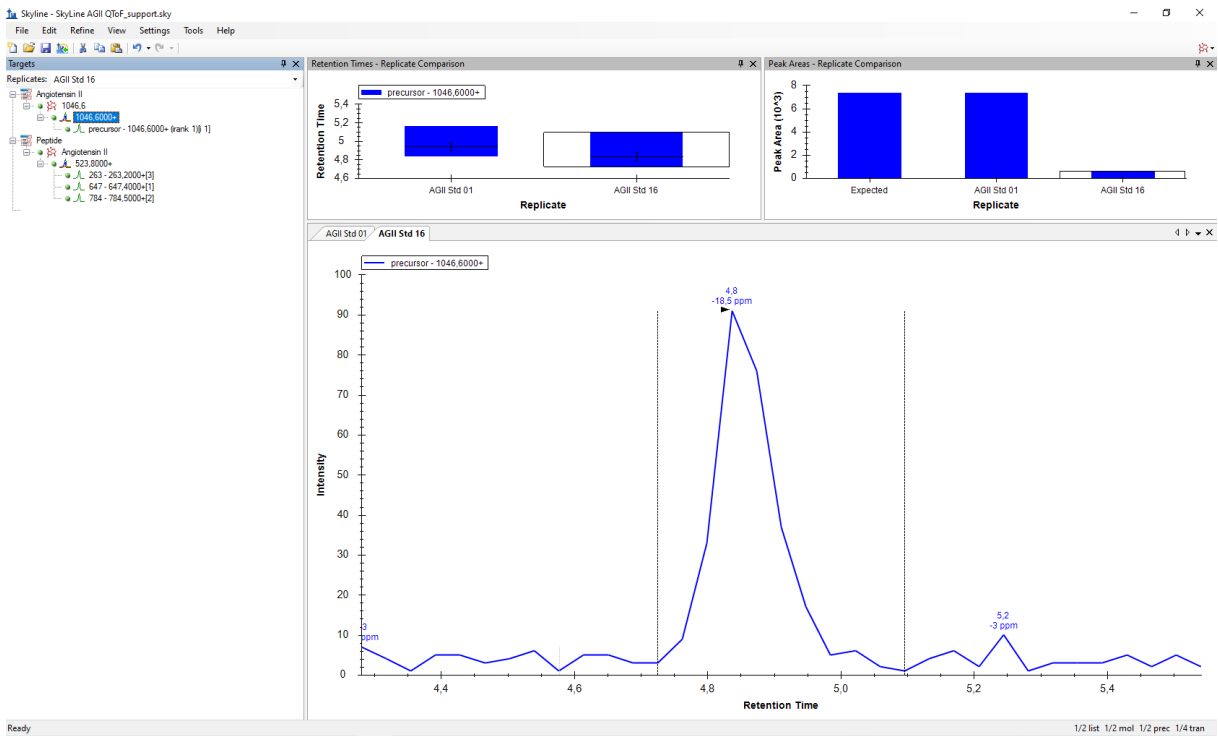
