

Services of the MS group

Biomolecules: Proteins and Peptides

Zuzana Demianová
MS group
IOCB AS CR v.v.i

Outline

- ◉ Service vs. Collaboration
- ◉ Service methodology
- ◉ Reports
- ◉ General problems

Service vs. Collaboration

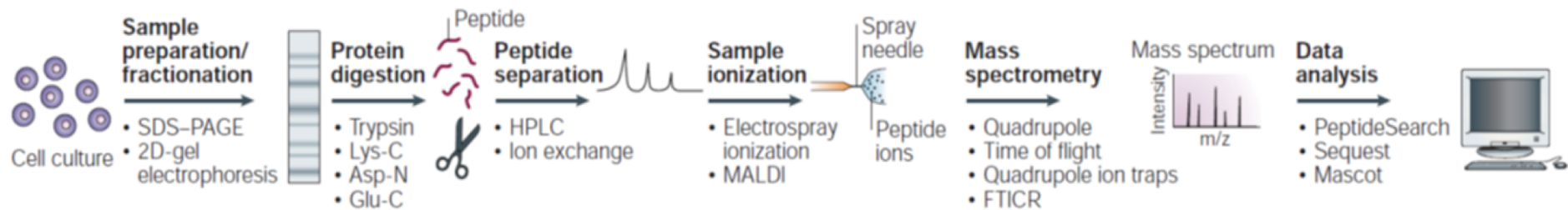
Service

- Routinely used methods
 - > Basic LC-MS
 - > Protein Identification

Collaboration

- Routinely used methods with adaptation/additional informations
 - > PTM and its position identification
 - > Quantification
- Developing a specific method for a particular sample
- Identification of cleavage site
- Identification of S-S bridges
- ...

Protein Identifications



General workflow

- Digestion of protein by specific proteases
- Separation of peptides by RP-nLC
- Mass Spectrometry detection
- Data analysis by Bioworks/Protein Pilot

MS instruments used in protein studies



BioWorks Report

Reference					P (pro)	Score	MW	Accession	Peptide (Hits)	
Scan(s)	Peptide	MH+	DeltaM (ppm)	z	Type	P (pep)	XC	Sp	RSp	Ions
<i>A42845 3-hydroxybutyrate dehydrogenase (EC 1.1.1.30)</i>										
1- human (fragment)										
2159 - 2176	K.YFDEK.I	701.31409	-0.22224	2	CID	9.24E-05	60.15	38112.3	345719	6 (6 0 0 0 0)
2297 - 2299	R.SPYC#ITK.F	868.42331	-0.65087	2	CID	1.40E-01	1.33	310.5	1	5/8
2349 - 2351	K.ELDSLNSDR.L	1048.49060	-0.07104	2	CID	3.26E-01	0.77	47.1	1	3/12
2558 - 2560	R.VVNISSM*LGR.M	1091.58775	-1.16992	2	CID	9.19E-04	1.93	210.6	1	7/16
2588 - 2590	R.YEM*YPLGVK.V	1115.54415	-0.58237	2	CID	9.24E-05	2.97	830.2	1	14/18
2967 - 2989	K.SFLPLIR.R	845.52435	-0.34074	2	CID	1.65E-03	1.95	268.5	1	8/16
<i>3-hydroxybutyrate dehydrogenase precursor; (R)-3-hydroxybutyrate</i>										
2 dehydrogenase [Homo sapiens]										
1444 - 1484	-.SSLKDPEK.-	903.47821	-0.80303	2	CID	1.68E-04	80.15	38132.5	17738292	8 (8 0 0 0 0)
2159 - 2176	K.YFDEK.I	701.31409	-0.22224	2	CID	9.44E-01	0.25	27.4	2	2/14
2297 - 2299	R.SPYC#ITK.F	868.42331	-0.65087	2	CID	2.40E-01	1.33	310.5	1	5/8
2326 - 2328	K.VVEIVR.H	714.45087	-0.31782	2	CID	5.11E-01	0.77	47.1	1	3/12
2349 - 2351	K.ELDSLNSDR.L	1048.49060	-0.07104	2	CID	6.80E-02	1.46	371.4	1	9/10
2558 - 2560	R.VVNISSM*LGR.M	1091.58775	-1.16992	2	CID	1.67E-03	1.93	210.6	1	7/16
2588 - 2590	R.YEM*YPLGVK.V	1115.54415	-0.58237	2	CID	1.68E-04	2.97	830.2	1	14/18
2967 - 2989	K.SFLPLIR.R	845.52435	-0.34074	2	CID	3.00E-03	1.95	268.5	1	8/16
<i>AAH11964 Unknown (protein for MGC:9788) [Homo</i>										
3 sapiens]										
						1.68E-04	80.15	38116.5	15080429	8 (8 0 0 0 0)
4 putative [Homo sapiens]										
						3.89E-01	20.09	2212.2	553734	2 (2 0 0 0 0)

Reference: huCD36 deglycosylated [MASS=54057]

