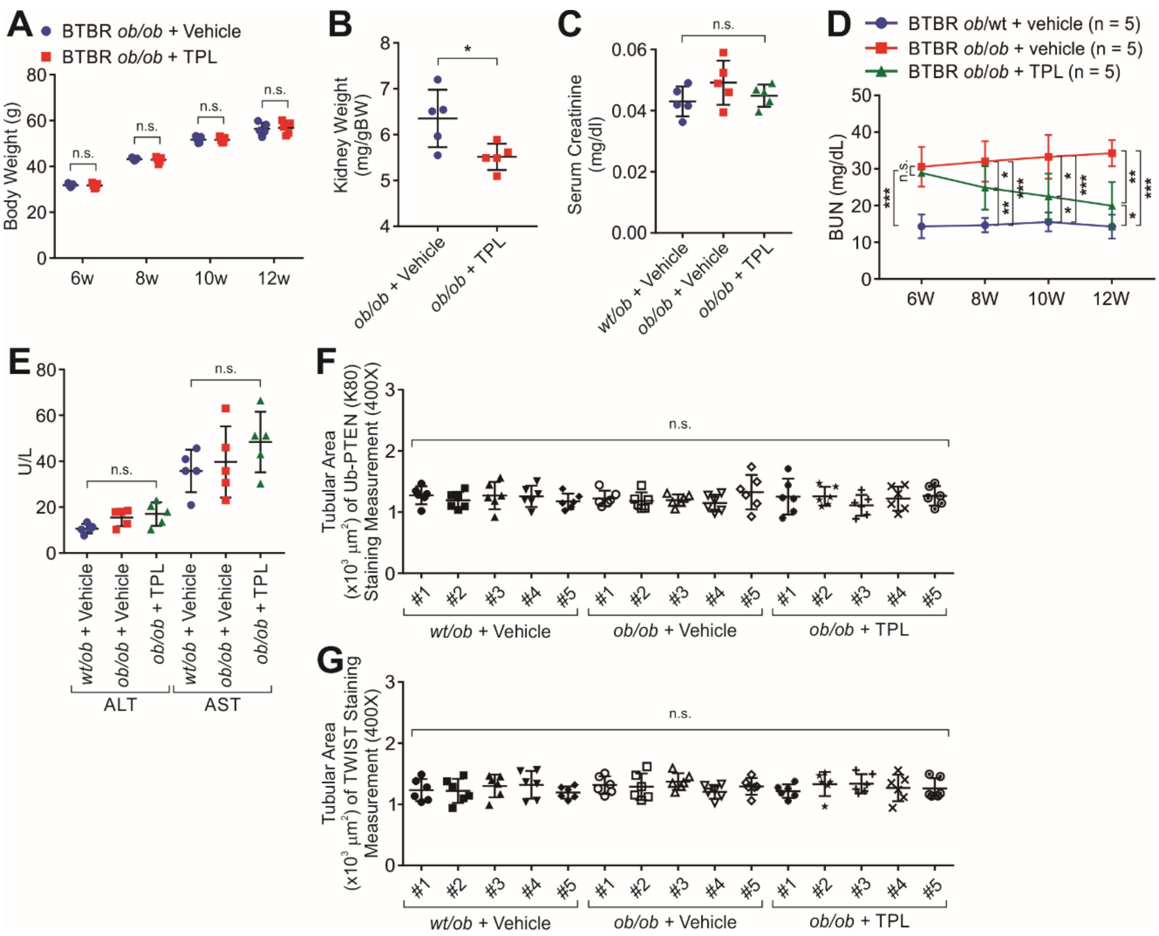
Supplemental Figure 11. Genetic inhibition of PTEN$^{K27\text{-}polyUb}$ reduces STZ-induced kidney injury.

(A) Blood glucose levels of *Pten$^{WT/K80R}$* and *Pten$^{K80R/K80R}$* mice 2 and 25 weeks after STZ injection (n=8, 8, 12, 9, 12, 11). **(B-G)** Body weight (n=5, 5, 5) (B), urine Ub-PTEN (K80) level (n=8, 8, 8) (C), measurement of BUN (n=8, 8, 12, 9, 12, 11) (D), normalized kidney weight (n=8, 9, 11) (E), serum ALT and AST levels (n=8, 8, 8) (F) and H&E staining of liver, lung, spleen, intestine and heart (G) in *Pten*$^{\mathrm{WT/K80R}}$ + vehicle, *Pten*$^{\mathrm{WT/K80R}}$ + STZ, or *Pten*$^{\mathrm{K80R/K80R}}$ + STZ animals. Scale bar: 100 µm. **(H-K)** The tubule area of measurement of α-SMA (H), Ub-PTEN (K80) (I), MEX3C (J) and TWIST (K) staining intensity per tubule of *Pten*$^{\mathrm{WT/K80R}}$ + vehicle, *Pten*$^{\mathrm{WT/K80R}}$ + STZ, or *Pten*$^{\mathrm{K80R/K80R}}$ + STZ kidneys. 6 independent area for each animal is shown, n=8 animals and 6 independent fields per experimental condition. All error bars, SD, n.s., $p>0.05$, *$p< 0.05$, **$p< 0.01$, ***$p<0.001$, and ****$p< 0.0001$, one-way ANOVA.



Supplemental Figure 12. Triptolide reduces STZ-induced kidney damage.

(A) Body weight of *Pten*$^{WT/K80R}$ +vehicle injection; *Pten*$^{WT/K80R}$ +STZ and *Pten*$^{K80R/K80R}$ +STZ animals 2 and 25 weeks after STZ injection (n=5, 5, 5). Error bars, SD, one-way ANOVA. **(B-F)** Blood glucose levels (n=8, 8, 12, 9, 12, 11) (B), normalized kidney weight (n=8, 8, 8) (C), serum creatinine measured by mass spectrometry (n=8, 8, 8) (D), serum ALT and AST levels (n=5, 5, 5) (E) and H&E staining of liver, lung, spleen, intestine and heart (F) in vehicle, STZ, or STZ + TPL treated animals Scale bar: 100 µm. Error bars, SD, one-way ANOVA. **(G-J)** Tubule area of measurement of α-SMA (G), Ub-PTEN (K80) (H), MEX3C (I) and TWIST (J) staining intensity per tubule of vehicle, STZ, or STZ + TPL kidneys. 6 independent area for each animal is shown. Error bars, SD, n=8 animals and 6 independent field per experimental condition. Error bars, SD, one-way ANOVA. (n.s., $p>0.05$, $*p< 0.05$, $**p< 0.01$, $***p<0.001$, and $****p< 0.0001$).



Supplemental Figure 13. Triptolide alleviates BTBR *ob/ob* kidney damage.

(A) Body weight of male BTBR *ob/ob* + vehicle and BTBR *ob/ob* + TPL animals at age of 6, 8, 10, 12 weeks (n=5, 5 animals). Error bars, SD, Student's t-test. **(B-C)** Normalized kidney weight (B), serum creatinine level measured by mass spectrometry (C) in BTBR *ob/wt* + vehicle, BTBR *ob/ob* + vehicle and BTBR *ob/ob* + TPL animals at age of 12 weeks (n=5 animal per group). Error bars, SD, Student's t-test (B) or one-way ANOVA (C). **(D)** Measurement of BUN in BTBR *ob/wt* + vehicle, BTBR *ob/ob* + vehicle and BTBR *ob/ob* + TPL animals at age of 6, 8, 10, 12 weeks (n=5, 5, 5 animals). Error bars, SD, one-way ANOVA. **(E)** Measurement of ALT and AST in BTBR *ob/wt* + vehicle, BTBR *ob/ob* + vehicle and BTBR *ob/ob* + TPL animals at age of 12 weeks (n=5 animal per group). Error bars, SD, one-way ANOVA. **(F-G)** Tubule area of measurement of Ub-PTEN (K80) (F) and TWIST (G) staining intensity per tubule of BTBR *ob/wt* + vehicle, BTBR *ob/ob* + vehicle and BTBR *ob/ob* + TPL kidneys. 6 independent area for each animal is shown, n=5 animals and 6 independent fields per experimental condition. Error bars, SD, one-way ANOVA (n.s., $p>0.05$, $^*p< 0.05$).

Supplemental Table Legends

Supplemental Table 1: Clinical information of tissue samples used in this study.

<u>Serum samples of healthy donors</u>: Human serum samples of healthy donors with BMI and medical information.

<u>Serum Samples of Diabetes</u>: Human serum samples of type 1 or type 2 diabetes with diagnosis and symptom shown.

<u>Serum samples of patients with diabetic nephropathy</u>: Human serum samples of diabetic nephropathy patients, with Blood glucose (BG) levels, diabetic condition and medications shown.

Fresh frozen kidney tissues within normal limits and patients with diabetic nephropathy: Fresh frozen sections of human kidney tissues within normal limits or diabetic nephropathy with case diagnosis, and cause of death shown.

Urine samples of Healthy Donors: Fresh frozen urine samples of healthy donors, with BMI, eGFR and medical information shown.

Urine samples of DKD patients: Fresh frozen urine samples of patients with diabetic kidney disease, with BMI, Creatinine, eGFR and medical histories shown.

Paired serum and urine samples: Fresh frozen paired serum and urine samples of healthy donor, type 2 diabetes and DKD, with diagnosis, and medical information shown.

Extended Data Table 2. Summary of protein identification of Biotin-TPL pulldown from fibrotic mouse kidneys.

Complete mass spectrometry results for Biotin-TPL associated proteins pulled down from *Col4a3*$^{-/-}$ fibrotic kidneys. This table has seven tabs, containing summary and six tabs corresponding to each band cut from silver staining of proteins in polyacrylamide gels. The number of unique and shared peptides and quarry numbers are shown.

Supplemental Table 1. Clinical information of human biospeciements used in this study.

Human Serum of Healthy Donors

KITID	DCMDATE	PATIENTID	GENDER	AGE	BMI	SURVEYID	TOBACCO	ETHNICITY	BSI_ID	MAT_TYPE	VOLUME
ONOIO	36731	G100013713	FEMALE	19	22.676	CONTROL_4_1	NO	HISPANIC/LATINO	GF083097 0002	B1	1000
FGB2H	36656	G100001925	MALE	21	18.365	CONTROL_4_1	NO	WHITE/CAUCSIAN(POLISH)	GF051739 0007	B1	1000
X9YLT	36724	G100014071	FEMALE	22	23.373	CONTROL_4_1	NO	WHITE/CAUCASIAN	GF112455 0002	B1	1000
UV494	36703	G100014110	MALE	22	23.590	CONTROL_4_1	NO	WHITE/CAUCASIAN	GF104399 0002	B1	1000
ODT4Y	36752	G100013137	FEMALE	32	20.889	CONTROL_4_1	NO	ASIAN	GF082148 0003	B1	1000
VOBL3	36991	G100063629	MALE	32	22.097	CONTROL_4_1	NO	WHITE/CAUCASIAN	GF107154 0003	B1	1000
6FQU8	36623	G100001621	FEMALE	40	23.309	CONTROL_4_1	NO	WHITE/CAUCSIAN(POLISH)	GF018569 0002	B1	1000
AYCBV	36804	G100014684	MALE	42	24.251	CONTROL_4_1	NO	BLACK/AFRICAN-AMERICAN	GF033970 0002	B1	1000
LDPGP	36696	G100002465	MALE	50	22.598	CONTROL_4_1	NO	WHITE/CAUCSIAN(POLISH)	GF071885 0006	B1	1000
YDZGT	36740	G100013372	FEMALE	50	24.977	CONTROL_4_1	NO	ASIAN	GF116345 0003	B1	1000

Human Serum of Diabetic type I and type II Patients

Sample ID	Date of collection	Sex	Age	Specimen type	Volume, mL	Ethnicity	Height, cm	Weight, kg	BMI	Diagnosis	Date of diagnosis	Blood Glucose level, mmol/L	Symptoms	Current medications	Smoking history
71356S	10/21/2013	M	71	serum	1x1mL	Caucasian	170	80	27.7	Diabetes Mellitus type 2	2011	7.5	dry skin, thirst, increased appetite	actropid, Protaphane, Captopril, Egilok, Furosemide	no
71357S	10/21/2013	F	80	serum	1x1mL	Caucasian	167	70	25.1	Diabetes Mellitus type 2	2005	7.6	excessive thirst, frequent urination, genital itching	actropid, Captopril, Egilok, Verospiron	no
71358S	10/21/2013	F	72	serum	1x1mL	Caucasian	169	67	23.5	Diabetes Mellitus type 2	2012	7.8	itchy skin, thirst, dizziness	actropid, Enalapril, Perindopril, Furosemide, Bisoprolol	no
71350S	10/16/2013	F	81	serum	1x1mL	Caucasian	167	80	28.7	Diabetes Mellitus type 2	2001	7.5	excessive thirst, skin itching, fatigue	Diabetone, Metformin, Egilok, Captopril, Hypothiazide	no
71351S	10/21/2013	F	75	serum	1x1mL	Caucasian	167	86	30.8	Diabetes Mellitus type 2	2004	7.6	excessive thirst, irritability, skin scratches	actropid, Enalapril, Bisoprolol, Nifecard, Verospiron	no
71352S	10/21/2013	F	80	serum	1x1mL	Caucasian	167	80	28.7	Diabetes Mellitus type 2	1998	7.6	excessive thirst, appetite, dry skin, headaches	insulin therapy, Captopril, Egilok, Hypothiazide	no
71354S	10/21/2013	F	73	serum	1x1mL	Caucasian	170	86	29.8	Diabetes Mellitus type 2	2003	7.7	dry skin, excessive thirst, fatigue	immunotherapy, Cordaflex, Egilok, Furosemide	no
71348S	10/16/2013	F	75	serum	1x1mL	Caucasian	170	86	29.8	Diabetes Mellitus type 2	2010	7.6	excessive thirst, dry skin, headache, fatigue	Diabetone, Metformin, Enalapril, Betaloc, Verospiron	no
71334S	8/20/2013	F	76	serum	1x1mL	Caucasian	170	89	30.8	Diabetes Mellitus type 2	2012	7.6	excessive thirst, dyspnea at rest, headaches, fatigue	anaprilin, Maninil, Metformin, Losartan, Perindopril, Verospiron	no
71338S	8/26/2013	M	72	serum	1x1mL	Caucasian	175	80	26.1	Diabetes Mellitus type 2	2012	7.6	headache, fatigue, itchy skin, excessive thirst	Diabetone, Metformin, Egilok, Losartan, Verospiron	no
71490S	9/10/2014	M	36	serum	1x1ml	Caucasian	180	80	24.7	Diabetes Mellitus type l	2007	8.6	excessive thirst, fatigue	insulin therapy, No-Spa, papaverine, platyphylline, arifon	12 years 1 pack/day
71492S	9/10/2014	F	40	serum	1x1ml	Caucasian	167	75	26.9	Diabetes Mellitus type l	2008	8.2	frequent urination	insulin therapy, pancreatin, Lozapine, arifon, No-Spa	no
71488S	9/10/2014	M	40	serum	1x1ml	Caucasian	168	80	28.3	Diabetes Mellitus type l	2008	8.6	headache, excessive thirst, increased appetite	actrapid, papaverine, platyphylline, enalapril, arifon	no
71479S	9/8/2014	F	40	serum	1x1ml	Caucasian	167	70	25.1	Diabetes Mellitus type l	2007	8.6	excessive thirst, frequent urination, fatigue, tiredness	insulin therapy, papaverine, platyphylline, mesim forte	no
71457S	6/3/2014	M	47	serum	1x1ml	Caucasian	167	75	26.9	Diabetes Mellitus type l	1998	8.5	headache, excessive thirst, increased appetite, itching, sleep disturbance	actrapid, Lozapine, enalapril, arifon	no
71458S	6/3/2014	M	45	serum	1x1ml	Caucasian	165	80	29.4	Diabetes Mellitus type l	1998	8.3	excessive thirst, increased appetite, frequent urination, headache, fatigue	insulin therapy, losartan, enalapril, arifon	no
71452S	5/27/2014	M	41	serum	1x1ml	Caucasian	170	75	26	Diabetes Mellitus type l	1996	8.2	excessive thirst, increased appetite, itching, sleep disturbance	insulin therapy, Prestarium, Lozapine, arifon	no

71448S	5/27/2014	M	50	serum	1x1ml	Caucasian	170	75	26	Diabetes Mellitus type I	1998	8.2	excessive thirst, increased appetite, itching, headache, tachycardia	insulin therapy, Digoxin, euphylline, verospiron, enalapril	20 years 1 pack/day
71446S	5/27/2014	F	44	serum	1x1ml	Caucasian	166	66	24	Diabetes Mellitus type I	2008	8.5	tachycardia, excessive thirst, increased appetite, frequent urination, fatigue	insulin therapy, monopril, egiloc, furosemide	no
71447S	5/27/2014	F	48	serum	1x1ml	Caucasian	167	70	25.1	Diabetes Mellitus type I	2009	8.2	excessive thirst, itching, blurry vision	actrapid, Physiotens, egiloc, arifon	no

Human Serum of Diabetic Patients with Nephropathy

study	sample_id	Mat_type	Volume	age	DIABETES_DIAG_age	Gender	BMI	ETHNIC_you	DIABETES_TYPE	BG_LEVEL	BG_UNIT	BG_TYPE	DIAB_CONDITION	Pres_Medications
DIABETES_4_1	YKNY6	Serum	2000	29	2	FEMALE	36.328	WHITE/CAUCASIAN ** AMERICAN INDIAN OR ALASKAN NATIVE	TYPE I	1300	mg/dL	RANDOM	EYE PROBLEMS (YES) ** DIABETIC NEUROPATHY (YES) ** DIABETIC NEPHROPATHY (YES) ** PERIPHERAL VASCULAR DISEASE (NO) ** ULCER OR INFECTION OF THE FOOT OR LEG (NO) ** LOWER EXTREMITY AMPUTATION (NO) ** VEIN GRAFT (NO) ** IMPOTENCE (NO) ** HEART ATTACK (NO)	INSULIN(1973) ** LOTENSIN(2000)
DIABETES_4_1	T6I5U	Serum	2000	32	11	FEMALE	36.934	WHITE/CAUCASIAN ** AMERICAN INDIAN OR ALASKAN NATIVE	TYPE I	700	mg/dL	FASTING	EYE PROBLEMS (YES) ** DIABETIC NEUROPATHY (YES) ** DIABETIC NEPHROPATHY (YES) ** PERIPHERAL VASCULAR DISEASE (NO) ** ULCER OR INFECTION OF THE FOOT OR LEG (NO) ** LOWER EXTREMITY AMPUTATION (NO) ** VEIN GRAFT (NO) ** IMPOTENCE (NO) ** HEART ATTACK (NO)	RHINOCORT(1999) ** CLARITIN(1998) ** PROZAC(1995) ** ALESSE(1999) ** INSULIN N(1978) ** INSULIN R(1978) ** MONOPRIL(1998)
DIABETES_4_1	21Q1F	Serum	1900	32	10	MALE	22.145	WHITE/CAUCASIAN	TYPE I	1200	mg/dL	FASTING	EYE PROBLEMS (YES) ** DIABETIC NEUROPATHY (YES) ** DIABETIC NEPHROPATHY (YES) ** PERIPHERAL VASCULAR DISEASE (YES) ** ULCER OR INFECTION OF THE FOOT OR LEG (NO) ** LOWER EXTREMITY AMPUTATION (NO) ** VEIN GRAFT (NO) ** IMPOTENCE (NO) ** HEART ATTACK (NO)	INSULIN(1978) ** PEPCID(1980)
DIABETES_4_1	QOQ3B	Serum	1000	40	9	MALE	26.026	WHITE/CAUCASIAN	TYPE I	600	mg/dL	FASTING	EYE PROBLEMS (YES) ** DIABETIC NEUROPATHY (YES) ** DIABETIC NEPHROPATHY (YES) ** PERIPHERAL VASCULAR DISEASE (YES) ** ULCER OR INFECTION OF THE FOOT OR LEG (NO) ** LOWER EXTREMITY AMPUTATION (NO) ** VEIN GRAFT (NO) ** IMPOTENCE (NO) ** HEART ATTACK (NO)	INSULIN(1969) ** PRESTARIUM(1998) ** CARDURA(1998) ** AMLOZEK(1999) ** POLFILIN(1999)
DIABETES_4_1	H9HPR	Serum	2000	43	36	FEMALE	22.032	WHITE/CAUCASIAN	TYPE II	570	mg/dL	FASTING	EYE PROBLEMS (YES) ** DIABETIC NEUROPATHY (YES) ** DIABETIC NEPHROPATHY (YES) ** PERIPHERAL VASCULAR DISEASE (NO) ** ULCER OR INFECTION OF THE FOOT OR LEG (NO) ** LOWER EXTREMITY AMPUTATION (NO) ** VEIN GRAFT (NO) ** IMPOTENCE (DON'T KNOW) ** HEART ATTACK (NO)	HUMULIN M3(1997)