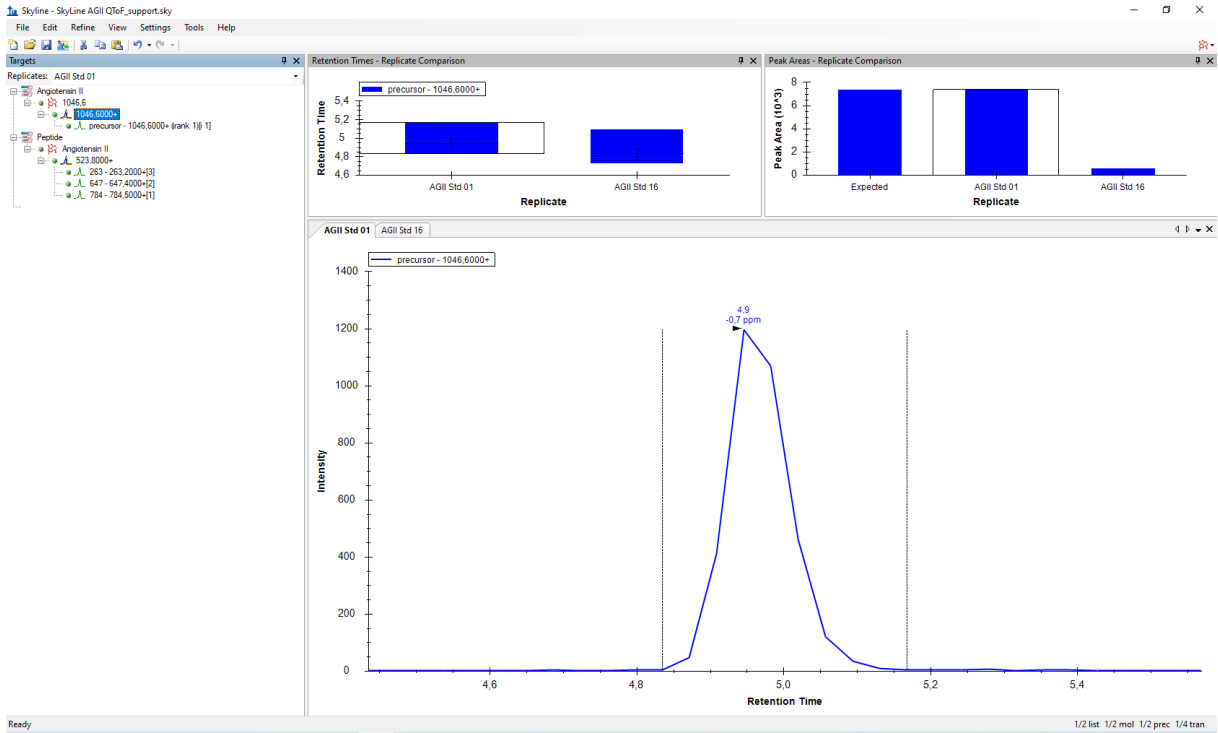
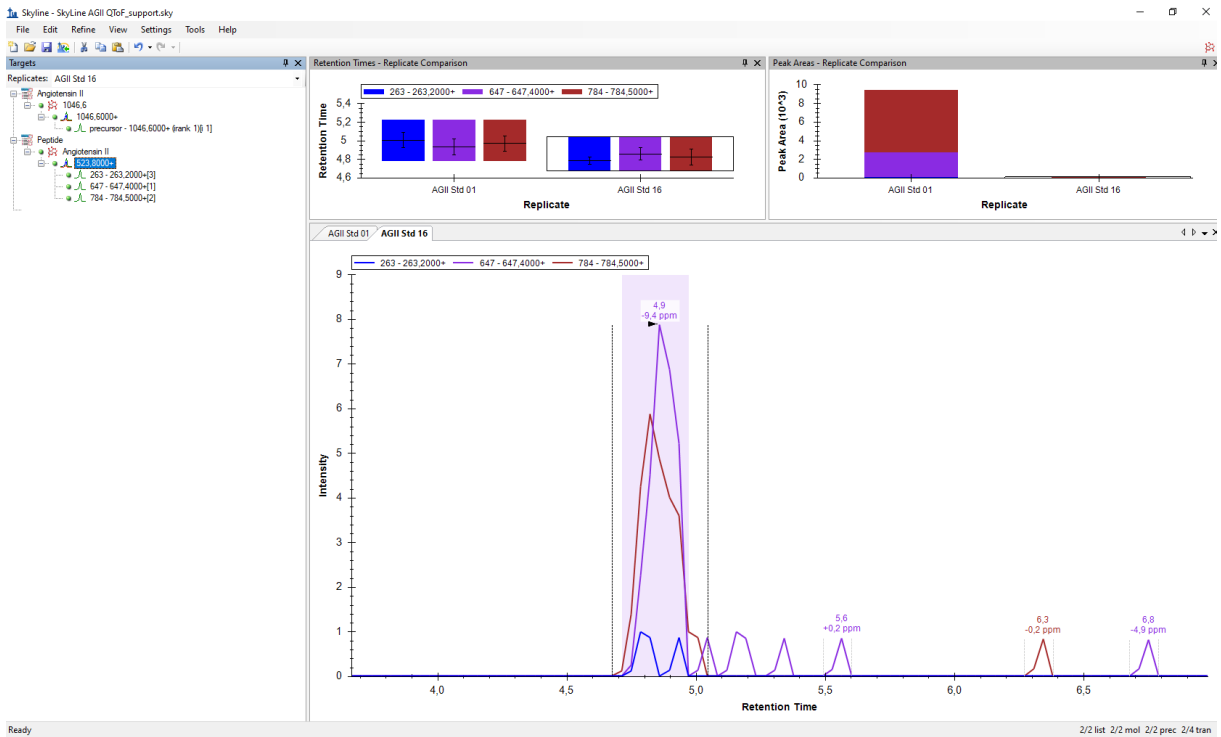
