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Abstract

Fast detection of bacteria in samples presumed to be un-contaminated, such as blood, is of great importance. Indeed, rapid diagnosis allows the set-up of appropriate antibiotic treatment. Besides clinical issues, there are many other domains, such as food processing or drug manufacturing, where the strict absence of any bacteria has to be assessed. Because the bacterial load found in most contaminated samples is often below the limit of detection for currently validated assays, a preliminary enrichment step is required to allow bacterial multiplication before proceeding to the analysis step, whatever it might be – cultural, immunological or molecular methods. In this study, we describe the use of a biosensor for single-step bacteria detection. The whole analysis is performed in less than 20 hours, during the growth phase of the micro-organisms, using an array of antimicrobial peptides (AMPs) coupled with a surface plasmon resonance imager (SPRI). A wide range of bacterial strains are assayed, showing differentiated affinity patterns with the immobilized peptides, which are confirmed by multivariate analysis. This work establishes the evidence that antimicrobial peptides, mostly used so far in the antibiotic drug industry, are suited for the wide-spectrum detection of unknown bacteria in samples, even at very low initial loads. Moreover, the small set of AMPs that were assayed provided a specific affinity profile for each pathogen, as confirmed by multivariate analyses. Furthermore, this work opens up the possibility of applying this method in more complex and relevant samples such as foodstuff, urine or blood.

Keywords

Antimicrobial Peptides; Bacteria Detection; Pathogens; Surface Plasmon Resonance imaging

Introduction

The presence of bacteria in a normally sterile environment is a huge issue for human health, since it can cause severe infections. Whether they originate in foodstuffs or bodily fluids such as blood or urine, the rapid and sensitive detection of pathogenic microorganisms is thus of great importance. Although fast diagnosis is vital during an infection, the early detection of pathogens is made difficult because of their low concentrations. For this reason, all samples drawn from patients are first diluted and cultured in a liquid medium to increase the bacterial concentration, before proceeding to the analysis of the enriched samples. So far, culture-based techniques have remained the gold standard in the process of diagnosing bacterial infections, though several alternative methods have emerged in recent decades to devise faster and more sensitive ways to achieve bacterial detection [1]. Assays based on DNA amplification have paved their way to a large use in clinics [2]. In spite of their faster response, these assays are still time-consuming, quite expensive, and require a high level of skills. Moreover, such methods may give false-positive results due to the presence of residual DNA, released from killed pathogenic bacteria in some samples, for instance after antibiotic treatment. Mass spectrometry has also become widely used for the precise identification of strains [3]. However, it requires isolated colonies of the pathogen to be grown on a solid medium and thus can only be performed several days after enrichment of the sample. Owing to these considerations, new technologies enabling faster diagnostics are still emerging, promising simple and low-cost on-field implementation [4,5]. Amongst other alternatives under research, biosensors able to detect whole viable cells directly from a suspect sample are very promising. Nevertheless, each of these exciting alternatives still require a preliminary enrichment step to increase the initial bacterial concentration above their limit of detection (10^3 to 10^6 CFU.ml^{-1}, depending on the method). Surprisingly, only a few approaches couple the enrichment step with the detection step. From this perspective, surface plasmon resonance imaging (SPRI) is a promising method. Indeed, this technique is based on the optical detection of interactions at the surface of a metallic layer, thus enabling the monitoring of molecular interactions without labels. Although SPRI-based molecular detections are less sensitive than ELISA for biomolecular interaction studies, SPRI has been used in versatile applications from molecular studies to whole cell or living bacteria detection, taking advantage of its real-time and label-free multiplexing abilities [6,7]. This optical method has already proven its ability to successfully detect and identify pathogens starting from food matrices or blood spiked with low bacterial concentrations (few CFU.ml^{-1}), using arrays of proteins and antibodies [8–11]. Such one-step approach enables sensitive detection during the enrichment phase, with a wide range of probes used in parallel that hence allow a high selectivity. However, although antibodies or other protein probes have been proven to have high efficiency as ligands (enabling strain or even serotype identification) they are known to present several difficulties such poor stability, difficulty of production, high cost, and/or burdensome handling. It is the reason why new sets of probes have been benched by researchers, the most prominent being aptamers, molecularly imprinted polymers, and peptides [12]. Aptamers and molecularly imprinted polymers usually show high specificity and reliability [13,14]. Nevertheless, to achieve wide spectrum detection, the multiplexing of large series of probing ligands remains an issue, which limits the extent of wide spectrum detection.

Antimicrobial peptides (AMPs) are a subset of peptides presenting outstanding bactericidal activity [15,16]. Their binding to bacteria mainly relies on physico-chemical interactions, due to their polycationic or amphiphilic characteristics. Hence, they can easily attach to negatively charged lipopolysaccharides (LPS) anchored in the membrane of Gram-negative bacteria *via* electrostatic interactions [17,18]. Conformational changes of their structure can also mediate the attachment to bacterial outer walls [19]. Although AMPs have so far mainly been investigated to design new drugs or antimicrobial applications [20], they are also promising ligands as potential alternatives to antibodies as large spectrum recognition elements towards bacteria [21,22]. Indeed, they have naturally evolved to interact with a wide range of pathogenic bacteria and they are not only easy to synthesize but also easier to handle than antibodies for instance, since they can resist harsh chemical conditions and air-drying for storage.

Surprisingly, the use of AMPs as recognition elements has only rarely been commented on in the literature [23–26]. Those studies relied on the specific recognition of particular groups of bacteria, for instance targeting either a bacterial genus or a Gram class. Herein, we demonstrate the use of AMPs in a multiplexed fashion, with several different peptidic probes exposed to a contaminated sample. Thanks to the development of antimicrobial peptides arrays, we expand the spectrum of detectable bacterial strains in a single one-step assay. Wide-spectrum sensing of bacterial pathogens would hence be achieved. A set of AMPs inspired by previous works on biosensors (see *Table 1*), has been produced by solid-phase synthesis and arrayed on the gold surface of SPRI prisms. Such arrays were then assayed with a series of samples spiked with pathogenic bacteria at low levels. Those strains are representative of major species encountered in both foodborne infections and bacteremia. We were thus able to assess the performance of such peptide-based sensors for wide-spectrum detection of bacteria.

