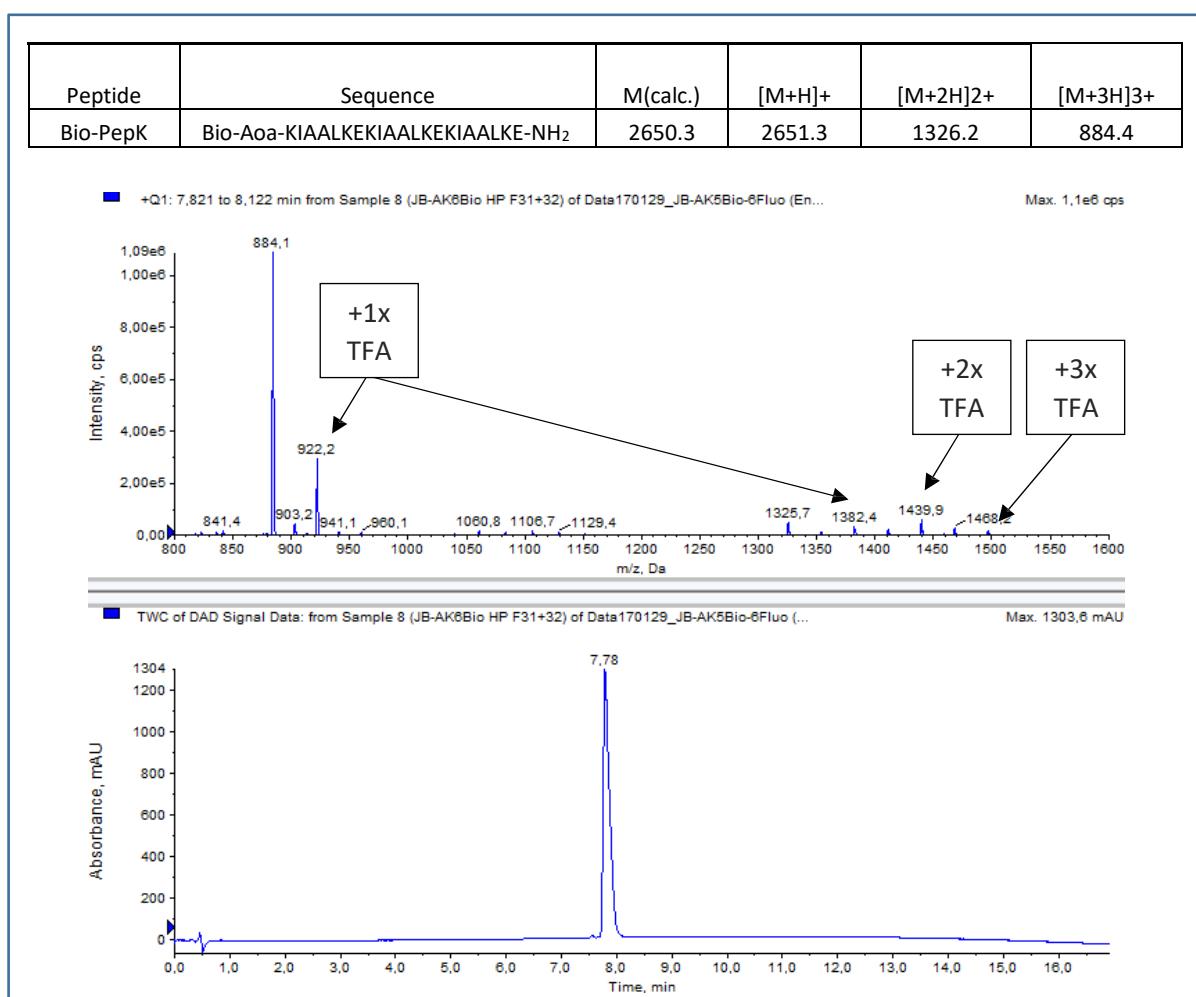


Electronic Supplementary Information

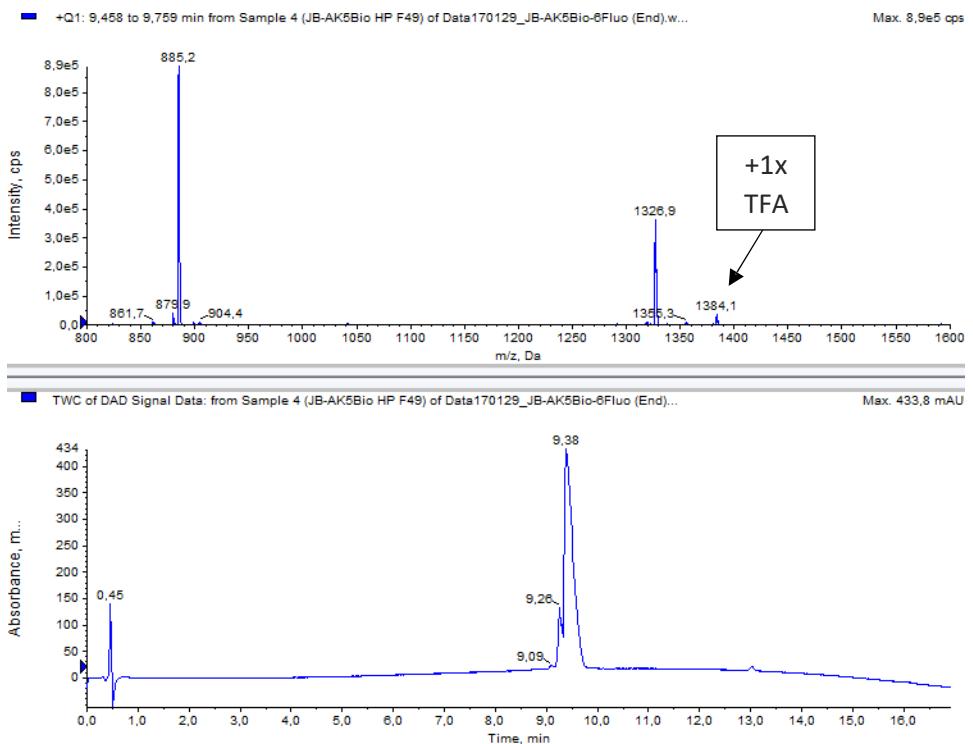
Bind&Bite: Covalently stabilized heterodimeric coiled-coil peptides for the stable, site-selective, cysteine-free chemical modification of proteins

Jannis Beutel, Pierre Tannig, Riccardo Di Vincenzo, Thomas Schumacher, Klaus Überla and Jutta Eichler

