**Table S1**. Prediction of amyloidogenic regions of the synthetized peptides.

| № | Peptide | Sequence | Algorithm and program for predicting amyloidogenic regions | | | |
|---|---|---|---|---|---|---|
| | | | **AGGRESCAN** [1] | **FoldAmyloid** [2] | **Waltz** [3] | **MetAmyl** [4] |
| 1 | G10G | GVVVRLANFG | 1-8 a.a. GVVVRLAN | 1-8 a.a. GVVVRLAN | 5-10 a.a. RLANFG | 1-7 a.a. GVVVRLA |
| 2 | Q10I | QQVNVKILGI | 5-10 a.a. VKILGI | 5-10 a.a. VKILGI | 3-10 a.a. VNVKILGI | 2-9 a.a. QVNVKILG |
| 3 | V10F | VVVHINGGKF | 1-5 a.a. VVVHI | Not found | 1-10 a.a. VVVHINGGKF | 1-8 a.a. VVVHINGG |
| 4 | V10I | VQGLVHISEI | 3-10 a.a. GLVHISEI | 2-9 a.a. QGLVHISE | 3-10 a.a. GLVHISEI | 1-10 a.a. VQGLVHISEI |
| 5 | R23F | RKKRRQRRRGG-Sar*(A)-GVVVHI-Asi**(D)GGKF | 12-18 a.a AGVVVHI | Not found | 18-23 a.a IDGGKF | 10-20 a.a. GGAGVVVHIDG |
| 6 | R23F | RKKRRQRRRGG-Sar(P)-GVVVHI-Asi(N)GGKF | 13-18 a.a. GVVVHI | Not found | 18-23 a.a IDGGKF | 11-20 a.a. GPGVVVHIDG |
| 7 | R23DI | RKKRRQRRRGG-Sar(A)-GLTQFGAFIDI | 18-23 a.a. GAFIDI | 18-23 a.a. GAFIDI | 11-23 a.a GAGLTQFGAFIDI | Not found |
| 8 | R23DI | RKKRRQRRRGG-Sar(P)-GLTQFGAFIDI | 18-23 a.a. GAFIDI | 18-23 a.a. GAFIDI | 16-23 a.a QFGAFIDI | Not found |
| 9 | R23EI | RKKRRQRRRGG-Sar(A)-GVQGLVHISEI | 15-23 a.a. QGLVHISEI | 16-20 a.a. GLVHI | 16-23 a.a GLVHISEI | 10-23 a.a. GGAGVQGLVHISEI |
| 10 | R23EI | RKKRRQRRRGG-Sar(P)-GVQGLVHISEI | 15-23 a.a. QGLVHISEI | 16-22 a.a. GLVHISE | 16-23 a.a GLVHISEI | 10-23 a.a. GGPGVQGLVHISEI |

* For calculations, sarcosine (Sar) was replaced by analogs similar in properties and structure: alanine (A) and proline (P).
** For calculations, aminosuccinimide (Asi) was replaced by analogs of similar properties and structure: asparagine (N).

**Table S2.** Prediction of the physicochemical properties of the peptides.

| № | Peptide | Sequence | Lenght | **ProtParam** [5] **(ExPASy Server)** | | | | | **DBAASP v3.0** [6] **(MF Scale)** | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | **Z** | **Theoretical pI** | **GRAVY** | **The instability index (II)** | **Aliphatic index (AI)** | **μHn** | **Hn** |
| 1 | G10G | GVVVRLANFG | 10 | +1.0 | 10.5 | 1.220 | -6.03 | 136 | 0.82 | -1.13 |
| 2 | Q10I | QQVNVKILGI | 10 | +1.0 | 9.82 | 0.640 | 20.12 | 175 | 0.56 | -0.55 |
| 3 | V10F | VVVHINGGKF | 10 | +1.0 | 10.09 | 0.850 | 41.76 | 126 | 0.29 | -0.47 |
| 4 | V10I | VQGLVHISEI | 10 | -1.0 | 5.14 | 0.980 | 91.46 | 175 | 0.83 | -0.91 |
| 5 | R23F | RKKRRQRRRGG-Sar*(A)- | 23 | +8.0 | 12.7 | -1.03 | 124.43 | 59.13 | 0.19 | 0.68 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | GVVVHI-Asi**(D)GGKF | | | | | | | | |
| 6 | R23F | RKKRRQRRRGG-Sar(P)-GVVVHI-Asi(N)GGKF | 23 | +8.0 | 12.4 | -1.417 | 129.28 | 54.78 | 0.25 | 0.61 |
| 7 | R23DI | RKKRRQRRRGG-Sar(A)-GLTQFGAFIDI | 23 | +7.0 | 12.3 | -1.110 | 94.56 | 59.57 | 0.29 | 0.23 |
| 8 | R23DI | RKKRRQRRRGG-Sar(P)-GLTQFGAFIDI | 23 | +7.0 | 12.7 | -1.260 | 98.25 | 55.22 | 0.25 | 0.16 |
| 9 | R23EI | RKKRRQRRRGG-Sar(A)-GVQGLVHISEI | 23 | +7.0 | 12.4 | -1.213 | 80.43 | 140.66 | 0.30 | 0.51 |
| 10 | R23EI | RKKRRQRRRGG-Sar(P)-GVQGLVHISEI | 23 | +7.0 | 12.4 | -1.361 | 144.35 | 76.09 | 0.25 | 0.44 |