Material and methods

Reagents

Phosphate Buffered Saline (PBS), Dimethyl Sulfoxide (DMSO), Bovine Serum Albumin (BSA), glycerol and Tryptic Soy Broth (TSB) culture medium were purchased from Sigma-Aldrich (Saint Quentin Fallavier, France). The solid culture medium Tryptone Soy Agar (TSA) was bought from bioMérieux (Lyon, France). Ultra-pure water (18,2 $M\Omega$ of resistivity) was obtained from an ELGA PURELAB flex dispenser (Veolia Water, France).

Peptides

Name	Sequence	Targets	Technique	Ref.
Clavanin A	VFQFLGKIIHHVGNFVHGFSHVF–spacer–C–NH_2	*E. coli*, *S. aureus* & *S. Typhimurium*	Electrochemical impedance	[27]
Magainin 1	GIGKFLHSAGKFGKAFVGEIMKS-spacer–C–NH_2	*E. coli* & *S. Typhimurium*	Fluorescence	[28]
		E. coli & *Salmonella*	Electrochemical capacitance	[24]
		E. coli	Fluorescence	[29]
		E. coli	Field-effect transistor	[30]
Pediocin Ped3	GKATTCIINNGAMA–spacer–C–NH_2	*Listeria*	Microcantilevers	[31]

		monocytogenes		
PGQ	GVLSNVIGYLKKLGTGALNAVLKQ–spacer–C–NH_2	*E. coli*	Fluorescence	[32]
Leucocin A 24	C–spacer–SVNWGEAFSAGVHRLANGGNGFW–OH	*Listeria monocytogenes* & *E. coli*	Electrochemical impedance	[25, 33]
Control peptide	C–spacer–RGEWFWGNLVVSAASFGNHNAGG–OH	Scrambled version of Leucocin A 24 (newly introduced)		

Table 1. Set of arrayed antimicrobial peptides. Sequences are listed along with the bacteria they can detect, the detection techniques that they were used in and literature references for each. Spacer is corresponding to AEEA.

All peptides were synthesized by Smart Bioscience (Saint Égrève, France) through standard Fmoc solid-phase method. A (2-(2-(amino)ethoxy)ethoxy)acetic acid (AEEA) spacer was inserted between the peptide sequence and the additional terminal cysteine. When this cysteine amino acid was added at the C-terminus, the supplier amidated this latter to achieve higher synthesis yields, otherwise the terminal amino acid was left free. The sequences of the chosen peptides are listed in *Table 1*. The certificates of analysis furnished by Smart Bioscience are given in the Electronic Supplementary Information to confirm peptide purities and molecular weights.

Bacterial strains

The *Salmonella enterica* subspecies *enterica* serovar Typhimurium (*S. Typhimirium*), CIP104474, was obtained from the Pasteur Institute (Paris, France). *Listeria monocytogenes* strain belonging to the molecular serotype IVc was acquired from the Institut Scientifique d'Hygiène et d'Analyse (ISHA, Massy, France). It had been isolated from chicken meat. The methicillin-resistant *Staphylococcus aureus* subspecies *aureus* (MRSA), ATCC43300, the *Staphylococcus epidermidis* strain, ATCC12228, and the *Escherichia coli* serovar O1:K1:H7 (isolated from urine), ATCC11775, were all purchased from the American Type Culture Collection (Manassas, Virginia, USA).

Culture conditions

Prior to each experiment, an individual bacterial colony was isolated on a TSA plate and resuspended in 4 mL of sterile TSB. This bacterial culture was then incubated for 18 hours at 37°C under constant agitation (180 rpm). Ten-fold serial dilutions of the bacterial suspension were then performed in TSB. 100 μL of one of the ten-fold dilution series was used for sample spiking. The 10^{-5} and 10^{-6} dilutions were plated (100 μL on TSA plates, in triplicates) to determine the initial bacterial concentration through manual colony counting. For each assay, sterility controls were performed.

Peptide arraying

Lyophilized peptides were resuspended in DMSO at 1 $mg.mL^{-1}$ and stored at -80C. Each peptide sequence was diluted at 100 μM in PBS 1x, with 5% (v/v) of glycerol ahead of arraying biochips. SPRi-biochips bought from Horiba Scientific (Palaiseau, France) consisted of glass prisms coated with a thin gold layer for direct functionalization using thiol moieties (see fig. S1 in the Electronic Supplementary Information for more details). Peptide biochips were prepared

using a sciFLEXARRAYER (Scienion, Berlin, Germany), a piezo-dispenser allowing arraying of 4 nL droplets per spot. Each array resulted in 12 spots with a 450 μm diameter, and a 800 μm pitch between each spot. All peptides were systematically arrayed in duplicate. This step was performed at room temperature under a humid atmosphere (75% relative humidity). After arraying, prisms were incubated for 18 hours at 25°C, under 94% humidity, to allow the complete formation of self-assembled monolayers of peptides onto gold. Chips were then rinsed with ultra-pure water, dried under an argon flow for a few seconds, and stored up to several weeks at +4°C until experiments. Effective surface functionalization was assessed by AFM comparison with bare gold surfaces (supplemental figure S2).

Biochip conditioning and sample processing

Prisms were systematically incubated with a sterile solution of PBS+1% BSA before each experiment to mimic interfering proteins of complex media such as blood, and to block non-specific interactions with gold. The surface of the prism was then rinsed with 3 mL of sterile PBS, before loading the biochip in the Surface Plasmon Resonance imager. 900 μL of sterile TSB were then injected in the culture chamber containing the AMP-array, followed by 100 μL of the bacterial dilution used for spiking. Interactions of bacteria on the surface of the prisms were observed in real-time with the SPRi-Lab+ system (Horiba Scientific, Palaiseau, France), at 37°C. The AMP-array was positioned so that its surface was vertical, on the sidewall of the culture chamber. This avoids any non-specific signal from sedimenting bacteria. Sensors were systematically discarded after use.