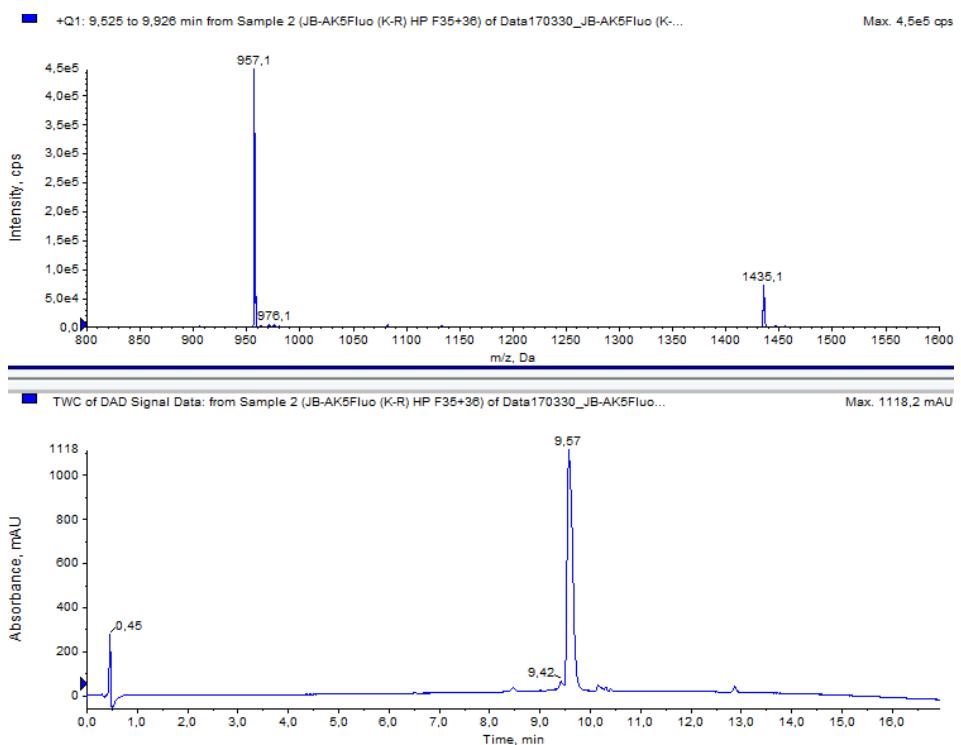
Analytical data of peptides



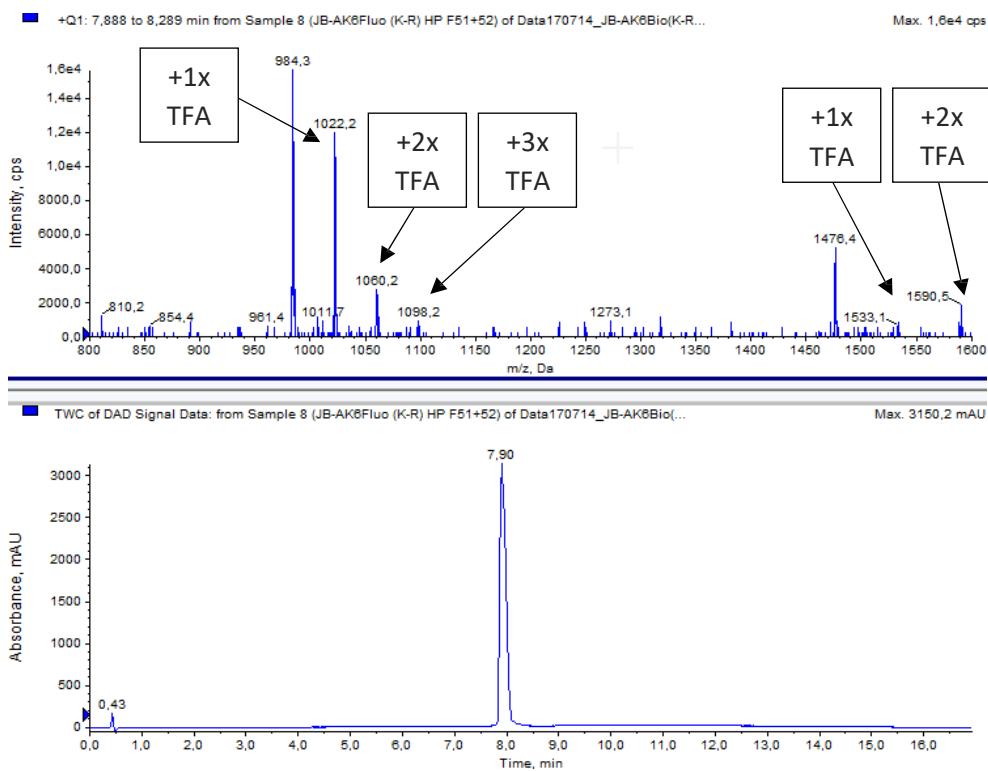
Peptide	Sequence	M(calc.)	[M+H]+	[M+2H]2+	[M+3H]3+
Bio-PepE	Bio-Aoa-EIAALEKEIAALEKEIAALEK-NH ₂	2653.1	2654.1	1327.6	885.4



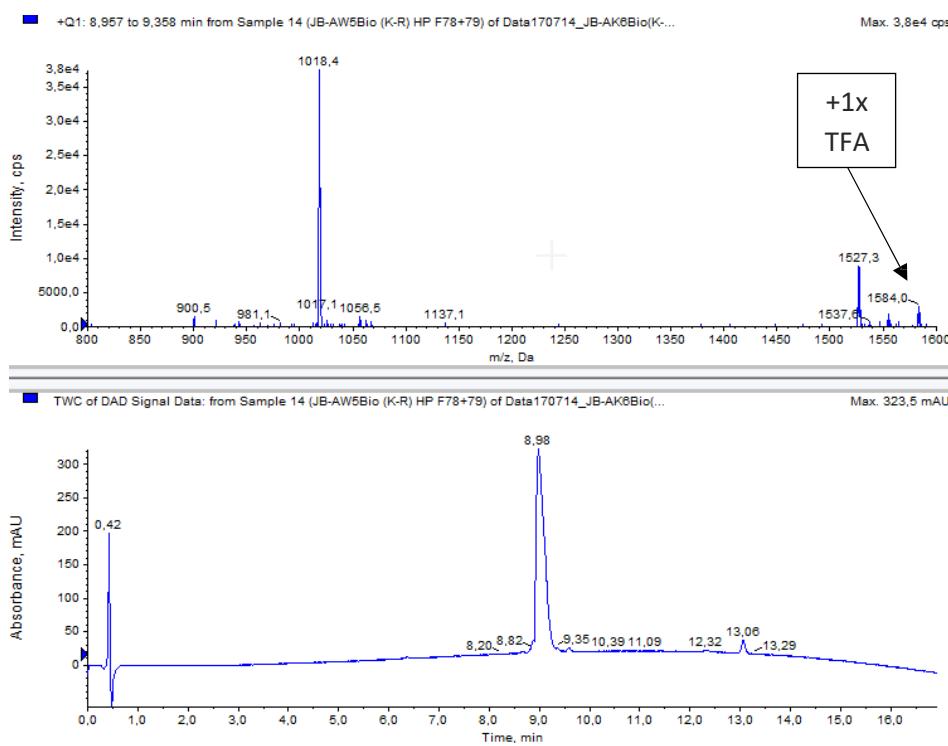
Peptide	Sequence	M(calc.)	[M+H]+	[M+2H]2+	[M+3H]3+
Fluo-PepE	Fluo-Aoa-EIAALEREIAALEREIAALER-NH ₂	2869.2	2870.2	1435.6	957.4



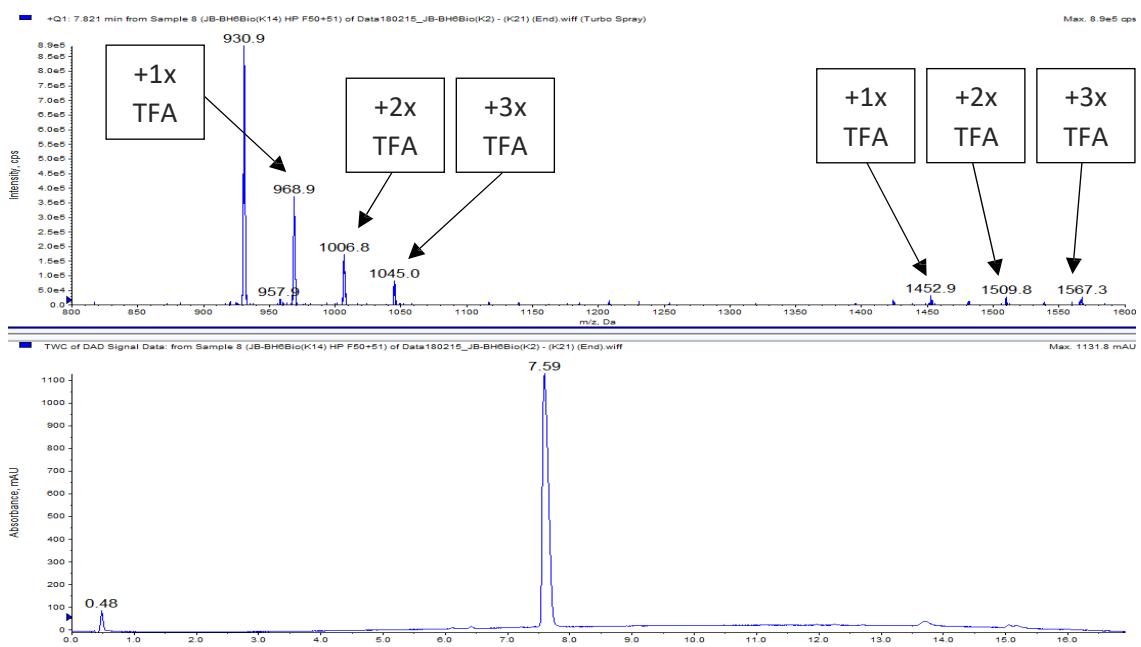
Peptide	Sequence	M(calc.)	[M+H]+	[M+2H]2+	[M+3H]3+
Fluo-PepK	Fluo-Aoa-RIAALRERIAALRERIAALRE-NH ₂	2953.3	2954.3	1477.7	985.4



