

Supplemental Material

An all-D amphipathic undecapeptide shows promising activity against colistin-resistant strains of *Acinetobacter baumannii* and a dual mode of action

Alberto Oddo,^{a#‡} Thomas T. Thomsen,^{b‡} Susanne Kjelstrup,^b Ciara Gorey,^a Henrik Franzyk,^a
Niels Frimodt-Møller,^c Anders Løbner-Olesen,^{b#} Paul R. Hansen^{a#}

Department of Drug Design and Pharmacology , University of Copenhagen, Copenhagen, Denmark^a; Dept. of Biology, Section for Functional Genomics and Center for Bacterial Stress Response (BASP), University of Copenhagen, Copenhagen, Denmark^b; Department of Clinical Microbiology, Rigshospitalet, Copenhagen, Denmark^c

#Address correspondence to Alberto Oddo, alberto.oddo@sund.ku.dk; Anders Løbner-Olesen, lobner@bio.ku.dk; Paul R. Hansen, prh@sund.ku.dk

‡These authors contributed equally to this work.

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Peptide characterization data

BP100: purity = 98.7%; t_R = 14.7 min; calculated m/z for $C_{72}H_{126}N_{17}O_{12}$ $[M+H]^+$ = 1420.97;
experimental m/z = 1420.72

BP143: purity = 95.5%; t_R = 15.0 min; calculated m/z for $C_{72}H_{126}N_{17}O_{12}$ $[M+H]^+$ = 1420.97;
experimental m/z = 1420.70

BP157: purity = 99.0%; t_R = 14.4 min; calculated m/z for $C_{72}H_{126}N_{17}O_{12}$ $[M+H]^+$ = 1420.97;
experimental m/z = 1420.58

RW-BP100: purity = 100%; t_R = 15.7 min; calculated m/z for $C_{74}H_{127}N_{28}O_{11}$ $[M+H]^+$ =
1584.02; experimental m/z = 1584.02

BP201: purity = 99.0%; t_R = 14.8 min; calculated m/z for $C_{72}H_{126}N_{21}O_{12}$ $[M+H]^+$ = 1476.98;
experimental m/z = 1476.59

BP202: purity = 99.0%; t_R = 14.8 min; calculated m/z for $C_{72}H_{126}N_{21}O_{12}$ $[M+H]^+$ = 1476.98;
experimental m/z = 1476.59

BP203: purity = 100%; t_R = 15.0 min; calculated m/z for $C_{72}H_{126}N_{19}O_{12}$ $[M+H]^+$ = 1448.98;
experimental m/z = 1448.76

BP204: purity = 99.9%; t_R = 14.7 min; calculated m/z for $C_{72}H_{126}N_{23}O_{12}$ $[M+H]^+$ = 1504.99;
experimental m/z = 1504.43

BP205: purity = 95.2%; t_R = 14.6 min; calculated m/z for $C_{72}H_{126}N_{21}O_{12}$ $[M+H]^+$ = 1476.98;
experimental m/z = 1476.86

BP206: purity = 98.5%; t_R = 15.0 min; calculated m/z for $C_{72}H_{126}N_{21}O_{12}$ $[M+H]^+$ = 1476.98;
experimental m/z = 1476.33

BP207: purity = 99.3%; t_R = 14.5 min; calculated m/z for $C_{72}H_{126}N_{17}O_{12}$ $[M+H]^+$ = 1420.97;
experimental m/z = 1420.46

BP208: purity = 98.4%; t_R = 14.2 min; calculated m/z for $C_{72}H_{126}N_{17}O_{12}$ $[M+H]^+$ = 1420.97;
experimental m/z = 1420.46

BP209: purity = 99.9%; t_R = 14.7 min; calculated m/z for $C_{76}H_{128}N_{27}O_{12}$ $[M+H]^+$ = 1404.97;
experimental m/z = 1404.55

BP210: purity = 95.1%; t_R = 15.7 min; calculated m/z for $C_{76}H_{128}N_{27}O_{12}$ $[M+H]^+$ = 1611.02;
experimental m/z = 1610.70

BP211: purity = 99.1%; t_R = 15.0 min; calculated m/z for $C_{72}H_{126}N_{19}O_{12}$ $[M+H]^+$ = 1448.98;
experimental m/z = 1448.51

BP212: purity = 100%; t_R = 15.7 min; calculated m/z for $C_{76}H_{128}N_{17}O_{12}$ $[M+H]^+$ = 1470.99;
experimental m/z = 1470.25

BP213 purity = 96.3%; t_R = 14.4 min; calculated m/z for $C_{72}H_{126}N_{19}O_{12}$ $[M+H]^+$ = 1448.98;
experimental m/z = 1448.51

BP214 purity = 96.8%; t_R = 14.6 min; calculated m/z for $C_{72}H_{126}N_{19}O_{12}$ $[M+H]^+$ = 1448.98;
experimental m/z = 1448.51

Reverse-phase HPLC Setup

For all experiments:

- **Buffer A:** 99.9% Water, 0.1% TFA
- **Buffer B:** 89.95% MeCN, 9.95% Water, 0.1% TFA

Analytical HPLC

- **Pump:** Waters™ 600 Pump
- **Detector:** Waters™ 2996 Photodiode Array Detector
- **Column:** Waters™ Symmetry™ C18, 4.6 x 250 mm, 5 μm

Gradient:

Time (min)	Flow (ml/min)	Buffer A	Buffer B
0.0	1.50	100%	0%
20.0	1.50	30%	70%
22.0	1.50	0%	100%
27.0	1.50	0%	100%
30.0	1.50	100%	0%

Equilibration delay between injections (both methods): 9 min with 100% Buffer A, 1.50 ml/min. The ApexTrack™ algorithm has been used for peak integration. Peaks having an area <0.01% were not included in the purity calculations. Spectra were processed as follows: the raw data were exported using the Waters Empower 3 software and imported in Microsoft Excel. The baseline (blank) was subtracted and negative absorbance values were corrected to 0 (zero).

Preparative HPLC

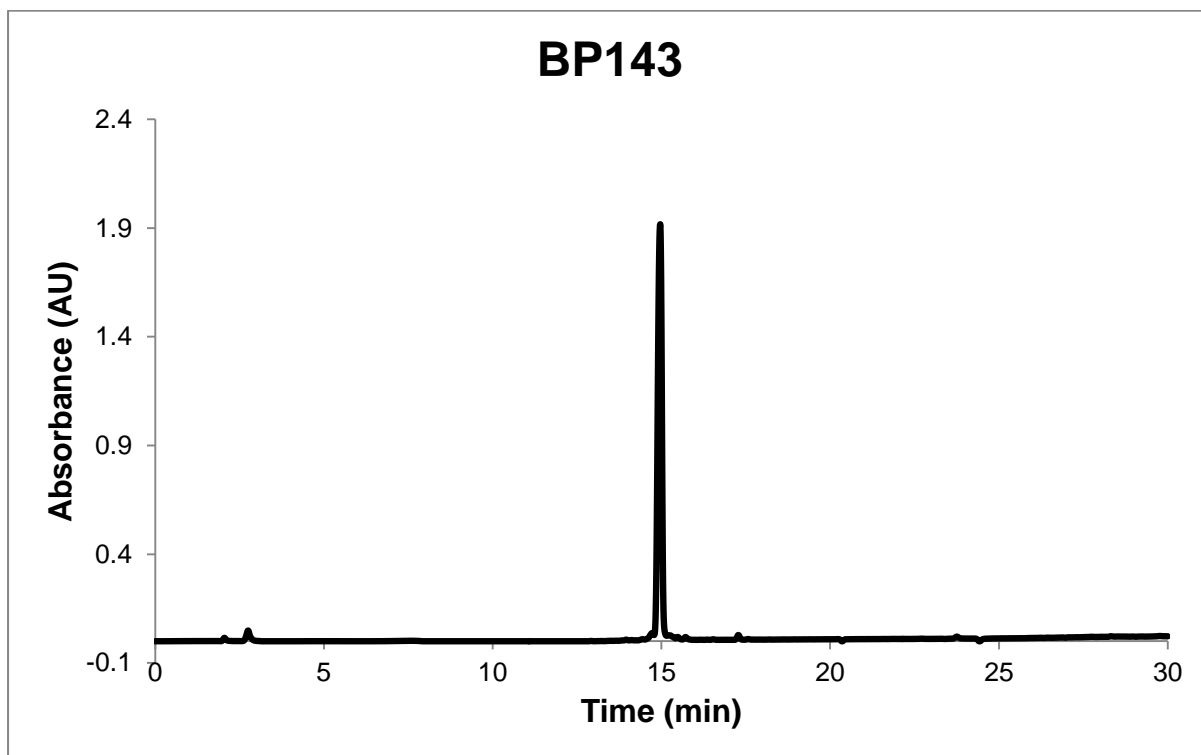
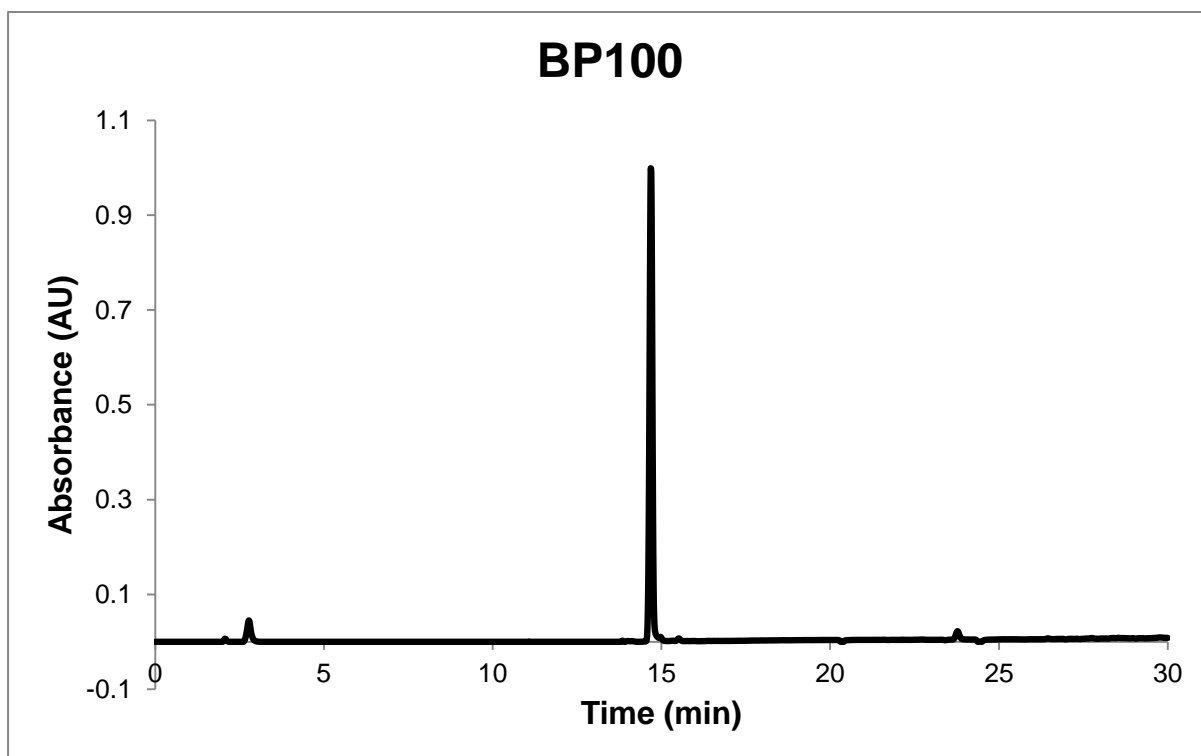
- **Pump:** Waters™ 600 Pump
- **Detector:** Waters™ 996 Photodiode Array Detector
- **Column:** Waters™ XBridge™ BEH130 C18, 10 x 250 mm, 5 μm

