

Supplementary material 1: Typical MS/MS data (Phenyx software output) with MS/MS spectrum and detailed coverage that was observed. Matching results from MS/MS with the corresponding transcript were then manually assessed and checked using Biolynx and the PepSeq module (Waters-Micromass).

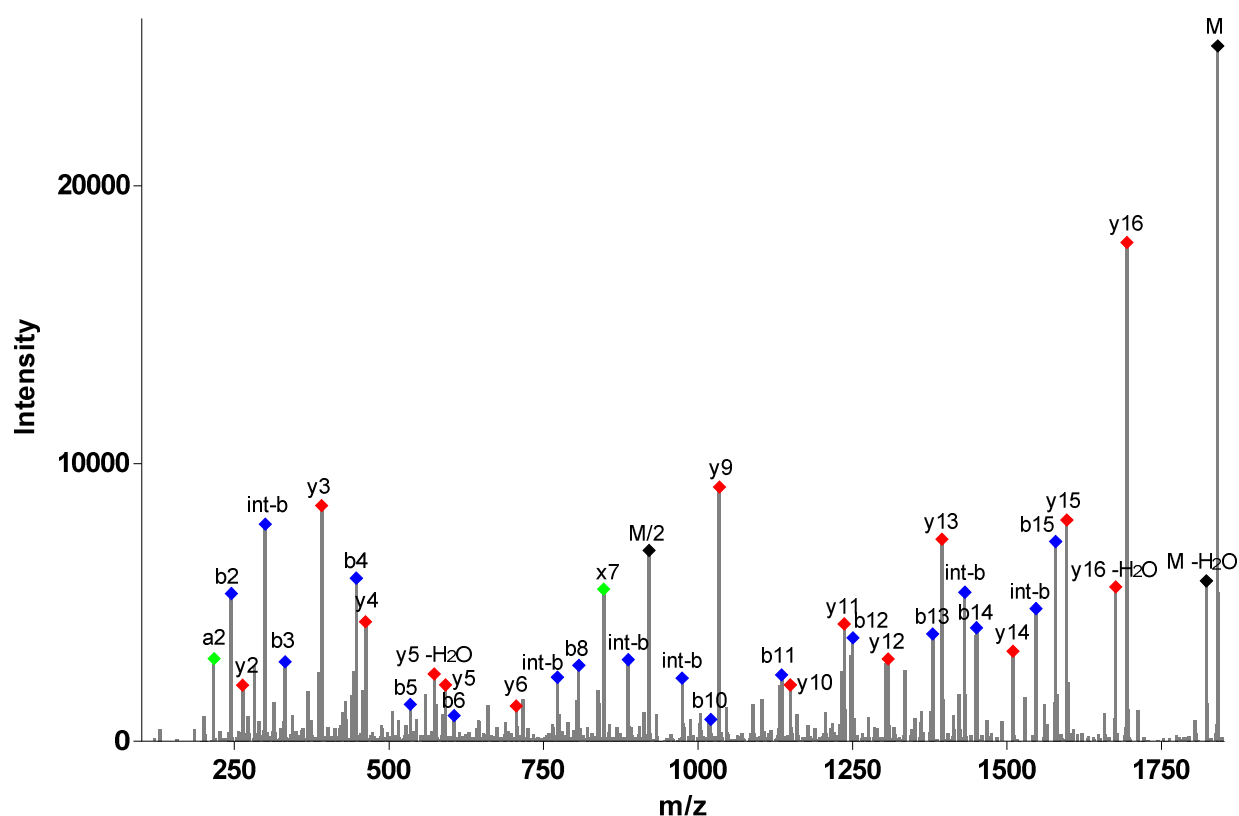
1) A-superfamily propeptide: FPSDSASDGRDDEAKDE

Peptide match details:

Theoretical mass: 1839.739

Experimental m/z: 920.874, charges: 2, # peaks: 1899

Match delta m/z: 0.003, score: 12.73, charge: 2



Ion series: ◆ b ions, ◆ y ions, ◆ other ions - Masses: ◆

Value Types : Delta Mass			Percentage of most intense peaks:										70<x<100		50<x<70		30<x<50		10<x<30		<10	
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17					
a		-0.006		0.003	-0.005	-0.018							-0.040	0.037								
a-H2O				-0.008	-0.006	0.011	0.043			0.023	0.030											
a-NH3										-0.144			0.003									
b		-0.002	-0.010	-0.013	-0.021	-0.013		0.006		-0.032	0.015	0.022	0.015	-0.098	0.067	0.054	0.036					
b-H2O			-0.000	-0.003	-0.001	-0.014	-0.022	0.035	0.016	-0.032	-0.036	0.031	-0.086	0.091	0.056	0.063	0.016					
b-NH3											0.078	-0.155	0.017									
sequence	F	P	S	D	S	A	S	D	G	R	D	D	E	A	K	D	E					
y	-0.073	0.038	0.016	0.014	0.007	0.005	-0.073	0.005	-0.032	-0.033	-0.004	-0.001	-0.008	-0.011	-0.008	-0.013						
y-H2O	0.036	0.048	0.015	0.033	0.036	0.014	0.037															
y-NH3	-0.240		-0.222	-0.164	-0.161			-0.052	-0.129													
	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1					

immonium ion	delta mass
R	-0.020

precursor	delta mass
1+	-0.073
2+	0.067

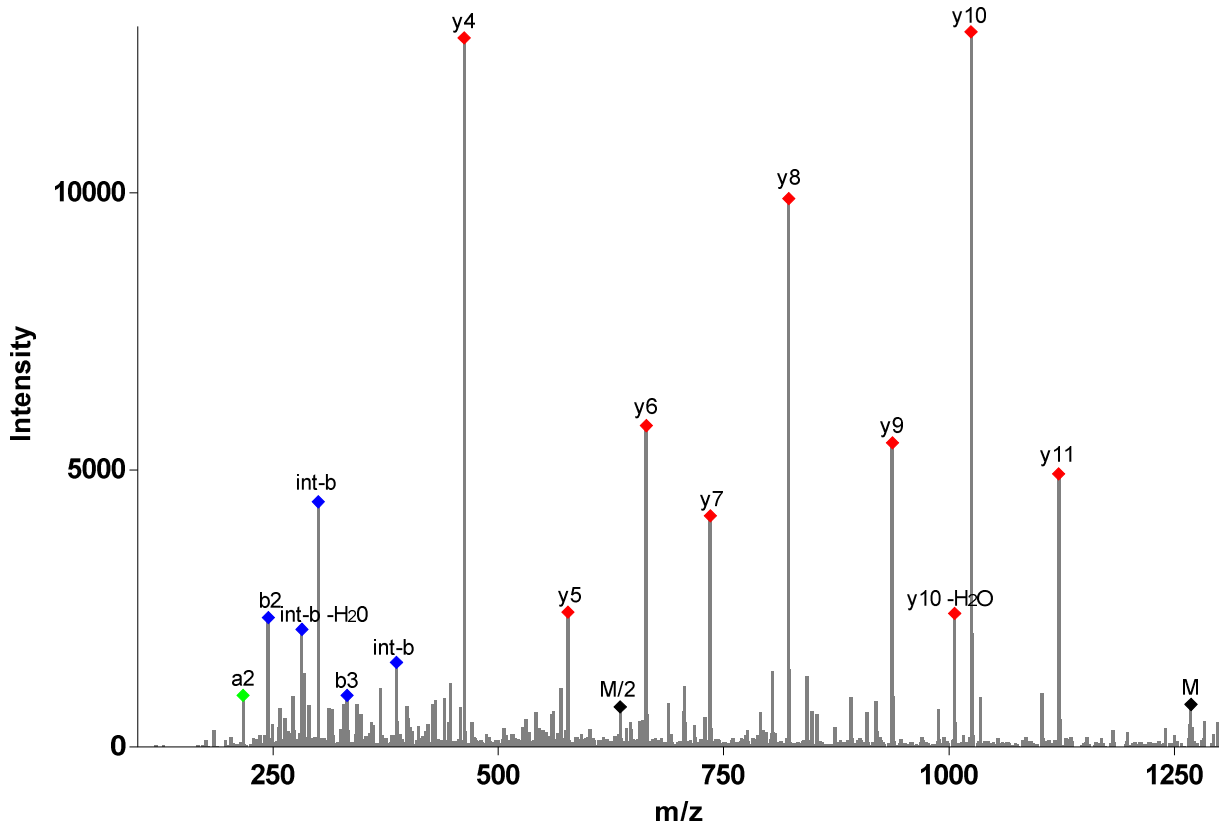
2) A-superfamily propeptide: FPSDSASDGRDD