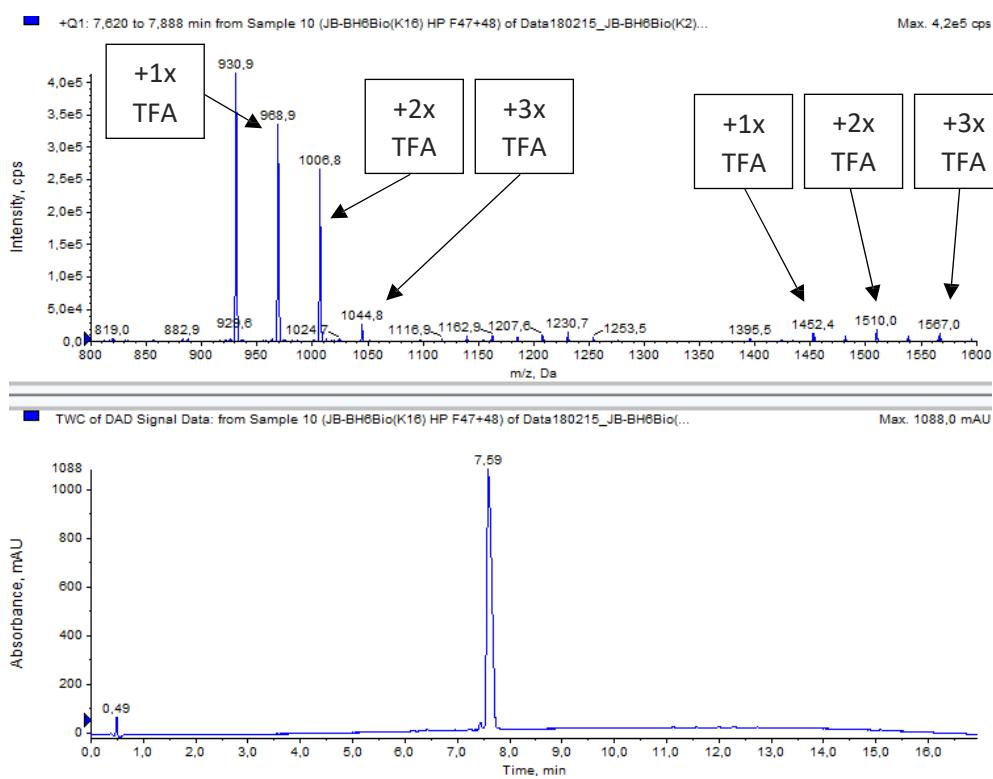
Peptide	Sequence	M(calc.)	[M+H]+	[M+2H]2+	[M+3H]3+
PepE-Bio	Ac-EIAALERERIAALEREIAALER-Aoa-Aoa-Lys(Bio)-NH ₂	3055.4	3056.4	1528.7	1019.5



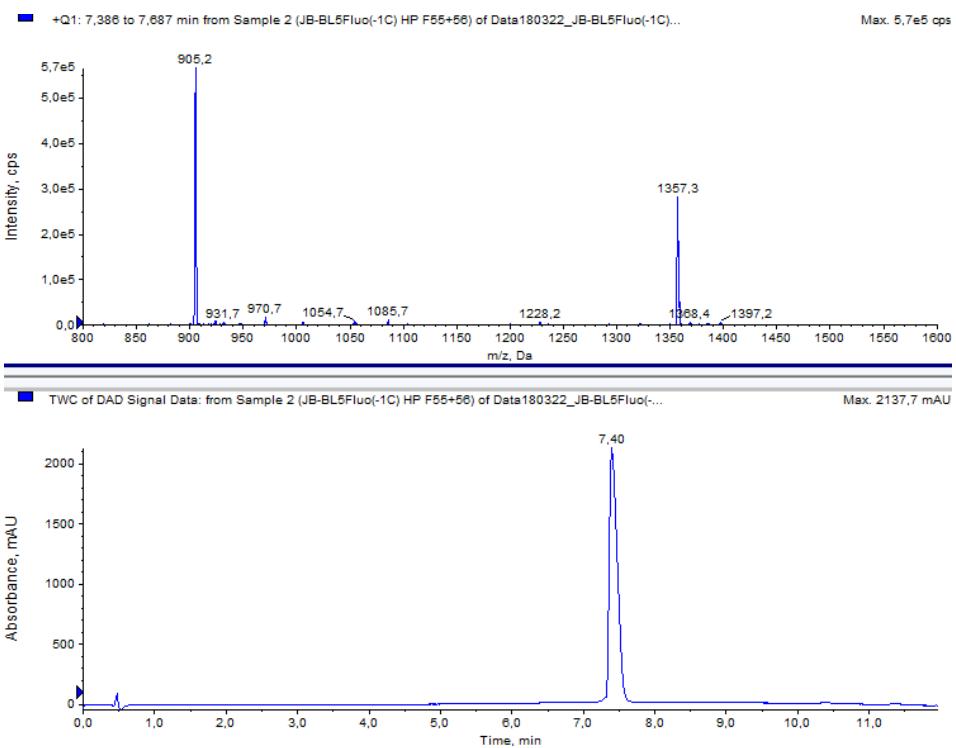
Peptide	Sequence	M(calc.)	[M+H]+	[M+2H]2+	[M+3H]3+
PepK(K13)	Bio-Aoa-RIAALKERIAALRERIAALRE-NH ₂	2791.3	2792.3	1396.7	931.4



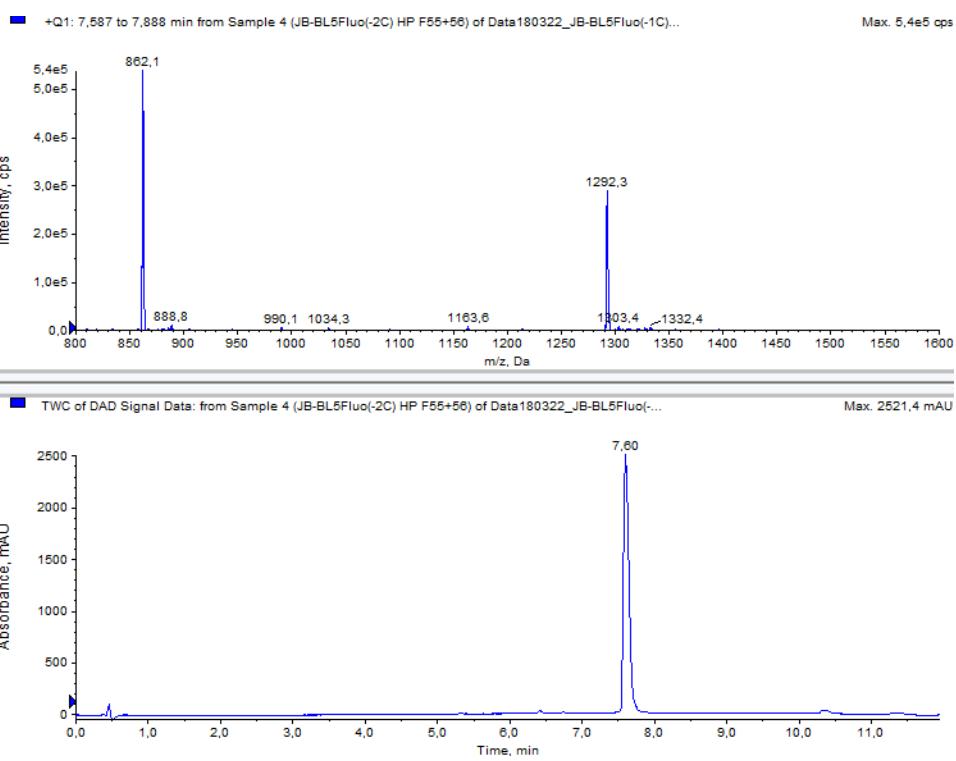
Peptide	Sequence	M(calc.)	[M+H]+	[M+2H]2+	[M+3H]3+
PepK(K6)	Bio-Aoa-RIAALKERIAALRERIAALRE-NH ₂	2791.3	2792.3	1396.7	931.4