* For calculations, sarcosine (Sar) was replaced by analogs similar in properties and structure: alanine (A) and proline (P).
** For calculations, aminosuccinimide (Asi) was replaced by analogs of similar properties and structure: asparagine (N). **Z** is the value of charge at pH 7, **pI** is the theoretical value of isoelectric point, **GRAVY** is the grand average of hydropathicity, **II** is the instability index, **AI** is the aliphatic index, **μHn** is the normalized hydrophobic moment, **Hn** is the normalized hydrophobicity [5,6].

**Table S3.** Prediction of antimicrobial properties of the peptides.

| № | Peptide | CAMP$_{R3}$ [7] | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | | SVM | | RF | | DA | | ANN |
| | | Class | AMP Probability | Class | AMP Probability | Class | AMP Probability | Class |
| 1 | G10G | NAMP§ | 0,05 | NAMP | 0,35 | NAMP | 0,40 | AMP§§ |
| 2 | Q10I | NAMP | 0,11 | NAMP | 0,44 | NAMP | 0,43 | AMP |
| 3 | V10F | NAMP | 0,4 | NAMP | 0,36 | AMP | 0,86 | AMP |
| 4 | V10I | NAMP | 0,04 | NAMP | 0,3 | NAMP | 0,09 | NAMP |
| 5 | R23F | NAMP | 0,02 | AMP | 0,5 | AMP | 0,99 | AMP |
| 6 | R23F | NAMP | 0.07 | AMP | 0.6 | AMP | 0.98 | AMP |
| 7 | R23DI | NAMP | 0.03 | AMP | 0.55 | AMP | 0.99 | AMP |
| 8 | R23DI | NAMP | 0.06 | AMP | 0.57 | AMP | 0.99 | AMP |
| 9 | R23EI | NAMP | 0.02 | AMP | 0.51 | AMP | 0.91 | AMP |
| 10 | R23EI | NAMP | 0.07 | NAMP | 0.5 | AMP | 0.87 | NAMP |

§ It is predicted as a peptide that does not exhibit antimicrobial activity. The prediction level is less than 0.5. §§ It is predicted as a peptide with antimicrobial activity. The prediction level is greater than 0.5. Antimicrobial activity was predicted using algorithms: **SVM** is a "support vector machine", **RF** is a "random forest", **DA** is a "discriminant analysis", **ANN** is an "artificial neural network" [7].

**Table S4.** Results of preliminary testing the antimicrobial properties of the VVVHINGGKF (V10F), GVVVRLANFG (G10G), VQGLVHISEI (V10I), QQVNVKILGI (Q10I) peptides against *S. aureus,* MRSA, *B. cereus,* and *E. coli* bacteria cells on agar.