DIABETES_4_1	28CSD	Serum	2000	46	46	FEMALE	50.712	AMERICAN INDIAN OR ALASKAN NATIVE	TYPE II	700	mg/dL	RANDOM	EYE PROBLEMS (YES) ** DIABETIC NEUROPATHY (YES) ** DIABETIC NEPHROPATHY (YES) ** PERIPHERAL VASCULAR DISEASE (YES) ** ULCER OR INFECTION OF THE FOOT OR LEG (NO) ** LOWER EXTREMITY AMPUTATION (NO) ** VEIN GRAFT (NO) ** IMPOTENCE (DON'T KNOW) ** HEART ATTACK (DON'T KNOW)	SYNTHROID(1976) ** ELAVIL(1994) ** PRILOSEC(2000) ** NITROSTAT(1996) ** COMPAZINE(1998) ** ALBUTEROL(1980) ** ALTACE(2000) ** PAXIL(1998) ** HUMALIN(2000) ** HUMALOG(2000) ** DYAZIDE(1999) ** ULTRAM(2000)			
DIABETES_4_1	EVWUK	Serum	2000	47	30	MALE	21.296	WHITE/CAUCASIAN	TYPE I	600	mg/dL	RANDOM	EYE PROBLEMS (YES) ** DIABETIC NEUROPATHY (YES) ** DIABETIC NEPHROPATHY (YES) ** PERIPHERAL VASCULAR DISEASE (YES) ** ULCER OR INFECTION OF THE FOOT OR LEG (YES) ** LOWER EXTREMITY AMPUTATION (YES) ** VEIN GRAFT (NO) ** IMPOTENCE (NO) ** HEART ATTACK (NO)	HUMALOG INSULIN(1984) ** ACIPHEX(1998) ** NORVASC(1998) ** FLOMAX(1998) ** LASIX(1998) ** PLAVIX(1998) ** ZAROXOLYN(1998)			
DIABETES_4_1	KOPLF	Serum	1750	50	30	FEMALE	28.197	WHITE/CAUCASIAN	TYPE I	800	mg/dL	RANDOM	EYE PROBLEMS (YES) ** DIABETIC NEUROPATHY (NO) ** DIABETIC NEPHROPATHY (YES) ** PERIPHERAL VASCULAR DISEASE (NO) ** ULCER OR INFECTION OF THE FOOT OR LEG (NO) ** LOWER EXTREMITY AMPUTATION (NO) ** VEIN GRAFT (NO) ** IMPOTENCE (NO) ** HEART ATTACK (NO)	LISINOPRIL(1992) ** LEVOTHROID(1998) ** PREMARIN(1999) ** MEDROXYPROGESTERONE (1999) ** LOVASTATIN(2000)			
DIABETES_4_1	IN7GU	Serum	2000	52	45	MALE	41.667	WHITE/CAUCASIAN	TYPE II	587	mg/dL	RANDOM	EYE PROBLEMS (YES) ** DIABETIC NEUROPATHY (YES) ** DIABETIC NEPHROPATHY (YES) ** PERIPHERAL VASCULAR DISEASE (NO) ** ULCER OR INFECTION OF THE FOOT OR LEG (NO) ** LOWER EXTREMITY AMPUTATION (NO) ** VEIN GRAFT (NO) ** IMPOTENCE (NO) ** HEART ATTACK (YES)	LOPRESSOR(1994) ** LIPITOR(1996) ** GLUCOPHAGE(1993) ** GLYNASE(1993) ** MONOPRIL(2000) ** ACTOS(2000)			
DIABETES_4_1	GRYKD	Serum	2000	53	41	FEMALE	29.997	WHITE/CAUCASIAN	TYPE II	566	mg/dL	0	EYE PROBLEMS (YES) ** DIABETIC NEUROPATHY (YES) ** DIABETIC NEPHROPATHY (YES) ** PERIPHERAL VASCULAR DISEASE (YES) ** ULCER OR INFECTION OF THE FOOT OR LEG (YES) ** LOWER EXTREMITY AMPUTATION (NO) ** VEIN GRAFT (NO) ** IMPOTENCE (DON'T KNOW) ** HEART ATTACK (NO)	HUMALOG(2001) ** GLUCOBAY(2001)			
DIABETES_4_1	8LK6I	Serum	2000	63	62	MALE	21.778	BLACK/AFRICAN-AMERICAN	TYPE II	800	mg/dL	RANDOM	EYE PROBLEMS (YES) ** DIABETIC NEUROPATHY (NO) ** DIABETIC NEPHROPATHY (YES) ** PERIPHERAL VASCULAR DISEASE (NO) ** ULCER OR INFECTION OF THE FOOT OR LEG (NO) ** LOWER EXTREMITY AMPUTATION (NO) ** VEIN GRAFT (NO) ** IMPOTENCE (NO) ** HEART ATTACK (NO)	0			
DIABETES_4_1	873U3	Serum	1000	69	58	MALE	31.02	BLACK/AFRICAN-AMERICAN	TYPE II	702	mg/dL	FASTING	EYE PROBLEMS (NO) ** DIABETIC NEUROPATHY (YES) ** DIABETIC NEPHROPATHY (YES) ** PERIPHERAL VASCULAR DISEASE (YES) ** ULCER OR INFECTION OF THE FOOT OR LEG (NO) ** LOWER EXTREMITY AMPUTATION (NO) ** VEIN GRAFT (NO) ** IMPOTENCE (YES) ** HEART ATTACK (NO)	TOPROL(1999) ** PROCARDIA(1998) ** ISOSORBIDE(1998) ** LASIX(1998) ** ACTOS(1999) ** ZOCOR(1998) ** HYDRALAZINE(1999) ** K-DUR(1999) ** PLETAL(1999)			

Fresh Frozen Human Kidney Tissues with or without Renal Disease

Sample ID	Sex	Age	Ethnic backg	Sample type	Matrix	Date of autopsy	PMI, hours	BMI	Diabetes yes / no	Cause of death	Renal disease	Weight, gm
052025A(4)	M	90	Caucasian	FF	kidney	06/19/2017	3	24.8	yes	coronary sclerosis, circulatory insufficiency	diabetic nephropathy	0.8
051980A(4)	F	61	Caucasian	FF	kidney	03/10/2017	2.5	41.5	yes	COPD, pneumonia, cardiovascular failure	diabetic nephropathy	0.8
051979A(1)	F	68	Caucasian	FF	kidney	03/03/2017	3	51.9	yes	heart failure	diabetic nephropathy	0.8
051937A(3)	F	69	Caucasian	FF	kidney	09/01/2016	2.5	25.7	yes	ischemic stroke, pulmonary embolism	diabetic nephropathy	0.9
051917A(4)	M	84	Caucasian	FF	kidney	06/09/2016	4.5	24.5	yes	discirculatory encephalopathy, pneumonia	diabetic nephropathy	0.7
051904A(3)	M	64	Caucasian	FF	kidney	04/29/2016	4	32.7	yes	ischemic stroke, cerebral edema	diabetic nephropathy	0.8
051727A(5)	F	58	Caucasian	FF	kidney	06/04/2015	5	32.9	yes	ischemic stroke	diabetic nephropathy	0.9
051707A(7)	M	57	Caucasian	FF	kidney	05/21/2015	6	27.5	yes	MI, asystole, renal falure	diabetic nephropathy	0.9
05771A(1)	F	72	Caucasian	FF	kidney	08/13/2011	5	N/A	yes	recurrent stroke, cerebral edema, brain stem dislocation	diabetic nephropathy	0.8
051982A(7)	F	44	Caucasian	FF	kidney	03/17/2017	2.5	26.0	no	peptic ulcer perforation, peritonitis	no	0.9
051918A(3)	M	67	Caucasian	FF	kidney	06/22/2016	4.5	26.1	no	hemorrhagic stroke, PE	no	0.7
051912A(3)	M	32	Caucasian	FF	kidney	05/12/2016	3	29.6	no	subarachnoid hemorrhage, cerebral edema, brain stem dislocation	no	0.8
051696A(5)	F	60	Caucasian	FF	kidney	04/13/2015	4.5	31.9	no	PE	no	0.5
051659A(8)	M	54	Caucasian	FF	kidney	12/09/2014	1.5	31.0	no	acute coronary syndrome	no	0.9
051617A(12)	M	34	Caucasian	FF	kidney	09/01/2014	2.5	22.8	no	poisoning by unspecified substance	no	0.6
051553A(13)	M	58	Caucasian	FF	kidney	06/19/2014	1.5	28.9	no	acute ethanol poisoning	no	0.8
051102A(1)	M	65	Caucasian	FF	kidney	02/19/2013	5.5	N/A	no	ischemic stroke, cerebral edema	no	0.45
051079A(3)	M	59	Caucasian	FF	kidney	01/24/2013	3	N/A	no	abscess of the anterior abdominal wall, intoxication	no	0.9

Urine Samples of Healthy Donors

Donor ID	Date collected	Sex	Age	Specimen type	Volume	Ethnicity	Height, cm	Weight, kg	BMI	Patient diagnosis	eGFR, mL/min/1.73m2	Smoking history	Medical history
D5715Ur	41613	F	56	urine	1 x 5mL	Caucasian	170	60	20.8	normal donor	136	no	no
D5714Ur	41613	F	54	urine	1 x 5mL	Caucasian	161	55	21.2	normal donor	157	no	no
D5712Ur	41613	M	53	urine	1 x 5mL	Caucasian	176	75	24.2	normal donor	124	no	no
D5711Ur	41613	M	55	urine	1 x 5mL	Caucasian	180	90	27.8	normal donor	117	no	no
D5745Ur	41617	F	57	urine	1 x 5mL	Caucasian	165	62	22.8	normal donor	142	no	no
D5744Ur	41617	F	60	urine	1 x 5mL	Caucasian	161	70	27	normal donor	139	no	no
D5743Ur	41617	F	51	urine	1 x 5mL	Caucasian	152	50	21.6	normal donor	116	no	no
D5741Ur	41617	M	50	urine	1 x 5mL	Caucasian	180	90	27.8	normal donor	128	no	no
D5967Ur	41668	F	55	urine	1 x 5mL	Caucasian	161	72	27.8	normal donor	133	no	no
D5964Ur	41668	F	47	urine	1 x 5mL	Caucasian	165	66	24.2	normal donor	141	no	no

Urine Samples of DKD Patients

Sample ID	Date of collection	Sex	Age	Specimen type	Volume	Ethnicity	Diagnosis	Date of diagnosis	Creatinine, μmol/L	eGFR, mL/min/1.73m2	Medical history	Smoking history	Height, cm	Weight, kg	BMI
60035Ur	41606	F	82	urine	1 x 5mL	Caucasian	DKD	2010	190	31	Diabetes mellitus type II, Diabetic Nephropathy, Diabetic Neuropathy	no	163	71	26.7
60036Ur	41607	F	64	urine	1 x 5mL	Caucasian	DKD	2012	210	29	Diabetes mellitus type II, Diabetic Nephropathy	no	169	79	27.7
60037Ur	41607	F	62	urine	1 x 5mL	Caucasian	DKD	2012	130	51	Diabetes mellitus type II, Diabetic Nephropathy	no	165	58	21.3
60038Ur	41607	M	65	urine	1 x 5mL	Caucasian	DKD	2011	190	44	Diabetes mellitus type II, Diabetic Nephropathy, Hypertension	no	178	86	27.1

60040Ur	41612	M	61	urine	1 x 5mL	Caucasian	DKD	2012	180	47	Diabetes mellitus type II, Diabetic Nephropathy, Coronary Artery Disease	no	179	87	27.2
60068Ur	41863	F	59	urine	1 x 5mL	Caucasian	DKD	2013	399	14	Diabetes mellitus type II, Diabetic Nephropathy, Diabetic Neuropathy, obesity	24 years 1 pack/day	162	98	37.3

Paired Serum and Urine Samples

Healthy donor

UID	**Donor #**	**Type**	**Volume (mL)**	**Hemolyzed (Approx. Level)**	**Viral Status (HIV, HBsAg, HCV**	**Age**	**Age Units**	**Gender**	**Race**	**Ethnicity**	**Country of Collection**	**Diagnosis**	**Medications**
337419	3	Serum	7	Non-Hemolyzed	Not Tested	64	Year(s)	Female	N/A	Hispanic	United States of America (USA)	Normal Donor	None
337420	3	Urine	5.5	Non-Hemolyzed	Not Tested	64	Year(s)	Female	N/A	Hispanic	United States of America (USA)	Normal Donor	None
339284	15	Serum	6.5	Non-Hemolyzed	Not Tested	41	Year(s)	Male	African	African American	United States of America (USA)	Normal Donor	None
339285	15	Urine	36.5	Non-Hemolyzed	Not Tested	41	Year(s)	Male	African	African American	United States of America (USA)	Normal Donor	None
413624	57	Serum	10.5	Non-Hemolyzed	Not Tested	50	Year(s)	Male	Caucasian	N/A	United States of America (USA)	Normal Donor	None
413575	57	Urine	2	Non-Hemolyzed	Not Tested	50	Year(s)	Male	Caucasian	N/A	United States of America (USA)	Normal Donor	None
Type 2 diabeties													
411578	32	Serum	13.5	Non-Hemolyzed	N/A	40	Year(s)	Female	Caucasian	N/A	United States of America (USA)	Type 2 Diabetes, Polycystic Ovary Syndrome (PCOS)	Metformin 500mg
411545	32	Urine	32.5	Non-Hemolyzed	N/A	40	Year(s)	Female	Caucasian	N/A	United States of America (USA)	Type 2 Diabetes, Polycystic Ovary Syndrome (PCOS)	Metformin 500mg
411521	119	Serum	6	Non-Hemolyzed	N/A	55	Year(s)	Female	Other	N/A	United States of America (USA)	Type 2 Diabetes	Lasix 40mg, Metformin 1000mg, Levothyroxine 0.075mg, Novolog 80units, Levemir 220mg, Omeprazole 40mg, Carvedilol 25mg
411480	119	Urine	24.5	Non-Hemolyzed	N/A	55	Year(s)	Female	Other	N/A	United States of America (USA)	Type 2 Diabetes	Lasix 40mg, Metformin 1000mg, Levothyroxine 0.075mg, Novolog 80units, Levemir 220mg, Omeprazole 40mg, Carvedilol 25mg
380715	72	Serum	11	Non-Hemolyzed	N/A	51	Year(s)	Male	N/A	Hispanic	United States of America (USA)	Type 2 Diabetes, Hypertension (HTN)	Losartan 25mg, Aspirin 81mg, Lisinopril 5mg, Metformin 500mg
380716	72	Urine	31.5	Non-Hemolyzed	N/A	51	Year(s)	Male	N/A	Hispanic	United States of America (USA)	Glucose >110, Hypertension (HTN), Type 2 Diabetes	Losartan 25mg, Aspirin 81mg, Lisinopril 5mg, Metformin 500mg
414123	101	Serum	15.5	Non-Hemolyzed	N/A	62	Year(s)	Male	Caucasian	N/A	United States of America (USA)	Type 2 Diabetes, Gouty Arthritis	Allopurinol 300mg, Benazepril 20mg, Atorvastatin 40mg, Clopidogrel 75mg, Cyclobenzaprine 10mg
414100	101	Urine	27.5	Non-Hemolyzed	N/A	62	Year(s)	Male	Caucasian	N/A	United States of America (USA)	Type 2 Diabetes, Gouty Arthritis	Allopurinol 300mg, Benazepril 20mg, Atorvastatin 40mg, Clopidogrel 75mg, Cyclobenzaprine 10mg
DKD													
177774	3	Serum	2	Non-Hemolyzed	Negative	60	Year(s)	Male	Caucasian	N/A	United States of America (USA)	Diabetic Nephropathy, Diabetic Neuropathy, Type 2 Diabetes, Dyslipidemia, Hypertension (HTN), Hypogonadism, Thyroid Goiter, Gastroesophageal Reflux Disease (GERD), Sleep Apnea, Erectile Dysfunction (ED), Chronic Lumbar Pain	Lantus 30units, Novolin 30units, Novolog 10units, Metformin 1000mg, Ultracet 37.5mg-325mg, Cymbalta 60mg, Jyrica 150mg, Loratadine 10mg, Lovastatin 40mg, Lisinopril 40mg

177792	3	Urine	1.5	Non-Hemolyzed	Negative	60	Year(s)	Male	Caucasian	N/A	United States of America (USA)	Diabetic Nephropathy, Diabetic Neuropathy, Type 2 Diabetes, Dyslipidemia, Hypertension (HTN), Hypogonadism, Thyroid Goiter, Gastroesophageal Reflux Disease (GERD), Sleep Apnea, Erectile Dysfunction (ED), Chronic Lumbar Pain	Lantus 30units, Novolin 30units, Novolog 10units, Metformin 1000mg, Ultracet 37.5mg-325mg, Cymbalta 60mg, Jyrica 150mg, Loratadine 10mg, Lovastatin 40mg, Lisinopril 40mg				
427574	4	Serum	15.5	Non-Hemolyzed	Not Tested	73	Year(s)	Male	Caucasian	N/A	United States of America (USA)	Coronary Artery Disease (CAD), Diabetic Nephropathy, Diabetic Neuropathy, Type 2 Diabetes, Umbilical Hernia, Gastric Polyp, Gastroesophageal Reflux Disease (GERD), Deviated Septum, Dyslipidemia, Erectile Dysfunction (ED), Obesity, Vitamin D Deficiency, Hypertension (HTN)	Novolin 2iu-40iu, Metformin 1000mg, Simvastatin 20mg, Omeprazole 20mg, Zetia 10mg, Aspirin 81mg, Amlodipine 10mg, Lisinopril 20mg				
427551	4	Urine	21.5	Non-Hemolyzed	Not Tested	73	Year(s)	Male	Caucasian	N/A	United States of America (USA)	Coronary Artery Disease (CAD), Diabetic Nephropathy, Diabetic Neuropathy, Type 2 Diabetes, Umbilical Hernia, Gastric Polyp, Gastroesophageal Reflux Disease (GERD), Deviated Septum, Dyslipidemia, Erectile Dysfunction (ED), Obesity, Vitamin D Deficiency, Hypertension (HTN)	Novolin 2iu-40iu, Metformin 1000mg, Simvastatin 20mg, Omeprazole 20mg, Zetia 10mg, Aspirin 81mg, Amlodipine 10mg, Lisinopril 20mg				
368259	30	Serum	5.5	Non-Hemolyzed	N/A	68	Year(s)	Male	Caucasian	N/A	United States of America (USA)	Diabetic Nephropathy, Hypertension (HTN), Dyslipidemia, Allergy to Penicillin, Vitamin D Deficiency, Erectile Dysfunction, Obesity, Lumbar Disc Disease, Coronary Artery Disease (CAD), Type 2 Diabetes, Benign Prostatic Hyperplasia (BPH), Gastroesophageal Reflux Disease (GERD)	Metaglip 5-500mg, Actos 15mg, Atenolol 25mg, Nitro 0.4mg, Lisinopril 20mg, Caduet 5-20mg, Omacor 1g, Ranitidine 150mg, Vitamin D 5000iu, Nexium 40mg, Zetia 10mg				
368260	30	Urine	8.5	Non-Hemolyzed	N/A	68	Year(s)	Male	Caucasian	N/A	United States of America (USA)	Diabetic Nephropathy, Hypertension (HTN), Dyslipidemia, Allergy to Penicillin, Vitamin D Deficiency, Erectile Dysfunction, Obesity, Lumbar Disc Disease, Coronary Artery Disease (CAD), Type 2 Diabetes, Benign Prostatic Hyperplasia (BPH), Gastroesophageal Reflux Disease (GERD)	Metaglip 5-500mg, Actos 15mg, Atenolol 25mg, Nitro 0.4mg, Lisinopril 20mg, Caduet 5-20mg, Omacor 1g, Ranitidine 150mg, Vitamin D 5000iu, Nexium 40mg, Zetia 10mg				
221111	1	Urine	2.5	Non-Hemolyzed	N/A	67	Year(s)	Male	N/A	Hispanic	United States of America (USA)	Diabetic Nephropathy, Type 2 Diabetes	Metformin 500mg, Lantus 15units				
221069	1	Serum	5	Non-Hemolyzed	N/A	67	Year(s)	Male	N/A	Hispanic	United States of America (USA)	Diabetic Nephropathy, Type 2 Diabetes	Metformin 500mg, Lantus 15units				

Supplemental Table 2: Summary of protein identification of Biotin-TPL pulldown from fibrotic mouse kidneys.