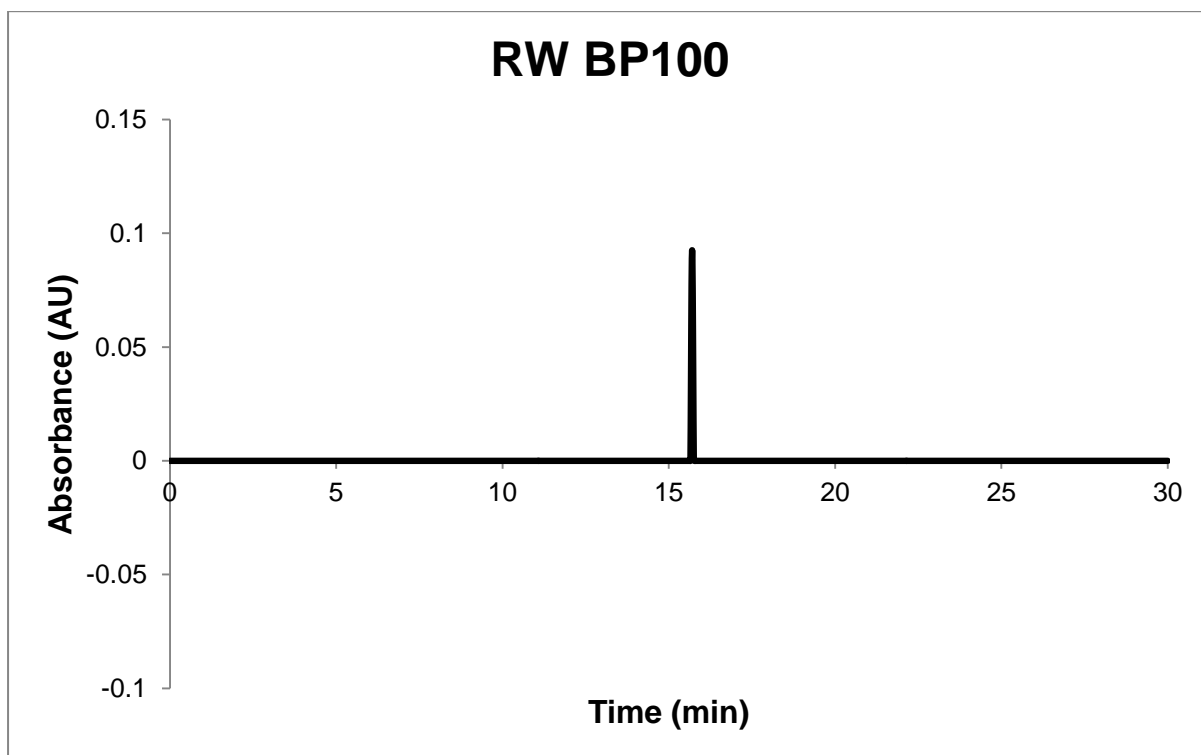
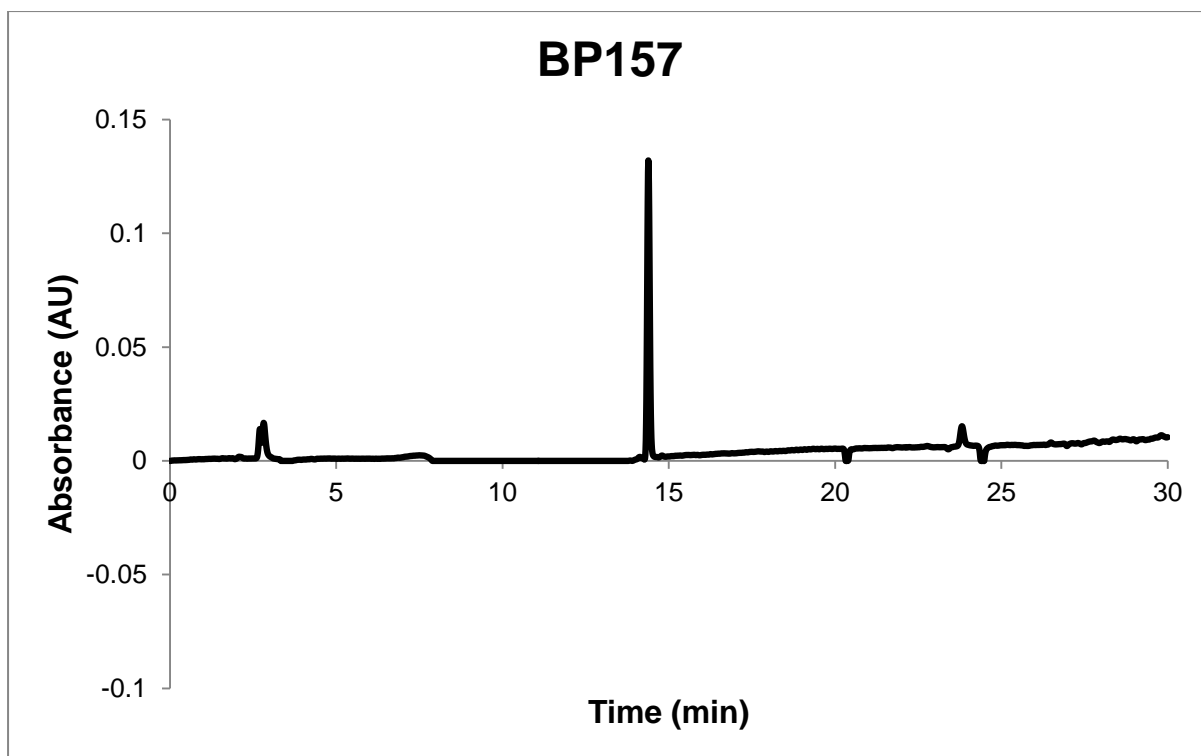
Gradient:

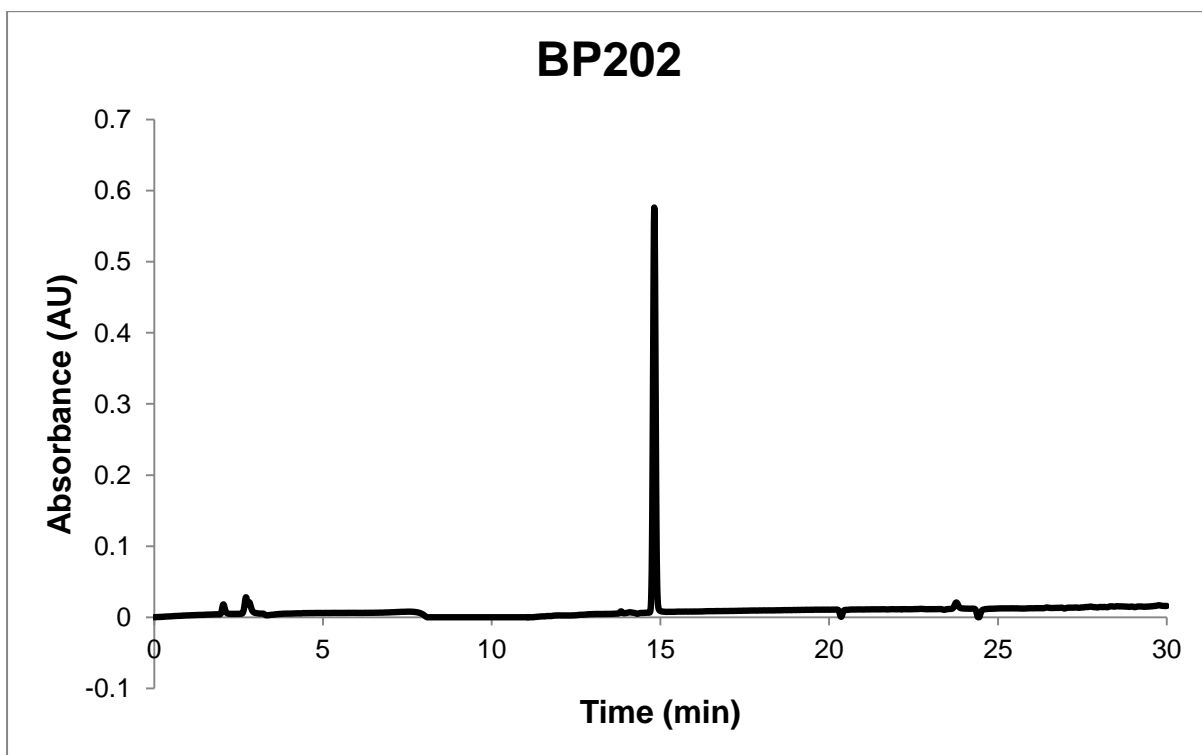
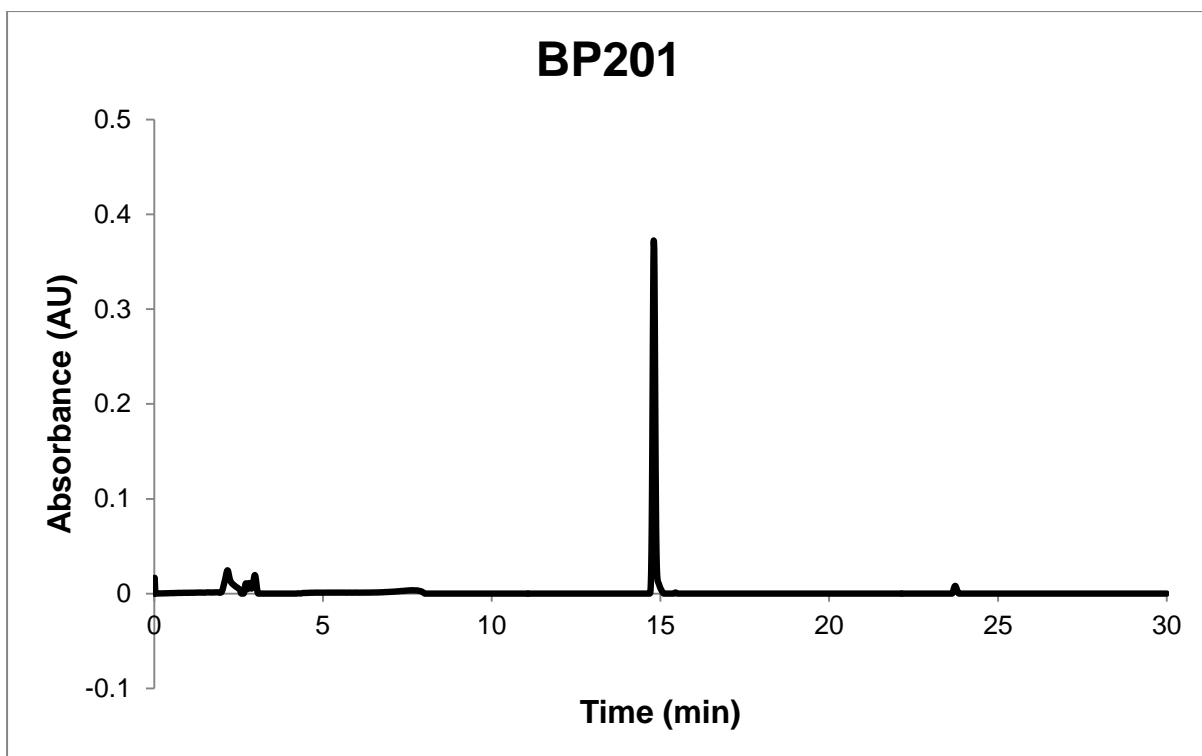
Time (min)	Flow (ml/min)	Buffer A	Buffer B
0.0	4.00	100%	0%
1.0	6.00	100%	0%
3.0	8.50	100%	0%
5.0	8.50	90%	10%
20.0	8.50	45%	55%
26.0	9.00	0%	100%
27.0	9.00	0%	100%
30.0	9.00	100%	0%
39.0	9.00	100%	0%

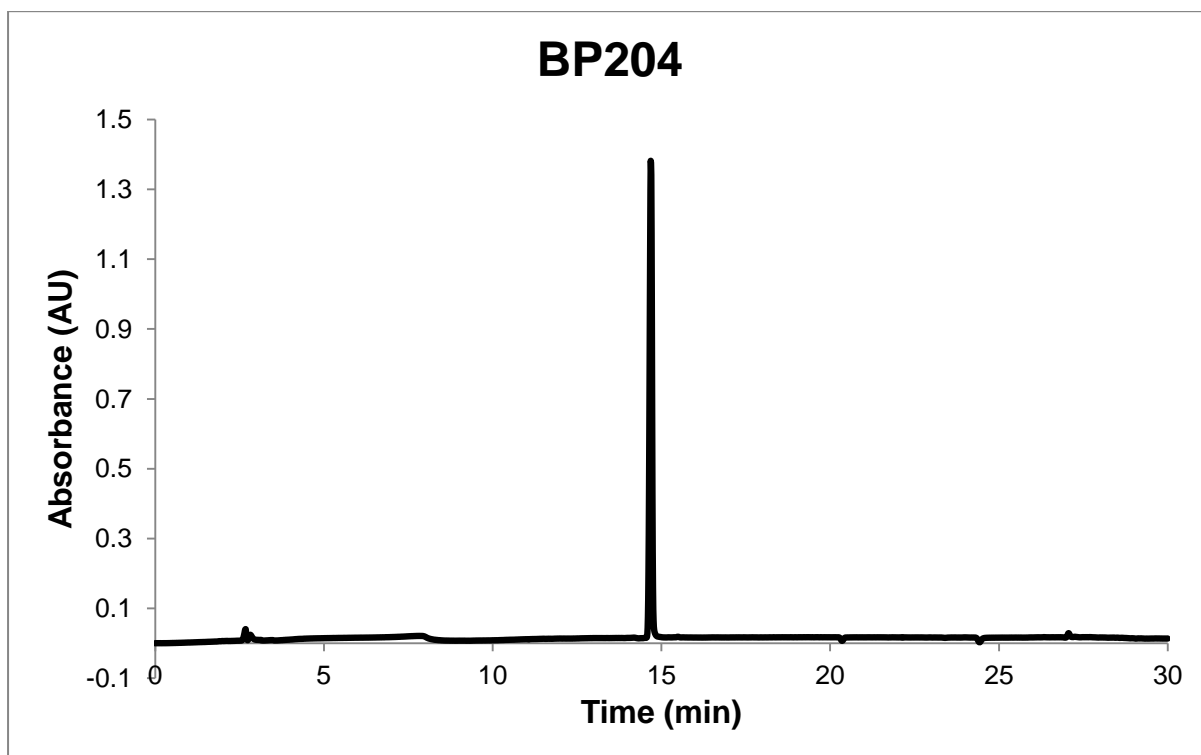
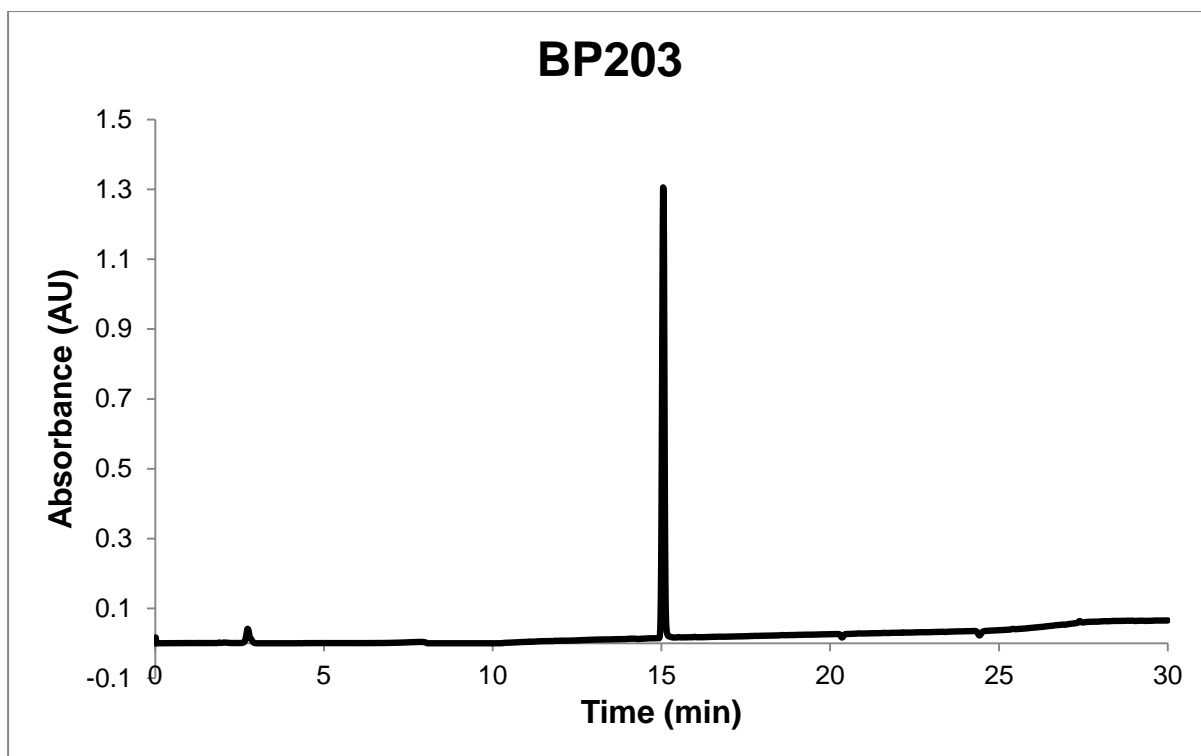
Purified fractions were collected manually.