SPR data analysis

Real-time monitoring of the SPR signal began when the bacteria were spiked into the sample. Regions of interest (ROI) were defined on each duplicate of AMP spots, in order to monitor the temporal change of reflectivity. Kinetics data were directly collected and processed in R programming language. Duplicate spots of each peptide were averaged, corrected with respect to the reference signal, and plotted. Peptide-free gold ROIs, coated with BSA, were chosen as reference signals for non-specific interactions. Reflectivity shifts as a function of time for each ROI allowed the assessment of the presence of bacteria in samples without further processing of the data, by the observation of a temporal response shift. Kinetics data were used to generate a database of interaction patterns between peptides and bacteria. For each spot, the first derivative of the smoothed temporal data was calculated. The maximum value of this derivative, as well as the corresponding smoothed reflectivity shift, were recorded. Unsupervised multivariate analysis was performed on this database thanks to the FactomineR package, embedded in the R software [34]. Names of targeted bacteria were used as a descriptive variable, and therefore did not affect the results of the Principal Components Analysis (PCA). As data were heterogeneous, they were centered and reduced. On one hand, PCA score plots were used to distinguish results from one bacterial strain to another. On the other hand, they also permitted a high level of repeatability of the process from different duplicates of the same assay. Hierarchical Clustering on Principal Components (HCPC) was also performed on the outcome of the PCA. This statistical method ensured that targeted bacteria were indeed discriminated from each other, based on the Euclidean distance separating the replicates in the PCA results.

Results and discussion

Bacterial growth monitoring by SPRI

The set of five bacterial strains to be detected with the peptide array has been chosen to represent the diversity of pathogens frequently involved in bloodstream or urinary tract infections, as well as food poisoning. The set also reflects microbial morphological diversity, with both Gram-positive and negative species, including bacilli and cocci.

Growth kinetics monitored by SPRI of the bacteria are depicted in fig. *1*, datasets retrieved from those results allow defining characteristic detection times of bacteria (Supplemental Table S1) and affinity patterns with the peptides.

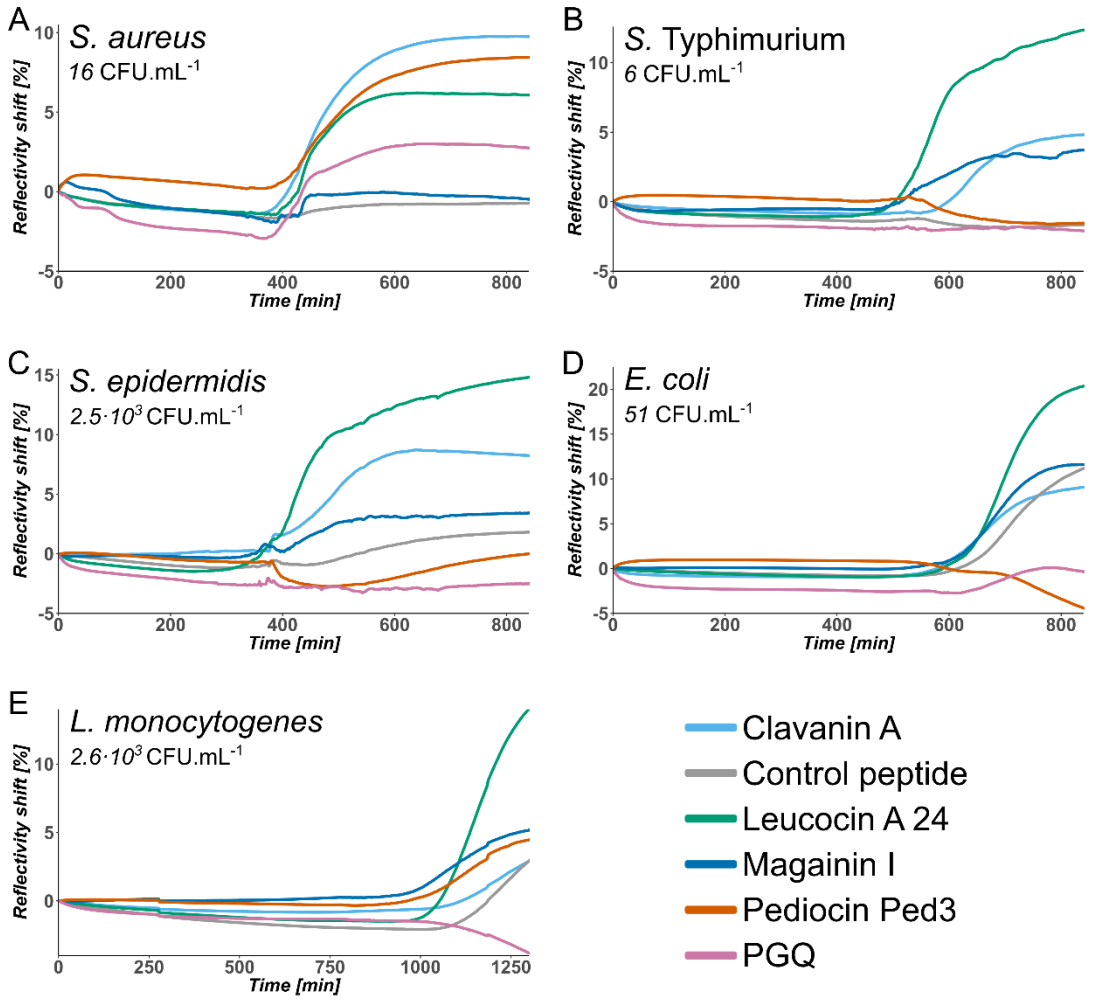

Figure 1. SPR kinetic data of the bacterial growth for five different bacterial strains cultured in tryptic soy broth at 37°C. Each curve is the average of duplicate spots for a given peptide arrayed on the sensor, with subtraction of the reference signal taken on peptide free gold.