Band	Description	Protein ID	Gene ID	Aliases
1	E3 ubiquitin-protein ligase TRIM71	LIN-41	TRIM71	LIN-41, LIN41
2	TFIIH basal transcription factor complex helicase XPB subunit	ERCC3	ERCC3	BTF2, GTF2H, RAD25, TFIIH, TTD2, XPB
3	RNA-binding E3 ubiquitin-protein ligase MEX3C	MEX3C	MEX3C	BM-013, RNF194, RKHD2
4	E3 ubiquitin-protein ligase TRIM63	TRI63	TRIM63	MuRF1, Rnf28, RF1
5	26S proteasome non-ATPase regulatory subunit	PSD10	PSMD10	
6	dCTP pyrophosphatase 1	DCTP1	DCTPP1	CDA03, RS21C6, XTP3TPA

Biotin-TPL pulldown Band #1											
1.	LIN41_MOUSE Mass: 91996 Score: 16348 Matches: 345(345) Sequences: 5(5) emPAI: 0.46										
	E3 ubiquitin-protein ligase TRIM71 OS=Mus musculus GN=Trim71 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1321	416.9032	1247.6879	1247.6874	0.40	0	(71)	7.3e-007	1	U	R.LPAPGGAGPAEALK.L 1314
	1322	624.8513	1247.6881	1247.6874	0.58	0	95	3.1e-009	1	U	R.LPAPGGAGPAEALK.L 1300 1301 1302 1303 1304 1305 1306 1307 1308 1309 1310 1312 1313 1315 1316 1317 1318 1319 1320
	3144	499.9510	1496.8311	1496.8311	0.05	0	(90)	6.4e-009	1	U	R.ALTIQLLADAQQGR.Q 3051 3053 3062 3063 3068 3069 3070 3081 3082 3083 3093 3094 3095 3096 3097 3098 3099 3115 3116 3117 3127 3128 3140 3141 3142 3143 3145 3153 3154 3165 3166 3170 3171 3172 3173 3174
	3176	749.4231	1496.8316	1496.8311	0.39	0	113	3.3e-011	1	U	R.ALTIQLLADAQQGR.Q 3044 3045 3046 3047 3048 3050 3052 3054 3055 3057 3058 3059 3060 3061 3064 3065 3066 3067 3071 3072 3073 3074 3075 3076 3077 3078 3079 3080 3084 3085 3086 3087 3088 3089 3090 3091 3092 3100 3101 3102 3103 3104 3105 3106 3107 3108 3109 3110 3111 3112 3113 3114 3118 3119 3120 3121 3122 3123 3124 3125 3129 3130 3131 3132 3133 3134 3135 3136 3137 3138 3139 3146 3147 3148 3149 3150 3151 3152 3155 3156 3157 3158 3160 3161 3162 3163 3164 3167 3168 3175 3177

	3870	528.6324	1582.8755	1582.8759	-0.25	0	(86)	2e-008	1	U	R.IQIFTFEGQFLLK.F 3785 3789 3790 3793 3794 3795 3798 3810 3811 3812 3813 3814 3815 3816 3817 3818 3819 3830 3831 3832 3833 3834 3835 3836 3838 3839 3840 3865 3866 3867 3868 3869 3871 3887 3888 3889 3890 3891 3892 3893 3910 3912 3913 3917 3918 3925 3926 3928 3929 3931 3934 3935
	3916	792.4452	1582.8759	1582.8759	0.02	0	115	2.6e-011	1	U	R.IQIFTFEGQFLLK.F 3786 3787 3788 3791 3792 3796 3797 3800 3801 3802 3803 3804 3805 3806 3807 3808 3809 3821 3822 3823 3824 3825 3826 3827 3828 3829 3841 3842 3843 3844 3845 3846 3847 3848 3849 3850 3851 3852 3853 3854 3855 3856 3857 3858 3859 3860 3861 3862 3863 3864 3872 3873 3874 3875 3876 3877 3878 3879 3880 3881 3882 3883 3884 3885 3894 3895 3896 3897 3898 3899 3900 3901 3902 3903 3904 3905 3906 3907 3908 3909 3914 3915 3919 3920 3921 3927 3932 3933
	4667	825.8285	1649.6425	1649.6418	0.43	0	(59)	2.3e-006	1	U	R.CLDCQEHLCDNCVR.A 4664 4666
	4668	550.8882	1649.6427	1649.6418	0.52	0	(49)	2e-005	1	U	R.CLDCQEHLCDNCVR.A 4662 4663 4665
	5022	849.8207	1697.6268	1697.6266	0.13	0	80	1.3e-008	1	U	R.CLDCQEHLCDNCVR.A
	5269	574.3162	1719.9268	1719.9269	-0.06	0	(69)	1.2e-006	1	U	R.IMFTPPDQALYLALK.S 5245 5253 5257 5258 5265 5268 5270 5271 5284 5289 5290

	5286	860.9709	1719.9272	1719.9269	0.17	0	(88)	1.3e-008	1	U	R.IMFTPPDQALYLALK.S 5250 5251 5252 5255 5256 5277 5278 5279 5285 5287 5293
	5422	868.9681	1735.9216	1735.9219	-0.15	0	99	1.1e-009	1	U	R.IMFTPPDQALYLALK.S 5412 5414 5415 5416 5421 5424 5425 5426 5428 5429 5430
	5423	579.6478	1735.9217	1735.9219	-0.11	0	(61)	7.2e-006	1	U	R.IMFTPPDQALYLALK.S 5417 5418 5419 5427
	5484	873.8128	1745.6110	1745.6113	-0.16	0	(63)	4.6e-007	1	U	R.CLDCQEHLCDNCVR.A 5485 5486
2.	DDB1_MOUSE Mass: 126772 Score: 71 Matches: 2(2) Sequences: 2(2) emPAI: 0.07										
	DNA damage-binding protein 1 OS=Mus musculus GN=Ddb1 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1584	651.3133	1300.6120	1300.6122	-0.11	0	63	4.7e-006	1	U	K.GAVYSMVEFNGK.L
	4394	548.6348	1642.8827	1642.8831	-0.26	0	30	0.0092	1	U	R.ALYYLQIHPQELR.Q
3.	CO6A6_MOUSE Mass: 246169 Score: 51 Matches: 2(2) Sequences: 1(1) emPAI: 0.02										
	Collagen alpha-6(VI) chain OS=Mus musculus GN=Col6a6 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	74	378.7158	755.4171	755.4177	-0.78	1	33	0.00053	1	U	K.QGKEAIK.A 75
4.	OLIG1_MOUSE Mass: 27124 Score: 50 Matches: 1(1) Sequences: 1(1) emPAI: 0.17										
	Oligodendrocyte transcription factor 1 OS=Mus musculus GN=Olig1 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	262	435.7931	869.5716	869.5698	2.09	0	50	1.7e-005	1	U	K.IATLLLAR.N
	OLIG2_MOUSE Mass: 32386 Score: 50 Matches: 1(1) Sequences: 1(1)										
	Oligodendrocyte transcription factor 2 OS=Mus musculus GN=Olig2 PE=1 SV=1										
	OLIG3_MOUSE Mass: 29488 Score: 50 Matches: 1(1) Sequences: 1(1)										
	Oligodendrocyte transcription factor 3 OS=Mus musculus GN=Olig3 PE=2 SV=1										
5.	HA23_MOUSE Mass: 29089 Score: 50 Matches: 2(2) Sequences: 1(1) emPAI: 0.16										
	H-2 class II histocompatibility antigen, E-U alpha chain OS=Mus musculus GN=H2-Ea PE=2 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide

	341	464.3030	926.5913	926.5913	0.08	0	35	0.00071	1	U	M.ATIGALLLR.F 339
6.	CCNF_MOUSE Mass: 86568 Score: 46 Matches: 2(2) Sequences: 1(1) emPAI: 0.05										
	Cyclin-F OS=Mus musculus GN=Ccnf PE=2 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	562	499.8214	997.6282	997.6284	-0.16	0	35	0.00068	1	U	R.LASAALLLAR.L 561
7.	COG2_MOUSE Mass: 81988 Score: 45 Matches: 1(1) Sequences: 1(1) emPAI: 0.05										
	Conserved oligomeric Golgi complex subunit 2 OS=Mus musculus GN=Cog2 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	340	464.3029	926.5912	926.5913	-0.12	0	45	6.5e-005	1	U	R.LTLQILAR.F
8.	NPA1P_MOUSE Mass: 254452 Score: 44 Matches: 2(2) Sequences: 1(1) emPAI: 0.02										
	Nucleolar pre-ribosomal-associated protein 1 OS=Mus musculus GN=Urb1 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	2284	704.8988	1407.7830	1407.7908	-5.50	2	34	0.0021	1	U	R.ATIIKLFKDMGR.F 2287
9.	EDC4_MOUSE Mass: 152389 Score: 38 Matches: 1(1) Sequences: 1(1) emPAI: 0.03										
	Enhancer of mRNA-decapping protein 4 OS=Mus musculus GN=Edc4 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	268	436.7328	871.4511	871.4512	-0.08	0	38	0.001	1	U	R.ALAEGQQR.G
10.	SMUF1_MOUSE Mass: 83303 Score: 36 Matches: 1(1) Sequences: 1(1) emPAI: 0.05										
	E3 ubiquitin-protein ligase SMURF1 OS=Mus musculus GN=Smurf1 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	2247	467.5773	1399.7100	1399.7096	0.29	0	36	0.0029	1	U	K.TDSITISVWNHK.K
11.	NBR1_MOUSE Mass: 109889 Score: 35 Matches: 1(1) Sequences: 1(1) emPAI: 0.04										
	Next to BRCA1 gene 1 protein OS=Mus musculus GN=Nbr1 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	666	531.7950	1061.5755	1061.5791	-3.34	1	35	0.0037	1	U	K.KDVLVPCLK.A
12.	DYSF_MOUSE Mass: 237759 Score: 34 Matches: 1(1) Sequences: 1(1) emPAI: 0.02										
	Dysferlin OS=Mus musculus GN=Dysf PE=1 SV=3										

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	248	431.7734	861.5323	861.5324	-0.06	0	34	0.00064	1	U	K.LQTIFLK.Y
13.	MK67I_MOUSE Mass: 36242 Score: 33 Matches: 1(1) Sequences: 1(1) emPAI: 0.13										
	MKI67 FHA domain-interacting nucleolar phosphoprotein OS=Mus musculus GN=Nifk PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	288	443.7591	885.5036	885.5032	0.41	0	33	0.004	1	U	K.ALTQIQGR.T
14.	PPR21_MOUSE Mass: 88282 Score: 31 Matches: 1(1) Sequences: 1(1) emPAI: 0.05										
	Protein phosphatase 1 regulatory subunit 21 OS=Mus musculus GN=Ppp1r21 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	576	501.8209	1001.6273	1001.6273	0.03	1	31	0.001	1	U	R.KILPYQLK.S
15.	RCOR3_MOUSE Mass: 49748 Score: 31 Matches: 3(3) Sequences: 1(1) emPAI: 0.19										
	REST corepressor 3 OS=Mus musculus GN=Rcor3 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	56	371.7083	741.4020	741.4021	-0.12	0	(16)	0.029	3	U	K.QVNSALK.Q
	81	380.2236	758.4326	758.4286	5.29	0	28	0.013	1	U	K.QVNSALK.Q 80
16.	ADRM1_MOUSE Mass: 42034 Score: 30 Matches: 1(1) Sequences: 1(1) emPAI: 0.11										
	Proteasomal ubiquitin receptor ADRM1 OS=Mus musculus GN=Adrm1 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	70	375.7127	749.4109	749.4105	0.52	1	30	0.002	1	U	R.AGKMSLK.G
17.	MTEF3_MOUSE Mass: 47328 Score: 30 Matches: 1(1) Sequences: 1(1) emPAI: 0.10										
	Transcription termination factor 3, mitochondrial OS=Mus musculus GN=Mterf3 PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	274	437.7916	873.5686	873.5688	-0.22	0	30	0.00093	1	U	K.QILLFLK.D
18.	CCL19_MOUSE Mass: 11903 Score: 30 Matches: 1(1) Sequences: 1(1) emPAI: 0.42										
	C-C motif chemokine 19 OS=Mus musculus GN=Ccl19 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	84	381.2495	760.4845	760.4807	5.02	2	30	0.00098	1	U	R.LKKSSAK.N

19.	VGLL3_MOUSE Mass: 35976 Score: 30 Matches: 1(1) Sequences: 1(1) emPAI: 0.13										
	Transcription cofactor vestigial-like protein 3 OS=Mus musculus GN=Vgll3 PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	909	571.7943	1141.5741	1141.5801	-5.32	0	30	0.009	1	U	R.IPAPQCDITK.T
20.	WDR12_MOUSE Mass: 47317 Score: 30 Matches: 1(1) Sequences: 1(1) emPAI: 0.10										
	Ribosome biogenesis protein WDR12 OS=Mus musculus GN=Wdr12 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	927	574.3108	1146.6071	1146.6073	-0.17	0	30	0.013	1	U	K.HVEFDFLIK.G
21.	MED1_MOUSE Mass: 167036 Score: 29 Matches: 1(1) Sequences: 1(1) emPAI: 0.03										
	Mediator of RNA polymerase II transcription subunit 1 OS=Mus musculus GN=Med1 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	3294	507.2599	1518.7578	1518.7579	-0.10	0	29	0.019	1	U	K.FNQNRPWSETIK.L
22.	XIRP2_MOUSE Mass: 427993 Score: 28 Matches: 1(1) Sequences: 1(1) emPAI: 0.01										
	Xin actin-binding repeat-containing protein 2 OS=Mus musculus GN=Xirp2 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	5161	856.9664	1711.9182	1711.9153	1.67	2	28	0.013	1	U	K.LKIVWPPCQEMPKK.N
23.	MMAD_MOUSE Mass: 32974 Score: 28 Matches: 1(1) Sequences: 1(1) emPAI: 0.14										
	Methylmalonic aciduria and homocystinuria type D homolog, mitochondrial OS=Mus musculus GN=Mmadhc PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	667	531.8132	1061.6119	1061.6155	-3.35	0	28	0.0066	1	U	K.LMILTVTQK.T
24.	PDIA6_MOUSE Mass: 48070 Score: 28 Matches: 1(1) Sequences: 1(1) emPAI: 0.09										
	Protein disulfide-isomerase A6 OS=Mus musculus GN=Pdia6 PE=1 SV=3										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	507	489.8103	977.6060	977.6096	-3.59	2	28	0.0029	1	U	R.KMKFALLK.G
25.	GT2D2_MOUSE Mass: 104511 Score: 28 Matches: 1(1) Sequences: 1(1) emPAI: 0.04										
	General transcription factor II-I repeat domain-containing protein 2 OS=Mus musculus GN=Gtf2ird2 PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	45	367.2157	732.4169	732.4204	-4.72	0	28	0.005	1	U	R.AAAMLIK.T

26.	BCAR1_MOUSE Mass: 94227 Score: 28 Matches: 2(2) Sequences: 1(1) emPAI: 0.05										
	Breast cancer anti-estrogen resistance protein 1 OS=Mus musculus GN=Bcar1 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1059	598.3398	1194.6650	1194.6682	-2.68	1	26	0.016	1	U	R.LKILVGMYDK.K 1057
27.	ARLY_MOUSE Mass: 51707 Score: 27 Matches: 1(1) Sequences: 1(1) emPAI: 0.09										
	Argininosuccinate lyase OS=Mus musculus GN=Asl PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1507	642.8795	1283.7445	1283.7561	-9.04	2	27	0.01	1	U	R.RLKELIGEAAGK.L
28.	ANCHR_MOUSE Mass: 43245 Score: 27 Matches: 1(1) Sequences: 1(1) emPAI: 0.10										
	Abscission/NoCut checkpoint regulator OS=Mus musculus GN=Zfyve19 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1071	599.3693	1196.7241	1196.7353	-9.36	2	27	0.0062	1	U	R.QERILALAKR.L
29.	ANR28_MOUSE Mass: 112826 Score: 27 Matches: 2(2) Sequences: 1(1) emPAI: 0.04										
	Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit A OS=Mus musculus GN=Ankrd28 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	4204	809.4370	1616.8595	1616.8443	9.36	0	26	0.029	1	U	R.AVASCSEEAVQILLK.H 4207
30.	ANGP4_MOUSE Mass: 57769 Score: 27 Matches: 1(1) Sequences: 1(1) emPAI: 0.08										
	Angiopoietin-4 OS=Mus musculus GN=Angpt4 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	312	455.2140	908.4134	908.4208	-8.11	0	27	0.012	1	U	R.QMLMQSR.E
31.	RGS9_MOUSE Mass: 76929 Score: 27 Matches: 1(1) Sequences: 1(1) emPAI: 0.06										
	Regulator of G-protein signaling 9 OS=Mus musculus GN=Rgs9 PE=1 SV=3										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	915	572.3058	1142.5970	1142.6084	-9.92	2	27	0.023	1	U	K.KDSYARYLK.S
32.	ADCY7_MOUSE Mass: 122628 Score: 27 Matches: 1(1) Sequences: 1(1) emPAI: 0.04										
	Adenylate cyclase type 7 OS=Mus musculus GN=Adcy7 PE=2 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide

	795	554.7768	1107.5390	1107.5304	7.79	0	27	0.022	1	U	K.MGLDICEAIK.Q
33.	ITPR3_MOUSE Mass: 304080 Score: 27 Matches: 2(2) Sequences: 2(2) emPAI: 0.03										
	Inositol 1,4,5-trisphosphate receptor type 3 OS=Mus musculus GN=Itpr3 PE=1 SV=3										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	81	380.2236	758.4326	758.4286	5.31	1	25	0.024	2	U	R.NAGEKIK.Y
	147	400.7221	799.4297	799.4300	-0.46	0	21	0.028	1	U	K.AAGLGAQGR.T
34.	CBX2_MOUSE Mass: 54885 Score: 27 Matches: 1(1) Sequences: 1(1) emPAI: 0.08										
	Chromobox protein homolog 2 OS=Mus musculus GN=Cbx2 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	173	409.7241	817.4337	817.4368	-3.77	0	27	0.026	1	U	K.CGLGLDLK.V
35.	HMCS2_MOUSE Mass: 56786 Score: 27 Matches: 1(1) Sequences: 1(1) emPAI: 0.08										
	Hydroxymethylglutaryl-CoA synthase, mitochondrial OS=Mus musculus GN=Hmgcs2 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	696	536.3113	1070.6081	1070.6019	5.86	1	27	0.019	1	U	-.MQRLLAPAR.R
36.	PKHG6_MOUSE Mass: 89093 Score: 27 Matches: 2(2) Sequences: 1(1) emPAI: 0.05										
	Pleckstrin homology domain-containing family G member 6 OS=Mus musculus GN=Plekhg6 PE=2 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	430	471.7902	941.5658	941.5658	-0.03	0	26	0.014	1	U	R.LTLAQLQR.M 429
37.	FAS_MOUSE Mass: 272257 Score: 26 Matches: 1(1) Sequences: 1(1) emPAI: 0.02										
	Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	170	408.7341	815.4537	815.4541	-0.52	0	26	0.032	1	U	R.WVSSPLK.H
38.	ZFAN4_MOUSE Mass: 81502 Score: 26 Matches: 2(2) Sequences: 1(1) emPAI: 0.05										
	AN1-type zinc finger protein 4 OS=Mus musculus GN=Zfand4 PE=4 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	193	416.2762	830.5378	830.5411	-4.01	2	22	0.013	1	U	K.MKLLKAK.M 192
39.	DSCR6_MOUSE Mass: 16954 Score: 26 Matches: 1(1) Sequences: 1(1) emPAI: 0.28										

	Protein ripply3 OS=Mus musculus GN=Ripply3 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	196	417.6836	833.3526	833.3515	1.28	0	26	0.0052	1	U	R.DSAQEER.A
40.	PDE7B_MOUSE Mass: 51304 Score: 26 Matches: 1(1) Sequences: 1(1) emPAI: 0.09										
	cAMP-specific 3',5'-cyclic phosphodiesterase 7B OS=Mus musculus GN=Pde7b PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	772	550.7341	1099.4536	1099.4460	6.86	0	26	0.012	1	U	K.CVCMLGDVR.L
41.	NIM1_MOUSE Mass: 49746 Score: 25 Matches: 1(1) Sequences: 1(1) emPAI: 0.09										
	Serine/threonine-protein kinase NIM1 OS=Mus musculus GN=Nim1k PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	246	431.7369	861.4593	861.4596	-0.33	0	25	0.026	1	U	R.QLTPFEK.L
42.	KI26A_MOUSE Mass: 196191 Score: 25 Matches: 1(1) Sequences: 1(1) emPAI: 0.02										
	Kinesin-like protein KIF26A OS=Mus musculus GN=Kif26a PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	309	451.7708	901.5269	901.5345	-8.36	2	25	0.033	1	U	R.SRSLKSPK.K
43.	CC162_MOUSE Mass: 104270 Score: 25 Matches: 1(1) Sequences: 1(1) emPAI: 0.04										
	Coiled-coil domain-containing protein 162 OS=Mus musculus GN=Ccdc162p PE=1 SV=4										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1625	656.8426	1311.6706	1311.6744	-2.88	1	25	0.035	1	U	R.EMTLFLSEKSK.E
44.	DLK1_MOUSE Mass: 41292 Score: 25 Matches: 1(1) Sequences: 1(1) emPAI: 0.11										
	Protein delta homolog 1 OS=Mus musculus GN=Dlk1 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	167	407.7608	813.5070	813.5072	-0.21	0	25	0.02	1	U	M.IATGALLR.V
45.	DYHC1_MOUSE Mass: 531710 Score: 25 Matches: 1(1) Sequences: 1(1) emPAI: 0.01										
	Cytoplasmic dynein 1 heavy chain 1 OS=Mus musculus GN=Dync1h1 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	148	401.2087	800.4029	800.4028	0.06	0	25	0.015	1	U	R.QNISPDK.I

46.	TEAN2_MOUSE Mass: 24185 Score: 25 Matches: 2(2) Sequences: 1(1) emPAI: 0.19										
	Transcription elongation factor A N-terminal and central domain-containing protein 2 OS=Mus musculus GN=Tceanc2 PE=2 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	136	396.2548	790.4950	790.4953	-0.31	0	20	0.011	1	U	R.ALVFTLK.H 138
47.	GOGA1_MOUSE Mass: 87284 Score: 25 Matches: 1(1) Sequences: 1(1) emPAI: 0.05										
	Golgin subfamily A member 1 OS=Mus musculus GN=Golga1 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	2929	740.3970	1478.7795	1478.7762	2.22	2	25	0.041	1	U	K.LQRELEALKTCK.A
48.	LBR_MOUSE Mass: 71395 Score: 24 Matches: 1(1) Sequences: 1(1) emPAI: 0.06										
	Lamin-B receptor OS=Mus musculus GN=Lbr PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	284	443.2795	884.5444	884.5443	0.09	1	24	0.018	1	U	R.REILQVK.L
49.	RPA1_MOUSE Mass: 193987 Score: 24 Matches: 1(1) Sequences: 1(1) emPAI: 0.02										
	DNA-directed RNA polymerase I subunit RPA1 OS=Mus musculus GN=Polr1a PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1222	614.8157	1227.6168	1227.6281	-9.24	1	24	0.035	1	U	R.SGYLQRCIIK.H
50.	M3K6_MOUSE Mass: 142964 Score: 24 Matches: 1(1) Sequences: 1(1) emPAI: 0.03										
	Mitogen-activated protein kinase kinase kinase 6 OS=Mus musculus GN=Map3k6 PE=1 SV=4										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	868	563.8506	1125.6867	1125.6771	8.60	1	24	0.009	1	U	R.IWRAILAQR.A
51.	PRP8_MOUSE Mass: 273443 Score: 24 Matches: 1(1) Sequences: 1(1) emPAI: 0.02										
	Pre-mRNA-processing-splicing factor 8 OS=Mus musculus GN=Prpf8 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	2129	692.8587	1383.7028	1383.7068	-2.86	0	24	0.046	1	U	R.QILMASGSTTFTK.I
52.	RIMS1_MOUSE Mass: 163061 Score: 24 Matches: 1(1) Sequences: 1(1) emPAI: 0.03										
	Regulating synaptic membrane exocytosis protein 1 OS=Mus musculus GN=Rims1 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	69	375.2315	748.4485	748.4483	0.20	0	24	0.004	1	U	R.LGAFITK.V