Database: C:\Xcalibur\database\CD36.fasta

Number of Amino Acids: 480 Monoisotopic MW: 54023.5 pI: 5.09

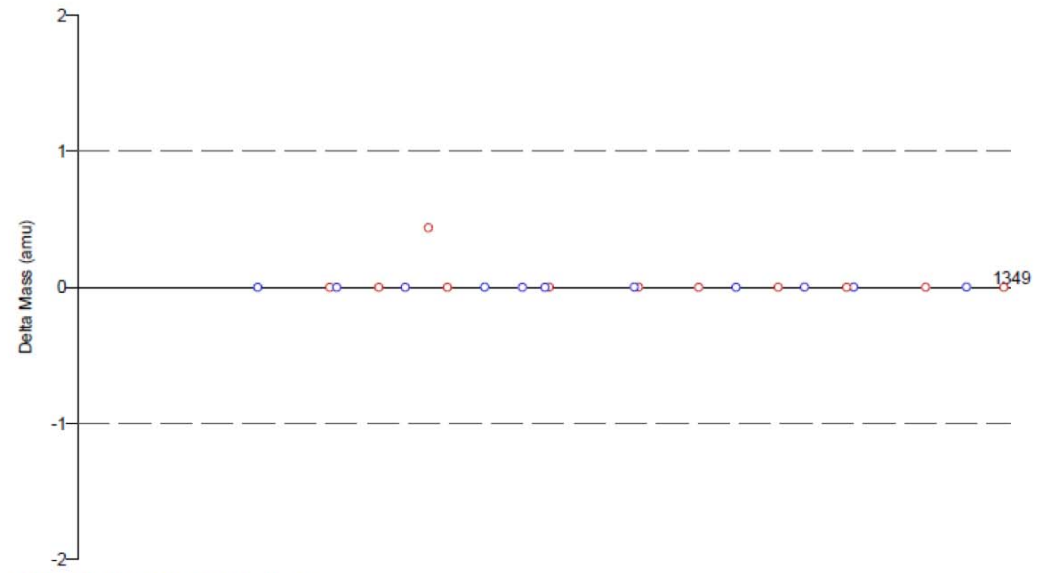


Protein:

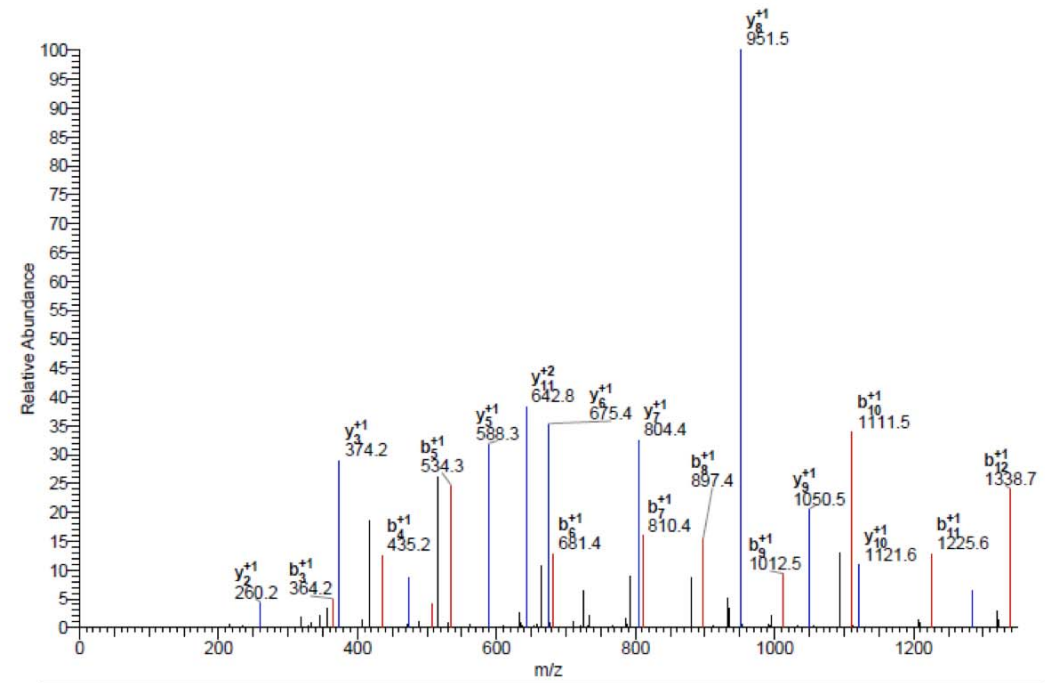
MGCDRNCGLI AGAVIGAVLA VFGGILMPVG DLIQKTIKK QVVLEEGTIA
 FKNWVKGTGE VYRQFWIPDV QNPQEVMMDS SNIQVKQRGP YTYRVRFLAK
 EDVTQDAEDN TVSFLQPNGA IFEPSSLVGT EADDFTVLNL AVAAASHIYQ
 NQFVQMILNS LINKSKSSMF QVRTLRELLW GYRDPFLSLV PYPVTTTVGL
 FYPYDNTADG VYKVFNGKDD ISKVAIIDTY KGKRDLSYWE SHCDMIDGTD
 AASFPFVVEK SQVLQFFSSD ICRSIYAVFE SDVNLKGIPV YRFVLPSKAF
 ASPVENPDNY CFCTEKIISK DCTSYGVLDI SKCKEGRPVY ISLPHFLYAS
 PDVSEPIDGL NPNEEEHRTY LDIEPITGFT LQFAKRLQVN LLVKPSEKIQ
 VLKLNLRNYI VPILWLDETG TIGDEKANMF RSQVTGKINL LGLIEMILLS
 VGVVMFVAFM ISYCACRSKT IKDYKDDDDK

Protein Coverage:

Sequence	MH+	% Mass	AA	% AA
KQVVLEEGTIAFK	1461.83	2.71	40 - 52	2.71
QVVLEEGTIAFK	1333.74	2.47	41 - 52	2.50
TGTEVYR	825.41	1.53	57 - 63	1.46
QFWIPDVQNPQEVMMDS SNIQVK	2783.32	5.15	64 - 86	4.79
GPYTYR	756.37	1.40	89 - 94	1.25
SSMPQVR	854.42	1.58	167 - 173	1.46
ELLWGYR	936.49	1.73	177 - 183	1.46
DPFLSLVPYPVTTTVGLFYPYDNTADGVYK	3352.67	6.21	184 - 213	6.25
VFNGKDDISK	1122.58	2.08	214 - 223	2.08
DLSYWESHCDMIDGTD AASFPFVVEK	2960.28	5.48	235 - 260	5.42
SQVLQFFSSD ICR	1529.74	2.83	261 - 273	2.71
SIYAVFESDVNLK	1484.76	2.75	274 - 286	2.71
GIPVYR	704.41	1.30	287 - 292	1.25
AFASPVENPDNYCFCTEK	2034.86	3.77	299 - 316	3.75
DCTSYGVLDISK	1300.61	2.41	321 - 332	2.50
PVYISLPHFLYASPDVSEPIDGLNPNEEEHR	3534.72	6.54	338 - 368	6.46
TYLDIEPITGFTLQFAK	1957.03	3.62	369 - 385	3.54
RLQVNLLVK	1082.70	2.00	386 - 394	1.88
RLQVNLLVKPSEK	1523.93	2.82	386 - 398	2.71
LQVNLLVK	926.60	1.72	387 - 394	1.67
LQVNLLVKPSEK	1367.83	2.53	387 - 398	2.50
NYIVPILWLDETGTIGDEK	2176.12	4.03	408 - 426	3.96
DYKDDDDK	1013.41	1.88	473 - 480	1.67
Totals:	31970.62	59.18	279	58.13



#2444-2444 RT:70.01-70.01 NL: 4.39E5

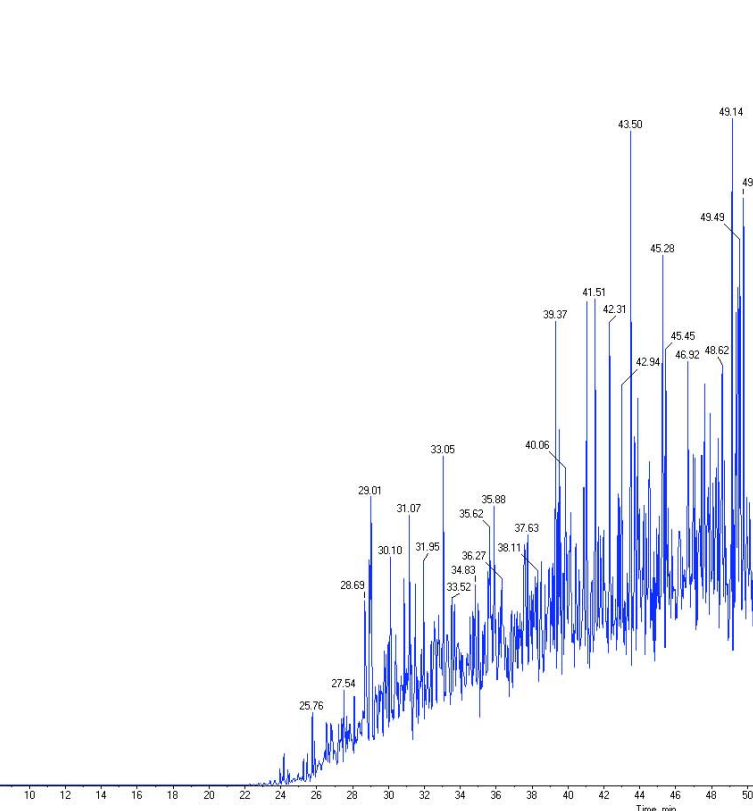


Protein Pilot Report / Protein

N	Total %Cov	%Cov		AccessionName	Species	Peptides (95%)	
		(50)	(95)				
1	77.88	59.57	54.61	54.61	sp P50440 GATM_HUMAN <i>Glycine amidinotransferase, mitochondrial OS=Homo sapiens GN=GATM PE=1 SV=1</i>	HUMAN	90
1	77.88	64.45	59.08	59.08	sp P50440-2 GATM_HUMAN <i>Isoform Cytoplasmic of Glycine amidinotransferase, mitochondrial OS=Homo sapiens GN=GATM</i>	HUMAN	90
2	51.36	43.72	43.72	43.72	sp P00761 TRYP_PIG <i>Trypsin OS=Sus scrofa PE=1 SV=1</i>	PIG	54
2	51.36	45.29	45.29	45.29	cont 000143 <i>polydocalin-1 (contaminant) [Sus scrofa (contaminant)]</i>	Sus scrofa (contaminant)	54
2	51.36	43.72	43.72	43.72	cont 000141 <i>spt P00761 Trypsin precursor (EC 3.4.21.4) [Sus scrofa (contaminant)]</i>	Sus scrofa (contaminant)	54
2	51.36	45.29	45.29	45.29	cont 000040 <i>gi 2914482 pdb 1TFX A Chain A, Complex Of The Second Kunitz Domain Of Tissue Factor Pathway Inhibitor With Porcine Trypsin [Sus scrofa (contaminant)]</i>	Sus scrofa (contaminant)	54
2	51.36	45.29	45.29	45.29	cont 000023 <i>gi 494360 pdb 1MCT A Chain A, Trypsin (E.C.3.4.21.4) Complexed With Inhibitor From Bitter Gourd [Sus scrofa (Contaminant)]</i>	Sus scrofa (Contaminant)	54
3	37.28	36.49	31.68	31.68	sp P04264 K2C1_HUMAN <i>Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6</i>	HUMAN	30
3	37.28	36.89	32.03	32.03	sp A5A6M6 K2C1_PANTR <i>Keratin, type II cytoskeletal 1 OS=Pan troglodytes GN=KRT1 PE=2 SV=1</i>	PANTR	30
3	37.28	36.49	31.68	31.68	cont 000135 <i>cra hCP1609934.2 keratin 1 (epidermolytic hyperkeratosis) [Homo sapiens (contaminant)]</i>	Homo sapiens (contaminant)	30
3	37.28	36.49	31.68	31.68	cont 000134 <i>rf NP_006112.2 keratin 1 [Homo sapiens (contaminant)]</i>	Homo sapiens (contaminant)	30
3	35.21	36.49	30.28	30.28	cont 000132 <i>sp P04264 K2C1_HUMAN Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytochrome b5 domain) [Homo sapiens (contaminant)]</i>	Homo sapiens (contaminant)	29
4	34.36	33.39	31.16	27.05	sp P13645 K1C10_HUMAN <i>Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6</i>	HUMAN	23
4	34.36	31.25	29.17	25.32	cont 000136 <i>cra hCP1812051 keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) [Homo sapiens (contaminant)]</i>	Homo sapiens (contaminant)	23
4	34.36	32.88	30.69	26.64	cont 000133 <i>pir KRHU0 keratin 10, type I, cytoskeletal - human [Homo sapiens (contaminant)]</i>	Homo sapiens (contaminant)	23
4	34.36	33.39	31.16	27.05	cont 000129 <i>trm Q8N175 Keratin 10 [Homo sapiens (contaminant)]</i>	Homo sapiens (contaminant)	23
4	34.36	32.88	30.69	26.64	cont 000122 <i>spt P13645 Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10) [Homo sapiens (contaminant)]</i>	Homo sapiens (contaminant)	23