Peptide match details:

Theoretical mass: 1267.495

Experimental m/z: 634.754, charges: 2, # peaks: 1300

Match delta m/z: 0.001, score: 10.12, charge: 2



Ion series: ◆ b ions, ◆ y ions, ◆ other ions - Masses: ◆

Value Types : Delta Mass Percentage of most intense peaks: 70<x<100 50<x<70 30<x<50 10<x<30 <10

	1	2	3	4	5	6	7	8	9	10	11	12
a		-0.006		0.033	0.005	0.032	0.044					
a-H2O				0.112	0.024	0.001	0.043					
a-NH3												
b		-0.002	0.000	-0.003	0.009	-0.023		0.006			-0.055	0.022
b-H2O			-0.000	0.007	-0.021	0.016						
b-NH3												
sequence	F	P	S	D	S	A	S	D	G	R	D	D
y	0.043	-0.006	0.011	0.019	0.012	-0.010	0.003	-0.009	-0.006	0.013	-0.008	
y-H2O	0.022	0.034	0.011	-0.011	0.012	0.010	0.003					
y-NH3		-0.143	-0.146	0.062	-0.115	-0.097	0.006	-0.016	-0.033	-0.014		
	12	11	10	9	8	7	6	5	4	3	2	1

precursor	delta mass
1+	0.043

3) A-superfamily peptide: QKDLVVTATTTCCGYNPMTICPPCMCTYSCPPKKKKP

Peptide match details:

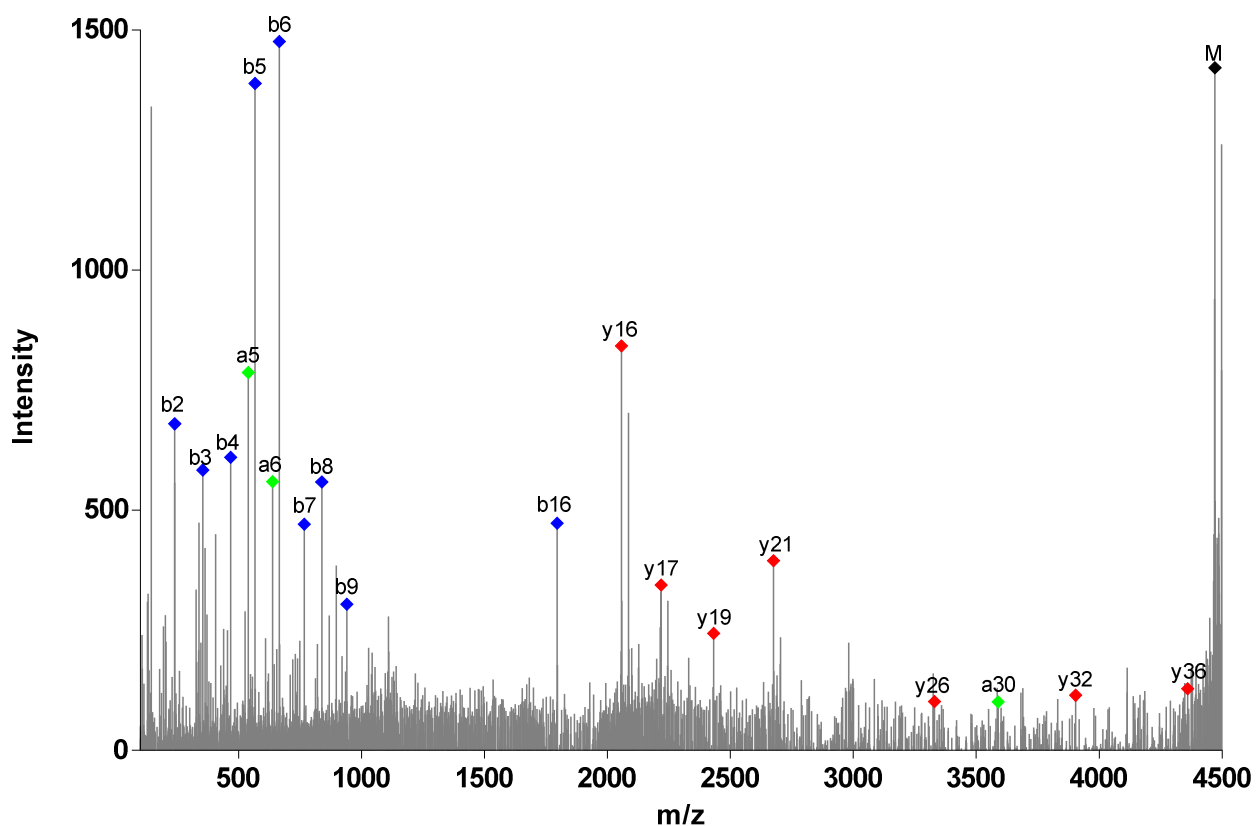
Theoretical mass: 4470.946

Experimental m/z: 895.182, charges: 5, # peaks: 4372

Match delta m/z: 0.015, score: 10.2, charge: 5

PTMs: Q1: Pyroglutamate; M18, M25: Oxidation; P22, P23, P31, P32: Hydroxyproline All C: Carboxamidomethyl-Cysteine

NB: The theoretical mass corresponds to the final peptide mass minus the mass of the combination of glycans



Ion series: ◆ b ions, ◆ y ions, ◆ other ions - Masses: ◆

Value Types : Delta Mass

Percentage of most intense peaks:

70<x<100 50<x<70 30<x<50 10<x<30 <10

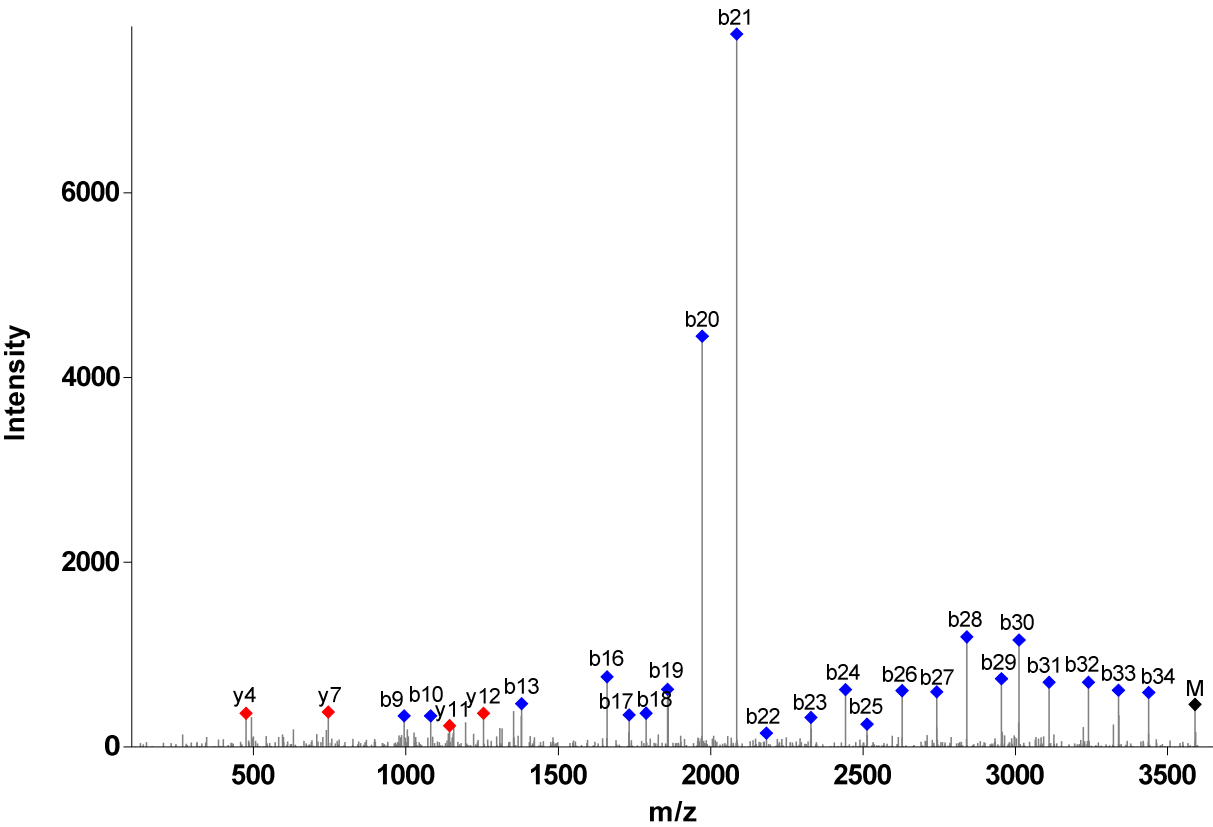
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37
a				-0.013	-0.016	-0.008	-0.020							0.090																							
a-H2O							0.008											0.021																			
a-NH3		0.072				-0.014					0.033									0.002																	
b		-0.007	-0.005	-0.017	-0.018	-0.022	-0.011	-0.014	-0.017	-0.001	-0.052			-0.046	0.001			0.001	-0.060									0.142									0.056
b-H2O							-0.033	-0.014	-0.018	-0.033	0.000																										0.131
b-NH3																																					
sequence	Q	K	D	L	V	V	T	A	T	T	T	C	C	G	Y	N	P	M	T	I	C	P	P	C	M	C	T	Y	S	C	P	K	K	K	K	P	
y	-0.291	0.065														-0.164					-0.040	-0.111															
y-H2O	0.056																				-0.050																
y-NH3																																					
	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1

immonium ion	delta mass
Y	-0.026

precursor	delta mass
1+	-0.291

4) T-superfamily peptide: FFSSIAKLVSQVAPALAGAIIPFIADLVNGVEVVE

Peptide match details:
Theoretical mass: 3584.027
Experimental m/z: 1195.676, charges: 3, # peaks: 1112
Match delta m/z: 0.007, score: 13.61, charge: 3



Ion series: ◆ b ions, ◆ y ions, ◆ other ions - Masses: ◆

Value Types : Delta Mass

Percentage of most intense peaks: 70<x<10050<x<7030<x<5010<x<30<10

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35
a		-0.003										0.066																							
a-H2O																																			
a-NH3																																			
b					0.012		-0.013		0.008	-0.017		0.002	0.011		0.003	0.002	0.021	0.007	-0.004	-0.006	0.001	0.020	0.001	0.083	0.012	0.013	-0.001	-0.003		0.345		0.015	0.024	0.031	
b-H2O																											-0.051				-0.006		0.342		
b-NH3																															0.003	-0.009		-0.076	
sequence	F	F	S	S	I	A	K	L	V	S	K	V	A	P	A	L	A	G	A	I	I	P	F	I	A	D	L	V	N	G	V	E	V	V	E
y		0.015				0.296	0.164																	0.005			0.004	-0.001	-0.006		-0.000	0.003			
y-H2O		0.326																																	
y-NH3																																			
	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1

precursor

delta mass

3+

0.010