53.	LMOD2_MOUSE Mass: 61980 Score: 24 Matches: 1(1) Sequences: 1(1) emPAI: 0.07										
	Leiomodin-2 OS=Mus musculus GN=Lmod2 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	185	413.7466	825.4786	825.4708	9.43	0	24	0.021	1	U	K.QPNNILK.E
54.	CD158_MOUSE Mass: 126748 Score: 24 Matches: 1(1) Sequences: 1(1) emPAI: 0.03										
	Coiled-coil domain-containing protein 158 OS=Mus musculus GN=Ccdc158 PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1639	657.3621	1312.7096	1312.7099	-0.25	1	24	0.045	1	U	R.TPSLGALEDRVR.D
55.	CC177_MOUSE Mass: 79809 Score: 23 Matches: 1(1) Sequences: 1(1) emPAI: 0.06										
	Coiled-coil domain-containing protein 177 OS=Mus musculus GN=Ccdc177 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1020	592.3615	1182.7085	1182.7197	-9.45	2	23	0.022	1	U	R.RELLQAIGRK.L
56.	IMP4_MOUSE Mass: 33635 Score: 23 Matches: 1(1) Sequences: 1(1) emPAI: 0.14										
	U3 small nucleolar ribonucleoprotein protein IMP4 OS=Mus musculus GN=Imp4 PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	791	554.3318	1106.6490	1106.6521	-2.82	2	23	0.016	1	U	R.LKMFAKELK.L
57.	RFX6_MOUSE Mass: 102501 Score: 23 Matches: 1(1) Sequences: 1(1) emPAI: 0.04										
	DNA-binding protein RFX6 OS=Mus musculus GN=Rfx6 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	197	417.7395	833.4644	833.4647	-0.36	0	23	0.033	1	U	R.AQDFLLK.W
58.	CAMP2_MOUSE Mass: 164230 Score: 23 Matches: 1(1) Sequences: 1(1) emPAI: 0.03										
	Calmodulin-regulated spectrin-associated protein 2 OS=Mus musculus GN=Camsap2 PE=1 SV=3										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	514	491.2738	980.5330	980.5365	-3.53	1	23	0.034	1	U	K.KMIEGLYK.Y
59.	BI1_MOUSE Mass: 26460 Score: 23 Matches: 1(1) Sequences: 1(1) emPAI: 0.18										
	Bax inhibitor 1 OS=Mus musculus GN=Tmbim6 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide

	1835	668.3874	1334.7602	1334.7632	-2.19	1	23	0.027	1	U	R.KLMLILAFNEK.D
60.	MSL2_MOUSE Mass: 62497 Score: 23 Matches: 1(1) Sequences: 1(1) emPAI: 0.07										
	E3 ubiquitin-protein ligase MSL2 OS=Mus musculus GN=Msl2 PE=2 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	570	501.1999	1000.3853	1000.3776	7.68	0	23	0.01	1	U	K.ACLDCICR.G
61.	LRIF1_MOUSE Mass: 82946 Score: 22 Matches: 1(1) Sequences: 1(1) emPAI: 0.05										
	Ligand-dependent nuclear receptor-interacting factor 1 OS=Mus musculus GN=Lrif1 PE=2 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	253	432.7505	863.4865	863.4865	0.01	0	22	0.032	1	U	K.IPAHAEVK.S
62.	SPD2B_MOUSE Mass: 101454 Score: 22 Matches: 1(1) Sequences: 1(1) emPAI: 0.04										
	SH3 and PX domain-containing protein 2B OS=Mus musculus GN=Sh3pxd2b PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	60	372.6979	743.3812	743.3814	-0.21	0	22	0.013	1	U	R.QDGLSPK.E
63.	KLDC3_MOUSE Mass: 43054 Score: 22 Matches: 1(1) Sequences: 1(1) emPAI: 0.11										
	Kelch domain-containing protein 3 OS=Mus musculus GN=Klhdc3 PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	260	435.7375	869.4604	869.4654	-5.69	2	22	0.028	1	U	K.GKGPCPRR.R
64.	CROCC_MOUSE Mass: 226809 Score: 22 Matches: 1(1) Sequences: 1(1) emPAI: 0.02										
	Rootletin OS=Mus musculus GN=Crocc PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1634	656.8827	1311.7509	1311.7623	-8.62	1	22	0.043	1	U	R.LLQERLGSLQR.A
65.	IQEC2_MOUSE Mass: 161687 Score: 22 Matches: 1(1) Sequences: 1(1) emPAI: 0.03										
	IQ motif and SEC7 domain-containing protein 2 OS=Mus musculus GN=Iqsec2 PE=1 SV=3										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	585	505.2713	1008.5280	1008.5314	-3.37	1	22	0.044	1	U	K.MKLDDFIK.N
66.	ATAD5_MOUSE Mass: 203783 Score: 22 Matches: 1(1) Sequences: 1(1) emPAI: 0.02										
	ATPase family AAA domain-containing protein 5 OS=Mus musculus GN=Atad5 PE=1 SV=1										

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	226	427.2627	852.5109	852.5069	4.72	1	22	0.023	1	U	R.KLPPSSPK.T
67.	TAF4B_MOUSE Mass: 90028 Score: 22 Matches: 1(1) Sequences: 1(1) emPAI: 0.05										
	Transcription initiation factor TFIID subunit 4B OS=Mus musculus GN=Taf4b PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	513	491.2737	980.5328	980.5365	-3.73	0	22	0.047	1	U	K.NFLSMLIK.L
68.	CLC1A_MOUSE Mass: 30938 Score: 21 Matches: 1(1) Sequences: 1(1) emPAI: 0.15										
	C-type lectin domain family 1 member A OS=Mus musculus GN=Clec1a PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	897	569.8289	1137.6432	1137.6506	-6.54	1	21	0.036	1	U	R.IAGRVVPGELQ.-
69.	LSG1_MOUSE Mass: 73111 Score: 21 Matches: 1(1) Sequences: 1(1) emPAI: 0.06										
	Large subunit GTPase 1 homolog OS=Mus musculus GN=Lsg1 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	225	427.2425	852.4705	852.4678	3.22	2	21	0.033	1	U	K.KHGNRNK.K
70.	RT18A_MOUSE Mass: 22307 Score: 21 Matches: 1(1) Sequences: 1(1) emPAI: 0.21										
	28S ribosomal protein S18a, mitochondrial OS=Mus musculus GN=Mrps18a PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	616	517.7977	1033.5808	1033.5709	9.59	1	21	0.042	1	U	R.YLTRWAPK.S
71.	AR13B_MOUSE Mass: 48114 Score: 21 Matches: 1(1) Sequences: 1(1) emPAI: 0.09										
	ADP-ribosylation factor-like protein 13B OS=Mus musculus GN=Arl13b PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	191	416.2706	830.5266	830.5225	4.90	2	21	0.024	1	U	K.KIDKSIK.K
72.	FAN_MOUSE Mass: 104479 Score: 21 Matches: 1(1) Sequences: 1(1) emPAI: 0.04										
	Protein FAN OS=Mus musculus GN=Nsmaf PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	2481	718.9109	1435.8072	1435.7935	9.53	1	21	0.038	1	U	K.LQLHEQYKIHK.E
73.	ATS16_MOUSE Mass: 136193 Score: 21 Matches: 2(2) Sequences: 1(1) emPAI: 0.03										

	A disintegrin and metalloproteinase with thrombospondin motifs 16 OS=Mus musculus GN=Adamts16 PE=2 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	675	533.7094	1065.4043	1065.4033	0.90	0	20	0.018	1	U	K.DGTPCSEDSR.N 676
74.	SSF1_MOUSE Mass: 52724 Score: 21 Matches: 1(1) Sequences: 1(1) emPAI: 0.09										
	Suppressor of SWI4 1 homolog OS=Mus musculus GN=Ppan PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	247	431.7552	861.4959	861.4994	-3.96	0	21	0.03	1	U	R.MTLQLIK.I
75.	NRAP_MOUSE Mass: 195633 Score: 20 Matches: 1(1) Sequences: 1(1) emPAI: 0.02										
	Nebulin-related-anchoring protein OS=Mus musculus GN=Nrap PE=1 SV=3										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	257	434.7663	867.5180	867.5112	7.84	1	20	0.027	1	U	R.RMLHALK.V
76.	ASH1L_MOUSE Mass: 331126 Score: 20 Matches: 1(1) Sequences: 1(1) emPAI: 0.01										
	Histone-lysine N-methyltransferase ASH1L OS=Mus musculus GN=Ash1l PE=1 SV=3										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1595	652.8823	1303.7500	1303.7500	-0.00	1	20	0.045	1	U	K.IPASKVFSLQSK.E
77.	ATR_MOUSE Mass: 300030 Score: 20 Matches: 1(1) Sequences: 1(1) emPAI: 0.01										
	Serine/threonine-protein kinase ATR OS=Mus musculus GN=Atr PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	280	441.7741	881.5337	881.5334	0.27	0	20	0.026	1	U	R.IHALTSLK.E
78.	TRRAP_MOUSE Mass: 291370 Score: 19 Matches: 2(2) Sequences: 2(2) emPAI: 0.03										
	Transformation/transcription domain-associated protein OS=Mus musculus GN=Trrap PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	79	379.7298	757.4451	757.4446	0.64	0	21	0.039	1	U	R.LATVQAR.G
	196	417.6836	833.3526	833.3524	0.22	0	16	0.05	2	U	K.ACVDPACR.Y
79.	ANR22_MOUSE Mass: 21895 Score: 19 Matches: 1(1) Sequences: 1(1) emPAI: 0.22										
	Ankyrin repeat domain-containing protein 22 OS=Mus musculus GN=Ankrd22 PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1603	654.3895	1306.7645	1306.7683	-2.86	1	19	0.027	1	U	R.LKFSQIALMLK.R

80. MICA1_MOUSE Mass: 116711 Score: 19 Matches: 1(1) Sequences: 1(1) emPAI: 0.04

[F-actin]-methionine sulfoxide oxidase MICAL1 OS=Mus musculus GN=Mical1 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
5037	850.4907	1698.9669	1698.9515	9.03	2	19	0.046	1	U	R.ELEAEGTKLELALRK.E

81. K22E_MOUSE Mass: 70880 Score: 19 Matches: 1(1) Sequences: 1(1) emPAI: 0.06

Keratin, type II cytoskeletal 2 epidermal OS=Mus musculus GN=Krt2 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2435	715.8023	1429.5901	1429.5818	5.75	0	19	0.04	1	U	R.GSGSGSGGGGYSSGGGSR.G

82. S27A2_MOUSE Mass: 70378 Score: 19 Matches: 1(1) Sequences: 1(1) emPAI: 0.06

Very long-chain acyl-CoA synthetase OS=Mus musculus GN=Slc27a2 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
462	480.7974	959.5802	959.5837	-3.66	1	19	0.038	1	U	R.IGMASLKIK.E

83. AKTIP_MOUSE Mass: 32921 Score: 18 Matches: 1(1) Sequences: 1(1) emPAI: 0.14

AKT-interacting protein OS=Mus musculus GN=Aktip PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
120	391.7442	781.4738	781.4698	5.14	0	18	0.037	1	U	K.QLPSIPK.N

84. NRIP1_MOUSE Mass: 126259 Score: 18 Matches: 1(1) Sequences: 1(1) emPAI: 0.03

Nuclear receptor-interacting protein 1 OS=Mus musculus GN=Nrip1 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
53	371.2291	740.4437	740.4432	0.64	0	18	0.023	1	U	K.IPGVDIK.E

85. CE042_MOUSE Mass: 358324 Score: 17 Matches: 1(1) Sequences: 1(1) emPAI: 0.01

Protein JBTS17 OS=Mus musculus GN=Jbts17 PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
8	353.2183	704.4221	704.4221	0.06	0	17	0.022	1	U	R.AGLFGLK.Q

86. TENA_MOUSE Mass: 231659 Score: 15 Matches: 1(1) Sequences: 1(1) emPAI: 0.02

Tenascin OS=Mus musculus GN=Tnc PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide

	684	535.2133	1068.4120	1068.4077	4.02	1	15	0.047	1	U	R.CPRDCSQR.G
87.	DDX1_MOUSE Mass: 82448 Score: 15 Matches: 1(1) Sequences: 1(1) emPAI: 0.05										
	ATP-dependent RNA helicase DDX1 OS=Mus musculus GN=Ddx1 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	110	388.2575	774.5005	774.4963	5.35	2	15	0.028	1	U	K.KGKTTIK.T
88.	ETAA1_MOUSE Mass: 96492 Score: 15 Matches: 2(2) Sequences: 2(2) emPAI: 0.09										
	Ewing's tumor-associated antigen 1 homolog OS=Mus musculus GN=Etaa1 PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	64	373.1829	744.3513	744.3515	-0.23	0	13	0.046	1	U	R.QAAADGGR.S
	70	375.7127	749.4109	749.4105	0.52	1	17	0.047	2	U	K.ASCTKLK.T
89.	MUC19_MOUSE Mass: 693090 Score: 15 Matches: 1(1) Sequences: 1(1) emPAI: 0.01										
	Mucin-19 OS=Mus musculus GN=Muc19 PE=2 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1013	590.7309	1179.4472	1179.4359	9.65	0	15	0.044	1	U	R.GCYCPVGMVR.N
90.	DOCK3_MOUSE Mass: 232760 Score: 15 Matches: 1(1) Sequences: 1(1) emPAI: 0.02										
	Dedicator of cytokinesis protein 3 OS=Mus musculus GN=Dock3 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	183	412.2554	822.4963	822.4963	-0.02	0	15	0.039	1	U	K.LPIPIDR.F
91.	FBXL8_MOUSE Mass: 41119 Score: 15 Matches: 1(1) Sequences: 1(1) emPAI: 0.11										
	F-box/LRR-repeat protein 8 OS=Mus musculus GN=Fbxl8 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	251	432.6706	863.3266	863.3266	0.02	0	15	0.035	1	U	R.CACPEDAR.A
92.	ACATN_MOUSE Mass: 61036 Score: 14 Matches: 1(1) Sequences: 1(1) emPAI: 0.07										
	Acetyl-coenzyme A transporter 1 OS=Mus musculus GN=Slc33a1 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	195	417.2782	832.5418	832.5422	-0.43	0	14	0.035	1	U	K.LLFSIIK.M
93.	STAB1_MOUSE Mass: 276074 Score: 14 Matches: 1(1) Sequences: 1(1) emPAI: 0.02										

	Stabilin-1 OS=Mus musculus GN=Stab1 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	4746	554.8760	1661.6061	1661.5967	5.66	0	14	0.046	1	U	K.CPQNSQCSAEAPTCK.C
94.	TSP1_MOUSE Mass: 129564 Score: 13 Matches: 1(1) Sequences: 1(1) emPAI: 0.03										
	Thrombospondin-1 OS=Mus musculus GN=Thbs1 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	30	361.1414	720.2682	720.2675	0.97	0	13	0.047	1	U	K.DSDGDGR.G

Biotin-TPL pulldown Band #2											
1.	ERCC3_MOUSE Mass: 89070 Score: 15598 Matches: 319(319) Sequences: 5(5) emPAI: 0.47										
	TFIIH basal transcription factor complex helicase XPB subunit OS=Mus musculus GN=Ercc3 PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1341	644.3686	1286.7226	1286.7235	-0.64	0	74	3.1e-007	1	U	K.TGVPDGIIQFIK.L 1334 1335 1340 1343 1344 1345 1346 1353 1354 1358 1359 1360
	1349	429.9150	1286.7231	1286.7235	-0.26	0	(63)	4.4e-006	1	U	K.TGVPDGIIQFIK.L 1348 1357
	3314	777.8713	1553.7280	1553.7283	-0.18	0	127	2.3e-012	1	U	K.LAGMEEEELAFSTK.E 3246 3247 3248 3249 3250 3251 3252 3253 3254 3255 3256 3257 3258 3259 3260 3261 3262 3263 3264 3265 3266 3267 3268 3269 3270 3271 3273 3275 3276 3277 3278 3281 3282 3283 3284 3285 3286 3287 3288 3289 3290 3291 3292 3293 3294 3296 3297 3298 3299 3300 3301 3302 3303 3304 3305 3306 3307 3308 3309 3310 3311 3312 3313 3315 3316 3317 3318 3319 3320 3321 3322 3323 3324 3325 3326 3327 3328 3329 3330 3331 3332 3333 3334 3335 3336 3337 3338 3339 3340 3341 3342 3343 3344 3345 3346 3347 3348 3349 3350 3351 3354 3356 3357 3358 3361 3362 3363 3364 3365 3366 3367 3368 3369 3370 3371 3372 3374 3376 3377
	3359	518.9167	1553.7284	1553.7283	0.09	0	(78)	1.7e-007	1	U	K.LAGMEEEELAFSTK.E 3373

	3479	524.2481	1569.7223	1569.7232	-0.56	0	(69)	1.1e-006	1	U	K.LAGMEEEELAFSTK.E 3530 3564 3565 3585 3586 3587 3622 3624 3625
	3529	785.8687	1569.7227	1569.7232	-0.29	0	(115)	3e-011	1	U	K.LAGMEEEELAFSTK.E 3465 3466 3467 3468 3469 3470 3471 3472 3473 3474 3476 3477 3478 3480 3482 3484 3485 3486 3487 3488 3489 3490 3491 3492 3493 3494 3495 3496 3497 3498 3499 3500 3501 3502 3503 3505 3506 3507 3508 3509 3510 3511 3512 3513 3515 3516 3517 3518 3519 3520 3521 3522 3523 3524 3525 3526 3527 3528 3531 3532 3533 3534 3536 3537 3538 3539 3540 3541 3542 3543 3544 3545 3547 3548 3549 3550 3551 3552 3553 3554 3555 3556 3557 3558 3559 3560 3561 3562 3563 3566 3567 3568 3569 3572 3573 3574 3575 3576 3577 3578 3579 3580 3581 3582 3583 3584 3588 3589 3590 3591 3592 3593 3594 3595 3596 3597 3598 3599 3600 3601 3602 3603 3604 3605 3606 3607 3608 3609 3610 3611 3612 3614 3615 3616 3618 3619 3620 3621 3623 3626
	4073	816.9242	1631.8338	1631.8341	-0.18	0	101	1.2e-009	1	U	R.CLVLGNSAVSVEQWK.A 4064 4066 4071 4072 4080 4087 4089 4090

	4078	544.9520	1631.8341	1631.8341	-0.02	0	(57)	2.3e-005	1	U	R.CLVLGNSAVSVEQWK.A 4058 4065 4074 4076 4077 4082
	4438	840.9165	1679.8184	1679.8189	-0.25	0	(88)	2.3e-008	1	U	R.CLVLGNSAVSVEQWK.A 4437
	4439	560.9468	1679.8187	1679.8189	-0.10	0	(34)	0.0051	1	U	R.CLVLGNSAVSVEQWK.A
	4655	861.9440	1721.8734	1721.8737	-0.16	0	75	3.9e-007	1	U	R.LNKPYIYGPTSQGER.M 4654
	4663	574.9655	1721.8745	1721.8737	0.50	0	(60)	1.5e-005	1	U	R.LNKPYIYGPTSQGER.M 4656 4658 4659 4660 4661
	5102	924.4386	1846.8626	1846.8633	-0.38	0	44	0.00037	1	U	R.CICLEYPLLAEYDFR.N
	5103	616.6284	1846.8633	1846.8633	-0.05	0	(38)	0.0015	1	U	R.CICLEYPLLAEYDFR.N
	5313	972.4235	1942.8324	1942.8328	-0.24	0	(41)	0.00043	1	U	R.CICLEYPLLAEYDFR.N
2.	LIN41_MOUSE Mass: 91996 Score: 333 Matches: 27(27) Sequences: 2(2) emPAI: 0.10										
	E3 ubiquitin-protein ligase TRIM71 OS=Mus musculus GN=Trim71 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	3697	792.4448	1582.8750	1582.8759	-0.60	0	68	1.1e-006	1	U	R.IQIFTFEGQFLLK.F
	4235	825.8281	1649.6417	1649.6418	-0.08	0	(47)	3.3e-005	1	U	R.CLDCQEHLCDNCVR.A 4249
	4247	550.8880	1649.6422	1649.6418	0.20	0	52	1.1e-005	1	U	R.CLDCQEHLCDNCVR.A 4225 4226 4227 4228 4229 4230 4232 4234 4236 4237 4238 4241 4245 4246 4251 4252 4253 4254 4255 4256 4257 4258 4261
3.	ZFAN1_MOUSE Mass: 30183 Score: 103 Matches: 6(6) Sequences: 1(1) emPAI: 0.15										
	AN1-type zinc finger protein 1 OS=Mus musculus GN=Zfand1 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	104	409.7604	817.5063	817.5095	-3.98	1	36	0.0008	1	U	K.VALMKLK.M 99 100 101 103 105
4.	MT21A_MOUSE Mass: 24271 Score: 43 Matches: 3(3) Sequences: 1(1) emPAI: 0.19										
	Protein N-lysine methyltransferase METTL21A OS=Mus musculus GN=Mettl21A PE=2 SV=1										

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	108	410.2524	818.4903	818.4902	0.12	0	30	0.0023	1	U	K.VALEFLK.S 106 107
5.	STXB4_MOUSE Mass: 61650 Score: 34 Matches: 1(1) Sequences: 1(1) emPAI: 0.07										
	Syntaxin-binding protein 4 OS=Mus musculus GN=Stxbp4 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	18	359.2107	716.4069	716.4068	0.06	0	34	0.0012	1	U	K.ETGLGLK.I
6.	COHA1_MOUSE Mass: 147884 Score: 32 Matches: 1(1) Sequences: 1(1) emPAI: 0.03										
	Collagen alpha-1(XVII) chain OS=Mus musculus GN=Col17a1 PE=1 SV=3										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	2929	755.8824	1509.7503	1509.7418	5.64	1	32	0.0069	1	U	K.EMELLIMTKDSGK.V
7.	UNC80_MOUSE Mass: 363275 Score: 30 Matches: 1(1) Sequences: 1(1) emPAI: 0.01										
	Protein unc-80 homolog OS=Mus musculus GN=Unc80 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	170	438.2711	874.5277	874.5276	0.13	0	30	0.0028	1	U	R.QLVQFIK.E
8.	ANPRB_MOUSE Mass: 116986 Score: 29 Matches: 1(1) Sequences: 1(1) emPAI: 0.04										
	Atrial natriuretic peptide receptor 2 OS=Mus musculus GN=Npr2 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	173	438.7632	875.5118	875.5116	0.19	0	29	0.0053	1	U	R.QVLFELK.H
9.	CDHR1_MOUSE Mass: 93969 Score: 28 Matches: 1(1) Sequences: 1(1) emPAI: 0.05										
	Cadherin-related family member 1 OS=Mus musculus GN=Cdhr1 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	182	444.2710	886.5275	886.5276	-0.12	0	28	0.017	1	U	R.APALPPPPK.M
10.	GRIP1_MOUSE Mass: 121982 Score: 28 Matches: 1(1) Sequences: 1(1) emPAI: 0.04										
	Glutamate receptor-interacting protein 1 OS=Mus musculus GN=Grip1 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	4307	553.6132	1657.8177	1657.8028	8.94	2	28	0.02	1	U	R.SLYSTSPRGTMMRR.R
11.	FMNL1_MOUSE Mass: 121983 Score: 28 Matches: 1(1) Sequences: 1(1) emPAI: 0.04										