AMP-based arrays have permitted the detection of pathogens present at low initial concentration in all samples, at most in 19 hours, and in even less than 12 hours in the majority of cases. All culture conditions being the same, variations of detection signal can come from dissimilarities in generation times of the different strains. Shortest detection times were for *S. aureus* and *S. epidermidis*, in about 6 to 7 hours. Similar conclusions with solid based culture methods are hitherto obtained in at least 24 hours. Compared to other biosensing methods using AMPs to analyze pre-enriched samples, we obtained a very low limit of detection of virtually one live bacterium per sample. The coupling of the enrichment step in our one-step process, not only improved the safety for the operator, but also significantly improved both the overall processing time and the limit of detection, by comparison to the two-steps methods described so far. Naturally, the lower limit of detection comes with a longer detection time to get bacterial concentrations sufficient for SPRI detection.

Individual peptide responses for bacterial pathogens detection

Peptides showed very distinct profiles of response depending on the targeted bacterial strains. Individual examination of their performances is thus interesting to understand underlying interactions with bacteria. Interestingly, Leucocin A 24 interacted strongly with all tested bacterial strains. Nonetheless, the scrambled version of Leucocin A 24, here used as a control peptide, displayed only weak to no interactions at all with any bacterial pathogen, suggesting that interactions of bacteria with tethered peptides are not only governed by physico-chemical mechanisms but more probably by structural interactions between peptides and bacterial membranes. Such observation has already been described for therapeutic peptides [35]. Clavanin A functionalized surfaces exhibited stronger SPRI responses with *Staphylococci spp.*, which are Gram-positive bacteria, although this peptide also enabled to successfully detect *Salmonella Typhimurium* and *E. coli*, although with weaker interactions. With our method, Magainin I only displayed mild interactions with all the tested bacteria, whatever their Gram coloration (except for *S. aureus* which gave a very low shift). On the contrary, Ped3, a Pediocin fragment, exhibited a moderate ability to detect *Listeria monocytogenes*, as previously described [31], but surprisingly Ped3 also displayed a potent interaction with MRSA in our assay. In the meantime it did not interact with *S. epidermidis*, although they belong to the same *genus*. This selective response might be caused by an association of the peptide with a peculiar receptor specific to the membrane of MRSA. PGQ displayed interactions with *E. coli*, which is consistent with the literature [32]. However it detected *S. aureus*, which is a Gram-positive strain, and had no apparent interactions with *Salmonella*, another Gram-negative bacterium, that also displays LPS, which is a hint that the interactions between PGQ and bacteria is not only mediated by interacting with the latter.

These results tend to show that AMPs keep a wide spectrum of affinity towards bacteria after tethering on a surface. Moreover, association of AMPs enabled to obtain various kinetic profiles depending on the bacterial strain. Interestingly, our SPRI detection method allowed to unravel interactions which remained unobserved with other methods [25]. This could be explained by the establishment of weaker interactions between bacteria and AMPs thanks to their longer exposure time to the cultured bacteria.

Multivariate analyses of kinetic results

Multivariate analyses were performed to objectively assess the discrimination values of our method. To do so, PCA was performed based on reflectivity shift and sensitivity values at the

maximum of the first derivative for each peptide (Figure 2*A*). Each bacterial strain was processed once on an AMP micro-array, giving 64 sets of values, from all possible combinations of peptide duplicates responses at the surface. This combinatorial analyzing method ensured that statistical variability of the overall response was totally represented, and that cherry picking of data was avoided. Experiments on different bacterial strains with the same set of AMPs gave clustered results in the PCA 2D-score plot. Moreover, those clusters of data points were well segregated from each other according to the monitored pathogen: results were repeatable regardless of the set of replicates in the same monitoring. The first two principal components represented only 70.3% of the total variance. This meant that the data were of high dimensionality, thus explaining why such a good discrimination between bacterial strains could be obtained. However, those first two components were sufficient in our case to clearly distinguish between distinct bacterial strains. Such results underlined potential identification ability of the method, although more experiments would be required to create an even more exhaustive database. Results of the PCA were also used to perform a Hierarchical Clustering on Principal Components (fig. 2B), leading again to a satisfying separation of the different strains in separate clusters. Such discriminated profiles came from the variety of affinities displayed by the peptides towards the tested bacteria. Due to different physicochemical properties and structures, each peptide interacted differently to Gram or genera, hence the overall combination discriminated the tested strains. Multivariate analyses with appropriate databases thus allow pathogen identification methods to be derived from the usual key-lock principle and enable cross-reactivity sensors as demonstrated by [36].

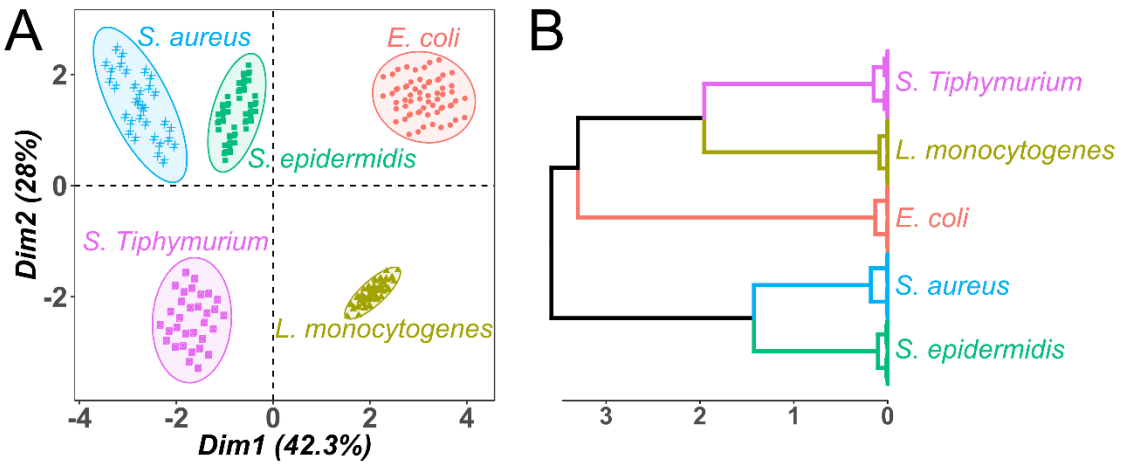

Figure 2. Multivariate data analyses for 5 bacterial strains processed on AMP-arrays. (A) 2D-score plot of the database generated from the kinetics of SPRI bacterial growth monitoring. Ellipses were annotated to represent the 95% confidence interval. (B) Hierarchical Clustering on Principal Components (HCPC) performed on the data from Fig. 2a. Distances between points are Euclidean.