| | **1 μM** | **10 μM** | **100 μM** | **1000 μM** | **10000 μM** |
|---|---|---|---|---|---|
| **VVVHINGGKF (V10F)** | | | | | |
| *S. aureus* (209P strain) | Non-AMP | Non-AMP | Non-AMP | Non-AMP | Non-AMP |
| MRSA (ATCC 43300 strain) | Non-AMP | Non-AMP | Non-AMP | Non-AMP | Non-AMP |

| | | | | | |
|---|---|---|---|---|---|
| MRSA (SA 180-F strain) | Non-AMP | Non-AMP | Non-AMP | Non-AMP | **AMP** |
| *E. coli* (K12 strain) | Non-AMP | Non-AMP | Non-AMP | Non-AMP | Non-AMP |
| *B. cereus* (IP-5812 strain) | Non-AMP | Non-AMP | Non-AMP | Non-AMP | Non-AMP |
| **GVVVRLANFG (G10G)** | | | | | |
| *S. aureus* (209P strain) | Non-AMP | Non-AMP | Non-AMP | Non-AMP | **AMP** |
| MRSA (ATCC 43300 strain) | Non-AMP | Non-AMP | Non-AMP | Non-AMP | Non-AMP |
| MRSA (SA 180-F strain) | Non-AMP | Non-AMP | Non-AMP | Non-AMP | Non-AMP |
| *E. coli* (K12 strain) | Non-AMP | Non-AMP | Non-AMP | Non-AMP | Non-AMP |
| *B. cereus* (IP-5812 strain) | Non-AMP | Non-AMP | Non-AMP | Non-AMP | Non-AMP |
| **VQGLVHISEI (V10I)** | | | | | |
| *S. aureus* (209P strain) | Non-AMP | Non-AMP | Non-AMP | Non-AMP | Non-AMP |
| MRSA (ATCC 43300 strain) | Non-AMP | Non-AMP | Non-AMP | Non-AMP | Non-AMP |
| MRSA (SA 180-F strain) | Non-AMP | Non-AMP | Non-AMP | Non-AMP | **AMP** |
| *E. coli* (K12 strain) | Non-AMP | Non-AMP | Non-AMP | Non-AMP | Non-AMP |
| *B. cereus* (IP-5812 strain) | Non-AMP | Non-AMP | Non-AMP | Non-AMP | Non-AMP |
| **QQVNVKILGI (Q10I)** | | | | | |
| *S. aureus* (209P strain) | Non-AMP | Non-AMP | Non-AMP | Non-AMP | Non-AMP |
| MRSA (ATCC 43300 strain) | Non-AMP | Non-AMP | Non-AMP | Non-AMP | Non-AMP |
| MRSA (SA 180-F strain) | Non-AMP | Non-AMP | Non-AMP | Non-AMP | Non-AMP |
| *E. coli* (K12 strain) | Non-AMP | Non-AMP | Non-AMP | Non-AMP | Non-AMP |
| *B. cereus* (IP-5812 strain) | Non-AMP | Non-AMP | Non-AMP | Non-AMP | Non-AMP |