	Formin-like protein 1 OS=Mus musculus GN=Fmnl1 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1252	637.8225	1273.6303	1273.6302	0.09	1	28	0.017	1	U	K.KAEQEVEQWK.K
12.	1A1L2_MOUSE Mass: 66086 Score: 27 Matches: 1(1) Sequences: 1(1) emPAI: 0.07										
	Probable inactive 1-aminocyclopropane-1-carboxylate synthase-like protein 2 OS=Mus musculus GN=Accsl PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	495	519.7846	1037.5547	1037.5579	-3.15	1	27	0.014	1	U	K.FVQEKMLK.F
13.	PLCD_MOUSE Mass: 43781 Score: 26 Matches: 1(1) Sequences: 1(1) emPAI: 0.10										
	1-acyl-sn-glycerol-3-phosphate acyltransferase delta OS=Mus musculus GN=Agpat4 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	85	401.2471	800.4796	800.4756	5.07	0	26	0.029	1	U	R.LGILGNSK.V
14.	PCAT2_MOUSE Mass: 60215 Score: 26 Matches: 1(1) Sequences: 1(1) emPAI: 0.07										
	Lysophosphatidylcholine acyltransferase 2 OS=Mus musculus GN=Lpcat2 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	118	416.2319	830.4493	830.4498	-0.54	0	26	0.031	1	U	K.NTINEIK.K
15.	P3C2A_MOUSE Mass: 190637 Score: 25 Matches: 1(1) Sequences: 1(1) emPAI: 0.02										
	Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit alpha OS=Mus musculus GN=Pik3c2a PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	2711	738.3326	1474.6507	1474.6585	-5.25	0	25	0.02	1	U	K.SCSFFSSNAMPLK.V
16.	AN34C_MOUSE Mass: 58135 Score: 25 Matches: 1(1) Sequences: 1(1) emPAI: 0.08										
	Ankyrin repeat domain-containing protein 34C OS=Mus musculus GN=Ankrd34c PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	484	517.2692	1032.5238	1032.5240	-0.21	0	25	0.035	1	U	K.VSASTPASWK.A
17.	KDM5D_MOUSE Mass: 176904 Score: 25 Matches: 1(1) Sequences: 1(1) emPAI: 0.02										
	Lysine-specific demethylase 5D OS=Mus musculus GN=Kdm5d PE=2 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	187	445.2791	888.5436	888.5466	-3.42	1	25	0.009	1	U	K.KLLVMGTK.V

18.	DHX36_MOUSE Mass: 113812 Score: 25 Matches: 1(1) Sequences: 1(1) emPAI: 0.04										
	ATP-dependent RNA helicase DHX36 OS=Mus musculus GN=Dhx36 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	325	470.2322	938.4499	938.4531	-3.49	0	25	0.028	1	U	K.LPSYGMQK.E
19.	AMER2_MOUSE Mass: 69890 Score: 24 Matches: 1(1) Sequences: 1(1) emPAI: 0.06										
	APC membrane recruitment protein 2 OS=Mus musculus GN=Amer2 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	27	365.2105	728.4065	728.4069	-0.46	0	24	0.008	1	U	K.TGDVPIK.T
20.	UBP24_MOUSE Mass: 293814 Score: 24 Matches: 1(1) Sequences: 1(1) emPAI: 0.01										
	Ubiquitin carboxyl-terminal hydrolase 24 OS=Mus musculus GN=Usp24 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	55	389.2106	776.4066	776.4028	4.91	0	24	0.019	1	U	R.QQSVSTK.D
21.	RYR2_MOUSE Mass: 564458 Score: 24 Matches: 1(1) Sequences: 1(1) emPAI: 0.01										
	Ryanodine receptor 2 OS=Mus musculus GN=Ryr2 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1483	652.8276	1303.6407	1303.6408	-0.07	1	24	0.041	1	U	K.SEGQVDVEKWK.F
22.	TRPM2_MOUSE Mass: 172092 Score: 23 Matches: 1(1) Sequences: 1(1) emPAI: 0.03										
	Transient receptor potential cation channel subfamily M member 2 OS=Mus musculus GN=Trpm2 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	49	388.7004	775.3863	775.3864	-0.15	0	23	0.028	1	U	R.VSEAWGK.T
23.	GVIN1_MOUSE Mass: 280637 Score: 23 Matches: 1(1) Sequences: 1(1) emPAI: 0.02										
	Interferon-induced very large GTPase 1 OS=Mus musculus GN=Gvin1 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1869	679.8872	1357.7599	1357.7605	-0.50	1	23	0.04	1	U	K.GSLPDLWTKITK.Q
24.	ADCYA_MOUSE Mass: 186290 Score: 23 Matches: 1(1) Sequences: 1(1) emPAI: 0.02										
	Adenylate cyclase type 10 OS=Mus musculus GN=Adcy10 PE=2 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	334	473.3101	944.6056	944.6059	-0.25	0	23	0.0049	1	U	R.LSKPLFLK.S

25.	CDC26_MOUSE Mass: 9755 Score: 23 Matches: 1(1) Sequences: 1(1) emPAI: 0.52										
	Anaphase-promoting complex subunit CDC26 OS=Mus musculus GN=Cdc26 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	339	473.7897	945.5648	945.5647	0.06	0	23	0.019	1	U	R.IGYKPQLK.S
26.	DJC21_MOUSE Mass: 61696 Score: 22 Matches: 1(1) Sequences: 1(1) emPAI: 0.07										
	DnaJ homolog subfamily C member 21 OS=Mus musculus GN=Dnajc21 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	2483	721.3292	1440.6439	1440.6554	-8.02	1	22	0.04	1	U	K.ELQEMEARYEK.E
27.	SMRC1_MOUSE Mass: 122813 Score: 22 Matches: 1(1) Sequences: 1(1) emPAI: 0.04										
	SWI/SNF complex subunit SMARCC1 OS=Mus musculus GN=Smarcc1 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	48	388.2575	774.5003	774.4963	5.22	2	22	0.0065	1	U	K.KTLAKSK.G
28.	PGFRB_MOUSE Mass: 122728 Score: 22 Matches: 1(1) Sequences: 1(1) emPAI: 0.04										
	Platelet-derived growth factor receptor beta OS=Mus musculus GN=Pdgfrb PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	89	402.7526	803.4907	803.4939	-3.97	1	22	0.017	1	U	K.VAVKMLK.S
	CSF1R_MOUSE Mass: 109110 Score: 22 Matches: 1(1) Sequences: 1(1)										
	Macrophage colony-stimulating factor 1 receptor OS=Mus musculus GN=Csf1r PE=1 SV=3										
	FGFR1_MOUSE Mass: 91922 Score: 22 Matches: 1(1) Sequences: 1(1)										
	Fibroblast growth factor receptor 1 OS=Mus musculus GN=Fgfr1 PE=1 SV=2										
	TYRO3_MOUSE Mass: 96147 Score: 22 Matches: 1(1) Sequences: 1(1)										
	Tyrosine-protein kinase receptor TYRO3 OS=Mus musculus GN=Tyro3 PE=1 SV=2										
29.	SKOR1_MOUSE Mass: 100183 Score: 21 Matches: 1(1) Sequences: 1(1) emPAI: 0.04										
	SKI family transcriptional corepressor 1 OS=Mus musculus GN=Skor1 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	411	498.7993	995.5841	995.5876	-3.51	2	21	0.029	1	U	R.RHLKLSDK.S
30.	VISTA_MOUSE Mass: 33538 Score: 21 Matches: 1(1) Sequences: 1(1) emPAI: 0.13										

	V-type immunoglobulin domain-containing suppressor of T-cell activation OS=Mus musculus GN=Vsir PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	3	353.2183	704.4221	704.4221	0.06	0	21	0.0088	1	U	R.GLVAAFK.V
31.	CADH1_MOUSE Mass: 98195 Score: 20 Matches: 2(2) Sequences: 1(1) emPAI: 0.04										
	Cadherin-1 OS=Mus musculus GN=Cdh1 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	316	466.3023	930.5901	930.5875	2.73	2	19	0.024	1	U	K.RHLKLHK.L 315
32.	NSE2_MOUSE Mass: 28213 Score: 20 Matches: 1(1) Sequences: 1(1) emPAI: 0.16										
	E3 SUMO-protein ligase NSE2 OS=Mus musculus GN=Nsmce2 PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	81	399.7106	797.4067	797.4031	4.48	0	20	0.033	1	U	R.AIESHNK.K
33.	GPX3_MOUSE Mass: 25409 Score: 20 Matches: 1(1) Sequences: 1(1) emPAI: 0.18										
	Glutathione peroxidase 3 OS=Mus musculus GN=Gpx3 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	16	358.7081	715.4016	715.3977	5.58	0	20	0.021	1	U	R.QAALSAR.G
34.	P66A_MOUSE Mass: 67292 Score: 19 Matches: 2(2) Sequences: 1(1) emPAI: 0.07										
	Transcriptional repressor p66 alpha OS=Mus musculus GN=Gatad2a PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	52	388.7550	775.4955	775.4956	-0.08	1	17	0.022	1	U	R.LKAAFVK.A 51
35.	RSPH9_MOUSE Mass: 31311 Score: 19 Matches: 1(1) Sequences: 1(1) emPAI: 0.14										
	Radial spoke head protein 9 homolog OS=Mus musculus GN=Rsph9 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1164	628.3923	1254.7700	1254.7812	-8.94	1	19	0.038	1	U	K.AVAIIPRGALFK.T
36.	GFRA1_MOUSE Mass: 51718 Score: 18 Matches: 1(1) Sequences: 1(1) emPAI: 0.09										
	GDNF family receptor alpha-1 OS=Mus musculus GN=Gfra1 PE=2 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	3983	541.8855	1622.6347	1622.6400	-3.26	1	18	0.032	1	U	K.ASDQCLKEQSCSTK.Y

37.	TICRR_MOUSE Mass: 208205 Score: 17 Matches: 1(1) Sequences: 1(1) emPAI: 0.02										
	Treslin OS=Mus musculus GN=Ticrr PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	333	472.8180	943.6214	943.6178	3.77	2	17	0.018	1	U	R.ILRSSKLK.E
38.	KALRN_MOUSE Mass: 336788 Score: 17 Matches: 1(1) Sequences: 1(1) emPAI: 0.01										
	Kalirin OS=Mus musculus GN=Kalrn PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	122	416.7682	831.5218	831.5218	-0.04	0	17	0.026	1	U	R.LAQLFIK.H
39.	HELZ_MOUSE Mass: 219742 Score: 16 Matches: 1(1) Sequences: 1(1) emPAI: 0.02										
	Probable helicase with zinc finger domain OS=Mus musculus GN=Helz PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	220	460.2842	918.5539	918.5538	0.10	0	16	0.037	1	U	R.IASFLQLK.N
40.	C16L2_MOUSE Mass: 18208 Score: 13 Matches: 1(1) Sequences: 1(1) emPAI: 0.26										
	CD164 sialomucin-like 2 protein OS=Mus musculus GN=Cd164l2 PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	2	350.1823	698.3499	698.3534	-4.89	0	13	0.048	1	U	-.MAAPGPR.A

Biotin-TPL pulldown Band #3

1. MEX3C_MOUSE Mass: 68531 Score: 3644 Matches: 106(106) Sequences: 8(8) emPAI: 0.86

RNA-binding E3 ubiquitin-protein ligase MEX3C OS=Mus musculus GN=Mex3c PE=2 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1121	549.2827	1096.5509	1096.5513	-0.37	0	71	6.5e-007	1	U	R.ATGLAPEEPGR.L 1118 1119 1120 1122 1123 1124 1125 1126 1127 1128 1129 1130
1651	602.3219	1202.6292	1202.6295	-0.25	0	91	9.9e-009	1	U	R.GEEPIFVVTGR.K 1648 1649 1650 1652 1653 1654 1655 1656 1657 1658 1660 1662 1663 1666 1667 1668
1664	401.8839	1202.6300	1202.6295	0.37	0	(46)	0.00036	1	U	R.GEEPIFVVTGR.K 1659 1661 1665
2420	672.3459	1342.6772	1342.6775	-0.22	0	99	1.3e-009	1	U	R.AAAVAAAAAAQCQAR.R 2419 2422 2423 2424 2425 2427
2428	448.5669	1342.6788	1342.6775	0.98	0	(90)	1.1e-008	1	U	R.AAAVAAAAAAQCQAR.R 2418 2421 2426
3392	500.6002	1498.7787	1498.7786	0.08	1	76	2.3e-007	1	U	R.AAAVAAAAAAQCQARR.A
3393	750.3967	1498.7788	1498.7786	0.11	1	(42)	0.00069	1	U	R.AAAVAAAAAAQCQARR.A
3420	752.3845	1502.7545	1502.7551	-0.42	0	94	5.8e-009	1	U	R.EILSAAEHFSMIR.A 3417 3434 3437 3438 3442 3443 3455 3461
3422	501.9255	1502.7545	1502.7551	-0.39	0	(43)	0.00062	1	U	R.EILSAAEHFSMIR.A 3416 3427 3433 3436 3440 3441 3446 3451 3454 3458
3566	760.3820	1518.7495	1518.7500	-0.36	0	(89)	1.7e-008	1	U	R.EILSAAEHFSMIR.A 3571
3574	507.2573	1518.7502	1518.7500	0.13	0	(32)	0.0086	1	U	R.EILSAAEHFSMIR.A 3568 3576
4309	836.4440	1670.8734	1670.8740	-0.38	0	86	2.8e-008	1		R.IQQQTHTYIVTPSR.D 4311 4312
4315	557.9657	1670.8753	1670.8740	0.75	0	(55)	3.1e-005	1		R.IQQQTHTYIVTPSR.D 4308 4310 4313 4314
4398	565.3014	1692.8823	1692.8835	-0.68	0	(38)	0.0019	1	U	R.LSPTFPESIEHPLAR.R 4400 4404 4406 4417 4420
4409	847.4491	1692.8836	1692.8835	0.09	0	72	6.5e-007	1	U	R.LSPTFPESIEHPLAR.R 4402 4410 4415

	4537	573.6067	1717.7982	1717.7981	0.06	0	(59)	1.2e-005	1		K.EPVFEVTGMPENVDR.A 4531 4536 4541
	4540	859.9065	1717.7984	1717.7981	0.17	0	(71)	9.1e-007	1		K.EPVFEVTGMPENVDR.A 4529 4530 4534 4538 4542
	4628	578.9381	1733.7925	1733.7931	-0.32	0	(63)	5e-006	1		K.EPVFEVTGMPENVDR.A 4632
	4630	867.9036	1733.7927	1733.7931	-0.20	0	92	6.7e-009	1		K.EPVFEVTGMPENVDR.A 4624 4625 4627
2.	MEX3B_MOUSE Mass: 61743 Score: 1601 Matches: 50(50) Sequences: 4(4) emPAI: 0.51										
	RNA-binding protein MEX3B OS=Mus musculus GN=Mex3b PE=2 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1564	595.3140	1188.6134	1188.6139	-0.45	0	75	4.4e-007	1	U	R.GEEPVFVVTGR.K
	3420	752.3845	1502.7545	1502.7551	-0.42	0	94	5.8e-009	1	U	R.EIISAAEHFSMIR.A 3417 3434 3437 3438 3442 3443 3455 3461
	3422	501.9255	1502.7545	1502.7551	-0.39	0	(43)	0.00062	1	U	R.EIISAAEHFSMIR.A 3416 3427 3433 3436 3440 3441 3446 3451 3454 3458
	3566	760.3820	1518.7495	1518.7500	-0.36	0	(89)	1.7e-008	1	U	R.EIISAAEHFSMIR.A 3571
	3574	507.2573	1518.7502	1518.7500	0.13	0	(32)	0.0086	1	U	R.EIISAAEHFSMIR.A 3568 3576
	4309	836.4440	1670.8734	1670.8740	-0.38	0	86	2.8e-008	1		R.IQQQTHTYIVTPSR.D 4311 4312
	4315	557.9657	1670.8753	1670.8740	0.75	0	(55)	3.1e-005	1		R.IQQQTHTYIVTPSR.D 4308 4310 4313 4314
	4537	573.6067	1717.7982	1717.7981	0.06	0	(59)	1.2e-005	1		K.EPVFEVTGMPENVDR.A 4531 4536 4541
	4540	859.9065	1717.7984	1717.7981	0.17	0	(71)	9.1e-007	1		K.EPVFEVTGMPENVDR.A 4529 4530 4534 4538 4542
	4628	578.9381	1733.7925	1733.7931	-0.32	0	(63)	5e-006	1		K.EPVFEVTGMPENVDR.A 4632
	4630	867.9036	1733.7927	1733.7931	-0.20	0	92	6.7e-009	1		K.EPVFEVTGMPENVDR.A 4624 4625 4627
3.	ERCC3_MOUSE Mass: 89070 Score: 104 Matches: 2(2) Sequences: 1(1) emPAI: 0.05										

	TFIIH basal transcription factor complex helicase XPB subunit OS=Mus musculus GN=Ercc3 PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	4123	544.9515	1631.8326	1631.8341	-0.93	0	(39)	0.0019	1	U	R.CLVLGNSAVSVEQWK.A
	4124	816.9241	1631.8336	1631.8341	-0.33	0	82	7.6e-008	1	U	R.CLVLGNSAVSVEQWK.A
4.	DCTP1_MOUSE Mass: 18783 Score: 84 Matches: 4(4) Sequences: 1(1) emPAI: 0.25										
	dCTP pyrophosphatase 1 OS=Mus musculus GN=Dctpp1 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	2856	705.3380	1408.6615	1408.6623	-0.58	0	43	0.00055	1	U	K.SDTEPGPQAWPPK.E 2857 2858 2859
5.	ROCK1_MOUSE Mass: 158072 Score: 52 Matches: 1(1) Sequences: 1(1) emPAI: 0.03										
	Rho-associated protein kinase 1 OS=Mus musculus GN=Rock1 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	4964	907.4464	1812.8781	1812.8781	0.01	0	52	9e-005	1	U	R.GILEEQYFELTQESK.K
6.	PTCD3_MOUSE Mass: 77747 Score: 48 Matches: 1(1) Sequences: 1(1) emPAI: 0.06										
	Pentatricopeptide repeat domain-containing protein 3, mitochondrial OS=Mus musculus GN=Ptcd3 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	5	350.7087	699.4028	699.4027	0.10	0	48	1.7e-005	1	U	M.AAAAVAAR.R
7.	LIN41_MOUSE Mass: 91996 Score: 47 Matches: 3(3) Sequences: 1(1) emPAI: 0.05										
	E3 ubiquitin-protein ligase TRIM71 OS=Mus musculus GN=Trim71 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	4213	550.8880	1649.6422	1649.6418	0.20	0	42	8.7e-005	1	U	R.CLDCQEHLCDNCVR.A 4212 4214
8.	TMM70_MOUSE Mass: 28256 Score: 33 Matches: 1(1) Sequences: 1(1) emPAI: 0.16										
	Transmembrane protein 70, mitochondrial OS=Mus musculus GN=Tmem70 PE=2 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	559	472.2458	942.4770	942.4770	0.01	0	33	0.0029	1	U	R.AASLAEPER.L
9.	MARCO_MOUSE Mass: 52697 Score: 30 Matches: 1(1) Sequences: 1(1) emPAI: 0.08										
	Macrophage receptor MARCO OS=Mus musculus GN=Marco PE=1 SV=1										

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	823	514.2826	1026.5506	1026.5458	4.68	0	30	0.0048	1	U	K.GESGVPGLVGR.K
10.	PTN6_MOUSE Mass: 67517 Score: 29 Matches: 1(1) Sequences: 1(1) emPAI: 0.07										
	Tyrosine-protein phosphatase non-receptor type 6 OS=Mus musculus GN=Ptpn6 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	232	418.2373	834.4601	834.4633	-3.84	0	29	0.0086	1	U	R.VIVMTTR.E
11.	SULF2_MOUSE Mass: 100433 Score: 29 Matches: 1(1) Sequences: 1(1) emPAI: 0.04										
	Extracellular sulfatase Sulf-2 OS=Mus musculus GN=Sulf2 PE=2 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	278	431.2323	860.4500	860.4538	-4.44	1	29	0.015	1	U	R.VKDLCQR.A
12.	PZRN3_MOUSE Mass: 119326 Score: 27 Matches: 1(1) Sequences: 1(1) emPAI: 0.04										
	E3 ubiquitin-protein ligase PDZRN3 OS=Mus musculus GN=Pdzrn3 PE=1 SV=3										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1160	553.7306	1105.4467	1105.4505	-3.42	1	27	0.0041	1	U	K.CAHAARGCGR.V
13.	ANR27_MOUSE Mass: 116735 Score: 27 Matches: 1(1) Sequences: 1(1) emPAI: 0.04										
	Ankyrin repeat domain-containing protein 27 OS=Mus musculus GN=Ankrd27 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	185	407.7243	813.4341	813.4345	-0.44	0	27	0.0075	1	U	R.SVPDLAGR.S
14.	KC1A_MOUSE Mass: 38890 Score: 27 Matches: 1(1) Sequences: 1(1) emPAI: 0.12										
	Casein kinase I isoform alpha OS=Mus musculus GN=Csnk1a1 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	2861	705.3566	1408.6987	1408.7054	-4.76	0	27	0.021	1	U	K.TVLMLADQMISR.I
15.	MSD3_MOUSE Mass: 32303 Score: 26 Matches: 1(1) Sequences: 1(1) emPAI: 0.14										
	Myb/SANT-like DNA-binding domain-containing protein 3 OS=Mus musculus GN=Msantd3 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	929	528.7934	1055.5722	1055.5658	6.11	2	26	0.016	1	U	K.KIMAHERR.E
16.	LRCC1_MOUSE Mass: 119094 Score: 26 Matches: 1(1) Sequences: 1(1) emPAI: 0.04										