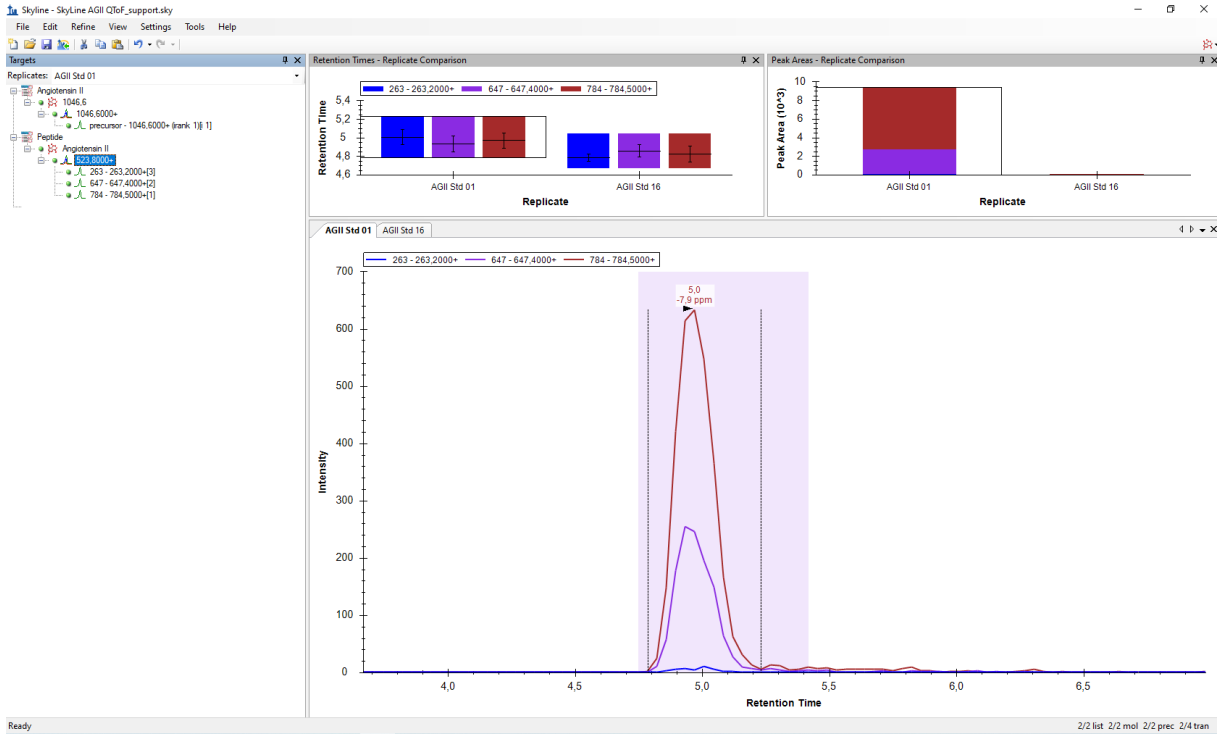