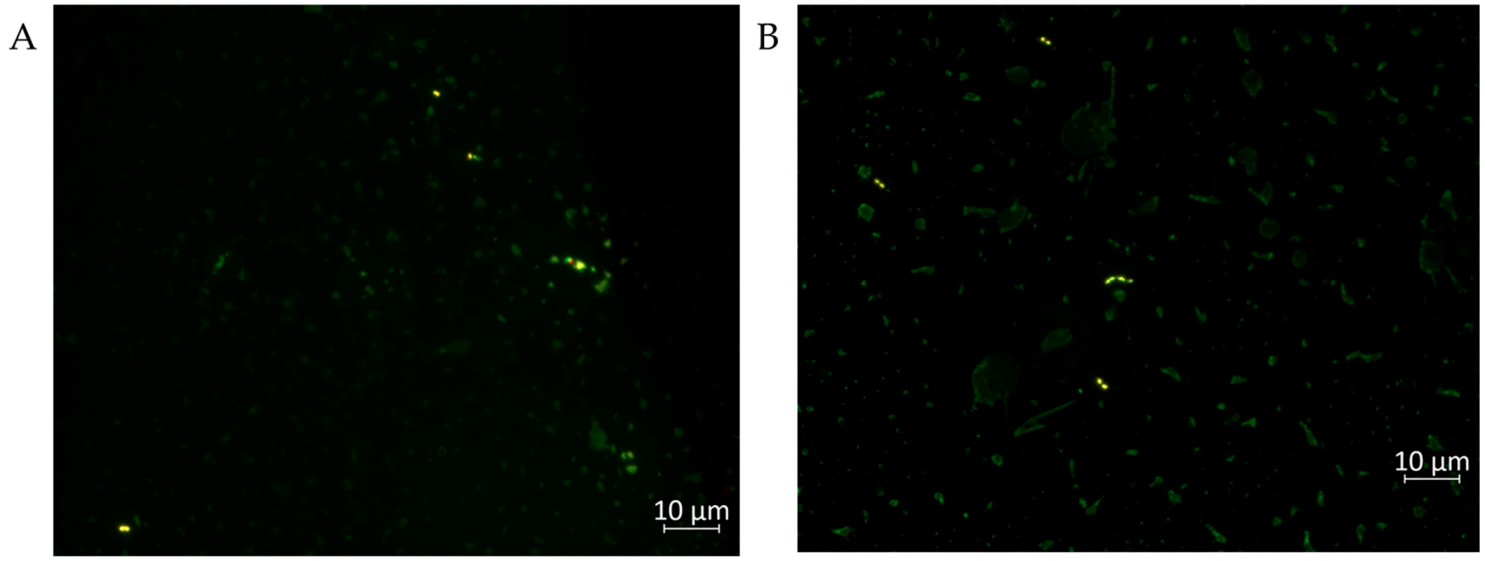



**Figure S1.** Fluorescence microscopic images of (**A**) MRSA cells (ATCC 43300 strain) and (**B**) *S. aureus* cells (209P strain) after one day of co-incubation with gentamicin sulfate concentration of 1700 μM. Bacterial cells stained with SYTO 9 (green) and propidium iodide (red). Green color indicates the living cells, yellow color, turning into red, indicates a violation of the vital functions of cells.