	Leucine-rich repeat and coiled-coil domain-containing protein 1 OS=Mus musculus GN=Lrrcc1 PE=2 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	303	439.7401	877.4657	877.4657	-0.02	1	26	0.025	1	U	K.DAIFKER.H
17.	PTTG1_MOUSE Mass: 21711 Score: 25 Matches: 1(1) Sequences: 1(1) emPAI: 0.21										
	Securin OS=Mus musculus GN=Pttg1 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	159	400.7350	799.4554	799.4552	0.29	0	25	0.02	1	U	K.LQVSTPR.V
18.	SUH_MOUSE Mass: 58500 Score: 24 Matches: 1(1) Sequences: 1(1) emPAI: 0.08										
	Recombining binding protein suppressor of hairless OS=Mus musculus GN=Rbpj PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	2888	707.3594	1412.7043	1412.7161	-8.31	1	24	0.04	1	U	M.PSGFPQSPRTSPR.A
19.	SBNO2_MOUSE Mass: 149200 Score: 24 Matches: 1(1) Sequences: 1(1) emPAI: 0.03										
	Protein strawberry notch homolog 2 OS=Mus musculus GN=Sbno2 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	379	452.7297	903.4449	903.4450	-0.15	0	24	0.036	1	U	K.WEEALTR.S
20.	AHDC1_MOUSE Mass: 167976 Score: 24 Matches: 1(1) Sequences: 1(1) emPAI: 0.03										
	AT-hook DNA-binding motif-containing protein 1 OS=Mus musculus GN=Ahdc1 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	54	371.2344	740.4543	740.4545	-0.19	0	24	0.0056	1	U	K.IPVSLGR.R
21.	KCJ10_MOUSE Mass: 42405 Score: 24 Matches: 1(1) Sequences: 1(1) emPAI: 0.11										
	ATP-sensitive inward rectifier potassium channel 10 OS=Mus musculus GN=Kcnj10 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1808	616.3378	1230.6611	1230.6568	3.50	1	24	0.048	1	U	K.EGSALSVRISNV.-
22.	MYO7B_MOUSE Mass: 240705 Score: 24 Matches: 1(1) Sequences: 1(1) emPAI: 0.02										
	Unconventional myosin-VIIb OS=Mus musculus GN=Myo7b PE=1 SV=3										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	64	374.1820	746.3495	746.3567	-9.72	0	24	0.0099	1	U	R.AAMPMAR.S

23.	LDB1_MOUSE Mass: 46472 Score: 23 Matches: 1(1) Sequences: 1(1) emPAI: 0.10										
	LIM domain-binding protein 1 OS=Mus musculus GN=Ldb1 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	203	412.2190	822.4235	822.4236	-0.08	0	23	0.027	1	U	K.TYSLSPR.D
24.	SPTB2_MOUSE Mass: 274052 Score: 23 Matches: 1(1) Sequences: 1(1) emPAI: 0.02										
	Spectrin beta chain, non-erythrocytic 1 OS=Mus musculus GN=Sptbn1 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	574	473.7712	945.5279	945.5317	-4.00	1	23	0.05	1	U	K.MKALAVEGK.R
25.	DISP1_MOUSE Mass: 170019 Score: 23 Matches: 1(1) Sequences: 1(1) emPAI: 0.03										
	Protein dispatched homolog 1 OS=Mus musculus GN=Disp1 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	874	520.7722	1039.5298	1039.5338	-3.89	0	23	0.038	1	U	K.ATLANYPYK.Y
26.	FHOD1_MOUSE Mass: 129520 Score: 23 Matches: 1(1) Sequences: 1(1) emPAI: 0.03										
	FH1/FH2 domain-containing protein 1 OS=Mus musculus GN=Fhod1 PE=1 SV=3										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	439	461.7590	921.5034	921.5032	0.22	0	23	0.036	1	U	K.HELSPALR.A
27.	ADCY7_MOUSE Mass: 122628 Score: 22 Matches: 1(1) Sequences: 1(1) emPAI: 0.04										
	Adenylate cyclase type 7 OS=Mus musculus GN=Adcy7 PE=2 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	103	387.7089	773.4032	773.4032	0.02	1	22	0.038	1	U	R.LKEGGDR.H
28.	PUF60_MOUSE Mass: 60211 Score: 20 Matches: 1(1) Sequences: 1(1) emPAI: 0.07										
	Poly(U)-binding-splicing factor PUF60 OS=Mus musculus GN=Puf60 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	245	421.7458	841.4770	841.4770	0.06	0	20	0.042	1	U	K.AIQALNGR.W
29.	CE030_MOUSE Mass: 23116 Score: 20 Matches: 1(1) Sequences: 1(1) emPAI: 0.20										
	UNC119-binding protein C5orf30 homolog OS=Mus musculus GN=D1Ertd622e PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	248	422.7172	843.4198	843.4272	-8.87	0	20	0.048	1	U	K.GEAMPALR.A

30. PTPRM_MOUSE Mass: 163549 Score: 20 Matches: 1(1) Sequences: 1(1) emPAI: 0.03

Receptor-type tyrosine-protein phosphatase mu OS=Mus musculus GN=Ptprm PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
793	509.7347	1017.4549	1017.4484	6.41	1	20	0.041	1	U	K.CADPMRGPR.K

31. PTHR_MOUSE Mass: 20088 Score: 18 Matches: 1(1) Sequences: 1(1) emPAI: 0.23

Parathyroid hormone-related protein OS=Mus musculus GN=Pthlh PE=2 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
19	359.1982	716.3817	716.3817	0.07	0	18	0.04	1	U	R.SVEGLGR.R

32. CDPF1_MOUSE Mass: 13292 Score: 18 Matches: 1(1) Sequences: 1(1) emPAI: 0.37

Cysteine-rich DPF motif domain-containing protein 1 OS=Mus musculus GN=Cdpf1 PE=3 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
145	396.2422	790.4698	790.4701	-0.37	0	18	0.044	1	U	R.FLVLGSR.C

33. KPYR_MOUSE Mass: 62270 Score: 17 Matches: 1(1) Sequences: 1(1) emPAI: 0.07

Pyruvate kinase PKLR OS=Mus musculus GN=Pklr PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
69	374.6905	747.3665	747.3697	-4.35	0	17	0.038	1	U	K.AGMNIAR.L

34. BRD7_MOUSE Mass: 73954 Score: 17 Matches: 1(1) Sequences: 1(1) emPAI: 0.06

Bromodomain-containing protein 7 OS=Mus musculus GN=Brd7 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
72	376.1921	750.3697	750.3694	0.40	0	17	0.045	1	U	R.LGMTTGR.L

Biotin-TPL pulldown Band #4											
1.	TRI63_MOUSE Mass: 39465 Score: 8683 Matches: 222(222) Sequences: 10(10) emPAI: 5.22										
	E3 ubiquitin-protein ligase TRIM63 OS=Mus musculus GN=Trim63 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	347	447.7085	893.4024	893.4025	-0.09	0	73	2.9e-007	1	U	R.GGSVSMSGGR.F 342 343 344 345 346 348 349
	392	455.7059	909.3973	909.3974	-0.15	0	(62)	2.8e-006	1	U	R.GGSVSMSGGR.F 385 389 390 391 393
	1533	588.2955	1174.5765	1174.5764	0.07	0	49	0.00016	1	U	K.QECSSRPLQK.G 1532 1534
	2506	664.3422	1326.6699	1326.6707	-0.62	0	93	6.3e-009	1	U	K.FDTLYAILDEK.K 2498 2501 2503 2504 2508 2509 2510 2511 2512 2513 2514 2515 2516 2518 2520
	2517	443.2307	1326.6704	1326.6707	-0.24	0	(26)	0.026	1	U	K.FDTLYAILDEK.K 2502 2505
	3225	479.2817	1434.8233	1434.8235	-0.11	0	(51)	2.6e-005	1	U	K.LGFIEALILQYR.E 3209 3219 3224 3232 3233 3242
	3228	718.4190	1434.8233	1434.8235	-0.08	0	83	1.6e-008	1	U	K.LGFIEALILQYR.E 3207 3210 3211 3212 3215 3216 3217 3218 3221 3222 3223 3227 3229 3230 3231 3234 3235 3237 3238 3239 3240 3241 3243 3246 3248

	3313	723.9132	1445.8119	1445.8129	-0.74	0	98	1.1e-009	1	U	R.NLLVENIIDIYK.Q 3304 3305 3306 3309 3311 3312 3314 3315 3316 3317 3320 3321 3322 3323 3325 3326 3327 3328 3329 3331 3332 3333 3334 3335 3336 3337 3339 3340 3341 3342 3343 3344 3345 3346 3347 3348 3349 3350 3351 3352 3354 3355 3356 3357 3358 3359 3360 3361 3362 3363 3364 3365 3367 3368 3369 3370 3371 3372 3373 3374 3375 3376 3377 3378 3379 3380 3381 3382 3383 3384 3385 3386 3387 3389 3390 3391 3392 3393 3394 3395 3396 3397 3398 3399 3400 3401 3403 3404 3405 3406 3407 3409 3410 3411 3413 3414 3415 3416 3417 3418
	3338	482.9447	1445.8123	1445.8129	-0.46	0	(56)	1.6e-005	1	U	R.NLLVENIIDIYK.Q 3308 3318 3324 3353
	3464	728.3895	1454.7644	1454.7657	-0.88	1	74	3.5e-007	1	U	K.FDTLYAILDEKK.S
	3465	485.9287	1454.7644	1454.7657	-0.88	1	(53)	4.8e-005	1	U	K.FDTLYAILDEKK.S 3467 3468
	3531	731.3898	1460.7650	1460.7657	-0.50	0	94	5.4e-009	1	U	R.VQTIISQLVDSCR.V 3528 3529 3530 3532 3533 3534
	3535	487.9293	1460.7660	1460.7657	0.22	0	(38)	0.0017	1	U	R.VQTIISQLVDSCR.V
	3878	755.3820	1508.7495	1508.7505	-0.64	0	(72)	8.2e-007	1	U	R.VQTIISQLVDSCR.V
	4268	529.9275	1586.7606	1586.7610	-0.22	0	(43)	0.00056	1	U	K.SGLIPDGNAMENLEK.Q 4267
	4271	794.3878	1586.7610	1586.7610	-0.01	0	98	1.6e-009	1	U	K.SGLIPDGNAMENLEK.Q 4266 4272 4273 4274 4275 4276
	4339	802.3854	1602.7563	1602.7559	0.26	0	(83)	5.8e-008	1	U	K.SGLIPDGNAMENLEK.Q 4335 4337 4338 4341
	4342	535.2595	1602.7567	1602.7559	0.52	0	(39)	0.0013	1	U	K.SGLIPDGNAMENLEK.Q

	4702	861.9108	1721.8071	1721.8076	-0.30	0	114	4.8e-011	1	U	K.TELSNCISMLVAGNDR.V 4701 4707
	4703	574.9430	1721.8071	1721.8076	-0.28	0	(61)	9.7e-006	1	U	K.TELSNCISMLVAGNDR.V 4704
	4738	869.9077	1737.8009	1737.8026	-0.97	0	(59)	1.7e-005	1	U	K.TELSNCISMLVAGNDR.V
	4739	580.2744	1737.8012	1737.8026	-0.76	0	(38)	0.002	1	U	K.TELSNCISMLVAGNDR.V
	4777	885.9026	1769.7907	1769.7924	-0.92	0	(25)	0.024	1	U	K.TELSNCISMLVAGNDR.V
	4778	590.9379	1769.7920	1769.7924	-0.23	0	(29)	0.011	1	U	K.TELSNCISMLVAGNDR.V
	4807	893.9003	1785.7861	1785.7873	-0.66	0	(43)	0.00042	1	U	K.TELSNCISMLVAGNDR.V
	4966	628.6208	1882.8405	1882.8420	-0.80	0	(48)	0.00013	1	U	K.CANDIFQAANPYWTNR.G 4971 4972 4973
	4970	942.4277	1882.8408	1882.8420	-0.67	0	92	4.7e-009	1	U	K.CANDIFQAANPYWTNR.G 4967 4974 4976
	5057	966.4207	1930.8269	1930.8268	0.05	0	(36)	0.0014	1	U	K.CANDIFQAANPYWTNR.G
2.	UB2G1_MOUSE Mass: 19497 Score: 415 Matches: 14(14) Sequences: 6(6) emPAI: 3.50										
	Ubiquitin-conjugating enzyme E2 G1 OS=Mus musculus GN=Ube2g1 PE=1 SV=3										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	691	493.2770	984.5394	984.5392	0.16	0	28	0.0093	1	U	K.DYPLRPPK.M 689 690 694
	1360	572.3403	1142.6660	1142.6659	0.08	0	55	2.7e-005	1	U	M.TELQSALLLR.R
	1503	585.7752	1169.5359	1169.5353	0.52	0	46	0.00018	1	U	K.YGYEKPEER.W
	2134	425.5757	1273.7054	1273.7064	-0.77	0	(38)	0.0013	1	U	-.MTELQSALLLR.R
	2135	637.8601	1273.7055	1273.7064	-0.65	0	97	1.8e-009	1	U	-.MTELQSALLLR.R 2133
	2258	645.8577	1289.7009	1289.7013	-0.30	0	(82)	6.2e-008	1	U	-.MTELQSALLLR.R 2259
	3806	749.8880	1497.7614	1497.7616	-0.11	0	49	0.00012	1	U	K.FITEIWHPNVDK.N
	3808	500.2612	1497.7619	1497.7616	0.17	0	(29)	0.014	1	U	K.FITEIWHPNVDK.N
	4715	575.9418	1724.8037	1724.8039	-0.16	0	42	0.00065	1	U	K.NGDVCISILHEPGEDK.Y
3.	P85A_MOUSE Mass: 83465 Score: 156 Matches: 6(6) Sequences: 4(4) emPAI: 0.23										
	Phosphatidylinositol 3-kinase regulatory subunit alpha OS=Mus musculus GN=Pik3r1 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1938	618.8269	1235.6392	1235.6397	-0.40	0	69	1.2e-006	1	U	R.TAIEAFNETIK.I 1939 1940
	3142	476.6060	1426.7961	1426.7966	-0.31	0	26	0.021	1	U	R.MNSIKPDLIQLR.K
	3605	737.3535	1472.6925	1472.6936	-0.76	0	29	0.01	1	U	R.GDFPGTYVEYIGR.K
	4204	787.4136	1572.8127	1572.8147	-1.27	0	40	0.0011	1	U	K.AIEILISTEWNER.Q

4.	PK3CG_MOUSE Mass: 126319 Score: 102 Matches: 5(5) Sequences: 3(3) emPAI: 0.15										
	Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit gamma isoform OS=Mus musculus GN=Pik3cg PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	421	459.7738	917.5331	917.5256	8.21	0	28	0.0098	1	U	K.IGMIEIVK.D
	3037	471.5991	1411.7754	1411.7758	-0.26	0	46	0.00019	1	U	K.IANNCIFIVIHR.G
	4590	557.6085	1669.8036	1669.8035	0.03	0	42	0.00067	1	U	R.HGDYVLHMWQISGK.A 4589
	4619	562.9401	1685.7985	1685.7984	0.07	0	(25)	0.036	1	U	R.HGDYVLHMWQISGK.A
5.	RASH_MOUSE Mass: 21285 Score: 61 Matches: 1(1) Sequences: 1(1) emPAI: 0.22										
	GTPase HRas OS=Mus musculus GN=Hras PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	593	478.3003	954.5860	954.5862	-0.23	0	61	2.1e-006	1	U	K.LVVVGAGGVGK.S
	RASK_MOUSE Mass: 21642 Score: 61 Matches: 1(1) Sequences: 1(1)										
	GTPase KRas OS=Mus musculus GN=Kras PE=1 SV=1										
	RASN_MOUSE Mass: 21186 Score: 61 Matches: 1(1) Sequences: 1(1)										
	GTPase NRas OS=Mus musculus GN=Nras PE=1 SV=1										
6.	LRC45_MOUSE Mass: 76337 Score: 46 Matches: 4(4) Sequences: 1(1) emPAI: 0.12										
	Leucine-rich repeat-containing protein 45 OS=Mus musculus GN=Lrrc45 PE=2 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	786	503.7290	1005.4435	1005.4437	-0.17	0	(24)	0.017	1	U	K.QNMEDLEK.L 789
	839	511.7265	1021.4384	1021.4386	-0.21	0	35	0.0012	1	U	K.QNMEDLEK.L 838
7.	SH2D6_MOUSE Mass: 31996 Score: 44 Matches: 3(3) Sequences: 1(1) emPAI: 0.14										
	SH2 domain-containing protein 6 OS=Mus musculus GN=Sh2d6 PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	288	438.7158	875.4171	875.4171	0.00	0	32	0.0048	1	U	R.NGAMDGALK.A 289 291
8.	KRT81_MOUSE Mass: 52829 Score: 42 Matches: 2(2) Sequences: 1(1) emPAI: 0.08										
	Keratin, type II cuticular Hb1 OS=Mus musculus GN=Krt81 PE=2 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1473	581.3182	1160.6219	1160.6223	-0.33	1	36	0.0027	1	U	K.CEEIKATVIR.H 1475

	KRT86_MOUSE Mass: 53217 Score: 42 Matches: 2(2) Sequences: 1(1)										
	Keratin, type II cuticular Hb6 OS=Mus musculus GN=Krt86 PE=2 SV=2										
9.	DC1L2_MOUSE Mass: 54185 Score: 40 Matches: 2(2) Sequences: 1(1) emPAI: 0.08										
	Cytoplasmic dynein 1 light intermediate chain 2 OS=Mus musculus GN=Dync1li2 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	299	439.7525	877.4904	877.4909	-0.50	0	36	0.001	1	U	K.NLDLLYK.Y 304
10.	RB33A_MOUSE Mass: 26523 Score: 38 Matches: 4(4) Sequences: 1(1) emPAI: 0.17										
	Ras-related protein Rab-33A OS=Mus musculus GN=Rab33a PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	178	408.2403	814.4660	814.4661	-0.06	1	31	0.0073	1	U	R.QQGKVQK.L 175 180 183
11.	PRP18_MOUSE Mass: 39865 Score: 36 Matches: 1(1) Sequences: 1(1) emPAI: 0.11										
	Pre-mRNA-splicing factor 18 OS=Mus musculus GN=Prpf18 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	199	415.2427	828.4708	828.4705	0.38	0	36	0.0017	1	U	R.NLLVENK.K
12.	ATF5_MOUSE Mass: 30312 Score: 35 Matches: 1(1) Sequences: 1(1) emPAI: 0.15										
	Cyclic AMP-dependent transcription factor ATF-5 OS=Mus musculus GN=Atf5 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	748	496.7869	991.5592	991.5590	0.28	0	35	0.0013	1	U	K.DLLIEVYK.A
13.	MPP8_MOUSE Mass: 97407 Score: 35 Matches: 2(2) Sequences: 1(1) emPAI: 0.04										
	M-phase phosphoprotein 8 OS=Mus musculus GN=Mphosph8 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	159	403.2501	804.4857	804.4857	-0.07	0	29	0.0028	1	U	K.LLIGAYR.V 158
14.	ARGAL_MOUSE Mass: 139898 Score: 35 Matches: 1(1) Sequences: 1(1) emPAI: 0.03										
	Rho guanine nucleotide exchange factor 10-like protein OS=Mus musculus GN=Arhgef10l PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	259	431.7608	861.5070	861.5072	-0.27	0	35	0.0015	1	U	K.GILLQYR.L

15.	CP250_MOUSE Mass: 276647 Score: 33 Matches: 1(1) Sequences: 1(1) emPAI: 0.02										
	Centrosome-associated protein CEP250 OS=Mus musculus GN=Cep250 PE=1 SV=4										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1239	559.8321	1117.6497	1117.6608	-9.84	1	33	0.0026	1	U	K.LQAKVLQYR.S
16.	FBXL2_MOUSE Mass: 46860 Score: 33 Matches: 1(1) Sequences: 1(1) emPAI: 0.10										
	F-box/LRR-repeat protein 2 OS=Mus musculus GN=Fbxl2 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	137	394.7291	787.4436	787.4440	-0.49	0	33	0.0045	1	U	R.VVENISK.R
	FXL20_MOUSE Mass: 48365 Score: 33 Matches: 1(1) Sequences: 1(1)										
	F-box/LRR-repeat protein 20 OS=Mus musculus GN=Fbxl20 PE=1 SV=3										
17.	DOCK3_MOUSE Mass: 232760 Score: 32 Matches: 1(1) Sequences: 1(1) emPAI: 0.02										
	Dedicator of cytokinesis protein 3 OS=Mus musculus GN=Dock3 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1990	623.3435	1244.6725	1244.6837	-9.01	1	32	0.0065	1	U	K.LQSIARTVDSR.L
18.	UB2E3_MOUSE Mass: 22898 Score: 29 Matches: 1(1) Sequences: 1(1) emPAI: 0.20										
	Ubiquitin-conjugating enzyme E2 E3 OS=Mus musculus GN=Ube2e3 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	331	444.2509	886.4871	886.4872	-0.07	0	29	0.014	1	U	R.KPSATQQK.K
19.	GLCE_MOUSE Mass: 70045 Score: 29 Matches: 1(1) Sequences: 1(1) emPAI: 0.06										
	D-glucuronyl C5-epimerase OS=Mus musculus GN=Glce PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1123	549.2969	1096.5792	1096.5805	-1.14	0	29	0.0083	1	U	K.DFIISFDLK.L
20.	INT5_MOUSE Mass: 108279 Score: 29 Matches: 1(1) Sequences: 1(1) emPAI: 0.04										
	Integrator complex subunit 5 OS=Mus musculus GN=Ints5 PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	65	375.2190	748.4235	748.4232	0.42	0	29	0.0016	1	U	R.LGLFSGR.F
21.	LRC71_MOUSE Mass: 61313 Score: 28 Matches: 1(1) Sequences: 1(1) emPAI: 0.07										