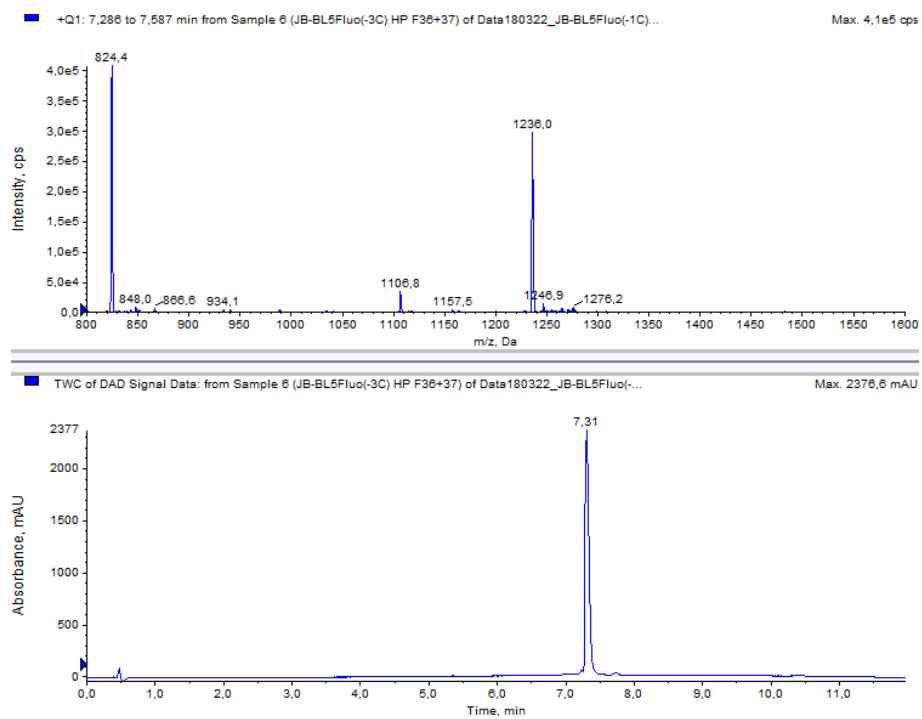
Peptide	Sequence	M(calc.)	[M+H]+	[M+2H]2+	[M+3H]3+
PepE(-1C)	Fluo-Aoa-EIAALEREIAALEREIAALE-NH ₂	2712.8	2713.8	1357.4	905.3



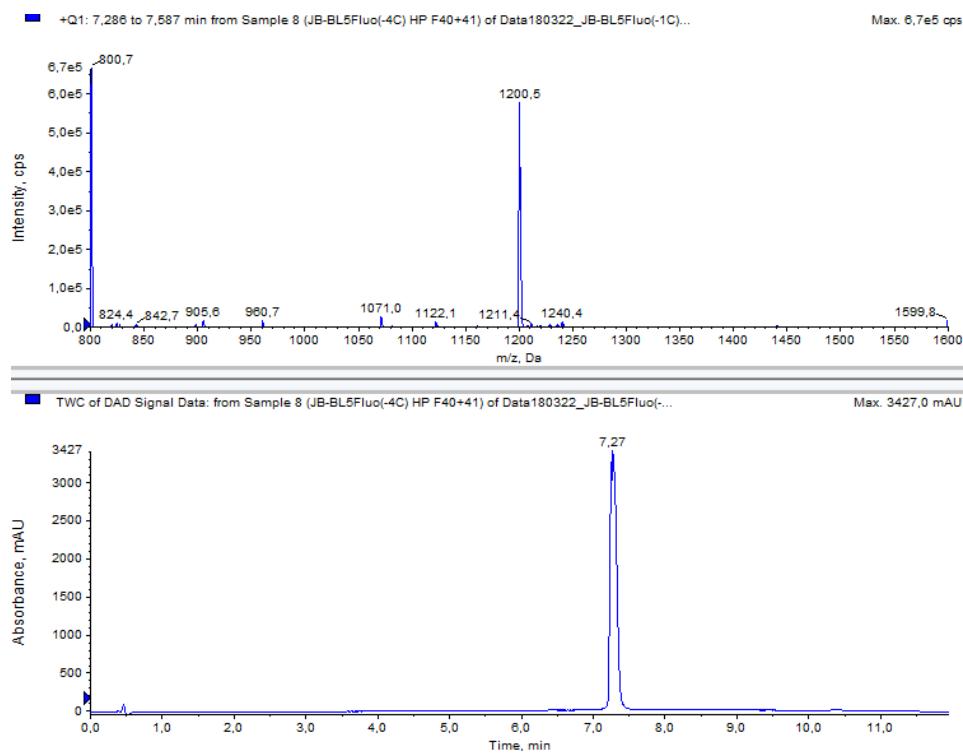
Peptide	Sequence	M(calc.)	[M+H]+	[M+2H]2+	[M+3H]3+
PepE(-2C)	Fluo-Aoa-EIAALEREIAALEREIAAL-NH ₂	2583.7	2584.7	1292.9	862.2



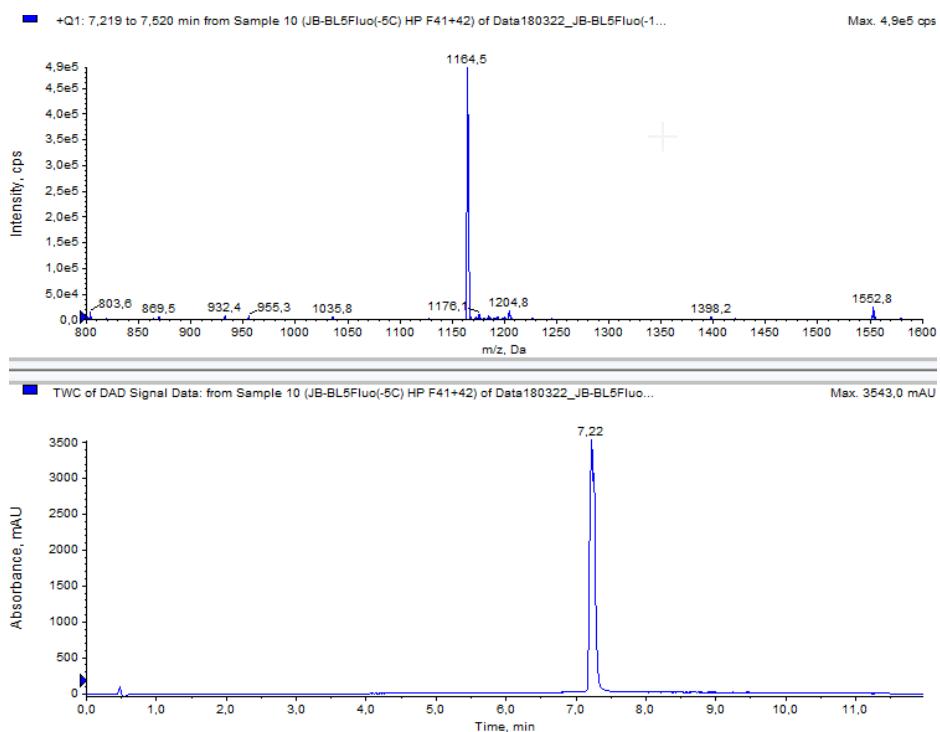
Peptide	Sequence	M(calc.)	[M+H]+	[M+2H]2+	[M+3H]3+
PepE(-3C)	Fluo-Aoa-EIAALEREIAALEREIAA-NH ₂	2470.5	2471.5	1236.3	824.5



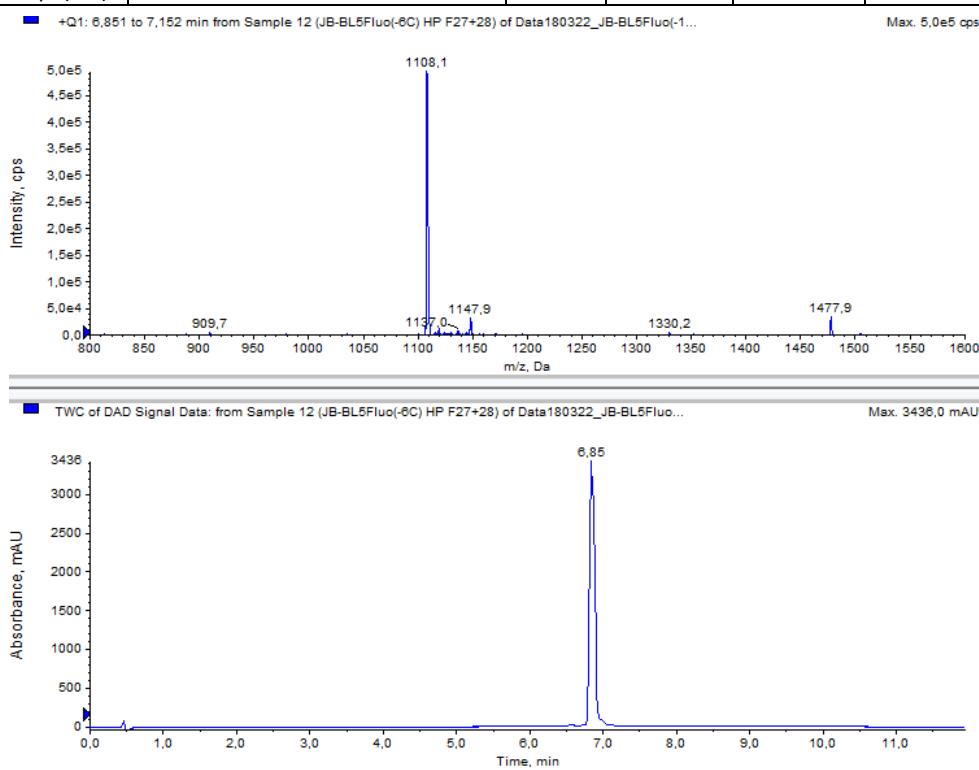
Peptide	Sequence	M(calc.)	[M+H]+	[M+2H]2+	[M+3H]3+
PepE(-4C)	Fluo-Aoa-EIAALEREIAALEREIA-NH ₂	2399.5	2400.5	1200.8	800.8