In this work, we demonstrated the suitability of AMP-arrays as powerful ligands of bacterial pathogens. Traditionally studied in the field of pharmacology and antimicrobial applications, AMPs were revealed to be potent ligands for pathogens in biosensing applications. Not only they are well-adapted for the detection of bacteria in a standard culture medium such as tryptic soy

broth, but compared to antibodies, the biochip functionalization and operation were less tedious, thanks to peptide resistance to air-drying without loss of activity in the process.

The use of AMPs in a multiplexed fashion allowed a fast and simple assessment of the presence of pathogens even at low concentrations. Detection times ranged from 6 to 19 hours, in a one-step assay. This is shorter than standard methods in blood or foodstuffs, which require enrichment times of usually 24 hours before confirmation of the culture positivity. Each tested bacterial strain resulted in different kinetic responses on the part of the AMP-array. Ped3 even exhibited a near-specific behavior, interacting almost uniquely with MRSA. Further studies could assess this point, which would be of importance in the detection of this prominent pathogen. Our results, for instance for Leucocin A24 and its scrambled version, showed that the recognition of bacteria by AMPs is not uniquely driven by physico-chemical interactions, but also by their secondary structuration. Moreover, tethering of the AMPs on the surface of our sensor did not seem to alter this interaction with bacteria in solution. The study of the whole set of AMPs interacting with live bacteria gave clearly different affinity profiles. This combined approach was preferred to a biomolecular study to enable the identification of several bacterial pathogens, with a single AMP set. The response to polymicrobial infections, which represent only 10% of bloodstream infections [37,38], is still to be investigated to check how AMPs responses might be deciphered to identify two, or more, pathogenic strains present in the same sample.

Furthermore, the small set of AMPs we used provided very distinct affinity profiles towards different pathogens, as multivariate analysis confirmed. Arrays presenting a larger collection of peptides could hence enable the possibility to create interaction profile libraries and therefore the identification of bacterial genus, species or strain of the infecting pathogen in a sample.

To the extent of our knowledge, the system we described is the first one-step biosensor assay using different multiplexed AMPs and enabling detection of several viable bacterial strains in biomedically relevant concentrations along with a discrimination capacity in a label-free assay. In the near future, this approach could be applied for the detection of any pathogen in samples such as foodstuff, urine or blood without any pre-requisite knowledge of the threat.

If these auspicious results are confirmed on a larger scale, it could permit the development of a one-step assay – not only able to detect common pathogens overnight – but also to identify them in reference to a database of affinity patterns.

Color should be used for any figures in print

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Competing interests statement

The authors declare no financial or non-financial competing interests.

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Supplementary Information:

Antimicrobial peptide arrays for wide spectrum sensing of pathogenic bacteria

Éric Pardoux[a,b], Agnès Roux[a], Raphaël Mathey[a], Didier Boturyn[b], Yoann Roupioz[a,*]

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Table S1. Detection times of the presence of the different bacterial strains are determined by the timestamp of the kinetics first derivative highest value. It thus corresponds to the middle of the jump between the baseline signal and the plateau. It is given for the shortest time for each bacterial strain, associated with the peptide giving this result. Only peptides giving a strong positive signal are included in the analysis. Times are given as the average over duplicates of each peptide.

Bacterial strain	**Initial concentration (CFU.mL^{-1})**	**Shortest detection time (min)**	**Peptide**
E. coli ATCC11775	51	677	Clavanin A
S. Typhimurium CIP104474	6	537	Magainin I
S. aureus ATCC43300	16	433	Leucocin A 24
S. epidermidis ATCC12228	$2.5 \cdot 10^3$	374	Leucocin A 24
L. monocytogenes IVc	$2.6 \cdot 10^3$	1160	Leucocin A 24

Figure S1. (A) Scaled scheme showing characteristic dimensions of the SPRi-biochip, including a representation of the observable field of view with the SPRi-Lab+. (B) Picture of a SPRi-biochip right after a spotting.