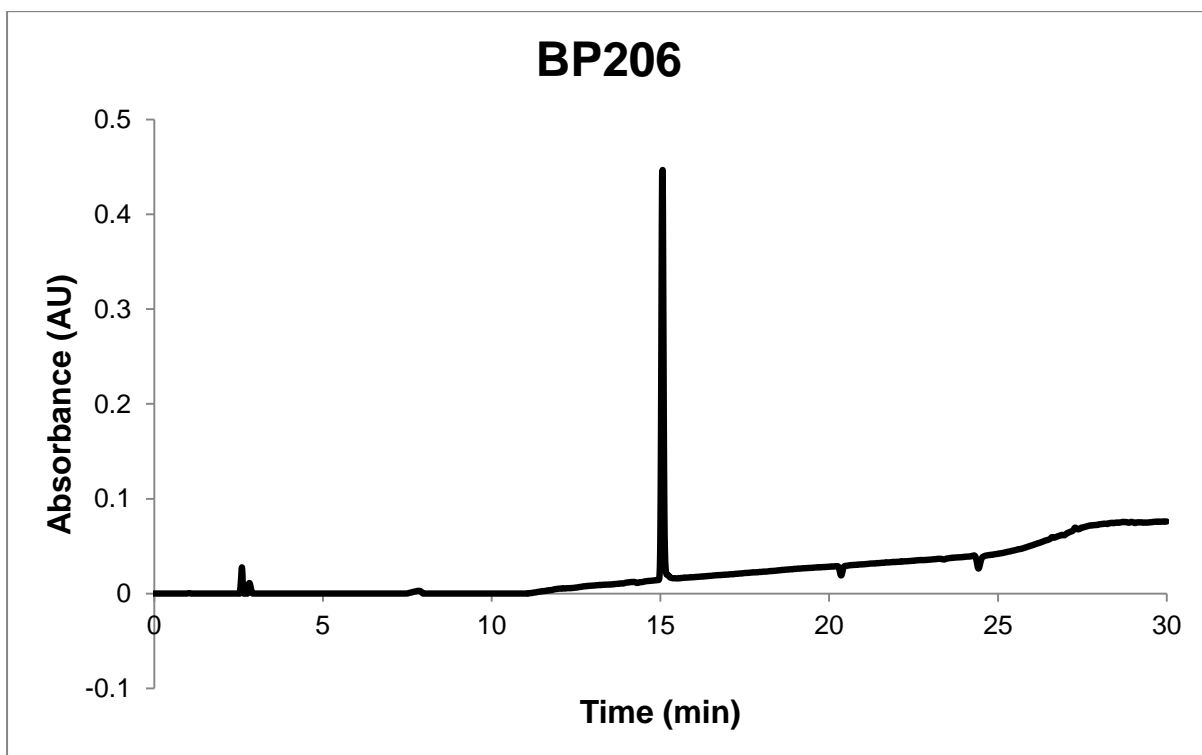
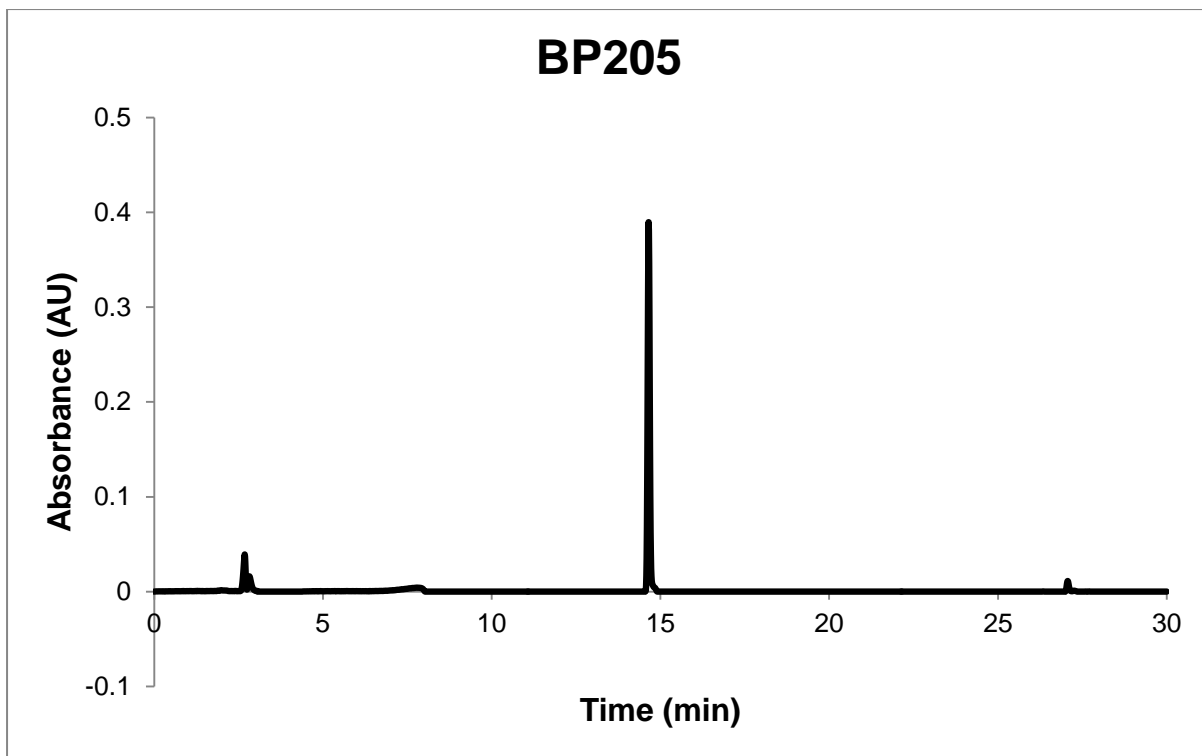
Analytical Chromatograms

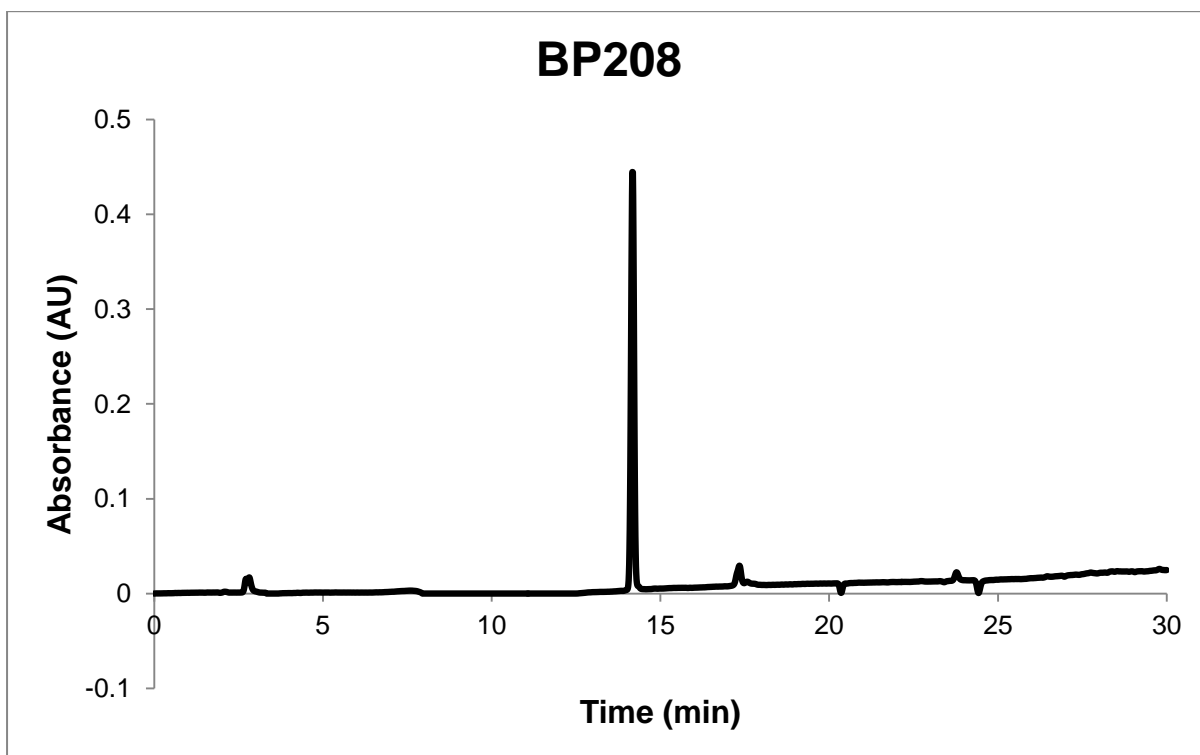
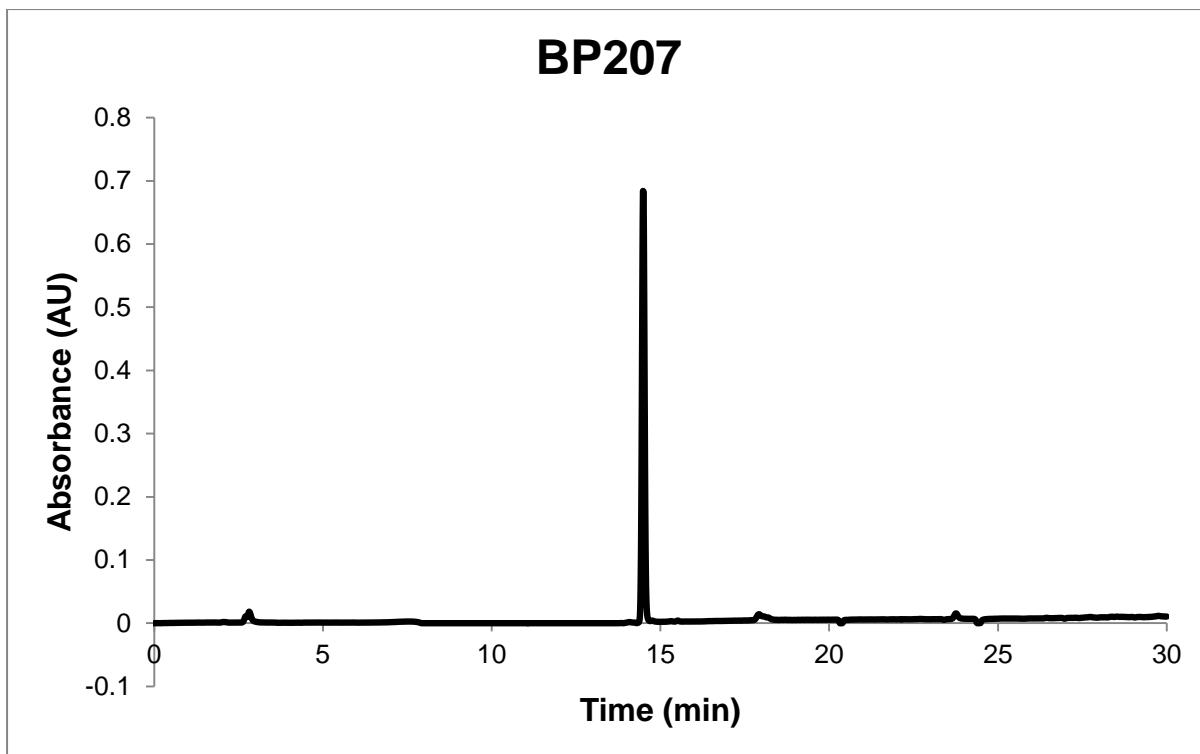