Protein Pilot Report / Peptide

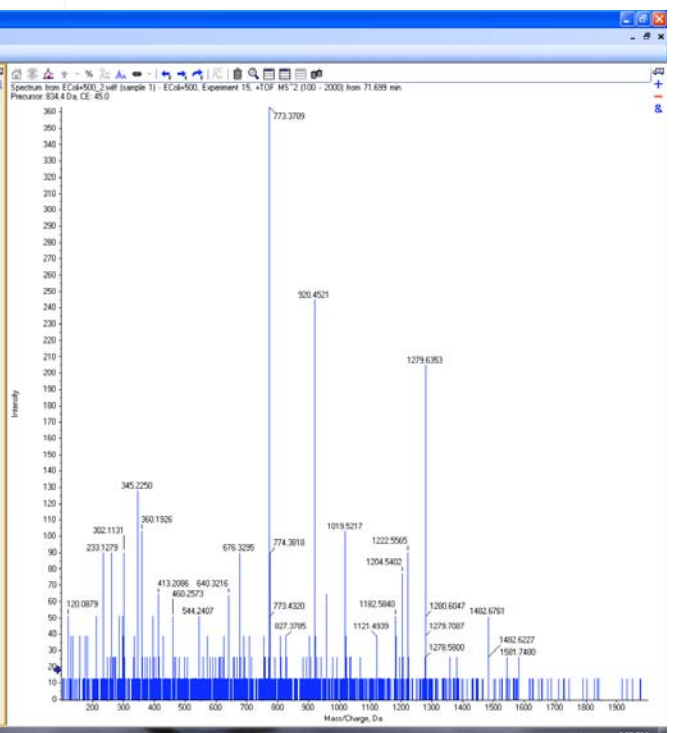
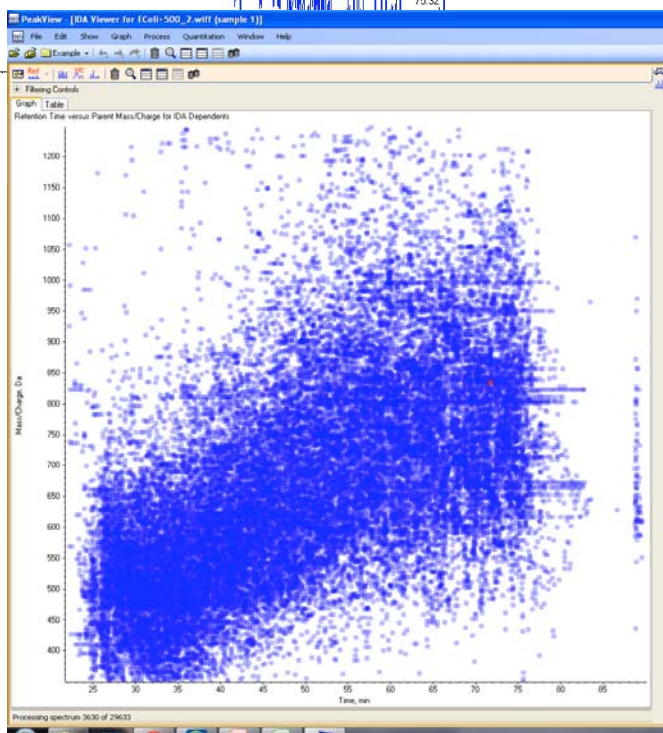
N	Name	Conf	Sequence	Prec dMass	MW	Theor Prec m/z	Theor MW	Theor m/z	Theor z	Sc	Spectrum	Time
	Glycine amidinotransferase, mitochondrial OS=Homo sapiens GN=GATM PE=1 SV=1; Isoform Cytoplasmic of Glycine amidinotransferase, mitochondrial OS=Homo sapiens GN=GATM											
1		99	AENACVPPFTIEVK	0.000875	1573.782	787.8983	1573.781	787.8978	2	231.1.1.3508.4		31.5673
1		99	AVAEIEEMCN	-0.00123	1180.473	591.2437	1180.474	591.2443	2	151.1.1.3299.6		23.5869
1		99	AVAEIEEMCNILK	-0.0003	1443.728	722.8711	1443.728	722.8712	2	181.1.1.3428.5		28.664
1		99	DFESTGLYSAMPR	-0.00074	1488.655	745.3347	1488.656	745.335	2	181.1.1.3418.3		28.3554
1		99	DPLEEVIVGR	0.002104	1125.605	563.8098	1125.603	563.8088	2	161.1.1.3523.2		32.1732
1		99	DPNPMHIDATF	-0.0007	1272.544	637.2792	1272.544	637.2795	2	141.1.1.3413.3		28.164
1		99	DPNPMHIDATFN	-0.00117	1386.586	694.3004	1386.587	694.301	2	181.1.1.3380.8		26.7868
1		99	FVTTEFPCFDAA	0.002738	1532.652	767.3333	1532.649	767.332	2	131.1.1.3766.2		36.5042
1		99	FVTTEFPCFDAADFIR	0.00625	2063.936	688.986	2063.93	688.9839	3	181.1.1.3869.3		38.5342
1		99	IIGPGIVLSNPDR	4.19E-05	1349.767	675.8906	1349.767	675.8906	2	161.1.1.3493.9		31.0142
1		99	KAVAEIEEMCN	-0.00266	1308.567	655.2905	1308.569	655.2917	2	161.1.1.3219.3		20.7267
1		99	KAVAEIEEMCNILK	-0.00017	1662.832	555.2846	1662.832	555.2846	3	161.1.1.3350.5		25.5352
1		99	MADELYNQDYPIHSVEDR	-0.00374	2209.955	737.6589	2209.958	737.6602	3	221.1.1.3401.3		27.6648
1		99	NANSLGGGFHCWTC	-0.00104	1579.629	790.8216	1579.63	790.8221	2	171.1.1.3444.4		29.1457
1		99	NANSLGGGFHCWTCDVR	-0.00268	1949.823	650.9484	1949.826	650.9493	3	161.1.1.3404.7		27.7844
1		99	NSCAADDKATEPLPK	-0.00167	1615.75	539.5905	1615.751	539.591	3	191.1.1.3164.2		19.6909
1		99	PCHQIDLFK	0.00205	1156.572	579.2933	1156.57	579.2922	2	151.1.1.3328.10		24.6557
1		99	PLEEVIVGR	0.001193	1010.577	506.2959	1010.576	506.2953	2	121.1.1.3389.4		27.1403
1		99	PNPMHIDATFN	-0.00055	1271.56	636.7872	1271.56	636.7875	2	141.1.1.3324.7		24.4978
1		99	PTMADELYNQDYPIH	0.000157	1821.788	608.27	1821.788	608.27	3	141.1.1.3441.2		28.9977
1		99	PTMADELYNQDYPIHSVEDR	-0.00455	2408.054	803.6921	2408.059	803.6936	3	151.1.1.3405.11		27.833
1		99	QGGHYFPK	0.001294	915.4253	458.7199	915.4239	458.7192	2	121.1.1.3268.4		22.3349
1		99	RPDPIDWSLK	0.004542	1241.645	414.8889	1241.64	414.8874	3	101.1.1.3388.3		27.0951