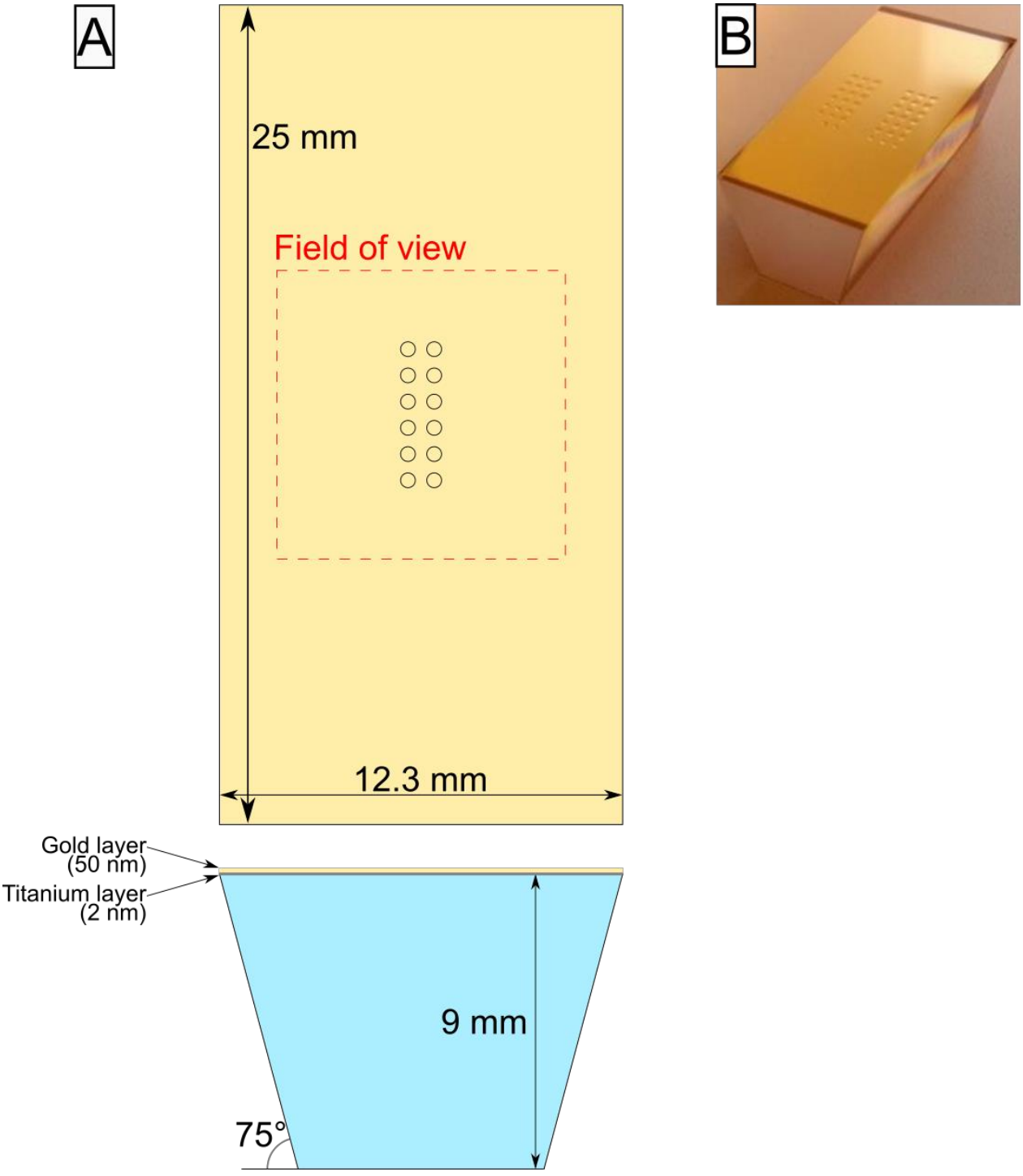
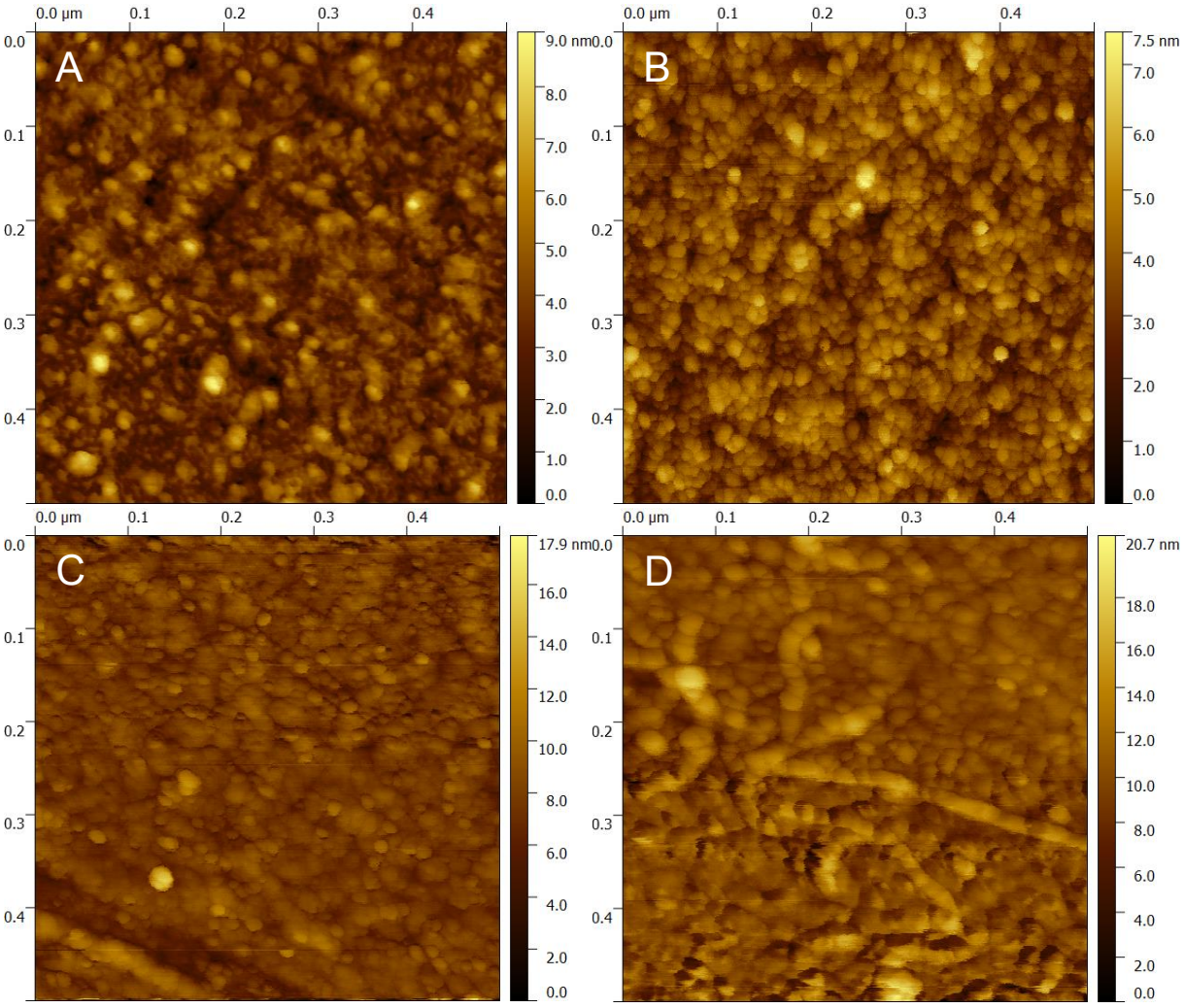