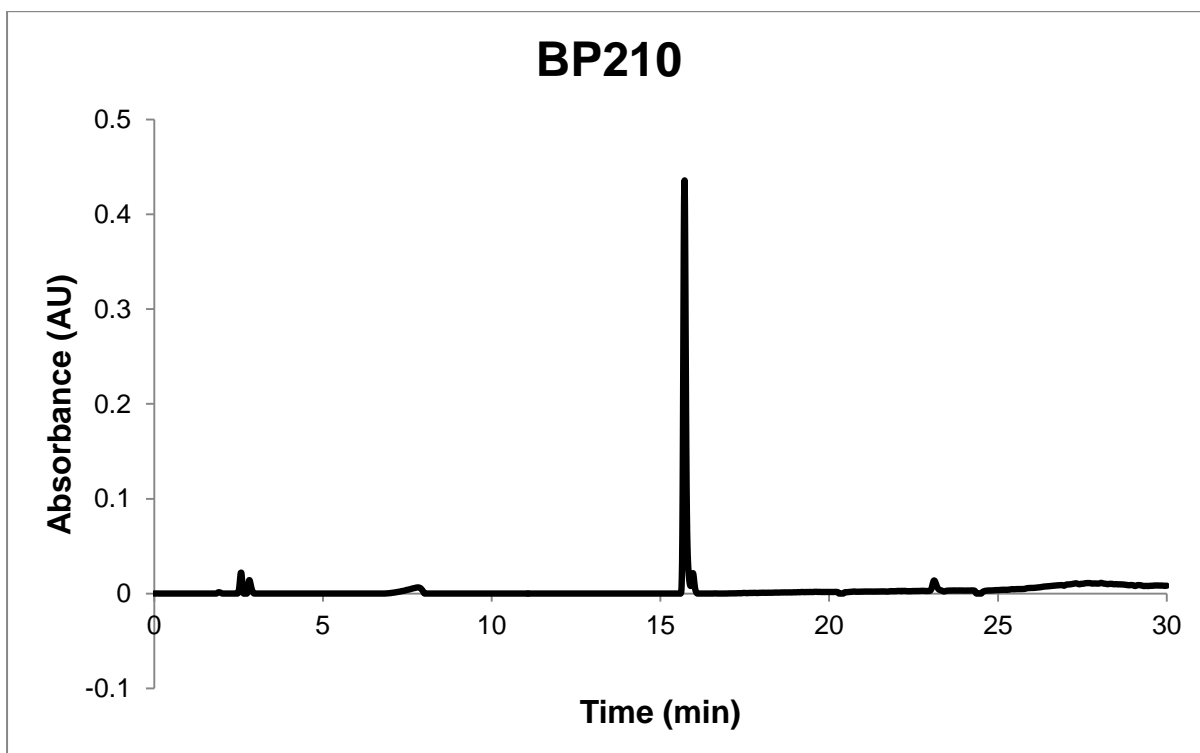
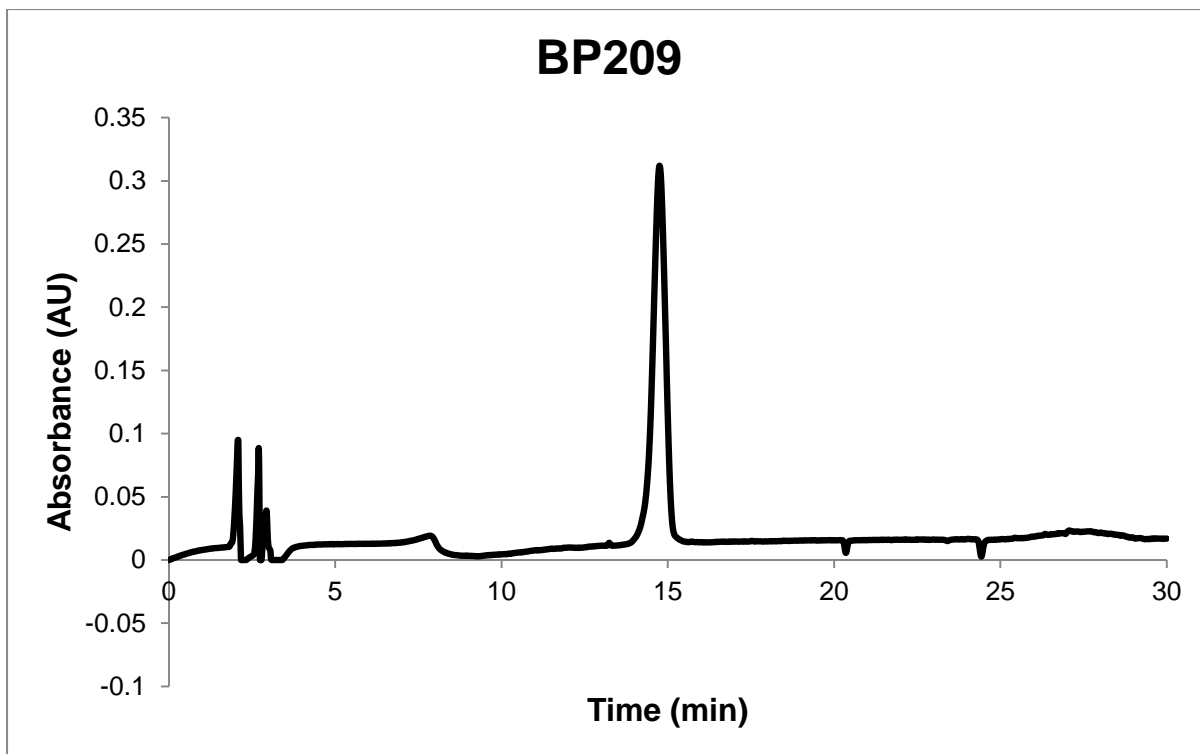


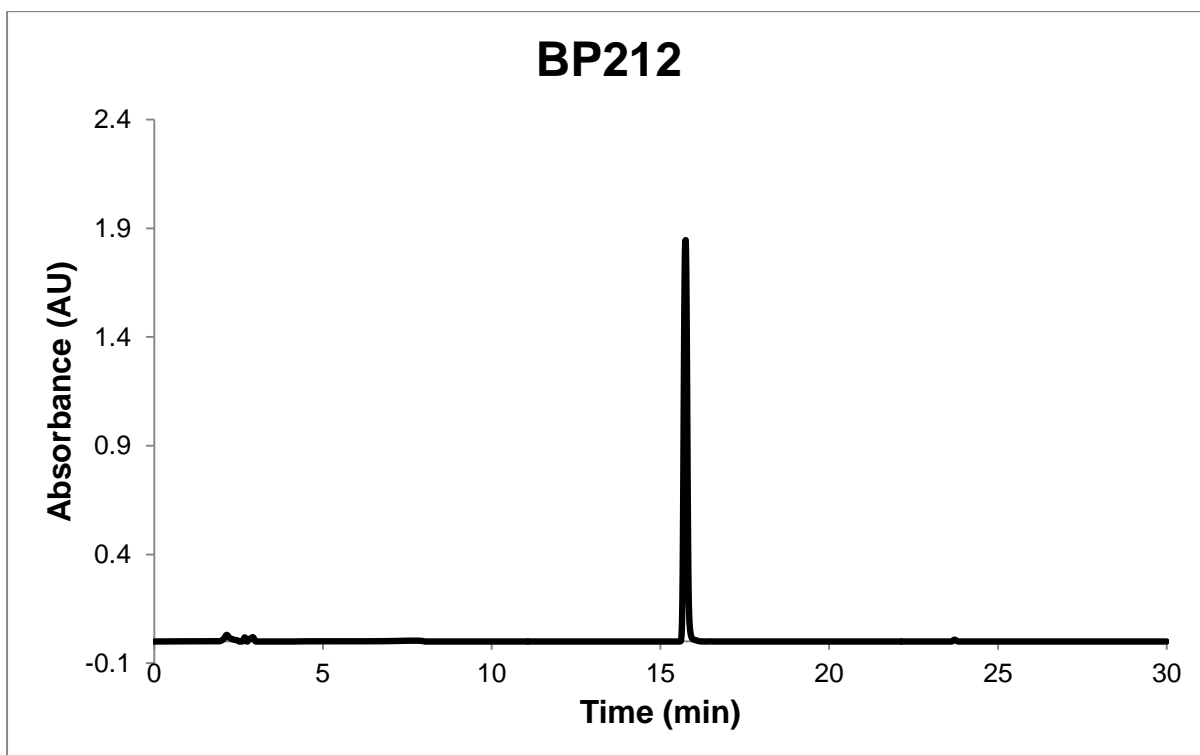
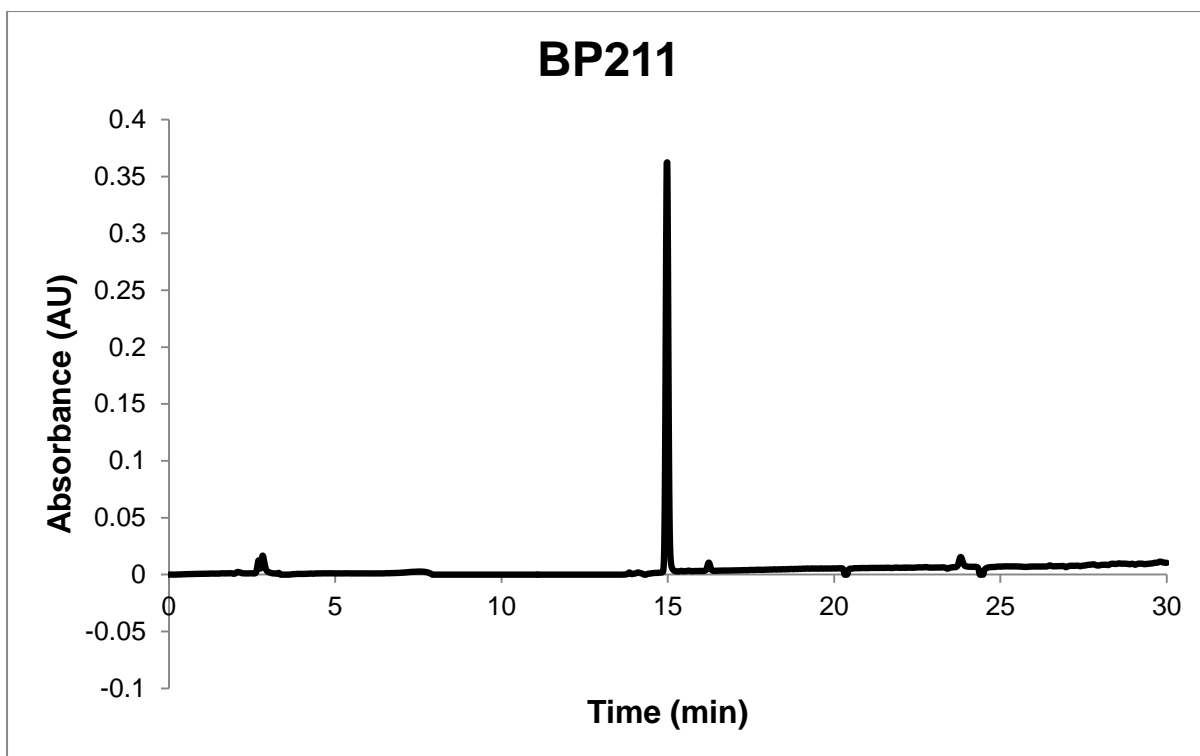


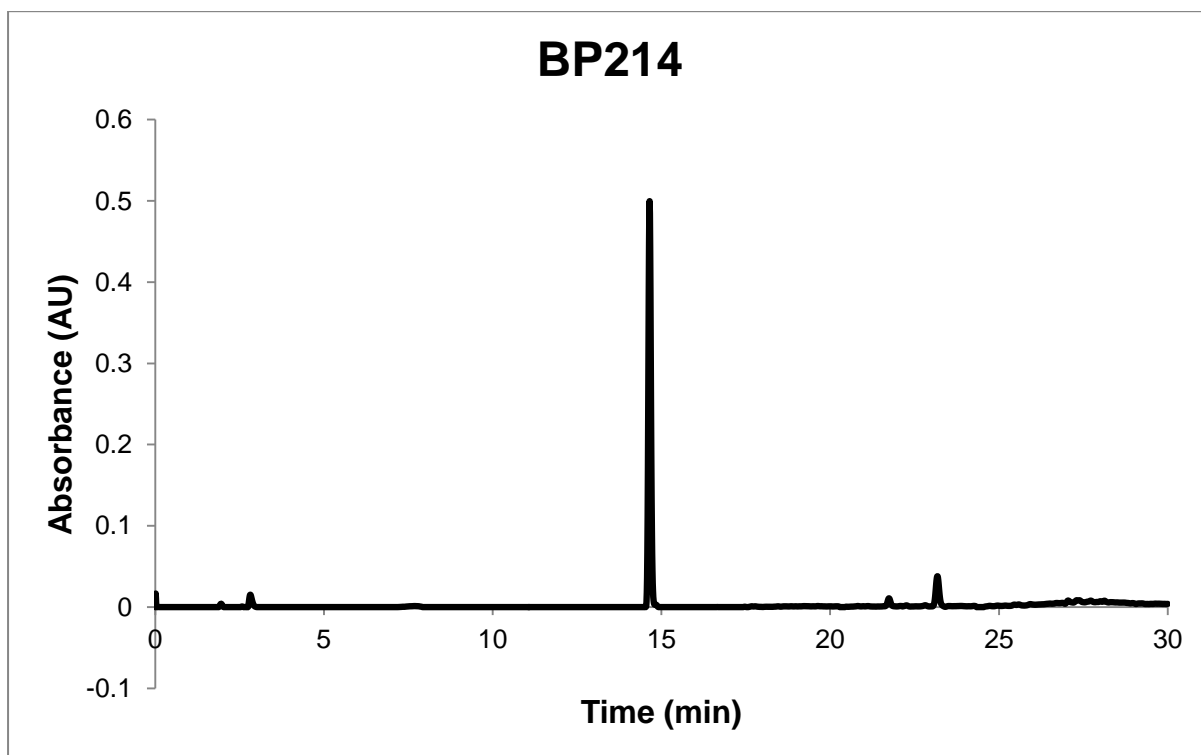
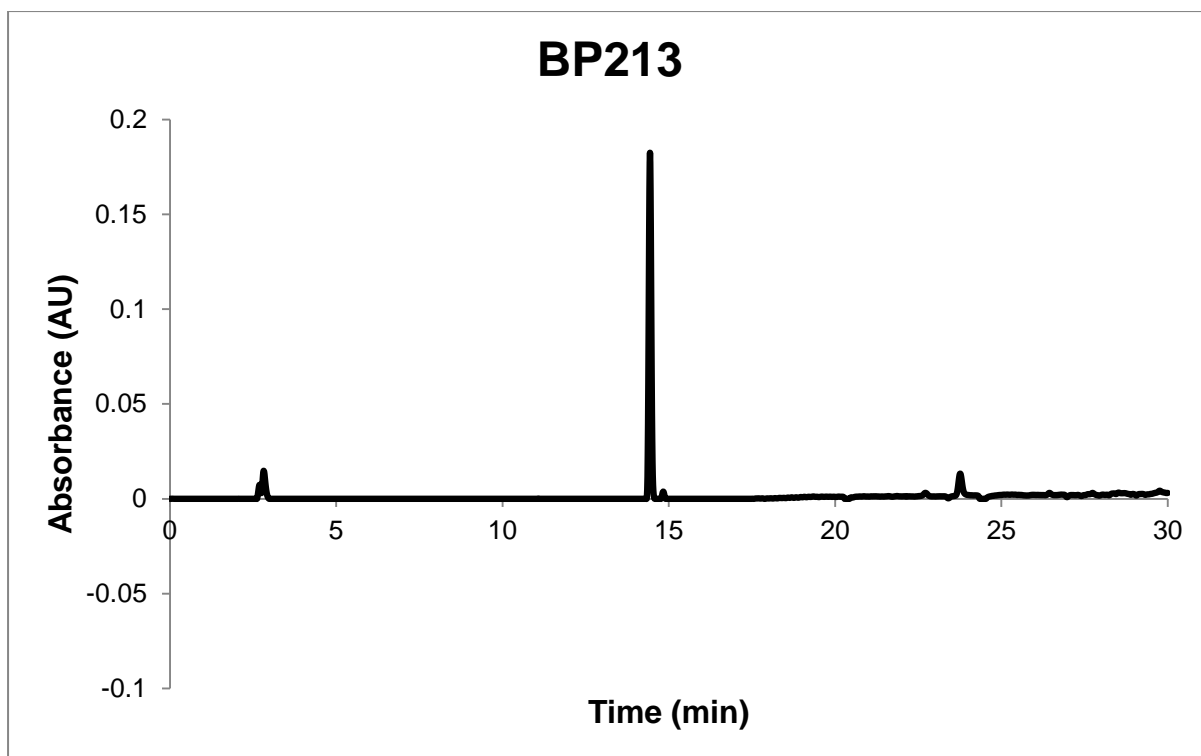