Proteins Identified at Critical False Discovery Rates

Number of Proteins Detected

Critical FDR	Local FDR	Global FDR	Global FDR from Fit
1.0%	920	951	957
5.0%	920	1057	1061
10.0%	920		



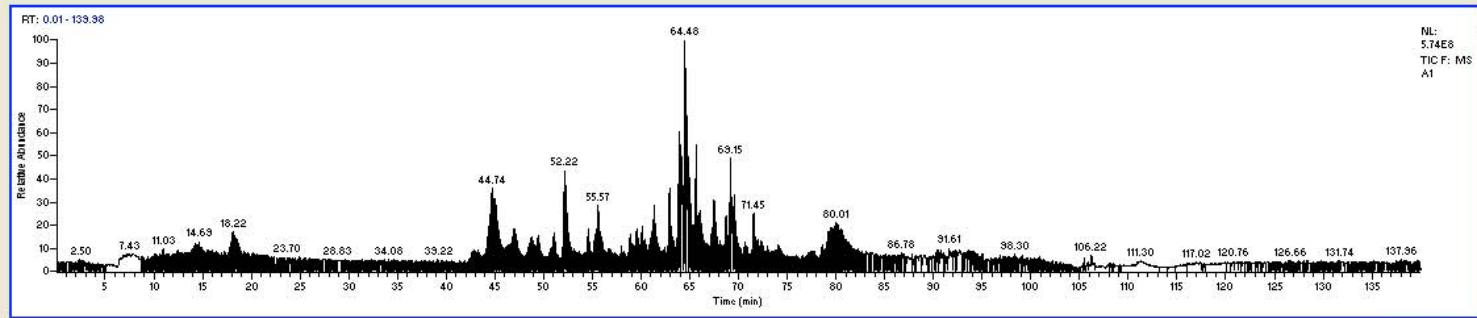
General Problems

- Contaminated Samples
- Mixture of Proteins/Peptides alias wrong separation condition prior LC-MS analyses



DTA Information:

Scans, Charge	Time (s)
2, +2	<0.1
4, +2	<0.1
8, +2	0.1
13, +3	<0.1
14, +2	<0.1
17, +2	<0.1
22, +2	<0.1
24, +2	0.1
31, +3	<0.1
32, +2	<0.1
34, +2	<0.1
36, +2	<0.1
38, +2	<0.1
44, +2	<0.1
57, +2	0.1
59, +2	<0.1
62, +2	<0.1
64, +2	<0.1
67, +2	<0.1
69, +2	<0.1
72, +2	0.1
73, +2	<0.1
77, +2	<0.1
80, +2	0.1
83, +2	<0.1
88, +2	<0.1
94, +2	<0.1
96, +2	<0.1
98, +2	<0.1
100, +2	<0.1
103, +2	0.1
104, +2	<0.1
106, +2	<0.1
110, +2	<0.1
113, +2	<0.1
114, +2	<0.1
120, +2	<0.1
129, +2	<0.1
134, +2	<0.1
142, +2	<0.1
148, +2	<0.1
150, +2	<0.1