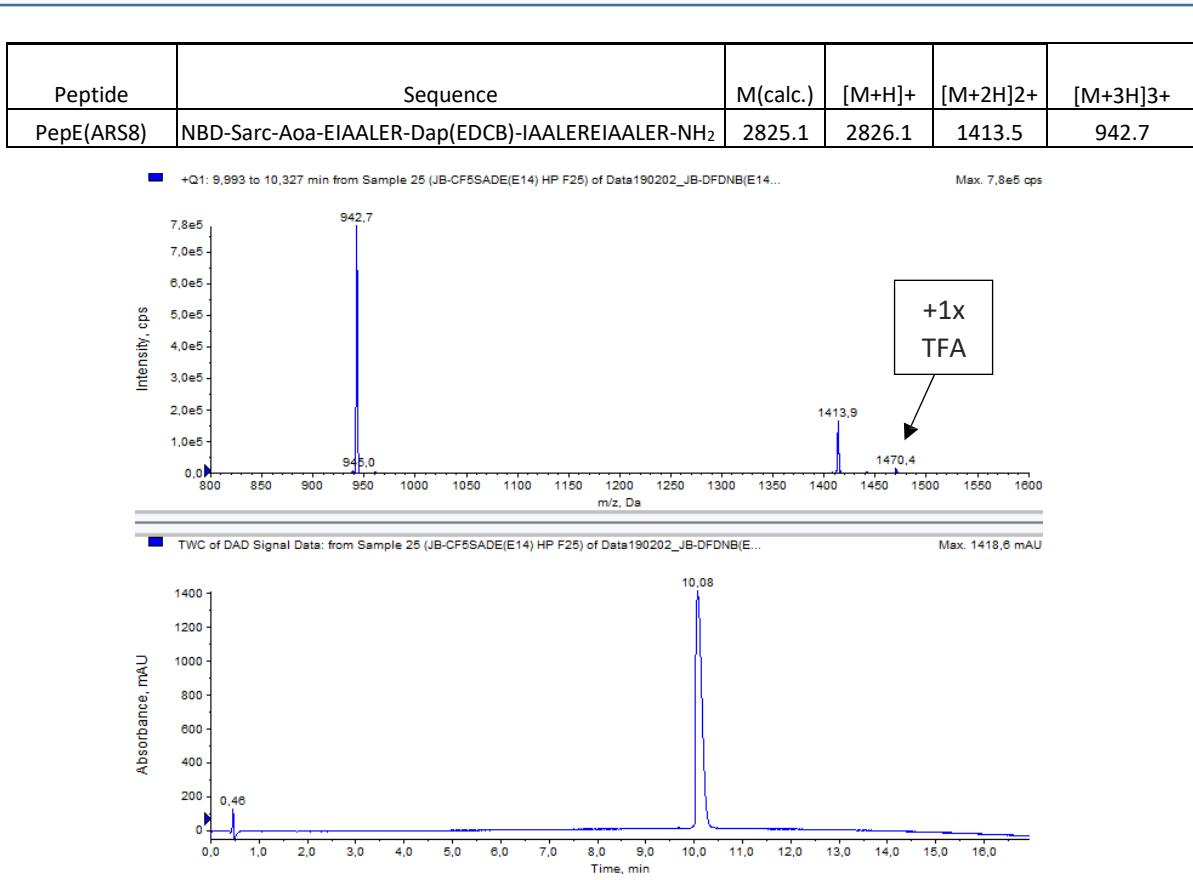
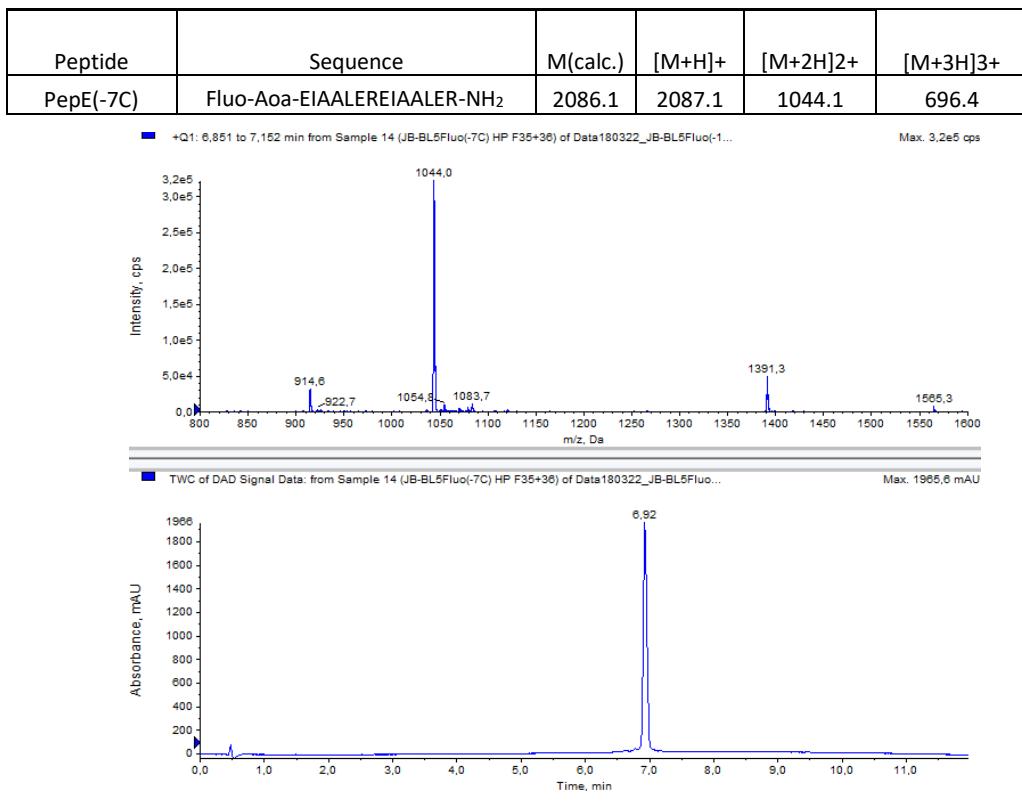


Peptide	Sequence	M(calc.)	[M+H]+	[M+2H]2+	[M+3H]3+
PepE(-5C)	Fluo-Aoa-EIAALEREIAALEREI-NH ₂	2328.4	2329.4	1165.2	777.1



Peptide	Sequence	M(calc.)	[M+H]+	[M+2H]2+	[M+3H]3+
PepE(-6C)	Fluo-Aoa-EIAALEREIAALEREI-NH ₂	2215.2	2216.2	1108.6	739.4