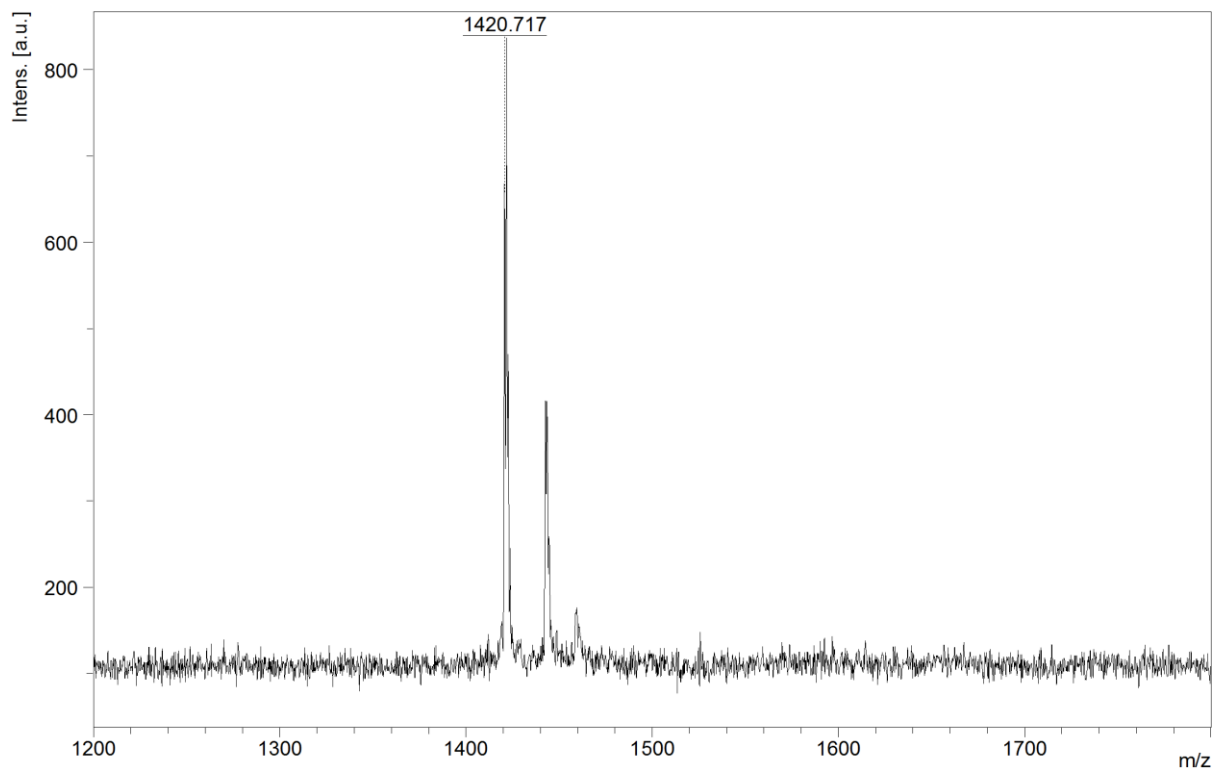
MALDI-ToF-MS Setup

Instrument: Bruker Microflex™

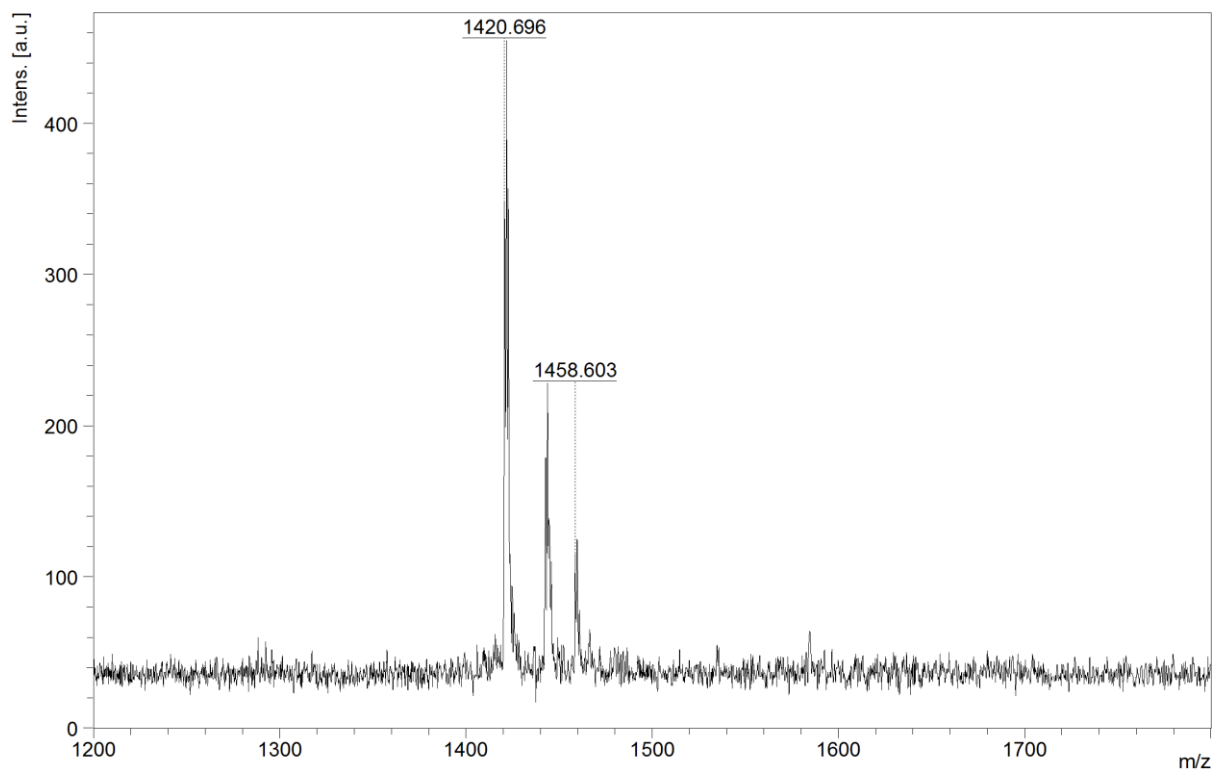
Matrix: α -cyano-4-hydroxycinnamic acid in MeCN:H₂O:TFA (50:47.5:2.5) (10 mg/ml).