Number of traces: 1

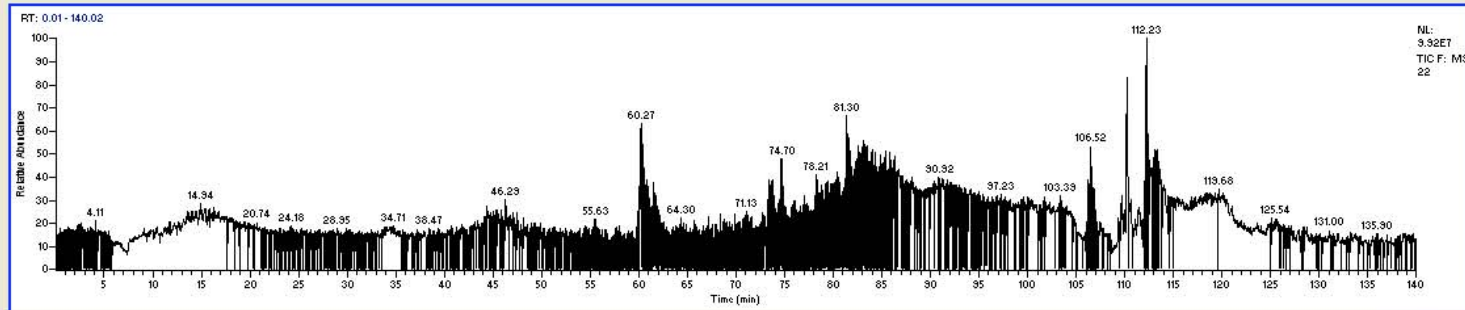
Database... indexed - CD36.fasta.hdr (10/26/2011) Filter(s)... distinct peptides ; protein probability<=0.5
 Mods: (M* +15.99491) (C# +57.02146) (ENVTDQ@ +266.26097)

Scan(s)	Peptide	Reference			z	Type	P (pro)	Score	Coverage	MW	Accession	Peptide (Hits)	
		MH+	ΔM (ppm)	ΔCn								ions	Count
414 - 416	K.DYKDDDDK.-	1013.40582	-0.2	2	CID	2.5e-004	1.997	-	352.9	1	9/14	6	
439	K.TGTEVYR.Q	825.41010	0.4	2	CID	2.0e-005	1.635	-	181.3	1	11/12	7	
465	K.VFNGKDDISK.V	1122.57898	-0.2	2	CID	2.2e-008	2.362	0.904	710.7	1	12/18	6	
511	R.GPYTYR.V	756.36749	0.2	2	CID	1.2e-004	1.446	-	348.0	1	7/10	7	
585	K.SSMFQVR.T	870.41381	0.6	2	CID	2.0e-005	1.375	-	534.9	1	10/12	7	
689	K.GIPVYR.F	704.40900	0.4	2	CID	2.2e-004	1.226	-	187.8	1	7/10	7	
1729	K.SSMFQVR.T	854.41888	0.7	2	CID	3.9e-005	2.150	-	864.5	1	11/12	7	
1841	K.RLQVNLVVKPSEK.I	1523.92676	0.8	3	CID	9.1e-007	6.069	-	1261.8	1	23/48	7	
1945	K.RLQVNLVVK.P	1082.70447	0.5	2	CID	7.9e-005	2.708	-	811.3	1	14/16	7	
1990	R.LQVNLVVKPSEK.I	1367.82568	0.7	2	CID	4.2e-007	3.559	-	836.8	1	14/22	7	
2081	K.KQVVLEEGTIAFK.N	1461.83118	0.8	3	CID	7.3e-005	4.476	-	1082.2	1	21/48	7	
2126	R.LQVNLVVK.P	926.60333	0.8	2	CID	8.7e-005	2.634	-	629.5	1	13/14	7	
2234	K.AFASPVENPDNYC#FC#TEK.I	2148.90011	1.6	3	CID	6.4e-011	6.744	-	1263.2	1	26/68	7	
2243	K.DCATSYGVLDISK.C	1357.63040	-0.3	2	CID	4.4e-008	3.410	0.974	1189.8	1	17/22	6	
2265	K.QVVLEEGTIAFK.N	1333.73621	-1.8	2	CID	2.4e-009	4.280	-	648.6	1	17/22	7	
2444	R.SIYAVFESDVNLK.G	1484.76318	1.4	2	CID	1.3e-010	3.961	-	1737.7	1	20/24	7	
2486	K.SQVLQFFSSDIC#R.S	1586.76315	0.8	2	CID	8.9e-011	3.498	-	2491.9	1	21/24	7	
2524	R.PVYISLPHFLYASPDVSEPIDGLNPNNEEHR.T	3534.71753	1.5	4	CID	1.1e-015	6.198	-	809.5	1	37/180	7	
2597	R.DLSYVESHCDMIDGTDAAASFPFVEK.S	3017.29680	2.1	3	CID	4.8e-005	1.250	-	28.4	1	6/10	6	
2612	R.QFVFDVQNPQEVMM'DSSNIQVK.Q	2799.31166	0.8	3	CID	4.1e-008	2.901	0.762	216.9	1	15/88	6	
2650	R.ELLWGYR.D	936.49377	0.5	2	CID	4.3e-004	1.053	-	133.7	1	5/12	7	
2663	R.QFVFDVQNPQEVMM'DSSNIQVK.Q	2799.31166	1.1	3	CID	1.3e-004	2.124	0.733	93.1	1	11/88	6	
2672	R.TYLDIEPTGFTLQFAK.R	1957.03174	0.8	3	CID	1.6e-014	6.567	-	3006.2	1	34/64	7	
2701	R.NYVILWLDDETGTIGDEK.A	2176.11719	1.6	2	CID	4.4e-015	5.172	0.814	1941.3	1	28/36	6	
2703	R.QFVFDVQNPQEVMM'DSSNIQVK.Q	2783.31665	1.2	3	CID	1.0e-010	3.538	-	367.0	1	20/88	6	