Figure S2. AFM images of monolayers of peptides prepared in the same conditions as SPRI biochips: (A) bare gold as a reference; (B) Magainin I; (C) Leucocin A 24; (D) Control peptide. They were recorded in air using the peak force mode of a Dimension Icon AFM (from Bruker, Santa Barbara, CA). The cantilevers were triangular and using a force contact of 0.1 N/m at a 70 kHz frequency and a 0.5 Hz scan rate. Image processing was performed using the Gwyddion microscopy software.



Certificate of analysis

Date	14/03/2016	Batch	849_s1p4f2
Product name	Magainin 1-Ncys	Catalog #	

Product specifications

AA sequence	C-AEEA-GIGKFLHSAGKFGKAFVGEIMKS-OH
Disulfide bond	0
Formula	$C_{121}H_{193}N_{31}O_{32}S_2$
Appearance	White powder
Theoritical average weight	2658,14 g/mol
CAS number	
Source	Synthetic
Counterion	TFA
Solubility (recommendation)	10% acetonrile solution 1 mg/mL

Handling & Storage

Storage	Shipped at ambient temperature under lyophilized powder. Store at -20°C (-4°F). Do not freeze-thaw. Aliquot sample if required and store at -80°C (-112°F).
Expiry date	Not defined
Handling and use restriction	Use with caution. Might be toxic. Product intented for research use only, not for use in diagnostic or therapeutic procedures.

Analytical results

Observed purity rate	97,60%	Observed monoisotopic mass [M+H+]+	2657,407 Da
		Theoritical monoisotopic mass	2656,38 Da

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Chromatogram

Sample Name : Sample #: 023 Page 1 of 1
FileName : C:\totalchrom\data\Peptide cea\linjer AEEA fevrier 2016\160308 magainin ncys 849s1p4f2.raw
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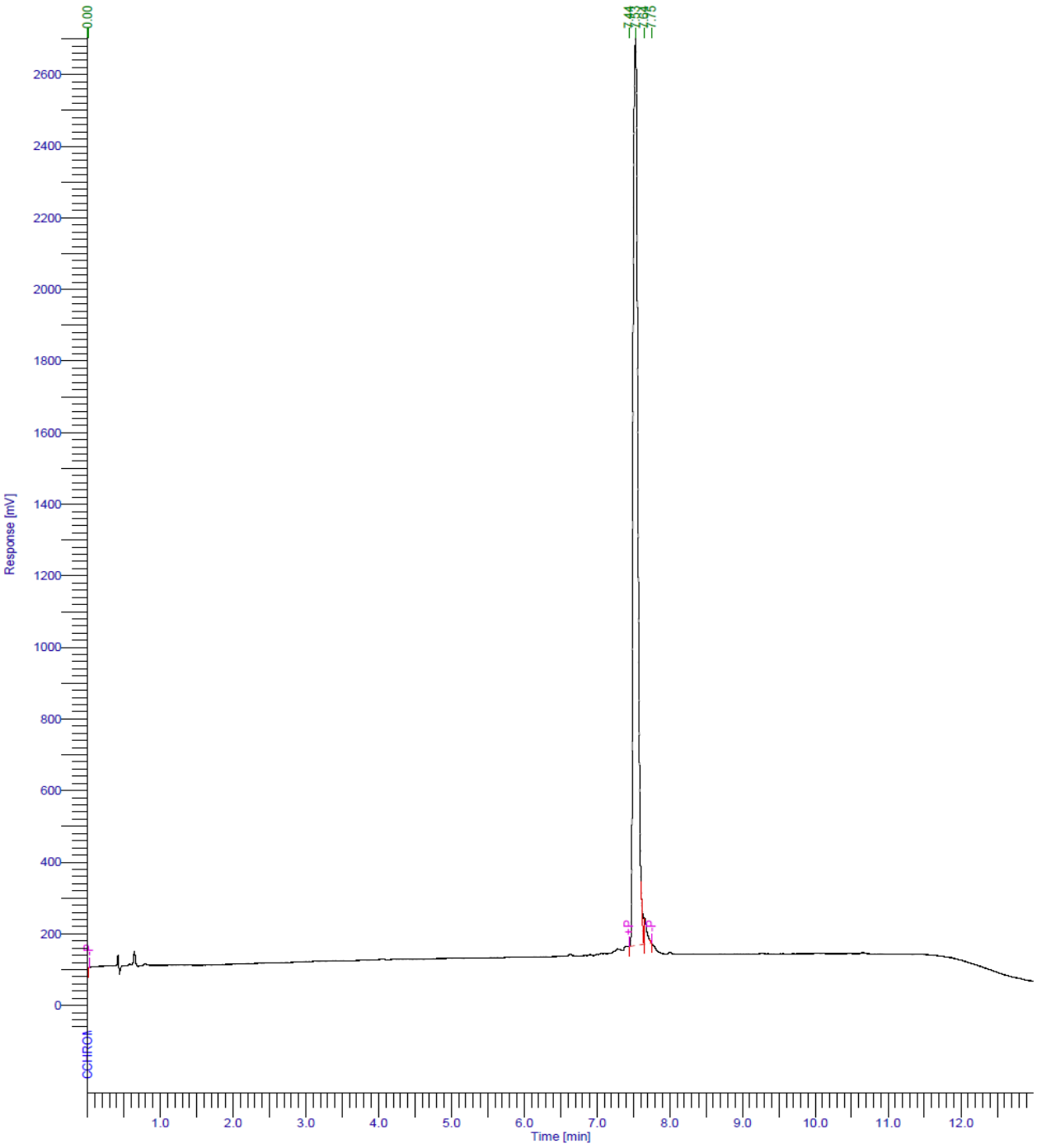