	Leucine-rich repeat-containing protein 71 OS=Mus musculus GN=Lrrc71 PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	372	451.7631	901.5116	901.5055	6.74	1	28	0.016	1	U	K.MQSLKAPK.T
22.	BLM_MOUSE Mass: 158266 Score: 27 Matches: 2(2) Sequences: 1(1) emPAI: 0.03										
	Bloom syndrome protein homolog OS=Mus musculus GN=Blm PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	428	460.7577	919.5008	919.4983	2.69	1	27	0.014	1	U	K.RLIMMEK.D 429
23.	SPA3G_MOUSE Mass: 48990 Score: 27 Matches: 2(2) Sequences: 1(1) emPAI: 0.09										
	Serine protease inhibitor A3G OS=Mus musculus GN=Serpina3g PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	857	515.7401	1029.4657	1029.4655	0.19	0	24	0.014	1	U	K.SEFYLDEK.R 856
24.	PCBP3_MOUSE Mass: 39269 Score: 27 Matches: 1(1) Sequences: 1(1) emPAI: 0.11										
	Poly(rC)-binding protein 3 OS=Mus musculus GN=Pcbp3 PE=1 SV=3										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1316	567.7702	1133.5258	1133.5313	-4.77	0	27	0.015	1	U	K.IANATEGSSER.Q
25.	BEND3_MOUSE Mass: 94096 Score: 27 Matches: 1(1) Sequences: 1(1) emPAI: 0.05										
	BEN domain-containing protein 3 OS=Mus musculus GN=Bend3 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	254	429.2455	856.4765	856.4767	-0.15	1	27	0.015	1	U	K.KQLDPTR.L
26.	DNJC1_MOUSE Mass: 63830 Score: 27 Matches: 1(1) Sequences: 1(1) emPAI: 0.07										
	DnaJ homolog subfamily C member 1 OS=Mus musculus GN=Dnajc1 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	537	471.3052	940.5959	940.5957	0.18	0	27	0.0072	1	U	K.LLVELVQK.K
27.	LIN41_MOUSE Mass: 91996 Score: 26 Matches: 1(1) Sequences: 1(1) emPAI: 0.05										
	E3 ubiquitin-protein ligase TRIM71 OS=Mus musculus GN=Trim71 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	2012	624.8510	1247.6873	1247.6874	-0.01	0	26	0.021	1	U	R.LPAPGGAGPAEALK.L

28.	CR025_MOUSE Mass: 26430 Score: 26 Matches: 1(1) Sequences: 1(1) emPAI: 0.17										
	Uncharacterized protein C18orf25 homolog OS=Mus musculus PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	91	382.1865	762.3585	762.3582	0.42	0	26	0.0051	1	U	K.MEEAVGK.V
29.	SPCS2_MOUSE Mass: 24962 Score: 26 Matches: 1(1) Sequences: 1(1) emPAI: 0.18										
	Signal peptidase complex subunit 2 OS=Mus musculus GN=Spcs2 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1507	585.8398	1169.6651	1169.6656	-0.38	1	26	0.015	1	U	K.IDDKPVKIDK.W
30.	DPYL3_MOUSE Mass: 61897 Score: 26 Matches: 2(2) Sequences: 1(1) emPAI: 0.07										
	Dihydropyrimidinase-related protein 3 OS=Mus musculus GN=Dpysl3 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	415	459.7451	917.4756	917.4818	-6.79	0	26	0.036	1	U	K.QEVQSLSK.E 416
31.	UN13A_MOUSE Mass: 193660 Score: 26 Matches: 1(1) Sequences: 1(1) emPAI: 0.02										
	Protein unc-13 homolog A OS=Mus musculus GN=Unc13a PE=1 SV=3										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	115	387.7214	773.4282	773.4283	-0.14	0	26	0.018	1	U	K.ELGQLSK.L
32.	RBP1_MOUSE Mass: 74997 Score: 26 Matches: 1(1) Sequences: 1(1) emPAI: 0.06										
	RalA-binding protein 1 OS=Mus musculus GN=Ralbp1 PE=1 SV=4										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	888	521.7921	1041.5697	1041.5706	-0.90	0	26	0.018	1	U	R.DLPENLLTK.E
33.	K1C28_MOUSE Mass: 50315 Score: 26 Matches: 1(1) Sequences: 1(1) emPAI: 0.09										
	Keratin, type I cytoskeletal 28 OS=Mus musculus GN=Krt28 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1222	557.2769	1112.5393	1112.5397	-0.35	1	26	0.022	1	U	-.MSLRFSGGSR.H
34.	TM11G_MOUSE Mass: 46584 Score: 26 Matches: 2(2) Sequences: 1(1) emPAI: 0.10										
	Transmembrane protease serine 11G OS=Mus musculus GN=Tmprss11g PE=2 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1464	580.3448	1158.6750	1158.6720	2.58	1	23	0.02	1	U	K.LQSSQSILKR.D 1466

35.	TCAL9_MOUSE Mass: 12656 Score: 26 Matches: 1(1) Sequences: 1(1) emPAI: 0.39										
	Transcription elongation factor A protein-like 9 OS=Mus musculus GN=Tceal9 PE=3 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	188	410.6972	819.3798	819.3796	0.20	0	26	0.013	1	U	K.MEGNLEK.E
36.	CTTB2_MOUSE Mass: 178662 Score: 26 Matches: 3(3) Sequences: 1(1) emPAI: 0.02										
	Cortactin-binding protein 2 OS=Mus musculus GN=Cttnbp2 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1000	533.2950	1064.5755	1064.5727	2.68	0	23	0.034	1	U	K.TIPHLNTNR.N 1002 1003
37.	DCLK1_MOUSE Mass: 84101 Score: 26 Matches: 1(1) Sequences: 1(1) emPAI: 0.05										
	Serine/threonine-protein kinase DCLK1 OS=Mus musculus GN=Dclk1 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1934	618.3293	1234.6441	1234.6557	-9.38	0	26	0.033	1	U	R.SFEALLADLTR.T
38.	PTK6_MOUSE Mass: 51939 Score: 25 Matches: 1(1) Sequences: 1(1) emPAI: 0.09										
	Protein-tyrosine kinase 6 OS=Mus musculus GN=Ptk6 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	3950	506.9473	1517.8201	1517.8202	-0.08	0	25	0.031	1	U	R.VSQKPGADYVLSVR.D
39.	PLXB3_MOUSE Mass: 208233 Score: 25 Matches: 1(1) Sequences: 1(1) emPAI: 0.02										
	Plexin-B3 OS=Mus musculus GN=Plxnb3 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	2072	631.3553	1260.6960	1260.7078	-9.31	0	25	0.032	1	U	R.LQQVAALVEYK.V
40.	ERCC3_MOUSE Mass: 89070 Score: 25 Matches: 1(1) Sequences: 1(1) emPAI: 0.05										
	TFIIH basal transcription factor complex helicase XPB subunit OS=Mus musculus GN=Ercc3 PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	4473	816.9244	1631.8342	1631.8341	0.05	0	25	0.043	1	U	R.CLVLGNSAVSVEQWK.A
41.	DDX54_MOUSE Mass: 97687 Score: 25 Matches: 1(1) Sequences: 1(1) emPAI: 0.04										
	ATP-dependent RNA helicase DDX54 OS=Mus musculus GN=Ddx54 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide

	4034	514.6291	1540.8654	1540.8685	-1.99	1	25	0.021	1	U	R.SAQTGARALILSPTR.E
42.	TRPC5_MOUSE Mass: 111387 Score: 25 Matches: 1(1) Sequences: 1(1) emPAI: 0.04										
	Short transient receptor potential channel 5 OS=Mus musculus GN=Trpc5 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	3426	483.2729	1446.7969	1446.8082	-7.80	0	25	0.029	1	U	K.EVVGAVELLLSYR.K
43.	DDIAS_MOUSE Mass: 99883 Score: 24 Matches: 1(1) Sequences: 1(1) emPAI: 0.04										
	DNA damage-induced apoptosis suppressor protein OS=Mus musculus GN=Ddias PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	2479	441.9213	1322.7421	1322.7380	3.07	2	24	0.018	1	U	R.CFSKIILESKR.F
44.	JHD2C_MOUSE Mass: 260479 Score: 24 Matches: 1(1) Sequences: 1(1) emPAI: 0.02										
	Probable JmjC domain-containing histone demethylation protein 2C OS=Mus musculus GN=Jmjd1c PE=1 SV=3										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	280	437.2429	872.4712	872.4716	-0.38	1	24	0.048	1	U	K.KQNDLQK.R
45.	ZDBF2_MOUSE Mass: 273578 Score: 24 Matches: 1(1) Sequences: 1(1) emPAI: 0.02										
	DBF4-type zinc finger-containing protein 2 homolog OS=Mus musculus GN=Zdbf2 PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	110	385.7295	769.4444	769.4446	-0.24	1	24	0.011	1	U	R.EGAIPKR.R
46.	BRE1A_MOUSE Mass: 113450 Score: 24 Matches: 1(1) Sequences: 1(1) emPAI: 0.04										
	E3 ubiquitin-protein ligase BRE1A OS=Mus musculus GN=Rnf20 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	4575	834.9477	1667.8808	1667.8856	-2.84	0	24	0.04	1	U	R.HLISSLQNHNHQLK.G
	BRE1B_MOUSE Mass: 113897 Score: 24 Matches: 1(1) Sequences: 1(1)										
	E3 ubiquitin-protein ligase BRE1B OS=Mus musculus GN=Rnf40 PE=1 SV=2										
47.	CMTA1_MOUSE Mass: 184202 Score: 24 Matches: 1(1) Sequences: 1(1) emPAI: 0.02										
	Calmodulin-binding transcription activator 1 OS=Mus musculus GN=Camta1 PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1686	602.3418	1202.6690	1202.6693	-0.18	0	24	0.04	1	U	K.MTQAAILIQSK.F

	CMTA2_MOUSE Mass: 131927 Score: 24 Matches: 1(1) Sequences: 1(1)										
	Calmodulin-binding transcription activator 2 OS=Mus musculus GN=Camta2 PE=2 SV=1										
48.	FA7_MOUSE Mass: 50244 Score: 24 Matches: 1(1) Sequences: 1(1) emPAI: 0.09										
	Coagulation factor VII OS=Mus musculus GN=F7 PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1684	601.8345	1201.6545	1201.6489	4.67	1	24	0.038	1	U	R.RVTQVIMPDK.Y
49.	RHG30_MOUSE Mass: 120040 Score: 24 Matches: 1(1) Sequences: 1(1) emPAI: 0.04										
	Rho GTPase-activating protein 30 OS=Mus musculus GN=Arhgap30 PE=1 SV=3										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	2671	449.8762	1346.6067	1346.6062	0.40	1	24	0.028	1	U	K.ADAEGGEAERSQK.V
50.	CF157_MOUSE Mass: 61010 Score: 23 Matches: 1(1) Sequences: 1(1) emPAI: 0.07										
	Cilia- and flagella-associated protein 157 OS=Mus musculus GN=Cfap157 PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	32	364.7240	727.4335	727.4341	-0.75	1	23	0.0097	1	U	K.KPNKGGK.E
51.	IL23R_MOUSE Mass: 73406 Score: 23 Matches: 1(1) Sequences: 1(1) emPAI: 0.06										
	Interleukin-23 receptor OS=Mus musculus GN=Il23r PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	298	439.7113	877.4080	877.4076	0.52	1	23	0.034	1	U	R.CQETGKR.N
52.	IQCD_MOUSE Mass: 53318 Score: 23 Matches: 1(1) Sequences: 1(1) emPAI: 0.08										
	IQ domain-containing protein D OS=Mus musculus GN=Iqcd PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	548	472.7797	943.5449	943.5450	-0.17	1	23	0.038	1	U	K.LNTIEAKR.I
53.	CH033_MOUSE Mass: 24450 Score: 23 Matches: 1(1) Sequences: 1(1) emPAI: 0.19										
	UPF0488 protein C8orf33 homolog OS=Mus musculus PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	221	422.2379	842.4612	842.4610	0.25	0	23	0.037	1	U	K.EQAVGAIR.T

54.	ZN330_MOUSE Mass: 35584 Score: 23 Matches: 1(1) Sequences: 1(1) emPAI: 0.13										
	Zinc finger protein 330 OS=Mus musculus GN=Znf330 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	2361	655.2871	1308.5597	1308.5631	-2.63	0	23	0.02	1	U	R.AFCYFCNSVQK.L
55.	PCYXL_MOUSE Mass: 54840 Score: 23 Matches: 1(1) Sequences: 1(1) emPAI: 0.08										
	Prenylcysteine oxidase-like OS=Mus musculus GN=Pcyox1l PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	669	489.2868	976.5591	976.5593	-0.22	0	23	0.025	1	U	R.VQIVVYEK.G
56.	ZFA_MOUSE Mass: 84603 Score: 23 Matches: 1(1) Sequences: 1(1) emPAI: 0.05										
	Zinc finger autosomal protein OS=Mus musculus GN=Zfa PE=3 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	207	419.1977	836.3809	836.3876	-7.90	0	23	0.027	1	U	K.SSNSSDLK.R
	ZFX_MOUSE Mass: 89969 Score: 23 Matches: 1(1) Sequences: 1(1)										
	Zinc finger X-chromosomal protein OS=Mus musculus GN=Zfx PE=1 SV=2										
	ZFY1_MOUSE Mass: 88174 Score: 23 Matches: 1(1) Sequences: 1(1)										
	Zinc finger Y-chromosomal protein 1 OS=Mus musculus GN=Zfy1 PE=2 SV=3										
	ZFY2_MOUSE Mass: 88071 Score: 23 Matches: 1(1) Sequences: 1(1)										
	Zinc finger Y-chromosomal protein 2 OS=Mus musculus GN=Zfy2 PE=2 SV=2										
57.	AT8A2_MOUSE Mass: 129333 Score: 23 Matches: 1(1) Sequences: 1(1) emPAI: 0.03										
	Phospholipid-transporting ATPase IB OS=Mus musculus GN=Atp8a2 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	350	448.7530	895.4914	895.4916	-0.27	0	23	0.034	1	U	K.LGFVFTGR.T
58.	IPO9_MOUSE Mass: 115978 Score: 22 Matches: 1(1) Sequences: 1(1) emPAI: 0.04										
	Importin-9 OS=Mus musculus GN=Ipo9 PE=1 SV=3										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1364	572.8578	1143.7011	1143.6975	3.15	1	22	0.013	1	U	R.LVSTLISKAGR.E
59.	E2F6_MOUSE Mass: 30833 Score: 22 Matches: 1(1) Sequences: 1(1) emPAI: 0.15										
	Transcription factor E2F6 OS=Mus musculus GN=E2f6 PE=2 SV=2										

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1758	606.8292	1211.6438	1211.6550	-9.29	0	22	0.048	1	U	R.FDVSLVYLTR.K
60.	SYCC_MOUSE Mass: 94800 Score: 22 Matches: 1(1) Sequences: 1(1) emPAI: 0.05										
	Cysteine--tRNA ligase, cytoplasmic OS=Mus musculus GN=Cars PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	2960	698.8887	1395.7629	1395.7762	-9.49	2	22	0.039	1	U	K.KLFEAQEKLYK.E
61.	VATE1_MOUSE Mass: 26141 Score: 22 Matches: 1(1) Sequences: 1(1) emPAI: 0.17										
	V-type proton ATPase subunit E 1 OS=Mus musculus GN=Atp6v1e1 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1834	610.3500	1218.6855	1218.6794	5.01	1	22	0.042	1	U	K.AAVQKAIPMYK.I
62.	NRX3A_MOUSE Mass: 173318 Score: 22 Matches: 1(1) Sequences: 1(1) emPAI: 0.03										
	Neurexin-3 OS=Mus musculus GN=Nrxn3 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	155	403.2320	804.4494	804.4415	9.76	0	22	0.048	1	U	K.GLMLDLK.Y
63.	SPI1_MOUSE Mass: 31329 Score: 22 Matches: 1(1) Sequences: 1(1) emPAI: 0.14										
	Transcription factor PU.1 OS=Mus musculus GN=Spi1 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	436	463.7564	925.4982	925.5055	-7.87	2	22	0.043	1	U	R.KKMTYQK.M
64.	MALD2_MOUSE Mass: 63622 Score: 22 Matches: 1(1) Sequences: 1(1) emPAI: 0.07										
	MARVEL domain-containing protein 2 OS=Mus musculus GN=Marveld2 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	316	441.2654	880.5162	880.5243	-9.15	1	22	0.035	1	U	K.LSHIKQR.I
65.	P_MOUSE Mass: 91810 Score: 21 Matches: 1(1) Sequences: 1(1) emPAI: 0.05										
	P protein OS=Mus musculus GN=Oca2 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	2582	667.8862	1333.7578	1333.7605	-2.06	0	21	0.031	1	U	R.LLTVKPATSNYK.L
66.	NMT2_MOUSE Mass: 60446 Score: 21 Matches: 1(1) Sequences: 1(1) emPAI: 0.07										

	Glycylpeptide N-tetradecanoyltransferase 2 OS=Mus musculus GN=Nmt2 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	2539	666.4000	1330.7855	1330.7972	-8.82	1	21	0.021	1	U	K.AVRELINIYLK.Q
67.	UIMC1_MOUSE Mass: 81427 Score: 21 Matches: 1(1) Sequences: 1(1) emPAI: 0.05										
	BRCA1-A complex subunit RAP80 OS=Mus musculus GN=Uimc1 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1022	536.2663	1070.5180	1070.5252	-6.72	2	21	0.045	1	U	R.KEKCYLCK.S
68.	MYOM1_MOUSE Mass: 185349 Score: 21 Matches: 1(1) Sequences: 1(1) emPAI: 0.02										
	Myomesin-1 OS=Mus musculus GN=Myom1 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	44	365.7083	729.4021	729.4021	-0.00	0	21	0.024	1	U	K.QAAIAEK.N
69.	HYAS3_MOUSE Mass: 63307 Score: 20 Matches: 1(1) Sequences: 1(1) emPAI: 0.07										
	Hyaluronan synthase 3 OS=Mus musculus GN=Has3 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	168	404.1926	806.3707	806.3671	4.44	0	20	0.039	1	U	K.SGWGTSGR.K
70.	LAMC2_MOUSE Mass: 130077 Score: 20 Matches: 1(1) Sequences: 1(1) emPAI: 0.03										
	Laminin subunit gamma-2 OS=Mus musculus GN=Lamc2 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	402	457.2949	912.5752	912.5756	-0.50	0	20	0.016	1	U	R.NLTALLIR.A
71.	KIF27_MOUSE Mass: 158858 Score: 20 Matches: 1(1) Sequences: 1(1) emPAI: 0.03										
	Kinesin-like protein KIF27 OS=Mus musculus GN=Kif27 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	22	360.6764	719.3383	719.3385	-0.23	0	20	0.013	1	U	R.CSLGAGGR.S
72.	PD1L1_MOUSE Mass: 32760 Score: 19 Matches: 2(2) Sequences: 1(1) emPAI: 0.14										
	Programmed cell death 1 ligand 1 OS=Mus musculus GN=Cd274 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	36	364.7243	727.4340	727.4341	-0.09	1	18	0.031	1	U	R.GRASLPK.D 40

73.	ACLY_MOUSE Mass: 119651 Score: 18 Matches: 1(1) Sequences: 1(1) emPAI: 0.04										
	ATP-citrate synthase OS=Mus musculus GN=Acly PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1089	545.3365	1088.6585	1088.6594	-0.76	1	18	0.035	1	U	R.VQILKDFVK.Q
74.	JPH1_MOUSE Mass: 71860 Score: 18 Matches: 1(1) Sequences: 1(1) emPAI: 0.06										
	Junctophilin-1 OS=Mus musculus GN=Jph1 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	85	378.7218	755.4290	755.4290	0.00	1	18	0.024	1	U	R.KGTTPPR.S

Biotin-TPL pulldown Band #5

1. PSD10_MOUSE Mass: 25068 Score: 11406 Matches: 478(478) Sequences: 4(4) emPAI: 2.25

26S proteasome non-ATPase regulatory subunit 10 OS=Mus musculus GN=Psmd10 PE=1 SV=3

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1551	388.5595	1162.6567	1162.6573	-0.48	0	(50)	7.2e-005	1	U	K.MVHILLFYK.A 1514 1516 1517 1522 1523 1529 1536 1537 1539 1541 1542 1543 1544 1546 1547 1548 1550 1552 1559 1561 1566 1567 1568 1571 1572 1575 1582 1583 1586 1587 1588 1591 1593 1598 1601 1602 1607 1610 1611 1612 1613 1614 1616 1617 1621 1623 1625 1627 1628 1629 1630 1632 1633 1634 1635 1636 1645 1646 1648 1649 1658 1659 1666 1669 1675 1676 1678 1679 1680 1681 1686 1687 1691
	1654	582.3361	1162.6576	1162.6573	0.27	0	61	4.2e-006	1	U	K.MVHILLFYK.A 1513 1515 1518 1519 1525 1530 1531 1532 1533 1555 1556 1557 1558 1563 1564 1565 1578 1579 1580 1596 1608 1619 1620 1642 1653 1655 1656 1657 1660 1661 1662 1663 1664 1672 1673 1683 1685 1688 1689 1692 1693
	1818	590.3333	1178.6519	1178.6522	-0.19	0	(53)	3.5e-005	1	U	K.MVHILLFYK.A 1816
	1822	393.8914	1178.6524	1178.6522	0.22	0	(30)	0.007	1	U	K.MVHILLFYK.A 1810 1819 1820 1821 1823