DTA Information:

Scans, Charge	Time (s)
<input type="checkbox"/> 6-, +2	<0.1
<input type="checkbox"/> 12, +2	1.2
<input type="checkbox"/> 15, +2	1.2
<input type="checkbox"/> 18, +2	0.7
<input type="checkbox"/> 22, +2	1.1
<input type="checkbox"/> 25, +2	1.0
<input type="checkbox"/> 27 - 29, +2	1.0
<input type="checkbox"/> 35, +2	<0.1
<input type="checkbox"/> 38, +2	1.1
<input type="checkbox"/> 42, +3	0.6
<input type="checkbox"/> 44, +2	<0.1
<input type="checkbox"/> 46, +2	1.0
<input type="checkbox"/> 48, +2	<0.1
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<input type="checkbox"/> 158, +3	<0.1



Number of traces: 1

Database... indexed - swissPROT_251011.fasta.hdr (10/25/2011)
 Mods: (M* +15.99491) (C# +57.02146)

Filter(s)... distinct peptides ; protein probability<=0.5

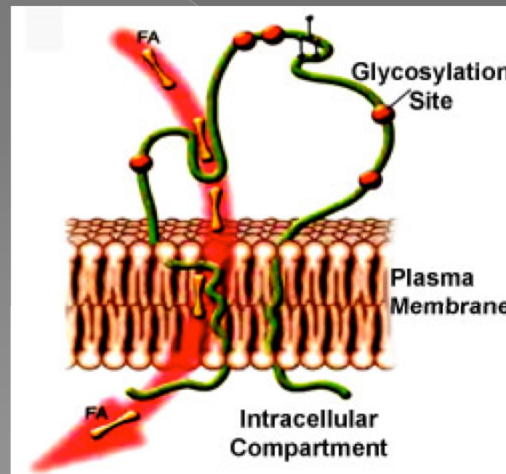
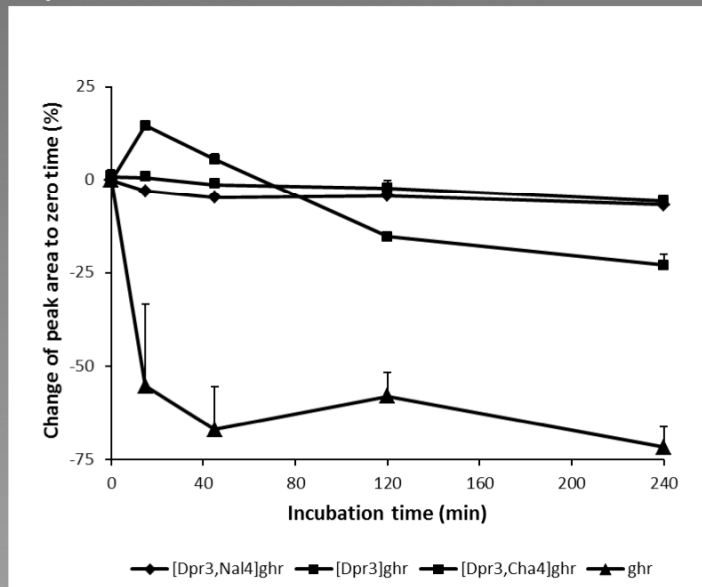
		Reference	P (pro)	Score	Coverage	MW	Accession	Peptide (Hits)				
Scan(s)	Peptide	MH+	ΔM (ppm)	z	Type	P (pep)	XC	ΔCn	Sp	RSp	Ions	Count
1	TRYP_PIG Trypsin OS=Sus scrofa PE=1 SV=1		4.2e-008	50.4		24393.8	P00761	5	(5 0 0 0 0)			
2	K2C1_HUMAN Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6		1.7e-007	150.2		65998.9	P04264	15	(15 0 0 0 0)			
3	K2C1_PANTR Keratin, type II cytoskeletal 1 OS=Pan troglodytes GN=KRT1 PE=2 SV=1		1.7e-007	140.2		65449.7	A5A6M6	14	(14 0 0 0 0)			
4	K1C10_CANFA Keratin, type I cytoskeletal 10 OS=Canis familiaris GN=KRT10 PE=2 SV=1		5.7e-007	100.1		57676.0	Q6E1Z0	10	(10 0 0 0 0)			
5	K1C10_MOUSE Keratin, type I cytoskeletal 10 OS=Mus musculus GN=Krt10 PE=1 SV=3		5.7e-007	70.1		57735.0	P02535	7	(7 0 0 0 0)			
6	K1C10_HUMAN Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6		7.7e-007	130.1		58791.6	P13645	13	(13 0 0 0 0)			
7	K22E_HUMAN Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2		8.0e-007	80.2		65393.2	P35908	8	(8 0 0 0 0)			
8	K2C1_CANFA Keratin, type II cytoskeletal 1 OS=Canis familiaris GN=KRT1 PE=2 SV=1		8.0e-007	60.2		63751.0	Q6E1Y9	6	(6 0 0 0 0)			
9	K22E_CANFA Keratin, type II cytoskeletal 2 epidermal OS=Canis familiaris GN=KRT2 PE=2 SV=1		8.0e-007	30.2		64529.4	Q6E1Z1	3	(3 0 0 0 0)			
10	K2C1_RAT Keratin, type II cytoskeletal 1 OS=Rattus norvegicus GN=Krt1 PE=2 SV=1		8.0e-007	30.2		64791.0	Q6IMF3	3	(3 0 0 0 0)			
11	K2C1_MOUSE Keratin, type II cytoskeletal 1 OS=Mus musculus GN=Krt1 PE=1 SV=4		8.0e-007	20.2		65565.2	P04104	2	(2 0 0 0 0)			
12	K2C1B_HUMAN Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=1 SV=3		8.0e-007	10.2		61863.5	Q7Z794	1	(1 0 0 0 0)			
13	K2C1B_MOUSE Keratin, type II cytoskeletal 1b OS=Mus musculus GN=Krt77 PE=1 SV=1		8.0e-007	10.2		61321.6	Q6IFZ6	1	(1 0 0 0 0)			
14	K2C1B_RAT Keratin, type II cytoskeletal 1b OS=Rattus norvegicus GN=Krt77 PE=2 SV=1		8.0e-007	10.2		57219.7	Q6IG01	1	(1 0 0 0 0)			
15	K2C71_MOUSE Keratin, type II cytoskeletal 71 OS=Mus musculus GN=Krt71 PE=1 SV=1		8.0e-007	10.2		57346.9	Q9R0H5	1	(1 0 0 0 0)			
16	K22E_MOUSE Keratin, type II cytoskeletal 2 epidermal OS=Mus musculus GN=Krt2 PE=1 SV=1		3.2e-005	20.1		70879.8	Q3TTY5	2	(2 0 0 0 0)			
17	K1C10_BOVIN Keratin, type I cytoskeletal 10 OS=Bos taurus GN=KRT10 PE=3 SV=1		4.1e-005	80.1		54815.1	P06394	8	(8 0 0 0 0)			
18	K1C15_SHEEP Keratin, type I cytoskeletal 15 OS=Ovis aries GN=KRT15 PE=2 SV=1		4.1e-005	20.1		48740.2	Q77727	2	(2 0 0 0 0)			
19	UP01_VITRO Unknown protein 1 (Fragment) OS=Vitis rotundifolia PE=1 SV=1		4.9e-005	10.1		1392.7	P86104	1	(1 0 0 0 0)			
20	UP18_PSEMZ Unknown protein 18 (Fragment) OS=Pseudotsuga menziesii PE=1 SV=1		4.9e-005	10.1		1392.7	P85925	1	(1 0 0 0 0)			
21	K1C10_RAT Keratin, type I cytoskeletal 10 OS=Rattus norvegicus GN=Krt10 PE=2 SV=1		7.3e-005	80.1		56470.6	Q6IFW6	8	(8 0 0 0 0)			
22	SCP_CHIOP Sarcoplasmic calcium-binding protein (Fragment) OS=Chionoecetes opilio PE=1 SV=1		5.1e-004	10.1		841.5	P86909	1	(1 0 0 0 0)			
23	TRY1_CANFA Cationic trypsin OS=Canis familiaris PE=2 SV=1		8.5e-004	10.1		26152.9	P06871	1	(1 0 0 0 0)			
24	K1C14_HUMAN Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4		8.8e-004	20.1		51529.4	P02533	2	(2 0 0 0 0)			
25	K1C15_MOUSE Keratin, type I cytoskeletal 15 OS=Mus musculus GN=Krt15 PE=1 SV=2		8.8e-004	20.1		49107.2	Q61414	2	(2 0 0 0 0)			
26	K1C14_MOUSE Keratin, type I cytoskeletal 14 OS=Mus musculus GN=Krt14 PE=1 SV=2		8.8e-004	10.1		52833.9	Q61781	1	(1 0 0 0 0)			