MALDI Spectra

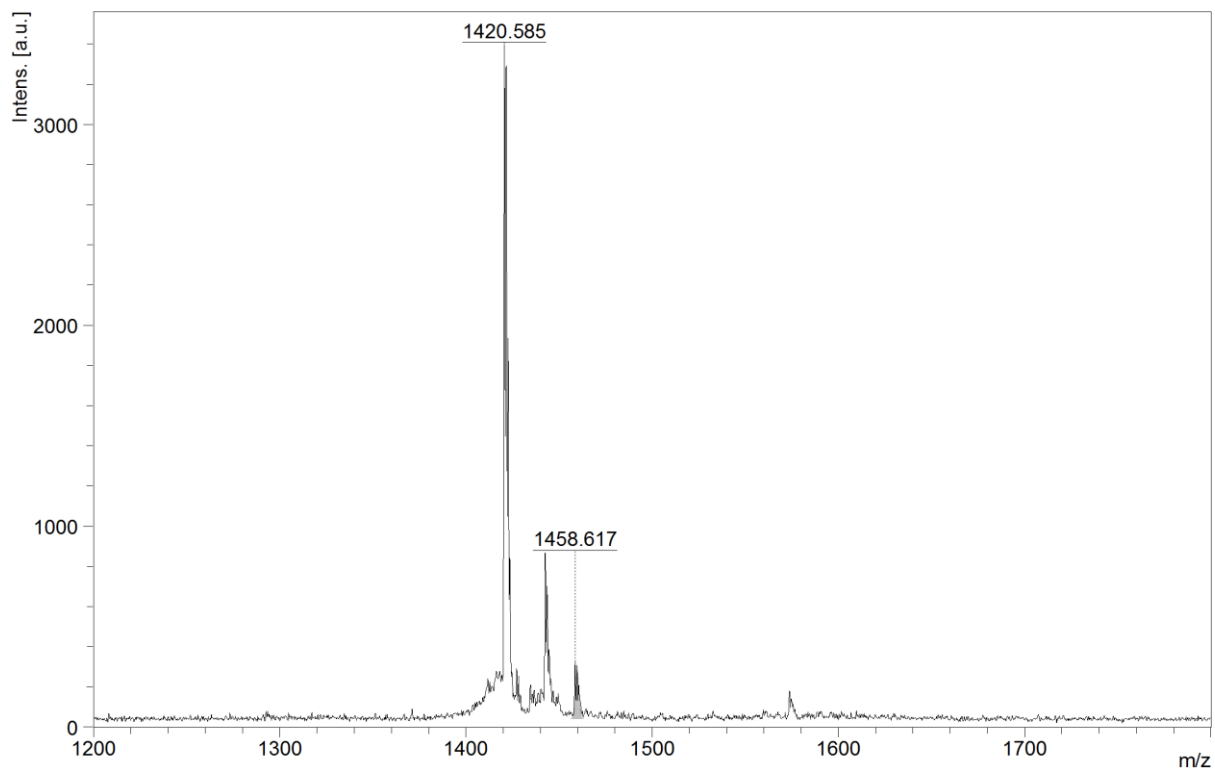
BP100



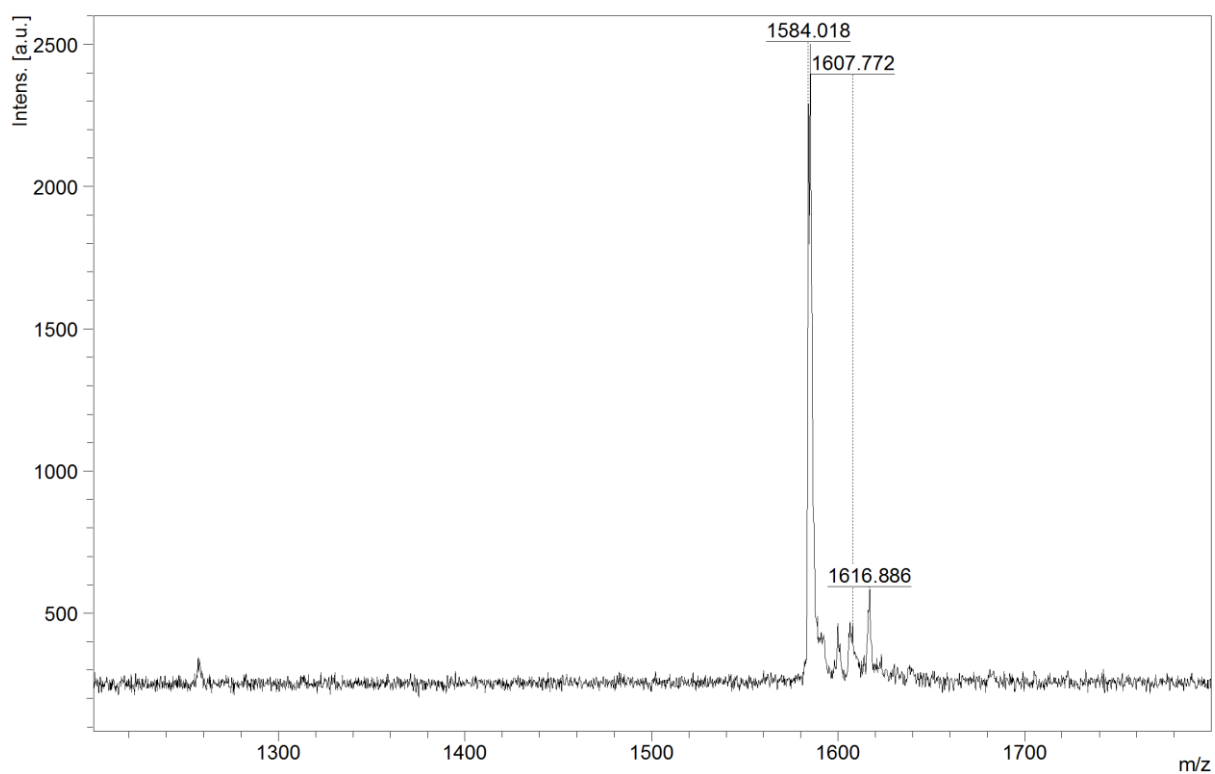
BP143



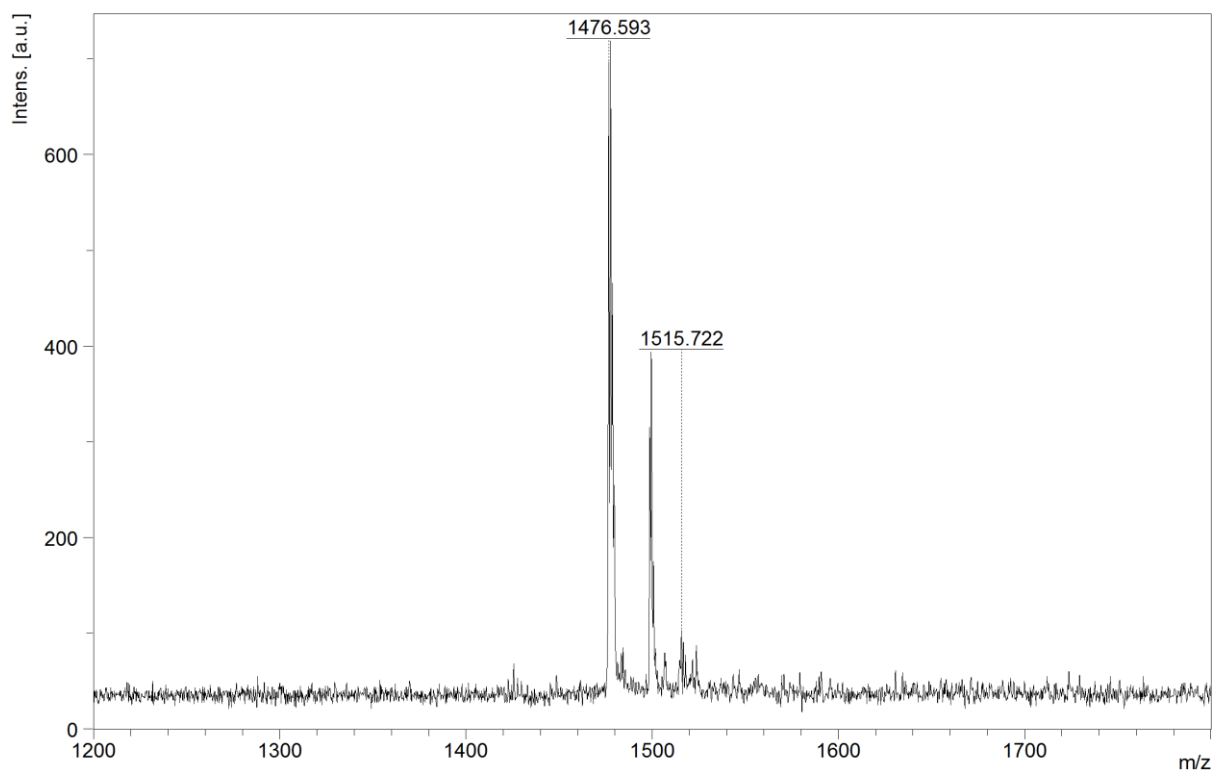
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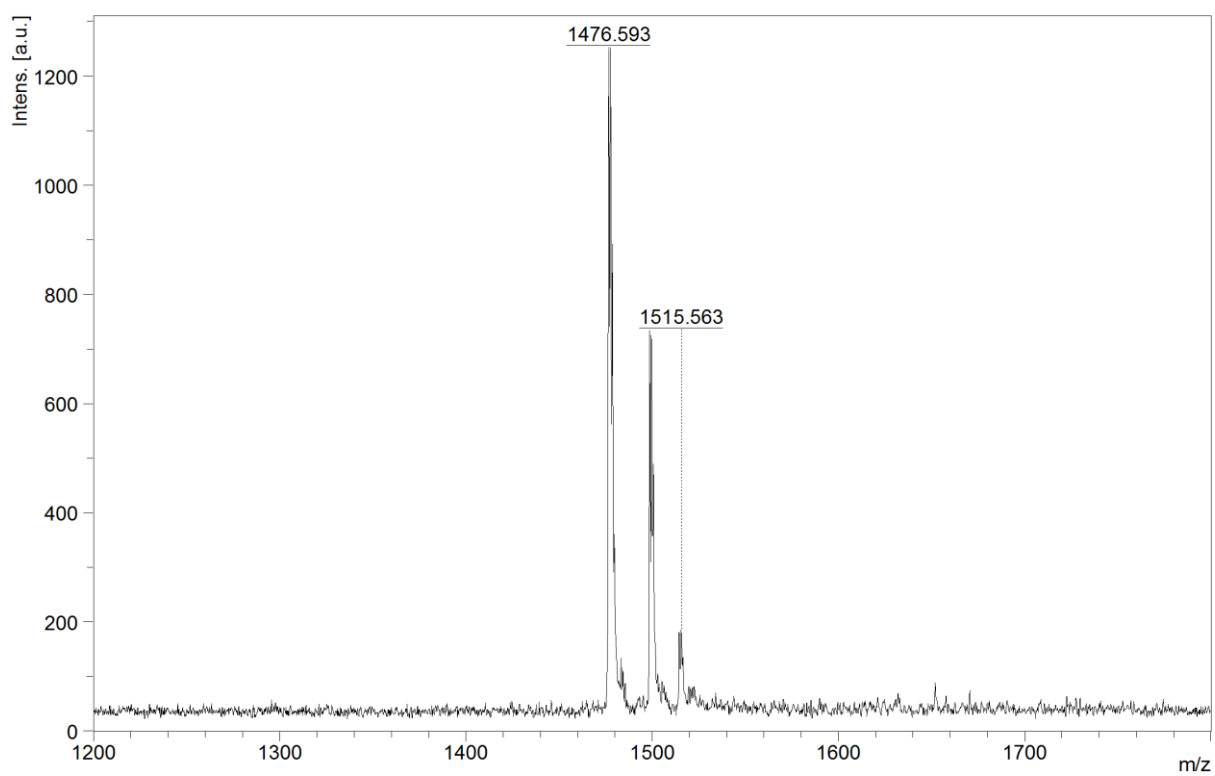
RW-BP100