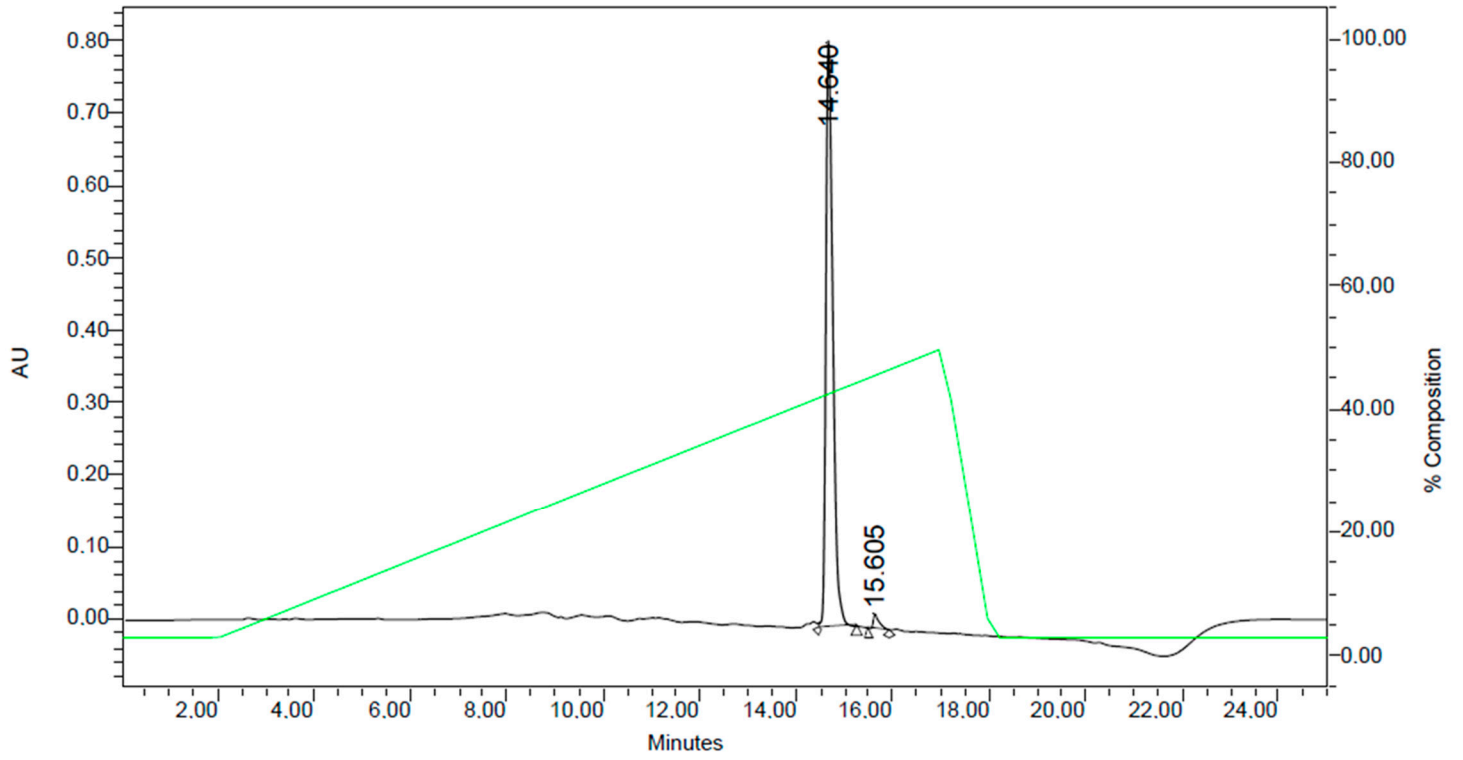



**Figure S2.** The chromatogram of sample R23F peptide (run time for peak of R23F was 14.640 min).

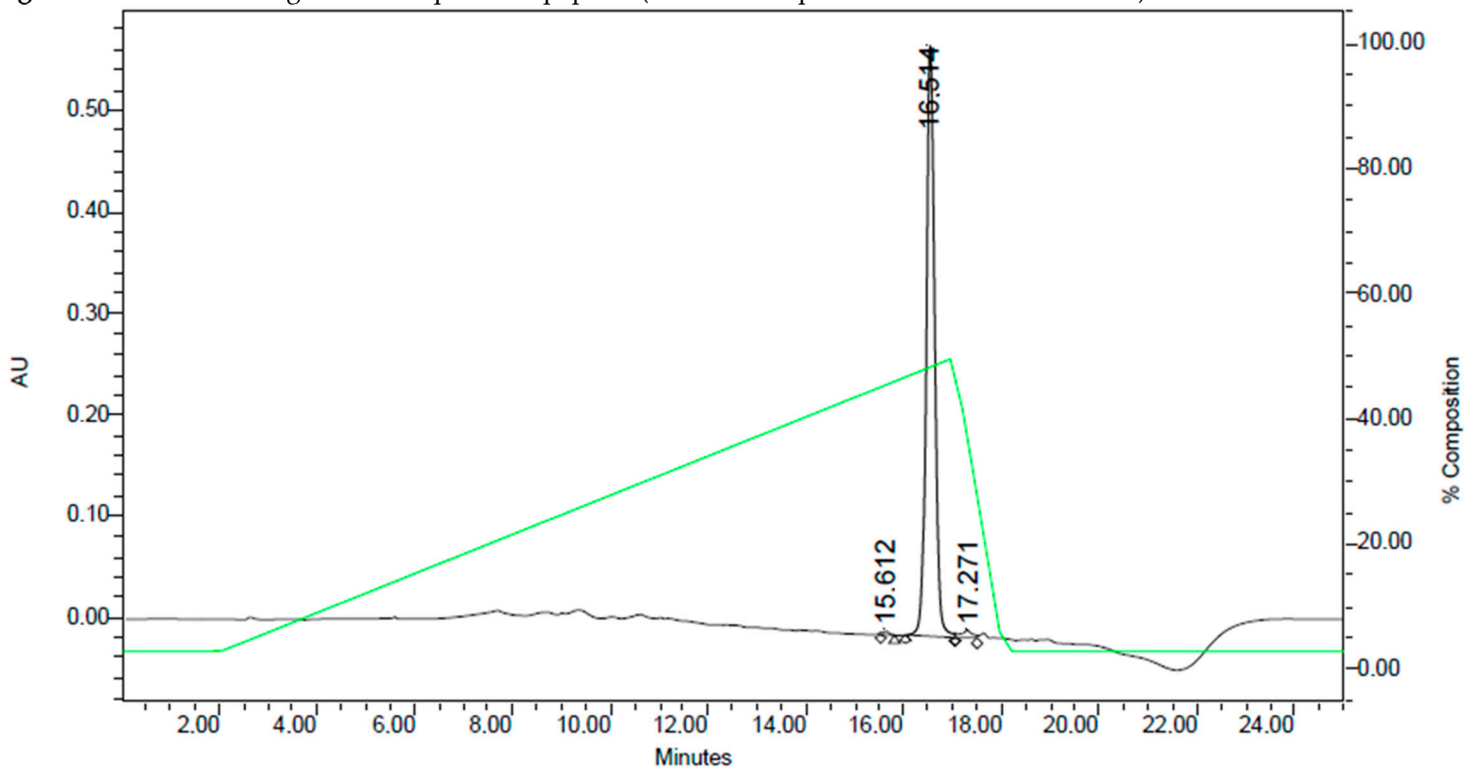



**Figure S3.** The chromatogram of sample R23DI peptide (run time for peak of R23DI was 16.514 min).

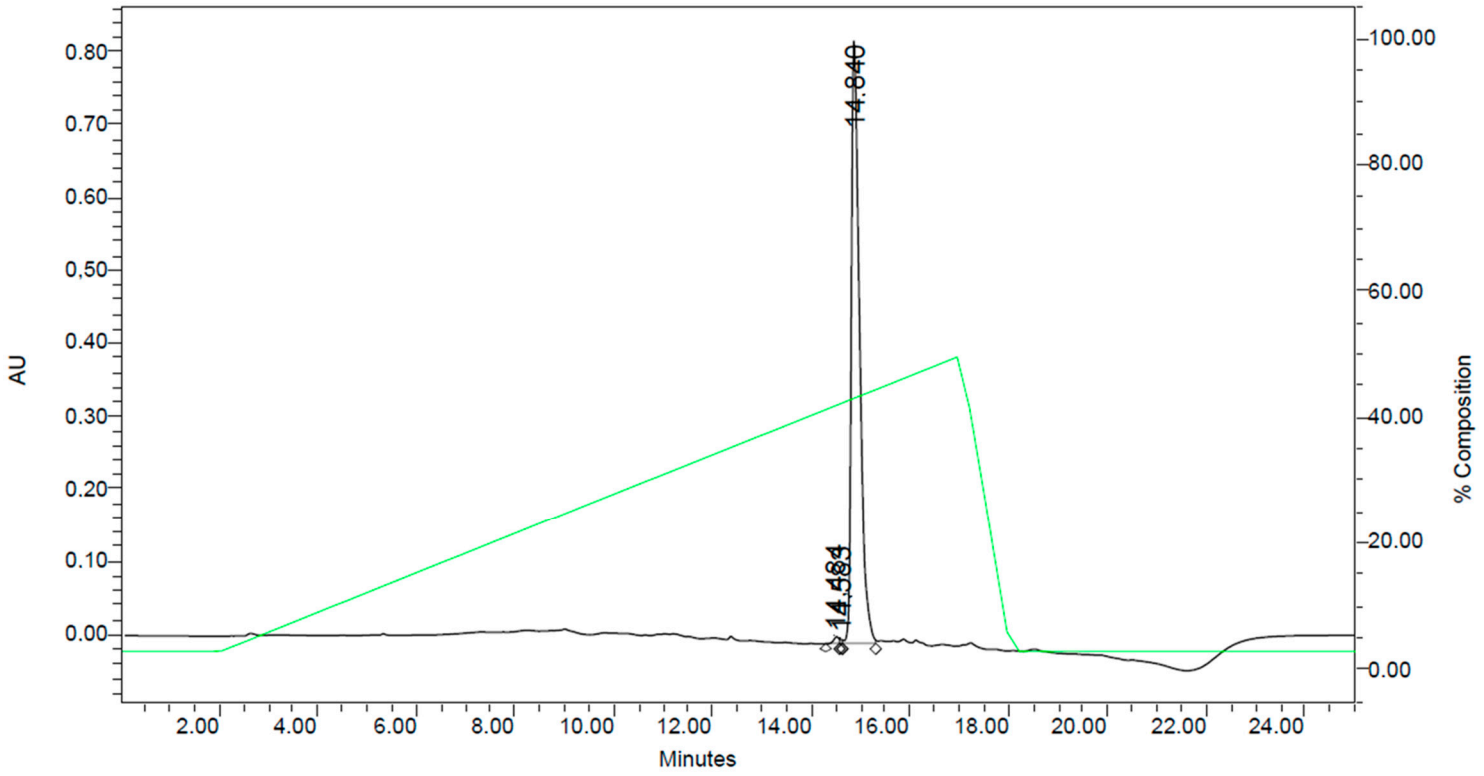



**Figure S4.** The chromatogram of sample R23EI peptide (run time for peak of R23DI was 14.840 min).

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