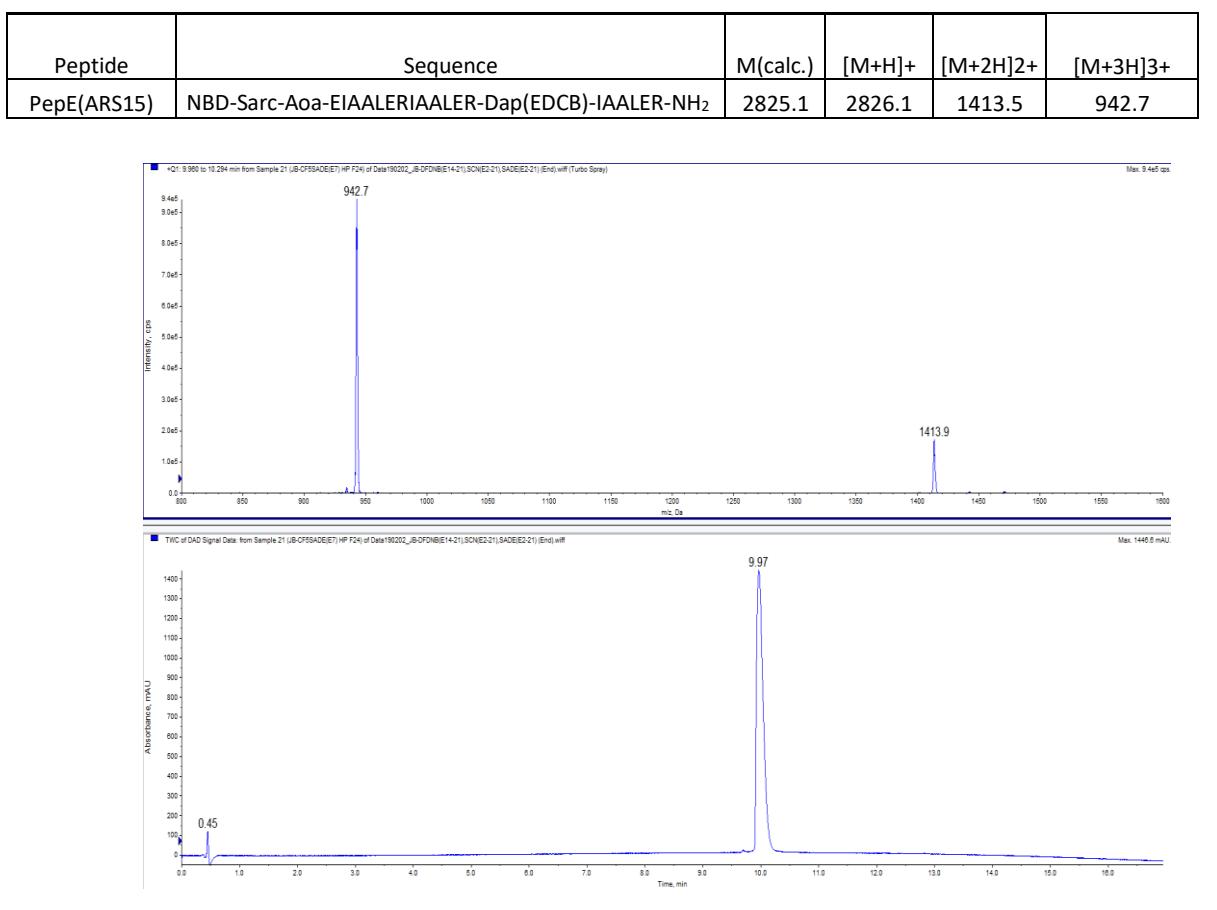
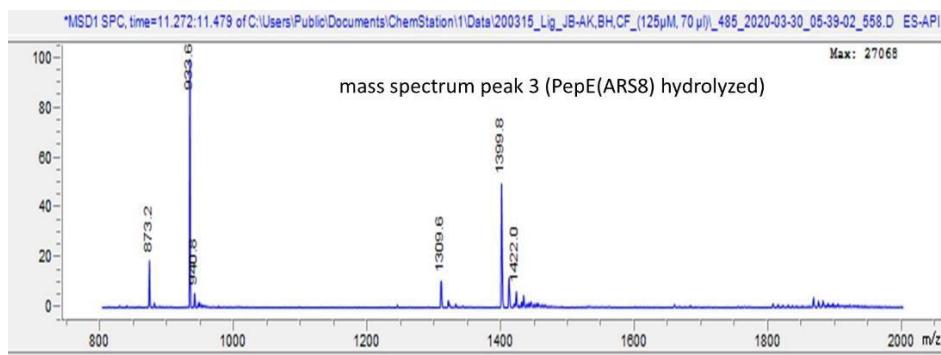
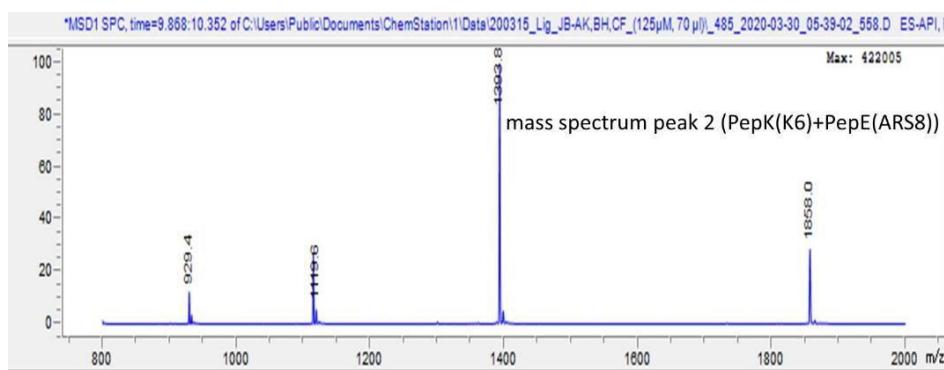
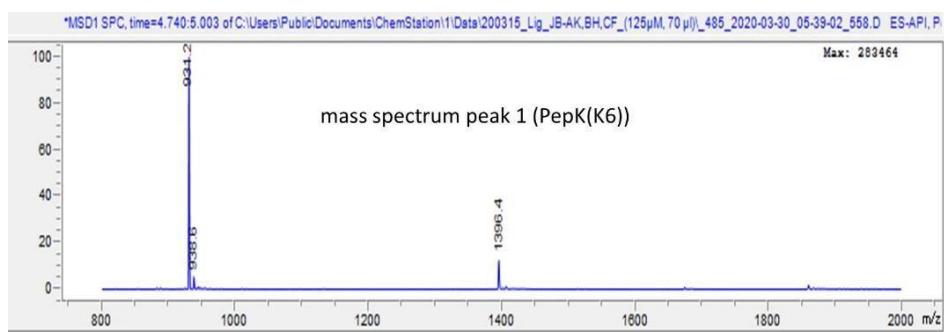
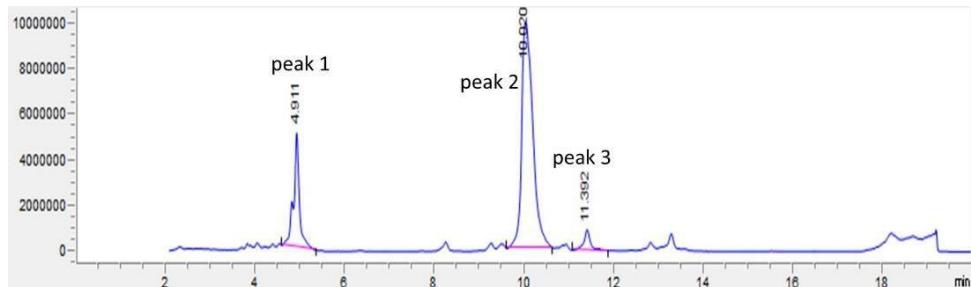


Figure S1. LC-MS data of peptides. Tables: ESI mass spectrometry data. Graphs: top: mass spectra, bottom: UV chromatograms (combined absorption at 220 and 280 nm). Masses of single, double and triple TFA adducts, which have been reported for arginine-rich peptides (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3397831/>), are marked accordingly.