NUM

Ongoing Projects

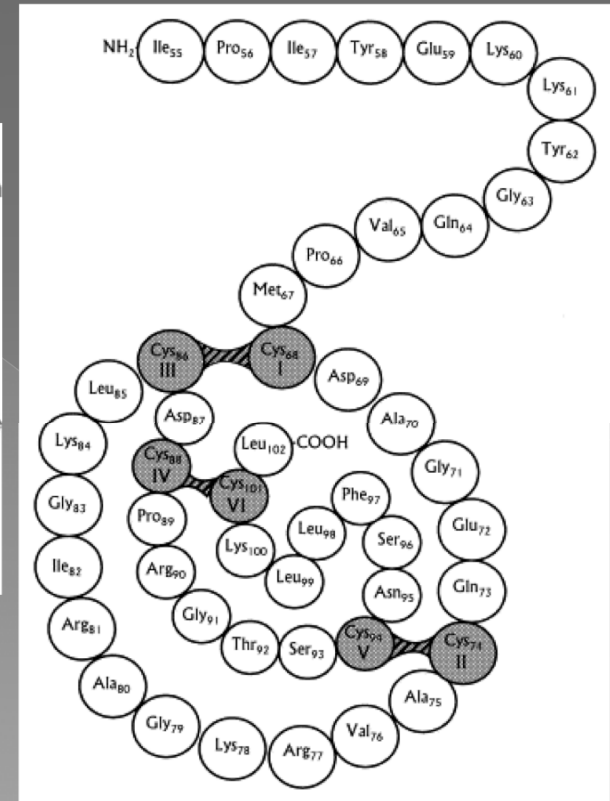
- Specificity of proteases
- Total Secretome Identification
- Searching for the lipase

Pharmacokinetics:
Degradation of molecule(s)
in plasma/serum



Looking for AA
with a specific
PTM

Identification of S-S bridges



Future Plans

- Protein Quantification by MS
 - > SILAC
 - > Labe-Free Quantification
- Implementation of 2-D LC-MS/MS
 - > IEX and RP-LC coupled to MS

Acknowledgements

- ◉ Dr. Cvačka and his team
- ◉ All creative scientists at the IOCB v.v.i or elsewhere!

Thank you for your attention!

any questions?