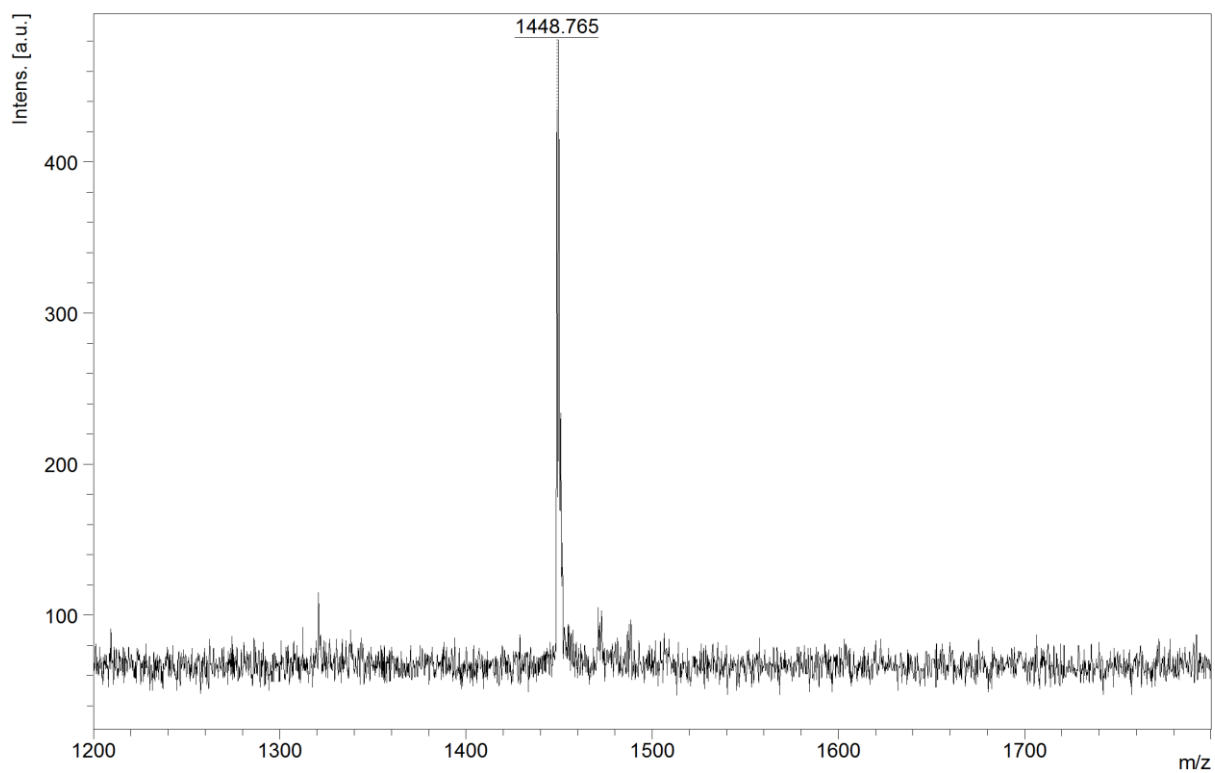
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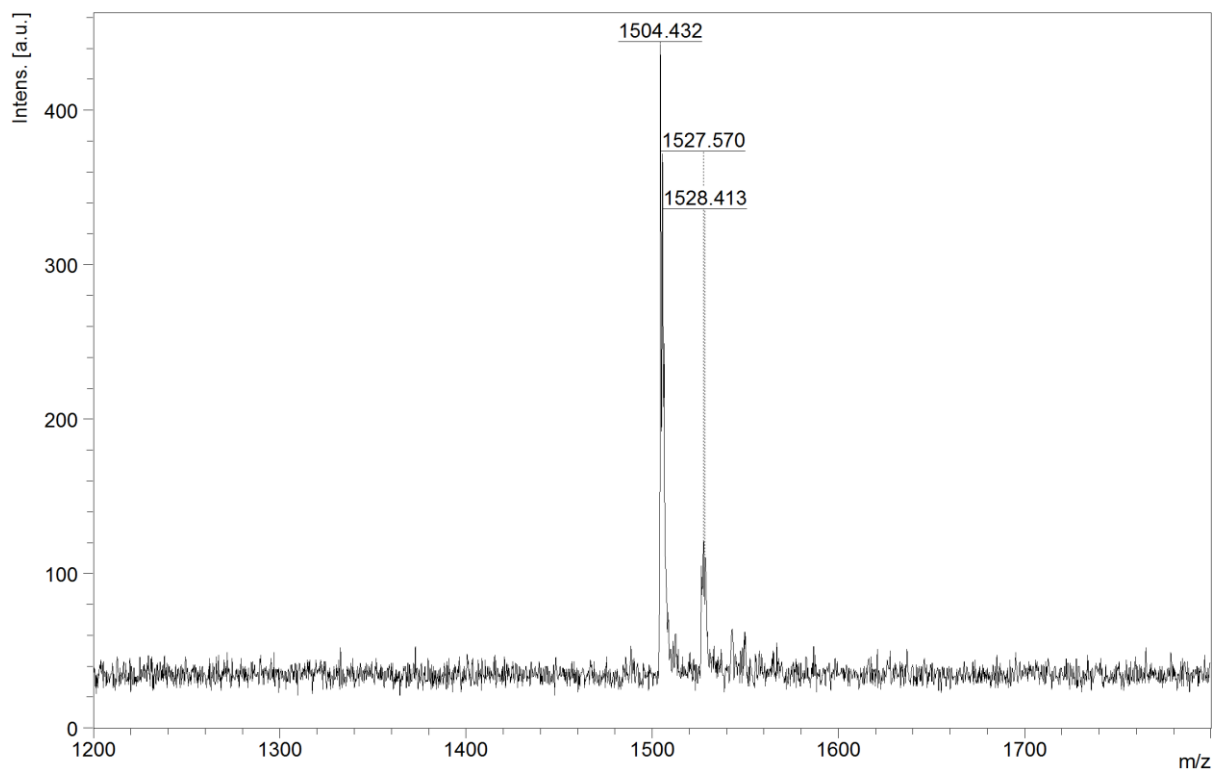
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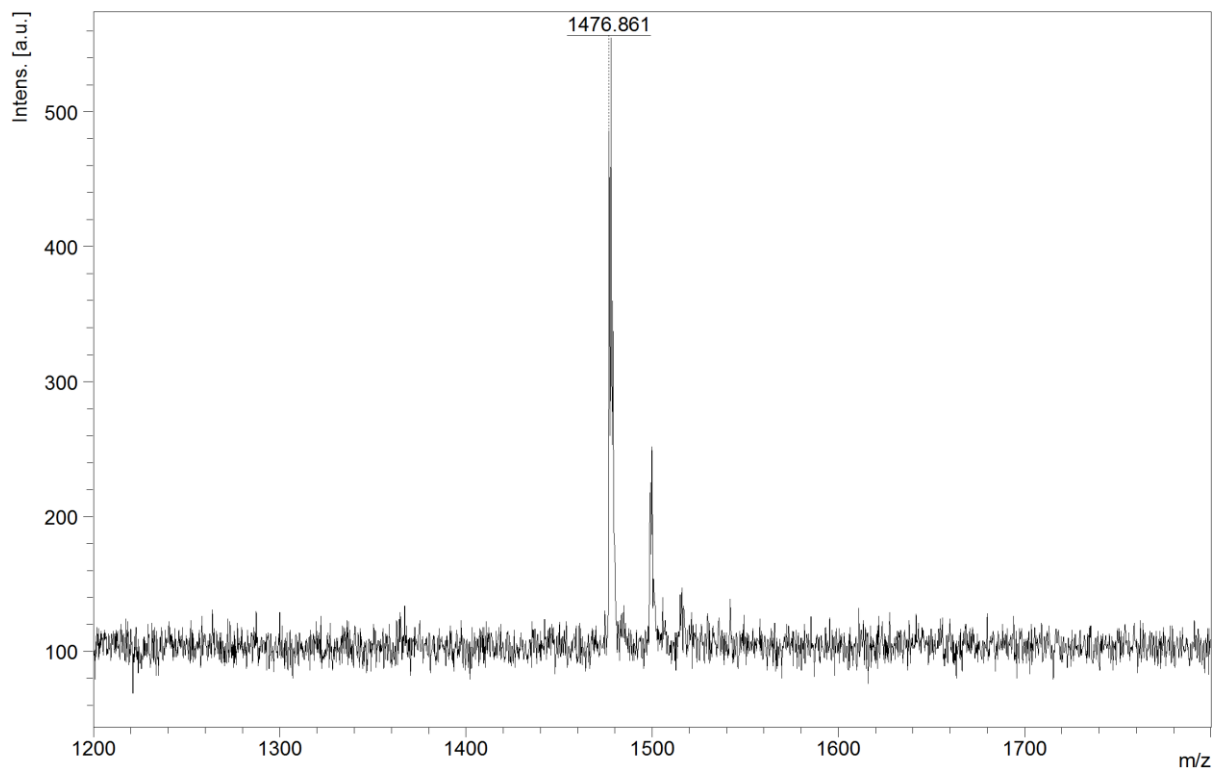
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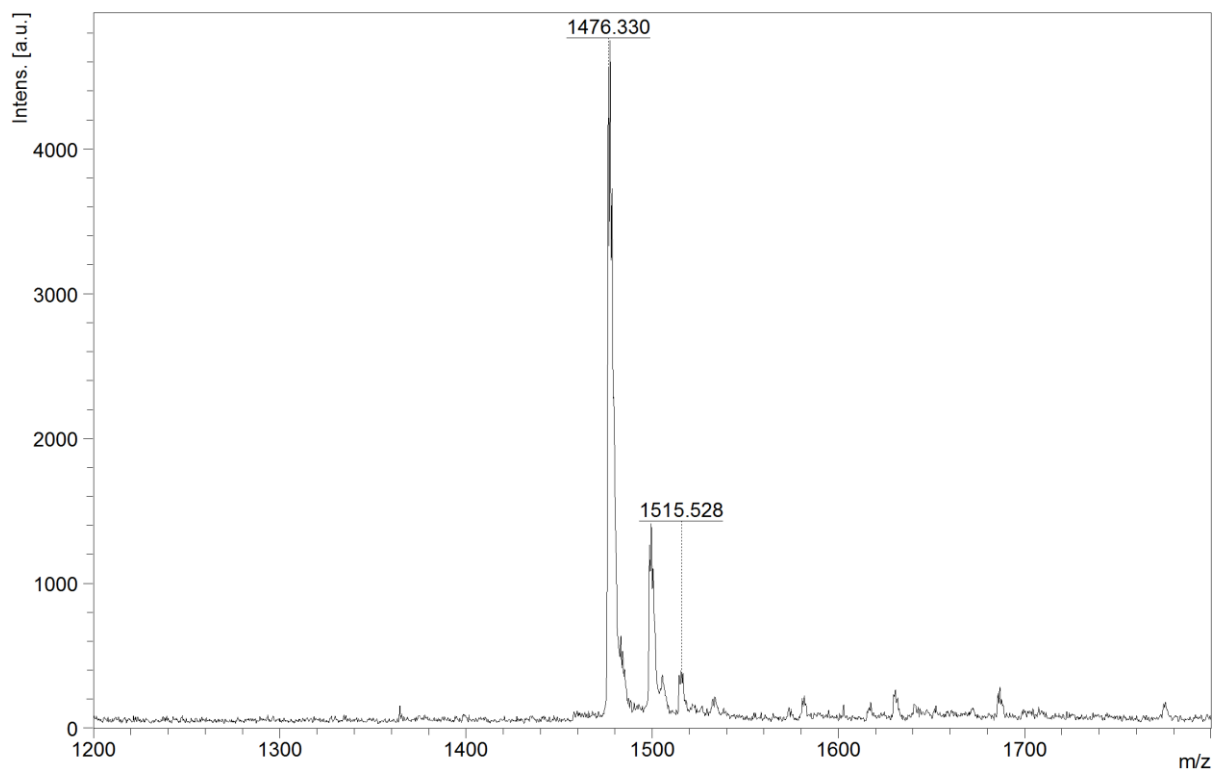
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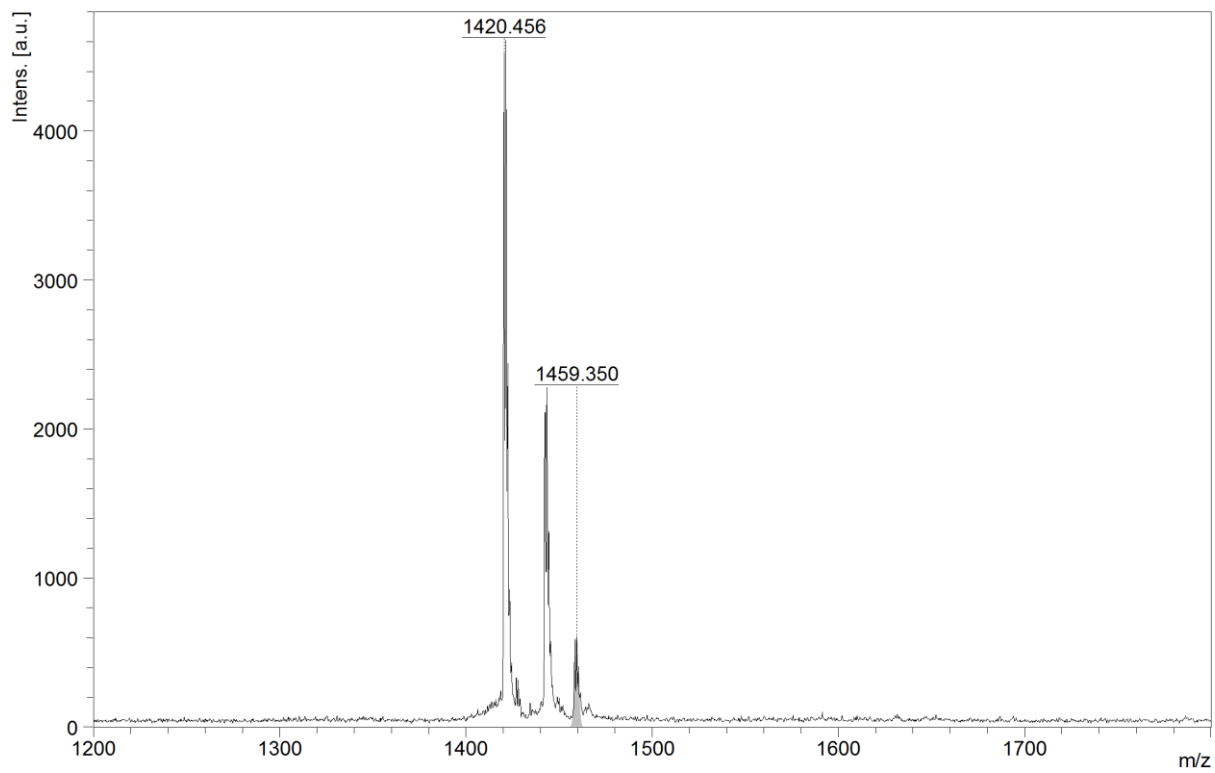
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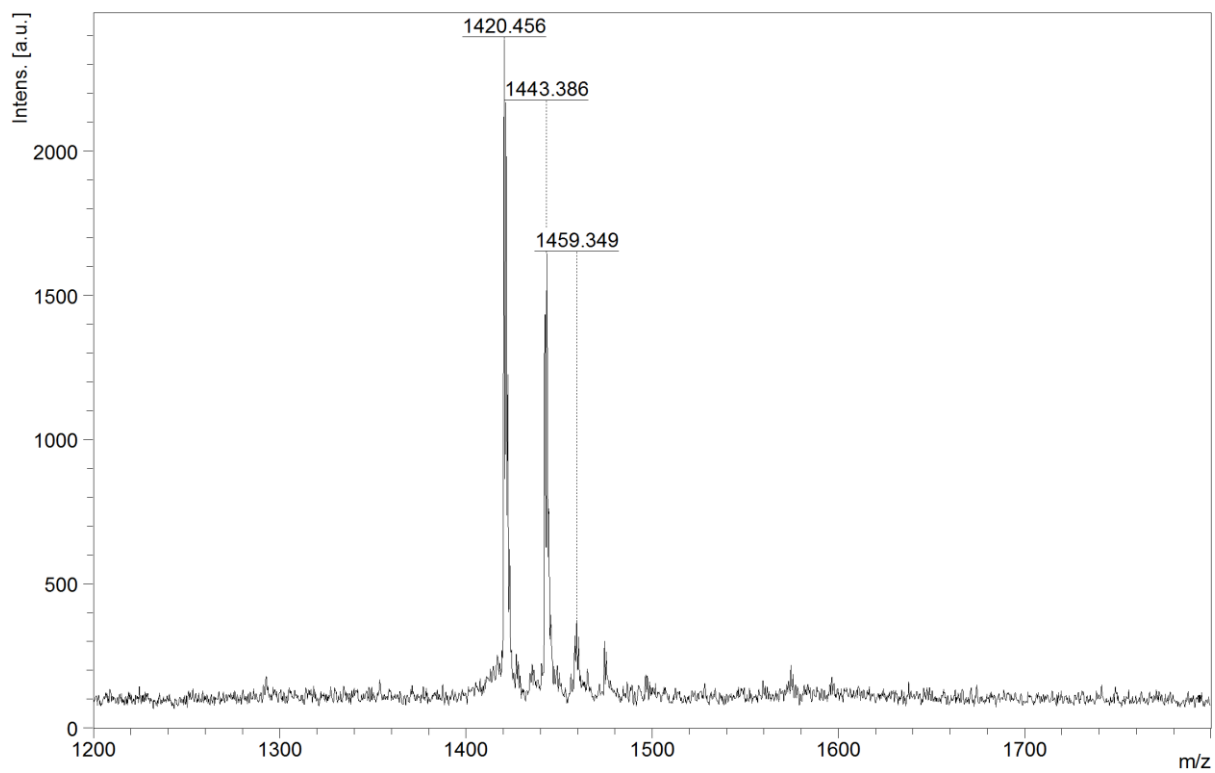
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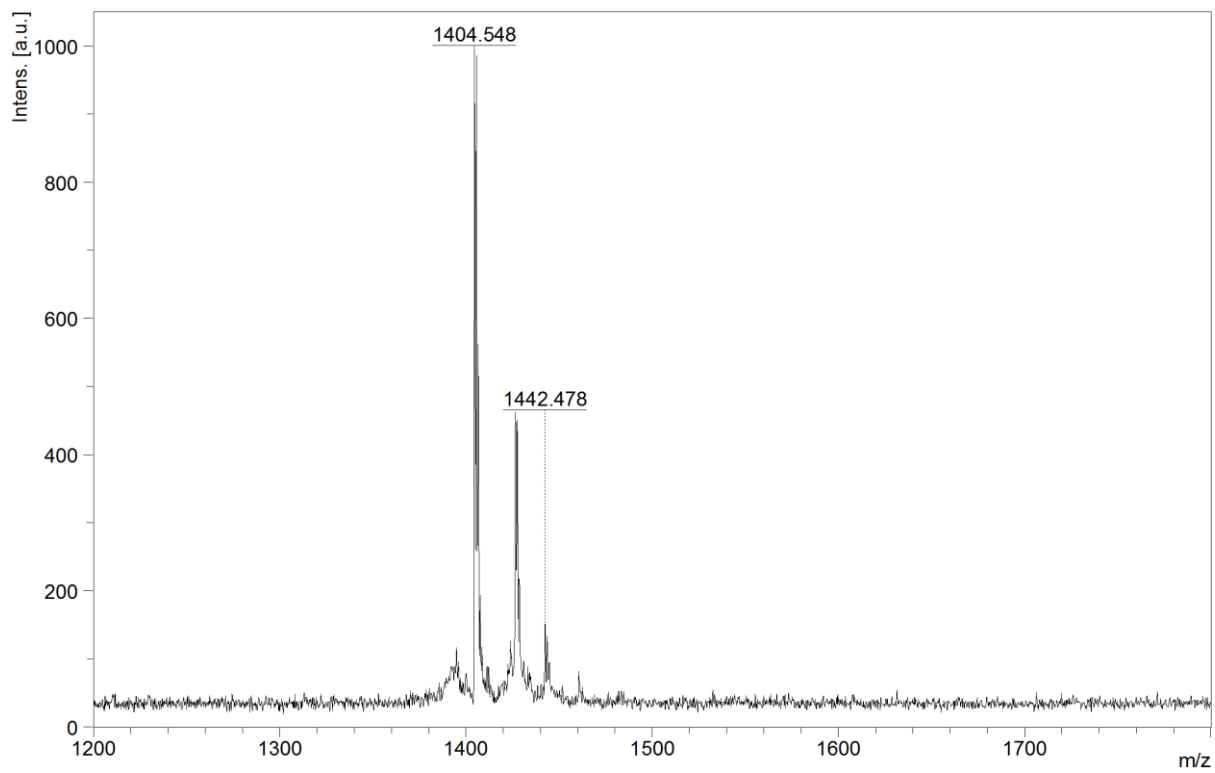
BP207