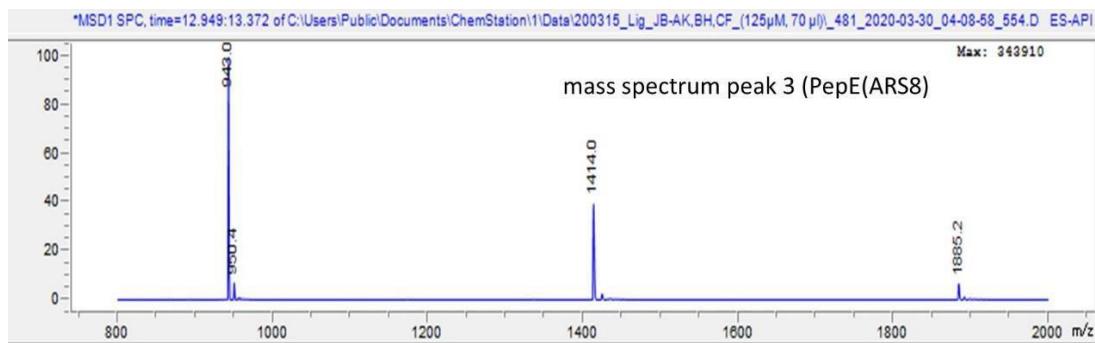
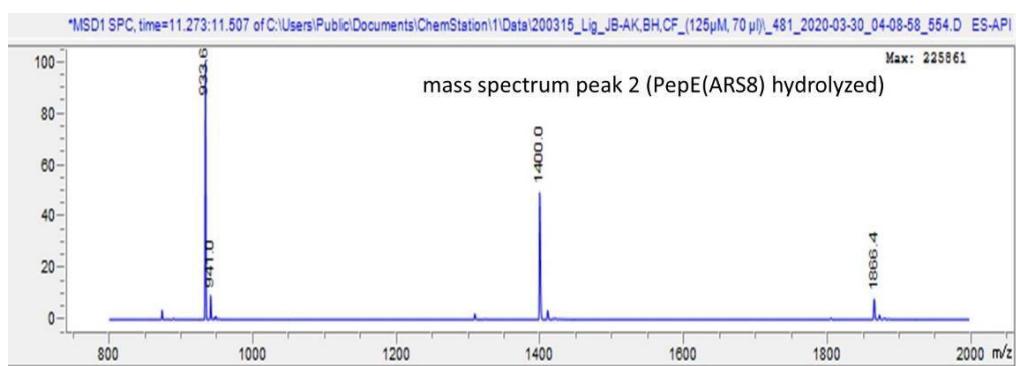
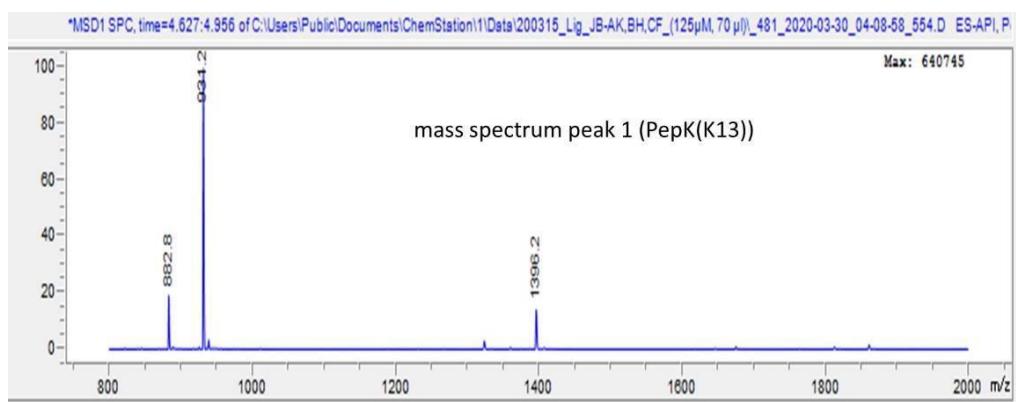
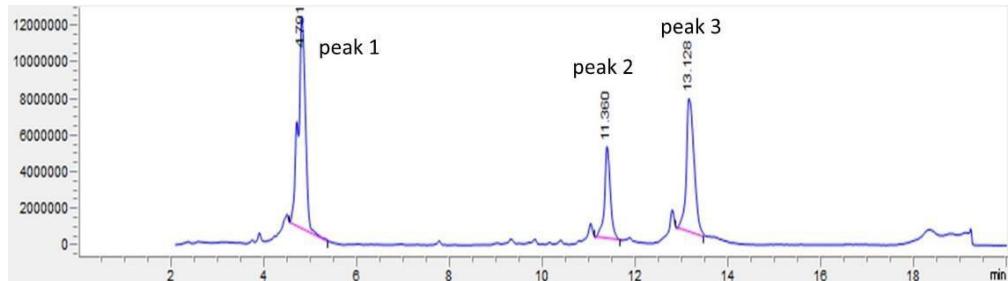
match 1: PepK(K6)+PepE(ARS8)

Chromatogram:



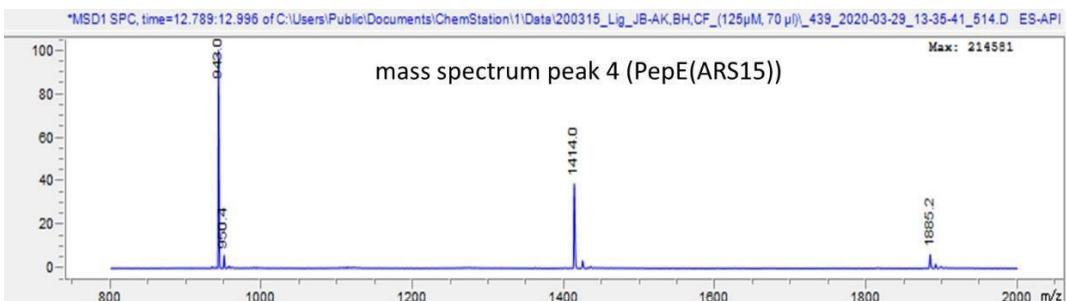
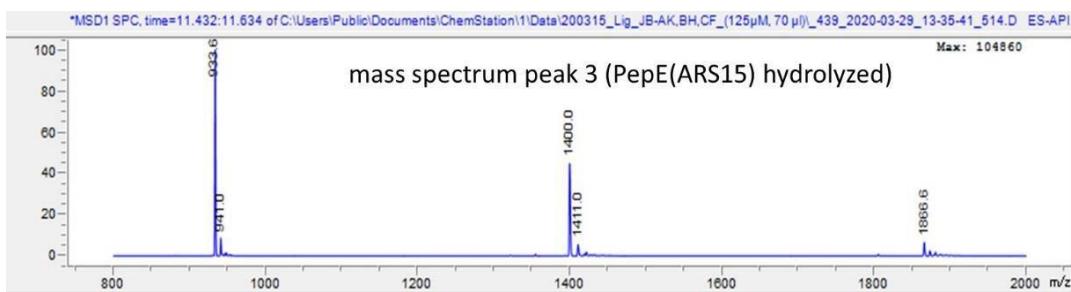
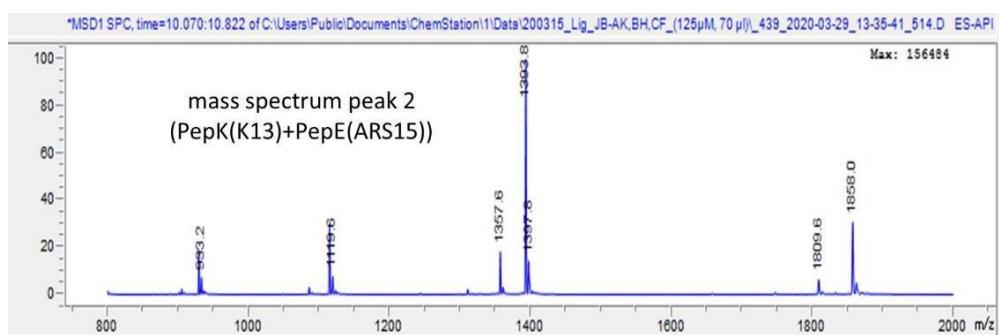
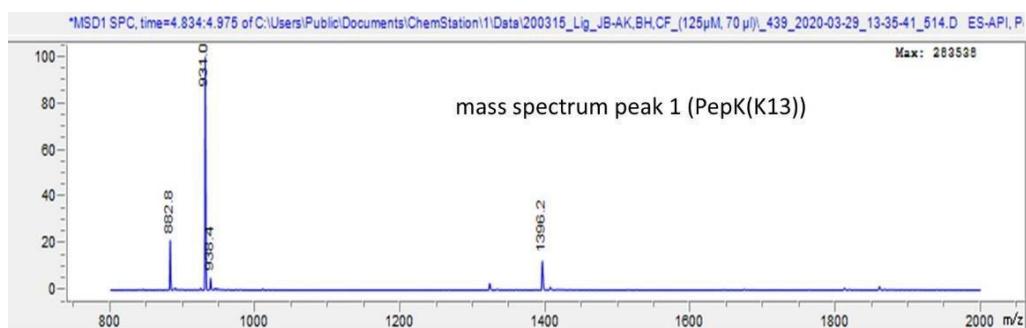
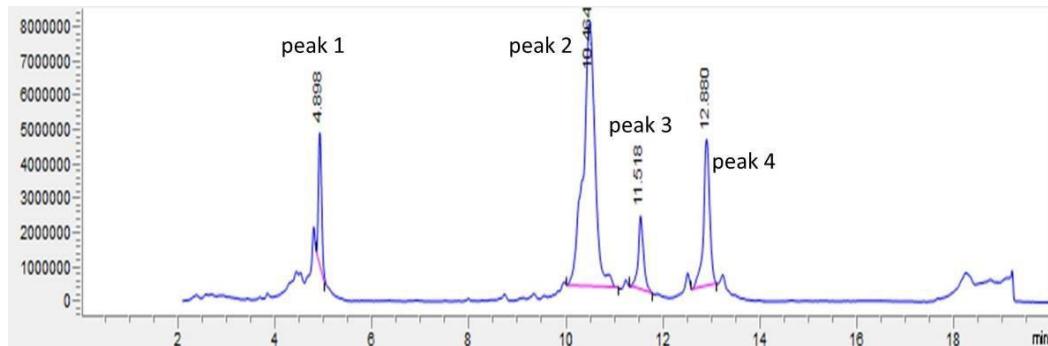
mismatch 1: + PepK(K13)+PepE(ARS8)