	2077	406.1768	1215.5085	1215.5091	-0.53	0	(61)	2.2e-006	1	U	K.DHYDATAMHR.A 2070 2071 2072 2073 2074 2076 2081 2082 2083 2085 2086 2089 2090 2091 2092 2095 2096 2097 2098 2100 2101 2102 2103 2104 2105 2106 2107 2109 2110 2111 2112 2113 2117 2118 2119 2120 2122 2123 2124 2126 2127 2129 2130 2131 2132 2133 2134 2137 2138
	2078	608.7615	1215.5085	1215.5091	-0.47	0	67	5.9e-007	1	U	K.DHYDATAMHR.A 2079 2087 2099 2114 2115 2116 2121 2128 2135 2136
	2267	616.7592	1231.5039	1231.5040	-0.10	0	(55)	9.6e-006	1	U	K.DHYDATAMHR.A 2249 2252 2266 2281 2282
	2285	411.5090	1231.5053	1231.5040	1.01	0	(44)	0.00012	1	U	K.DHYDATAMHR.A 2253 2254 2257 2258 2259 2262 2264 2265 2268 2269 2271 2272 2273 2274 2275 2277 2283
	4248	528.2873	1581.8402	1581.8402	-0.01	0	(53)	4.9e-005	1	U	K.FLVTQGASIYIENK.E 4178 4180 4190 4223 4224 4231 4247 4252 4270 4271 4285 4286 4307 4308

	4260	791.9275	1581.8404	1581.8402	0.12	0	109	1.2e-010	1	U	K.FLVTQGASIYIENK.E 4176 4181 4182 4183 4185 4186 4187 4188 4189 4191 4192 4193 4194 4195 4196 4197 4198 4200 4202 4203 4204 4205 4206 4208 4209 4210 4211 4212 4213 4214 4216 4217 4218 4219 4220 4221 4222 4227 4228 4229 4230 4232 4233 4234 4235 4236 4237 4238 4239 4240 4241 4242 4243 4244 4245 4249 4250 4251 4253 4254 4256 4257 4258 4259 4262 4265 4266 4267 4268 4272 4274 4275 4276 4277 4279 4280 4281 4282 4283 4287 4289 4290 4292 4293 4294 4295 4297 4302 4304 4306 4309 4310 4311

	4925	588.9695	1763.8866	1763.8876	-0.55	0	(69)	1.8e-006	1	U	R.HEIAVMLLEGGANPDAK.D 4902 4903 4904 4906 4907 4910 4911 4914 4915 4916 4917 4919 4920 4921 4922 4923 4924 4926 4930 4931 4932 4933 4934 4935 4936 4937 4938 4939 4940 4941 4942 4945 4946 4947 4948 4949 4950 4951 4952 4953 4956 4957 4958 4959 4960 4961 4962 4967 4968 4969 4970 4971 4973 4974 4975 4976 4978 4979 4980 4981 4982 4983 4985 4986 4987 4990 4991 4992 4993 4994 4995 4996 4997 4999 5000 5002 5003 5004 5005 5006 5007 5008 5009 5012 5013 5014 5015 5016 5017 5018 5019 5020 5022 5023 5024 5025 5026 5027 5028 5029 5030 5033 5034 5035 5036 5037 5038 5039 5042 5043 5044 5045 5046 5047 5048 5050 5051 5052 5053
	4943	882.9507	1763.8868	1763.8876	-0.44	0	150	1.5e-014	1	U	R.HEIAVMLLEGGANPDAK.D 4901 4909 4912 4913 4927 4929 4944 4954 4955 4963 4965 4966 4989 5011 5021 5041
	4964	441.9791	1763.8873	1763.8876	-0.17	0	(49)	0.00022	1	U	R.HEIAVMLLEGGANPDAK.D 5040
	5107	890.9486	1779.8827	1779.8825	0.09	0	(137)	3e-013	1	U	R.HEIAVMLLEGGANPDAK.D 5099 5102 5106 5109 5112 5113
	5114	594.3018	1779.8835	1779.8825	0.53	0	(74)	5.7e-007	1	U	R.HEIAVMLLEGGANPDAK.D 5095 5096 5097 5098 5100 5101 5103 5104 5108 5110 5111 5115 5116

2.	LIN41_MOUSE Mass: 91996 Score: 77 Matches: 2(2) Sequences: 2(2) emPAI: 0.10										
	E3 ubiquitin-protein ligase TRIM71 OS=Mus musculus GN=Trim71 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	2413	624.8510	1247.6875	1247.6874	0.08	0	72	5.3e-007	1	U	R.LPAPGGAGPAEALK.L
	4559	550.8879	1649.6420	1649.6418	0.09	0	22	0.0093	1	U	R.CLDCQEHLCDNCVR.A
3.	MED1_MOUSE Mass: 167036 Score: 59 Matches: 1(1) Sequences: 1(1) emPAI: 0.03										
	Mediator of RNA polymerase II transcription subunit 1 OS=Mus musculus GN=Med1 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	4512	819.9240	1637.8335	1637.8334	0.03	0	59	1.6e-005	1	U	K.MYLALQSLEQDLSK.M
4.	VP13C_MOUSE Mass: 419824 Score: 36 Matches: 2(2) Sequences: 1(1) emPAI: 0.01										
	Vacuolar protein sorting-associated protein 13C OS=Mus musculus GN=Vps13c PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	2028	604.8301	1207.6457	1207.6448	0.75	2	35	0.0031	1	U	K.EAKKDTFLEK.L 2026
5.	KNTC1_MOUSE Mass: 250198 Score: 29 Matches: 1(1) Sequences: 1(1) emPAI: 0.02										
	Kinetochore-associated protein 1 OS=Mus musculus GN=Kntc1 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	4355	797.9270	1593.8394	1593.8436	-2.61	1	29	0.012	1	U	K.EMSLKNFVGTDIIK.G
6.	KSYK_MOUSE Mass: 71331 Score: 26 Matches: 1(1) Sequences: 1(1) emPAI: 0.06										
	Tyrosine-protein kinase SYK OS=Mus musculus GN=Syk PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	559	486.2433	970.4720	970.4719	0.09	0	26	0.015	1	U	K.NEANDPALK.D
7.	NHRF1_MOUSE Mass: 38577 Score: 26 Matches: 1(1) Sequences: 1(1) emPAI: 0.12										
	Na(+)/H(+) exchange regulatory cofactor NHE-RF1 OS=Mus musculus GN=Slc9a3r1 PE=1 SV=3										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	4627	556.6187	1666.8341	1666.8275	3.99	1	26	0.032	1	U	K.QHGDVVSAIKGGGDEAK.L
8.	ATG2B_MOUSE Mass: 231253 Score: 26 Matches: 1(1) Sequences: 1(1) emPAI: 0.02										
	Autophagy-related protein 2 homolog B OS=Mus musculus GN=Atg2b PE=1 SV=3										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	826	526.7756	1051.5366	1051.5298	6.46	0	26	0.029	1	U	R.IEHVPENSK.T

9. WRN_MOUSE Mass: 157104 Score: 25 Matches: 1(1) Sequences: 1(1) emPAI: 0.03

Werner syndrome ATP-dependent helicase homolog OS=Mus musculus GN=Wrn PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1038	546.3085	1090.6025	1090.6056	-2.83	1	25	0.023	1	U	K.MLLENKSIK.K

10. KDM5B_MOUSE Mass: 175442 Score: 23 Matches: 1(1) Sequences: 1(1) emPAI: 0.02

Lysine-specific demethylase 5B OS=Mus musculus GN=Kdm5b PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1321	568.3091	1134.6036	1134.6067	-2.70	1	23	0.05	1	U	R.CDIGLLGLKR.K

11. SMC2_MOUSE Mass: 134156 Score: 23 Matches: 1(1) Sequences: 1(1) emPAI: 0.03

Structural maintenance of chromosomes protein 2 OS=Mus musculus GN=Smc2 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2965	662.3249	1322.6353	1322.6353	0.00	1	23	0.049	1	U	K.AEEKYEALENK.M

12. PCLO_MOUSE Mass: 550496 Score: 22 Matches: 1(1) Sequences: 1(1) emPAI: 0.01

Protein piccolo OS=Mus musculus GN=Pclo PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
589	492.7589	983.5033	983.5036	-0.34	0	22	0.04	1	U	K.SPAQQPGTAK.L

13. SYT1_MOUSE Mass: 47388 Score: 22 Matches: 1(1) Sequences: 1(1) emPAI: 0.09

Synaptotagmin-1 OS=Mus musculus GN=Syt1 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
35	368.2055	734.3964	734.3963	0.14	0	22	0.014	1	U	R.YVPTAGK.L

14. BRNP2_MOUSE Mass: 89171 Score: 22 Matches: 1(1) Sequences: 1(1) emPAI: 0.05

BMP/retinoic acid-inducible neural-specific protein 2 OS=Mus musculus GN=Brinp2 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
888	532.3108	1062.6071	1062.6107	-3.33	1	22	0.032	1	U	R.MLLTLKSNK.Y

15. GRM2_MOUSE Mass: 95826 Score: 19 Matches: 1(1) Sequences: 1(1) emPAI: 0.05

Metabotropic glutamate receptor 2 OS=Mus musculus GN=Grm2 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
136	400.2190	798.4235	798.4236	-0.08	0	19	0.033	1	U	R.GAVAEGPAK.K

16.	TRI50_MOUSE Mass: 54573 Score: 19 Matches: 1(1) Sequences: 1(1) emPAI: 0.08										
	E3 ubiquitin-protein ligase TRIM50 OS=Mus musculus GN=Trim50 PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	295	448.2860	894.5575	894.5538	4.06	0	19	0.016	1	U	K.VLPAPASLK.L
17.	TOPB1_MOUSE Mass: 168754 Score: 18 Matches: 1(1) Sequences: 1(1) emPAI: 0.03										
	DNA topoisomerase 2-binding protein 1 OS=Mus musculus GN=Topbp1 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	2194	610.7476	1219.4806	1219.4816	-0.81	0	18	0.021	1	U	K.SSDNSECFFK.A
18.	TR150_MOUSE Mass: 108114 Score: 14 Matches: 1(1) Sequences: 1(1) emPAI: 0.04										
	Thyroid hormone receptor-associated protein 3 OS=Mus musculus GN=Thrap3 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	86	387.6819	773.3492	773.3416	9.82	0	14	0.047	1	U	R.SSSNHSR.V
19.	ARI2_MOUSE Mass: 57659 Score: 14 Matches: 1(1) Sequences: 1(1) emPAI: 0.08										
	E3 ubiquitin-protein ligase ARIH2 OS=Mus musculus GN=Arih2 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	29	364.2084	726.4022	726.4024	-0.34	0	14	0.038	1	U	K.VSHSVAK.L

Biotin-TPL pulldown Band #6

1. DCTP1_MOUSE Mass: 18783 Score: 14079 Matches: 428(428) Sequences: 4(4) emPAI: 4.98

dCTP pyrophosphatase 1 OS=Mus musculus GN=Dctpp1 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1262	605.7973	1209.5800	1209.5812	-0.95	1	87	1.9e-008	1	U	R.GSACKYTDLPR.G 1257 1261 1272 1276 1277 1282 1283 1298 1299 1302 1303 1304 1308 1319 1324 1339 1340 1342 1344 1349 1350 1352
1265	404.2007	1209.5801	1209.5812	-0.88	1	(45)	0.00036	1	U	R.GSACKYTDLPR.G 1258 1259 1263 1264 1269 1270 1271 1273 1274 1275 1281 1285 1286 1287 1288 1290 1292 1293 1294 1295 1301 1306 1307 1309 1310 1313 1314 1315 1316 1317 1321 1322 1331 1333 1334 1335 1337 1341 1343
1630	420.1957	1257.5652	1257.5659	-0.57	1	(33)	0.0031	1	U	R.GSACKYTDLPR.G
1633	629.7901	1257.5656	1257.5659	-0.23	1	(60)	7.5e-006	1	U	R.GSACKYTDLPR.G 1631 1632 1634 1636
1707	634.3080	1266.6015	1266.6027	-0.89	1	(26)	0.029	1	U	R.GSACKYTDLPR.G
1711	423.2079	1266.6019	1266.6027	-0.58	1	(28)	0.018	1	U	R.GSACKYTDLPR.G

	1996	437.2357	1308.6853	1308.6860	-0.51	0	(58)	1.6e-005	1	U	R.CHVDLPQAVISK.M 1965 1967 1969 1970 1975 1976 1977 1978 1979 1980 1981 1982 1983 1984 1985 1991 1992 1993 1994 1995 1997 1998 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2059 2060 2061 2062 2063 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2235 2236 2237 2238 2239 2240 2241 2253 2254 2255 2256 2257 2265 2272 2273 2274 2279 2280 2281 2285

	2075	655.3502	1308.6858	1308.6860	-0.18	0	(82)	6.5e-008	1	U	R.CHVDLPQAVISK.M 1964 1966 1968 1971 1972 1973 1974 1986 1987 1988 1989 1990 1999 2000 2001 2002 2003 2004 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2076 2077 2078 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2230 2231 2232 2233 2234 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2258 2259 2260 2261 2262 2263 2264 2266 2267 2268 2269 2270 2271 2275 2276 2277 2278 2282 2283 2284
	2603	679.3422	1356.6699	1356.6707	-0.63	0	91	8.4e-009	1	U	R.CHVDLPQAVISK.M 2604 2606 2608
	2672	683.8610	1365.7074	1365.7075	-0.08	0	(25)	0.036	1	U	R.CHVDLPQAVISK.M
	2673	456.2431	1365.7075	1365.7075	-0.00	0	(28)	0.015	1	U	R.CHVDLPQAVISK.M 2671 2674

	2988	470.5613	1408.6621	1408.6623	-0.13	0	(54)	4.4e-005	1	U	K.SDTEPGPQAWPPK.E 2978 2981 2982 2984 2985 2989 2990 2996
	2995	705.3385	1408.6624	1408.6623	0.11	0	92	7.3e-009	1	U	K.SDTEPGPQAWPPK.E 2977 2979 2980 2986 2987 2993 2994 2997 2998
	4110	521.2617	1560.7633	1560.7645	-0.73	0	50	0.00013	1	U	R.GTVGQEDSAAARPFR.F 4108 4109 4115 4118
	4113	781.3891	1560.7636	1560.7645	-0.52	0	(36)	0.0032	1	U	R.GTVGQEDSAAARPFR.F 4106 4107
2.	PSD10_MOUSE Mass: 25068 Score: 82 Matches: 5(5) Sequences: 3(3) emPAI: 0.66										
	26S proteasome non-ATPase regulatory subunit 10 OS=Mus musculus GN=Psmd10 PE=1 SV=3										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1061	388.5598	1162.6576	1162.6573	0.30	0	25	0.014	1	U	K.MVHILLFYK.A 1060
	1062	582.3361	1162.6577	1162.6573	0.37	0	(23)	0.025	1	U	K.MVHILLFYK.A
	1393	406.1770	1215.5092	1215.5091	0.06	0	35	0.00083	1	U	K.DHYDATAMHR.A
	4712	588.9698	1763.8877	1763.8876	0.08	0	48	0.00025	1	U	R.HEIAVMLLEGGANPDAK.D
3.	ERCC3_MOUSE Mass: 89070 Score: 34 Matches: 1(1) Sequences: 1(1) emPAI: 0.05										
	TFIIH basal transcription factor complex helicase XPB subunit OS=Mus musculus GN=Ercc3 PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	4387	816.9244	1631.8342	1631.8341	0.05	0	34	0.005	1	U	R.CLVLGNSAVSVEQWK.A
4.	NEUA_MOUSE Mass: 48028 Score: 32 Matches: 3(3) Sequences: 1(1) emPAI: 0.09										
	N-acylneuraminate cytidylyltransferase OS=Mus musculus GN=Cmas PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1778	638.8486	1275.6826	1275.6857	-2.40	1	28	0.015	1	U	K.QTLSALKLDCK.T 1775 1777
5.	CG057_MOUSE Mass: 32875 Score: 28 Matches: 1(1) Sequences: 1(1) emPAI: 0.14										
	Uncharacterized protein C7orf57 homolog OS=Mus musculus GN=Gm11992 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	64	371.7265	741.4385	741.4385	0.06	0	28	0.0033	1	U	K.LPAINSK.N
6.	LCA5_MOUSE Mass: 80113 Score: 27 Matches: 1(1) Sequences: 1(1) emPAI: 0.05										

	Lebercilin OS=Mus musculus GN=Lca5 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	84	378.7344	755.4543	755.4541	0.28	1	27	0.0026	1	U	R.LPKSSPK.K
7.	SOCS6_MOUSE Mass: 59040 Score: 27 Matches: 1(1) Sequences: 1(1) emPAI: 0.07										
	Suppressor of cytokine signaling 6 OS=Mus musculus GN=Socs6 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	190	412.2394	822.4642	822.4599	5.20	1	27	0.0077	1	U	R.KSFNLSK.S
8.	PLIN4_MOUSE Mass: 139328 Score: 26 Matches: 2(2) Sequences: 1(1) emPAI: 0.03										
	Perilipin-4 OS=Mus musculus GN=Plin4 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	82	373.6932	745.3719	745.3719	0.01	0	22	0.014	1	U	R.ASVAQDR.L 81
9.	EST1A_MOUSE Mass: 160396 Score: 26 Matches: 1(1) Sequences: 1(1) emPAI: 0.03										
	Telomerase-binding protein EST1A OS=Mus musculus GN=Smg6 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1875	646.8368	1291.6590	1291.6482	8.38	0	26	0.032	1	U	R.IGMETFPAVAEK.V
10.	PKRI1_MOUSE Mass: 21478 Score: 24 Matches: 1(1) Sequences: 1(1) emPAI: 0.22										
	PRKR-interacting protein 1 OS=Mus musculus GN=Prkrip1 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	383	460.7658	919.5171	919.5161	1.10	2	24	0.037	1	U	K.KMKLEQK.K
11.	ZBT18_MOUSE Mass: 58348 Score: 23 Matches: 1(1) Sequences: 1(1) emPAI: 0.08										
	Zinc finger and BTB domain-containing protein 18 OS=Mus musculus GN=Zbtb18 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	122	392.7498	783.4850	783.4854	-0.49	0	23	0.0075	1	U	K.LNILPSK.R
12.	SWP70_MOUSE Mass: 68953 Score: 23 Matches: 2(2) Sequences: 1(1) emPAI: 0.06										
	Switch-associated protein 70 OS=Mus musculus GN=Swap70 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	73	372.2185	742.4225	742.4225	0.06	0	21	0.016	1	U	R.LIEPGSK.N 72

13.	SGPL1_MOUSE Mass: 63636 Score: 23 Matches: 1(1) Sequences: 1(1) emPAI: 0.07										
	Sphingosine-1-phosphate lyase 1 OS=Mus musculus GN=Sgpl1 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	175	409.7606	817.5066	817.5062	0.49	0	23	0.016	1	U	R.VAIQFLK.D
14.	MTUS2_MOUSE Mass: 147266 Score: 23 Matches: 1(1) Sequences: 1(1) emPAI: 0.03										
	Microtubule-associated tumor suppressor candidate 2 homolog OS=Mus musculus GN=Mtus2 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	168	407.2452	812.4759	812.4756	0.42	0	23	0.013	1	U	K.KPAVSSPK.R
15.	MCM10_MOUSE Mass: 98344 Score: 23 Matches: 3(3) Sequences: 1(1) emPAI: 0.04										
	Protein MCM10 homolog OS=Mus musculus GN=Mcm10 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	237	428.2685	854.5224	854.5225	-0.11	1	18	0.026	1	U	R.LPQIKEK.M 235 236
16.	APOB_MOUSE Mass: 509113 Score: 22 Matches: 1(1) Sequences: 1(1) emPAI: 0.01										
	Apolipoprotein B-100 OS=Mus musculus GN=Apob PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	43	364.2265	726.4385	726.4388	-0.44	0	22	0.007	1	U	K.GVVSIPR.L
17.	RASA3_MOUSE Mass: 95926 Score: 20 Matches: 1(1) Sequences: 1(1) emPAI: 0.05										
	Ras GTPase-activating protein 3 OS=Mus musculus GN=Rasa3 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	85	379.7421	757.4696	757.4698	-0.14	1	20	0.032	1	U	R.IKIGEAK.N
18.	RABL6_MOUSE Mass: 79782 Score: 20 Matches: 1(1) Sequences: 1(1) emPAI: 0.05										
	Rab-like protein 6 OS=Mus musculus GN=Rabl6 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	263	431.6987	861.3828	861.3828	0.06	1	20	0.026	1	U	K.EEGKEDR.K
19.	AKAP4_MOUSE Mass: 93735 Score: 20 Matches: 1(1) Sequences: 1(1) emPAI: 0.05										
	A-kinase anchor protein 4 OS=Mus musculus GN=Akap4 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	71	372.2184	742.4222	742.4225	-0.37	0	20	0.021	1	U	K.LPEVSAK.A

20.	DYSF_MOUSE Mass: 237759 Score: 18 Matches: 1(1) Sequences: 1(1) emPAI: 0.02										
	Dysferlin OS=Mus musculus GN=Dysf PE=1 SV=3										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	103	385.7168	769.4190	769.4195	-0.62	1	18	0.017	1	U	K.RSSAPPR.K
21.	MET14_MOUSE Mass: 52090 Score: 18 Matches: 1(1) Sequences: 1(1) emPAI: 0.09										
	N6-adenosine-methyltransferase subunit METTL14 OS=Mus musculus GN=Mettl14 PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	56	370.7188	739.4229	739.4228	0.17	1	18	0.018	1	U	K.SPPPKSK.S
22.	STPG1_MOUSE Mass: 37475 Score: 17 Matches: 1(1) Sequences: 1(1) emPAI: 0.12										
	O(6)-methylguanine-induced apoptosis 2 OS=Mus musculus GN=Stpg1 PE=2 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	44	364.2392	726.4638	726.4640	-0.24	0	17	0.02	1	U	R.LGPIISK.N
23.	CASP_MOUSE Mass: 77222 Score: 15 Matches: 1(1) Sequences: 1(1) emPAI: 0.06										
	Protein CASP OS=Mus musculus GN=Cux1 PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	101	384.7524	767.4902	767.4905	-0.39	0	15	0.029	1	U	K.QVAPLLK.S