1. Data evaluated with SkyLine software:

1.1 Analysis of full scan data with $[M+H]^+$ at m/z 1046.6



1.2 Analysis of MS/MS data regarding three fragments (m/z 784.5; 647.4 and 263.2) derived from $[M+2H]^{2+}$ at m/z 523.8

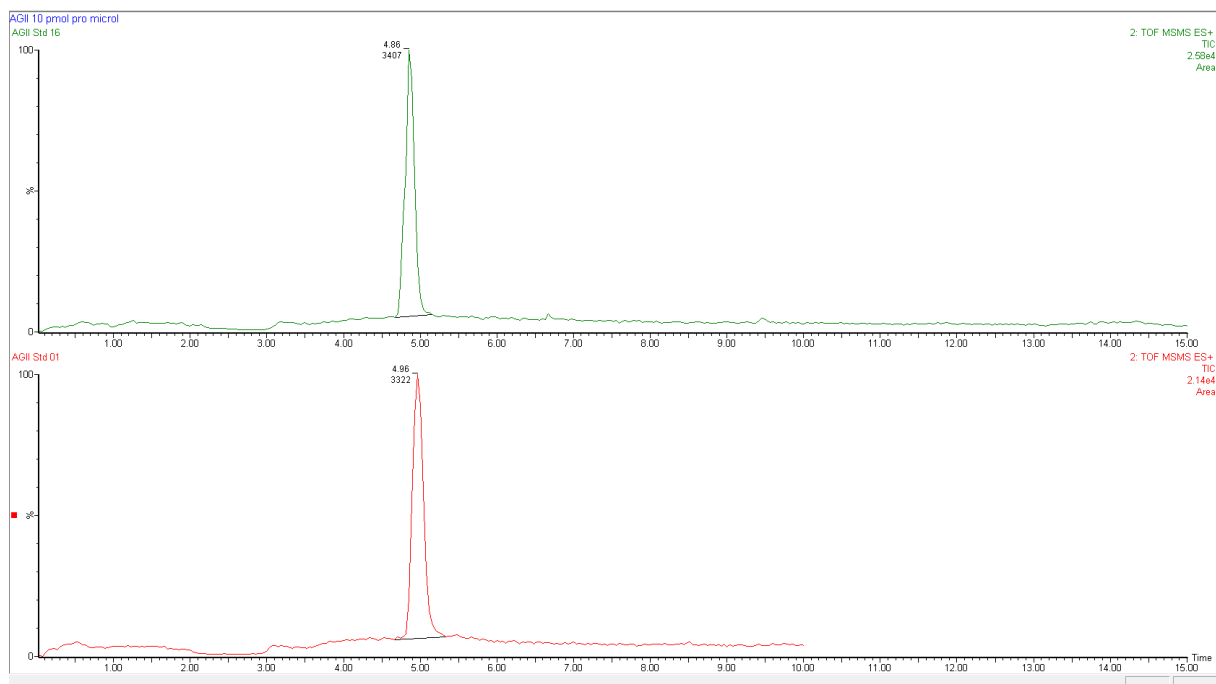


Peak areas are:

	Protein Name	Total Area	Precursor Neutral Mass	Retention Time	File Name
▶	Angiotensin II	596	1046,600549	4,84	AGII Std 16.raw
	Angiotensin II	7381	1046,600549	4,95	AGII Std 01.raw
	Peptide	126	523,800549	4,79	AGII Std 16.raw
	Peptide	9444	523,800549	5,01	AGII Std 01.raw

Looks like analysis 01 is much more intensive than analysis 16, but in MassLynx both raw data sets are nearly the same...

2. Data evaluated with MassLynx software, only MS/MS data



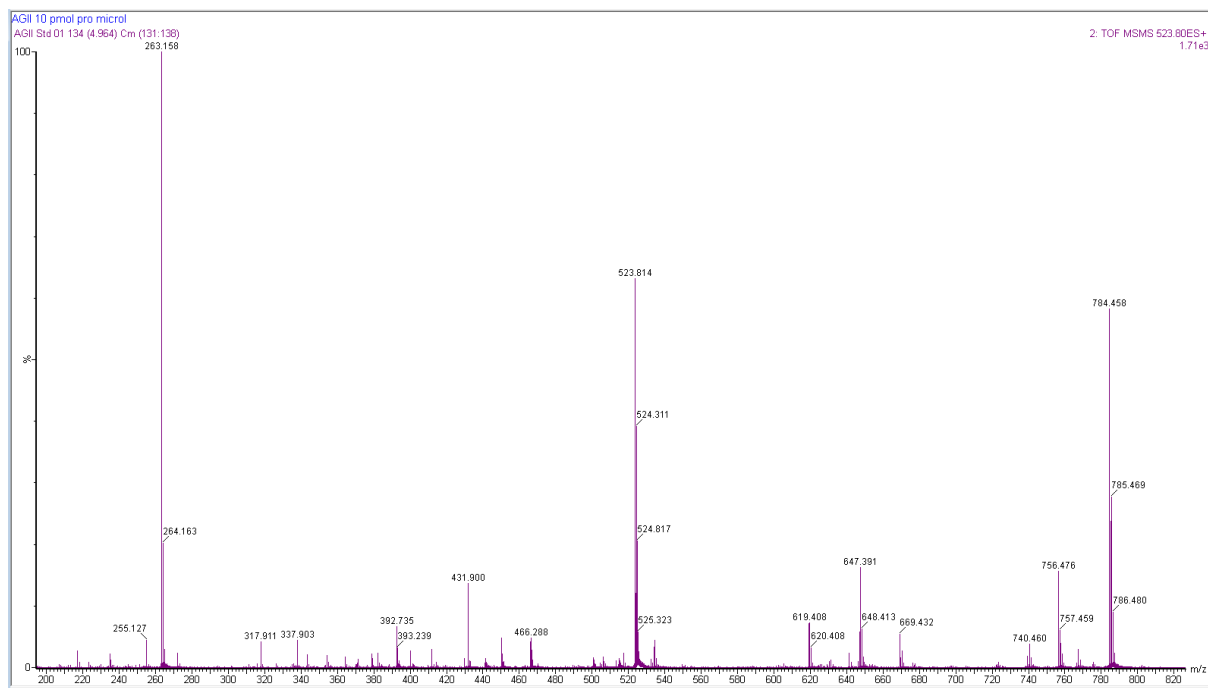
Peak areas are 3322 for analysis 01

3407 for analysis 16

Retention time is stable $\Delta = 0.1$ min.

Measured spectra are:

Analysis 01



Analysis 16