Chromatogram:



match 2: PepK(K13)+PepE(ARS15)

Chromatogram:



mismatch 2: PepK(K6)+PepE(ARS15)

Chromatogram:

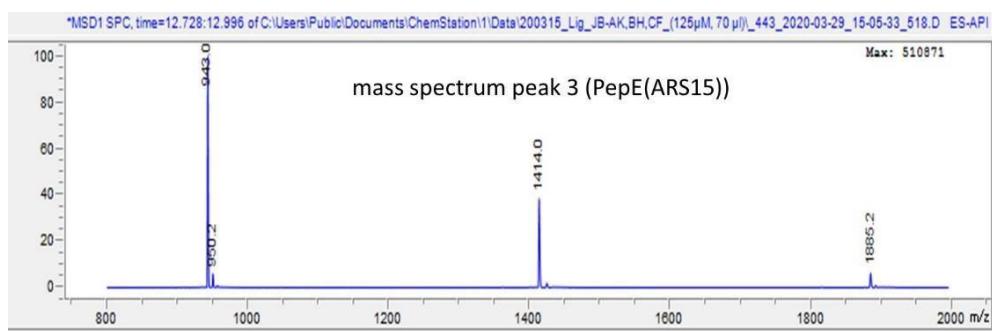
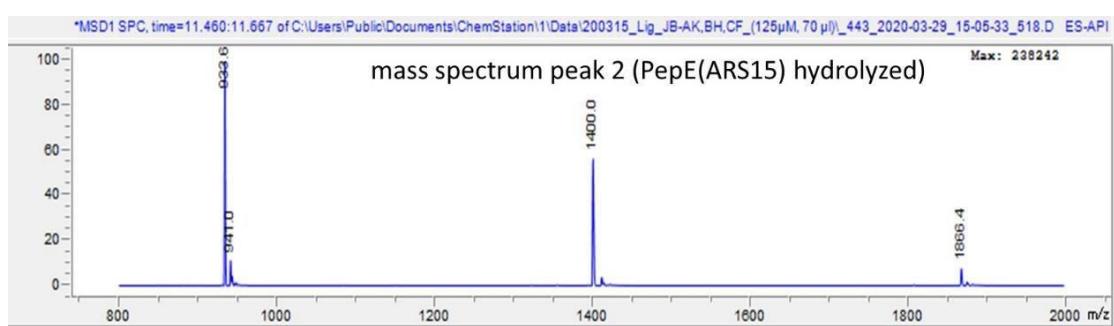
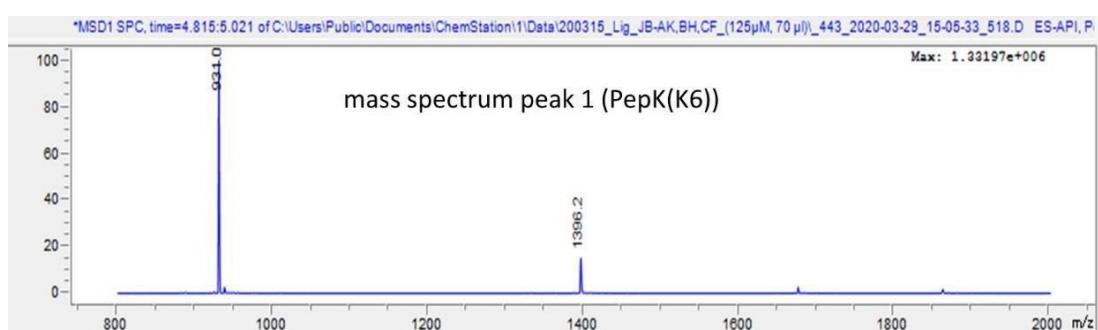
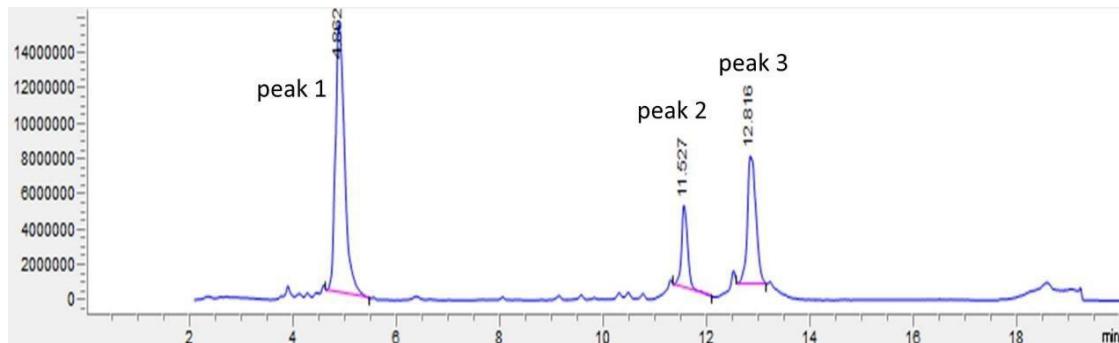


Figure S2. LC-MS data (TIC chromatograms and mass spectra of individual peaks of all match and mismatch reaction products of orthogonal pairs of coiled-coil peptides.

Peptide	Sequence	M(calc.)	[M+H]+	[M+2H]2+	[M+3H]3+	[M+4H]4+	[M+5H]5+
PepE-Bio + Bio-PepK (1 isopeptide bond)	Ac-EIAALEREIAALER-EIAALER-Aoa-Aoa-Lys(Bio)-NH2 + Bio-Aoa-KIAALKEKIAALKEKIAALK-E-NH2	5685.2		1895.7	1422.1	1137.8	948.4
PepE-Bio + Bio-PepK (2 isopeptide bonds)	Ac-EIAALEREIAALER-EIAALER-Aoa-Aoa-Lys(Bio)-NH2 + Bio-Aoa-KIAALKEKIAALKEKIAALK-E-NH2	5667.2		1889.7	1417.6	1134.2	945.4

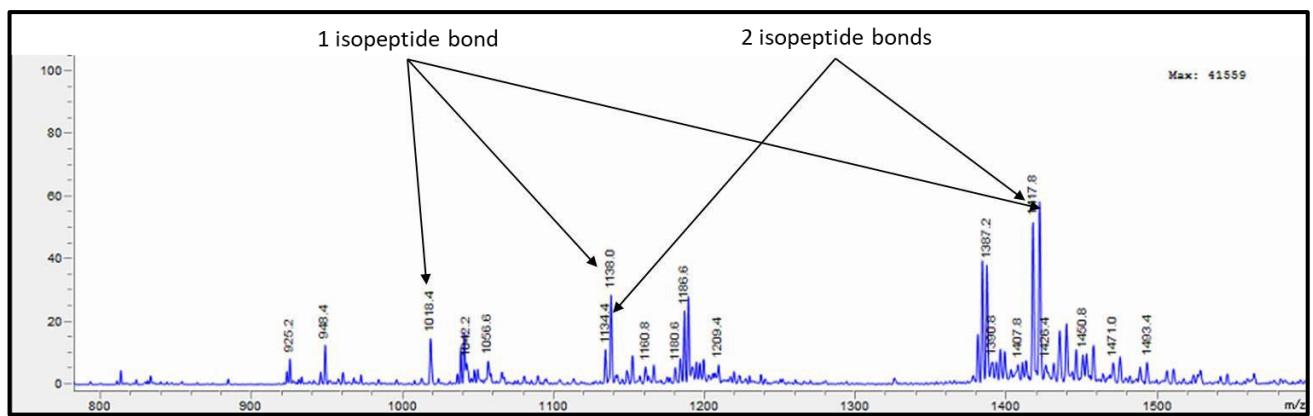


Figure S3. Mass spectrum of the product of the reaction of pre-activated PepE-Bio with Bio-PepK.