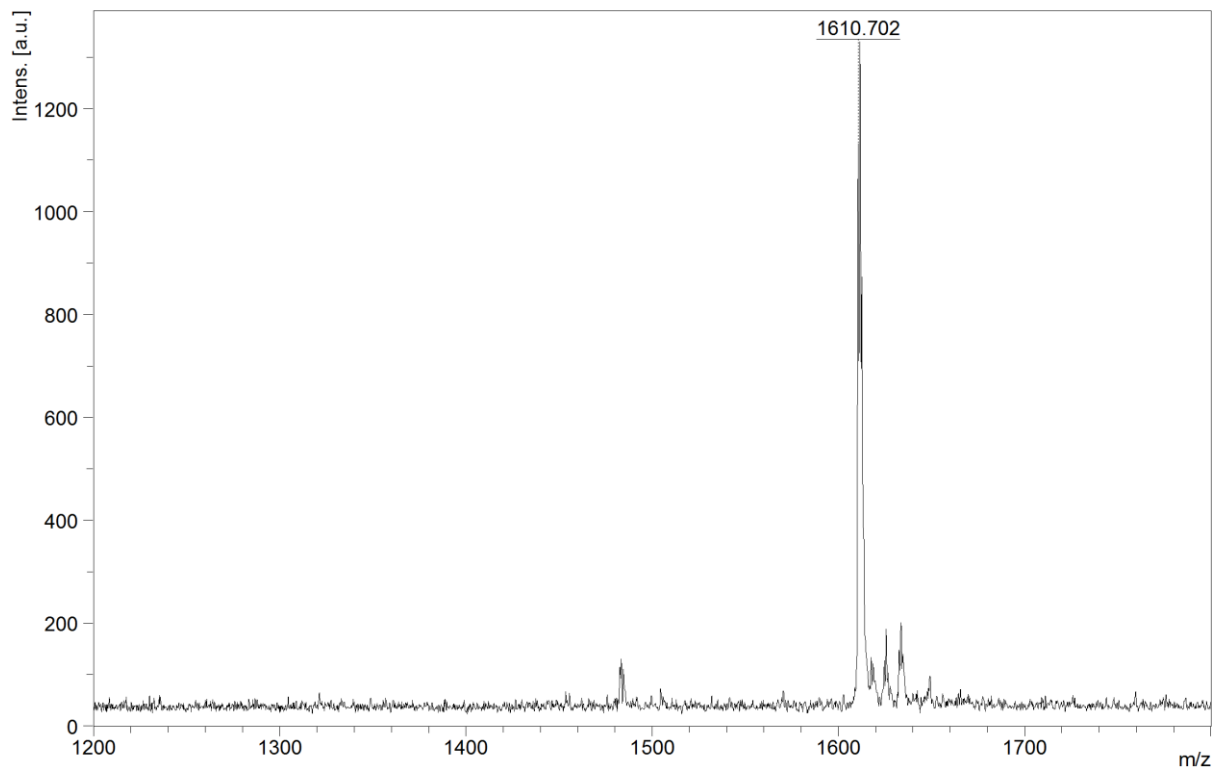
BP208



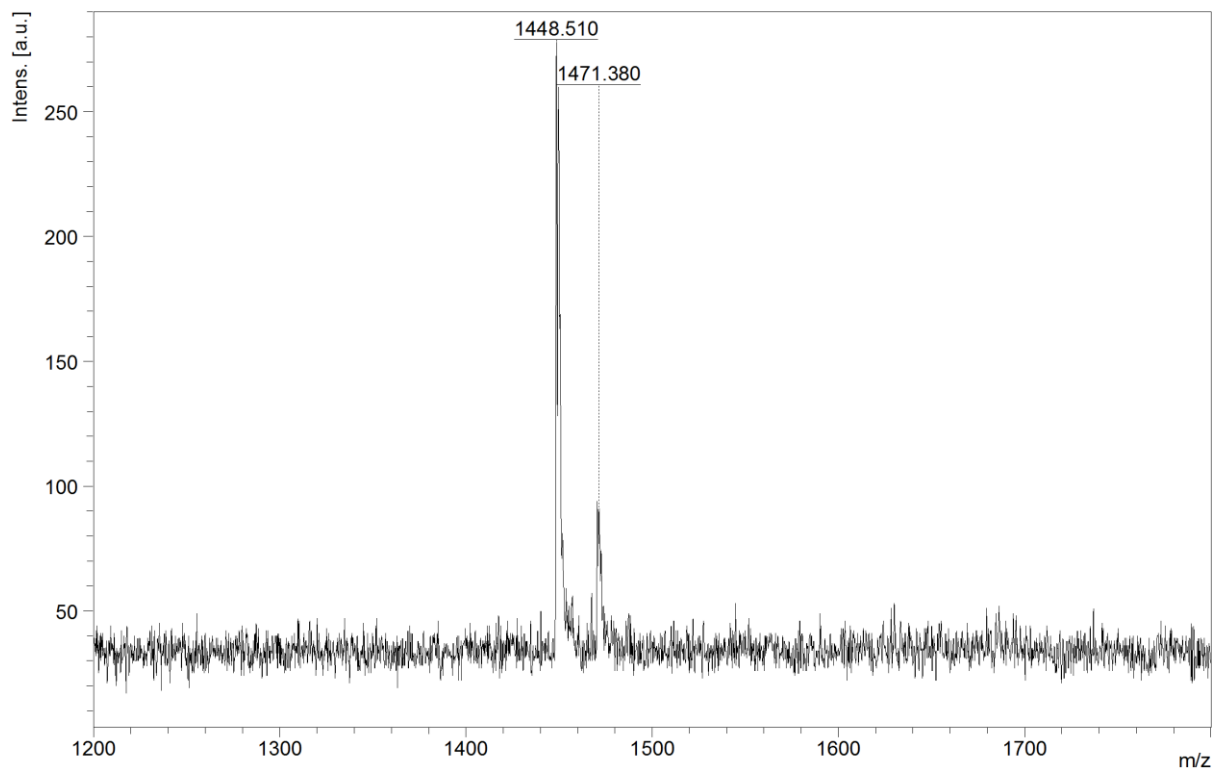
BP209



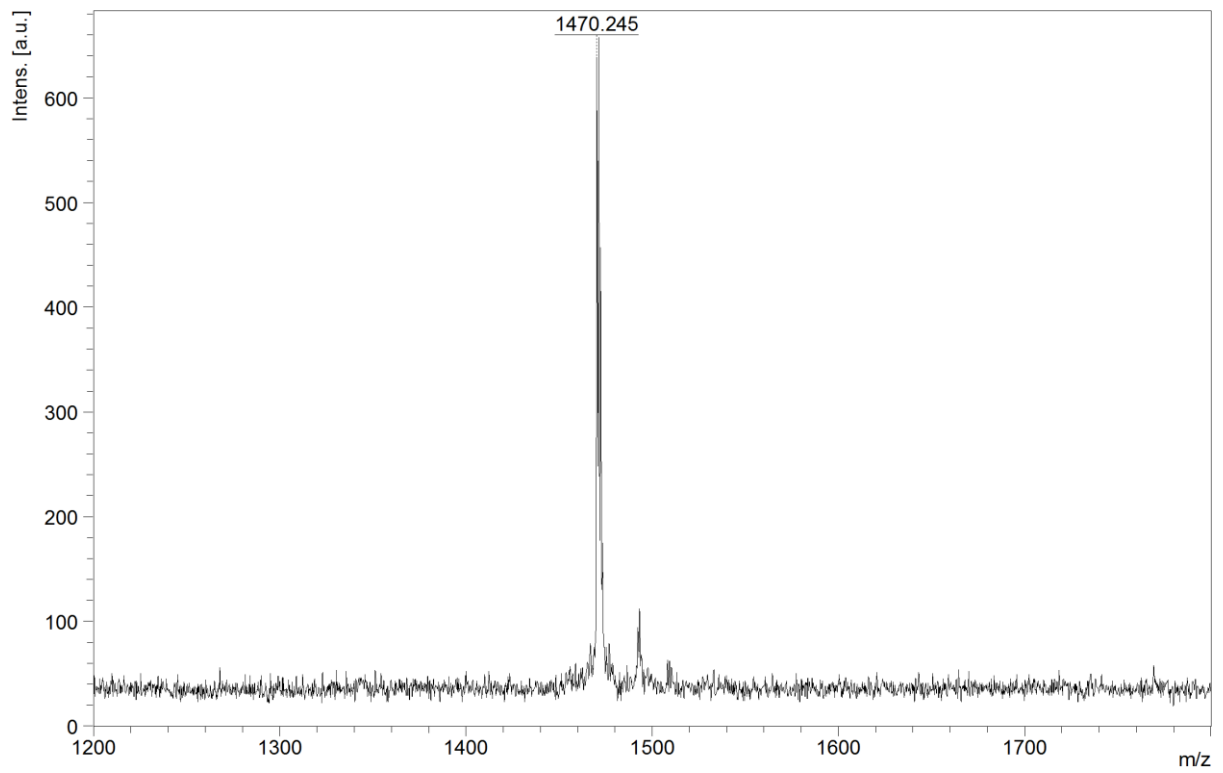
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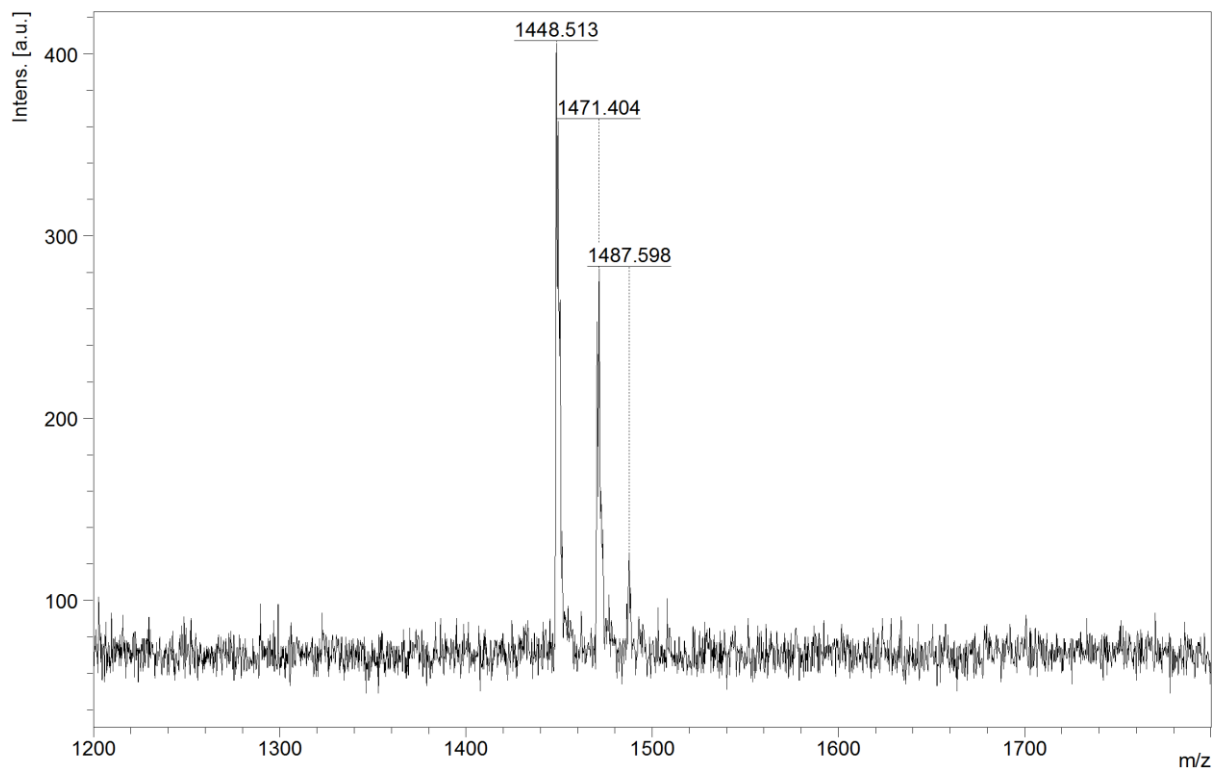
BP211



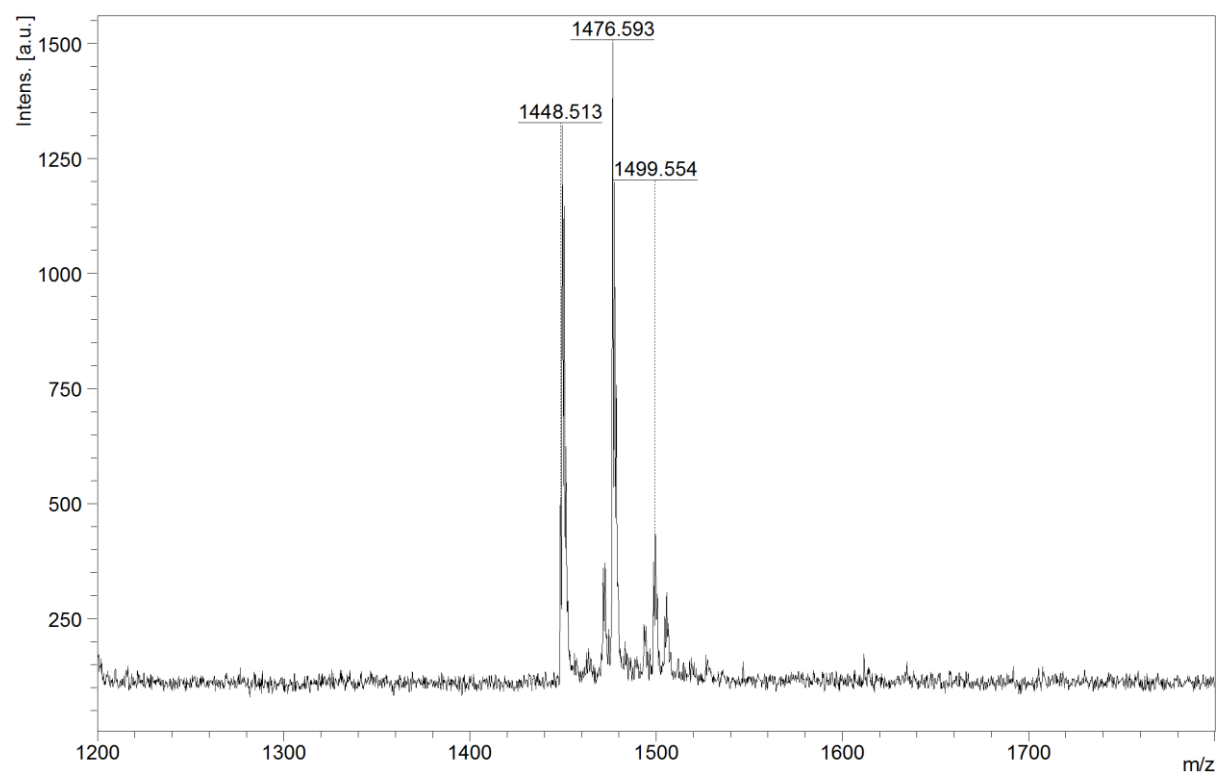
BP212



BP213



BP214



Haemolysis Assays

The hemolytic process took place in a V-shaped polypropylene 96-well plate (NUNC Cat# 249946). Each plate accommodated 4 peptides to be tested in triplicate.

Preparation

Melittin precoating. The night before the test, 150 μ l of melittin 5 μ M in water were added to the positive control wells. The day of the test, the solution was discarded and the wells were washed 3 times with the same volume of PBS. Then 75 μ l of a freshly-prepared 2.50 μ M melittin solution in PBS were transferred to the same wells.

RBC suspension. Freshly-drawn human whole blood (type O⁺, 1 ml) in EDTA was mixed gently with 3 ml of PBS and then centrifuged. The supernatant was discarded and the washing procedure was repeated twice. A 0.5 % v/v RBC suspension was prepared by mixing 40 μ l of RBC pellets with 8 ml of PBS.

Peptides: samples were dissolved in 500 μ l of PBS.

Test procedure

150 μ l of peptide solution were transferred to wells A₁₋₁₂ as follows:

- **Peptide 1:** A₁₋₃
- **Peptide 2:** A₄₋₆
- **Peptide 3:** A₇₋₉
- **Peptide 4:** A₁₀₋₁₂

75 μ l of PBS were transferred to all the wells from B₁ to G₁₂, and to H₇₋₁₂. A dilution series was obtained by transferring 75 μ l from row A to row B, mixing, then transferring 75 μ l from row B to row C, etc.; 75 μ l were discarded from row G after mixing.

75 μ l of RBC suspension were added to each well and mixed with the peptide solution. The plate was covered with a Biorad Microseal film (Cat# MSF1001) and incubated at 37 °C for 1h. After such time the plate was centrifuged in order to precipitate the RBC, then 60 μ l of supernatant from each well were transferred into a clear polystyrene flat-bottomed 96-well ELISA plate (Corning Costar Cat# 3370).

Absorbance at $\lambda = 414$ nm was determined with a Molecular Devices VersaMax spectrophotometer.

Interpretation

Results were normalized with respect of the averaged positive (100%) and negative (0%) controls. The formula applied is:

$$\%Hemolysis = \frac{Abs(sample) - Abs(NegAvg)}{Abs(PosAvg) - Abs(sample)} * 100$$

Abs(sample) = absorbance of the sample;

Abs(NegAvg) = averaged absorbance of the negative controls;

Abs(PosAvg) = averaged absorbance of the positive controls.

Finally, the three results for each peptide concentration were averaged. The EC₅₀ was determined by plotting peptide concentration against hemolysis percentage and then reading the interception of the curve with the y-axis value for hemolysis = 50%. A noise level of ~4% was observed; for such reason hemolysis values inferior to twice the noise level are reported as "<8%".