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Peak #	Time [min]	Area [µV·s]	Height [µV]	Area [%]	Norm. Area [%]	BL	Area/Height [s]
-	0.001	0.00	0.00	0.00	0.00		----------
1	0.002	33.34	325.09	0.00	0.00	BV	0.1025
2	0.005	39.66	338.72	0.00	0.00	VV	0.1171
3	0.007	18.23	286.91	0.00	0.00	VV	0.0636
4	0.010	29.97	341.26	0.00	0.00	VB	0.0878
5	0.012	24.20	256.27	0.00	0.00	BV	0.0944
6	0.015	19.32	190.70	0.00	0.00	VB	0.1013
7	0.017	8.71	188.02	7e-05	7e-05	BV	0.0463
8	0.018	11.78	221.95	0.00	0.00	VB	0.0531
9	7.444	13.25	278.45	0.00	0.00	BV	0.0476
10	7.447	67.80	709.43	0.00	0.00	VV	0.0956
11	7.450	161.57	1440.70	0.00	0.00	VV	0.1121
12	7.530	11494288.40	2.54e+06	97.60	97.60	VE	4.5342
13	7.645	80123.98	70666.35	0.68	0.68	EV	1.1338
14	7.647	9323.03	72519.37	0.08	0.08	VV	0.1286
15	7.650	11590.99	72555.12	0.10	0.10	VV	0.1598
16	7.653	12378.38	72682.91	0.11	0.11	VV	0.1703
17	7.655	11828.25	72501.87	0.10	0.10	VV	0.1631
18	7.657	156665.19	72211.00	1.33	1.33	VE	2.1695
19	7.749	482.05	363.95	0.00	0.00	*EB	1.3245
		11777108.11	2.97e+06	100.00	100.00		

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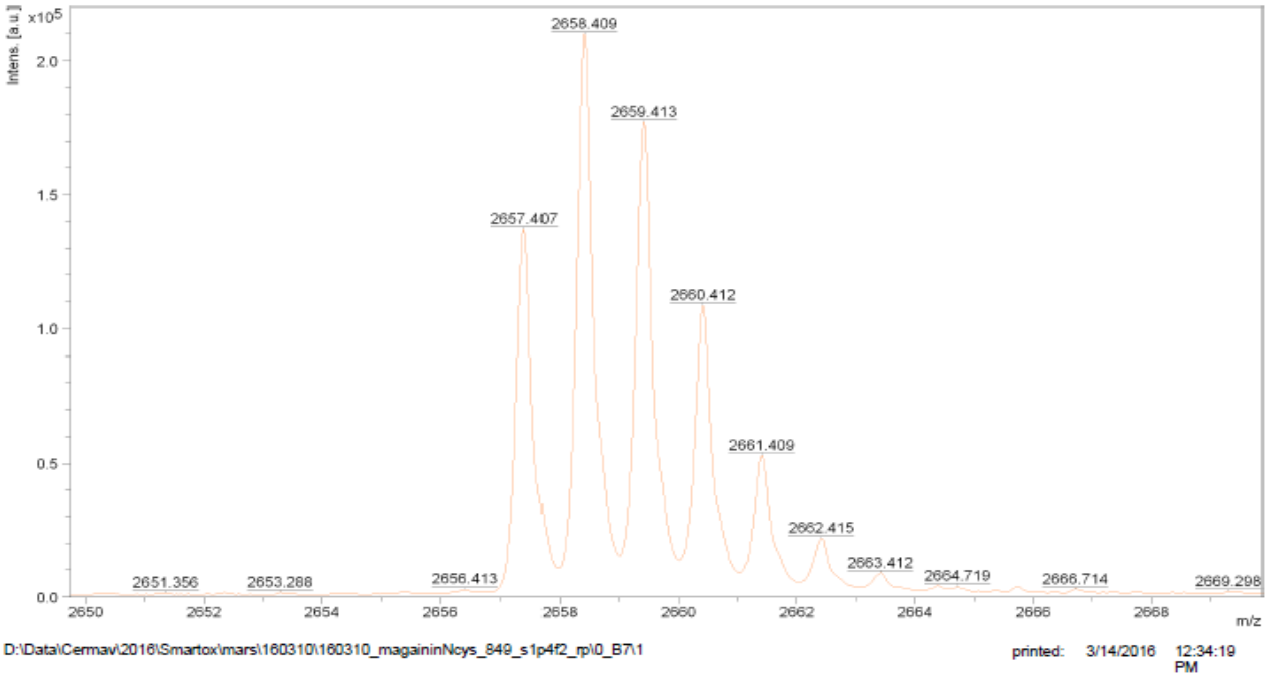

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Certificate of analysis

Date	21/03/2016	Batch	847_s1p1f1
Product name	clavaninA	Catalog #	

Product specifications

AA sequence	VFQFLGKIIHHVGNFVHGFSHVF-AEEA-C-NH2
Disulfide bond	0
Formula	$C_{140}H_{201}N_{37}O_{30}S$
Appearance	White powder
Theoritical average weight	2914,39 g/mol
CAS number	
Source	Synthetic
Counterion	TFA
Solubility (recommendation)	50% of Acetonitrile solution 1 mg/mL

Handling & Storage

Storage	Shipped at ambient temperature under lyophilized powder. Store at -20°C (-4°F). Do not freeze-thaw. Aliquot sample if required and store at -80°C (-112°F).
Expiry date	Not defined
Handling and use restriction	Use with caution. Might be toxic. Product intented for research use only, not for use in diagnostic or therapeutic procedures.

Analytical results

Observed purity rate	93,47%	Observed monoisotopic mass [M+H+]+	2913,41 Da
		Theoritical monoisotopic mass	2912,50 Da

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Chromatogram

Sample Name : Sample #: 022 Page 1 of 1
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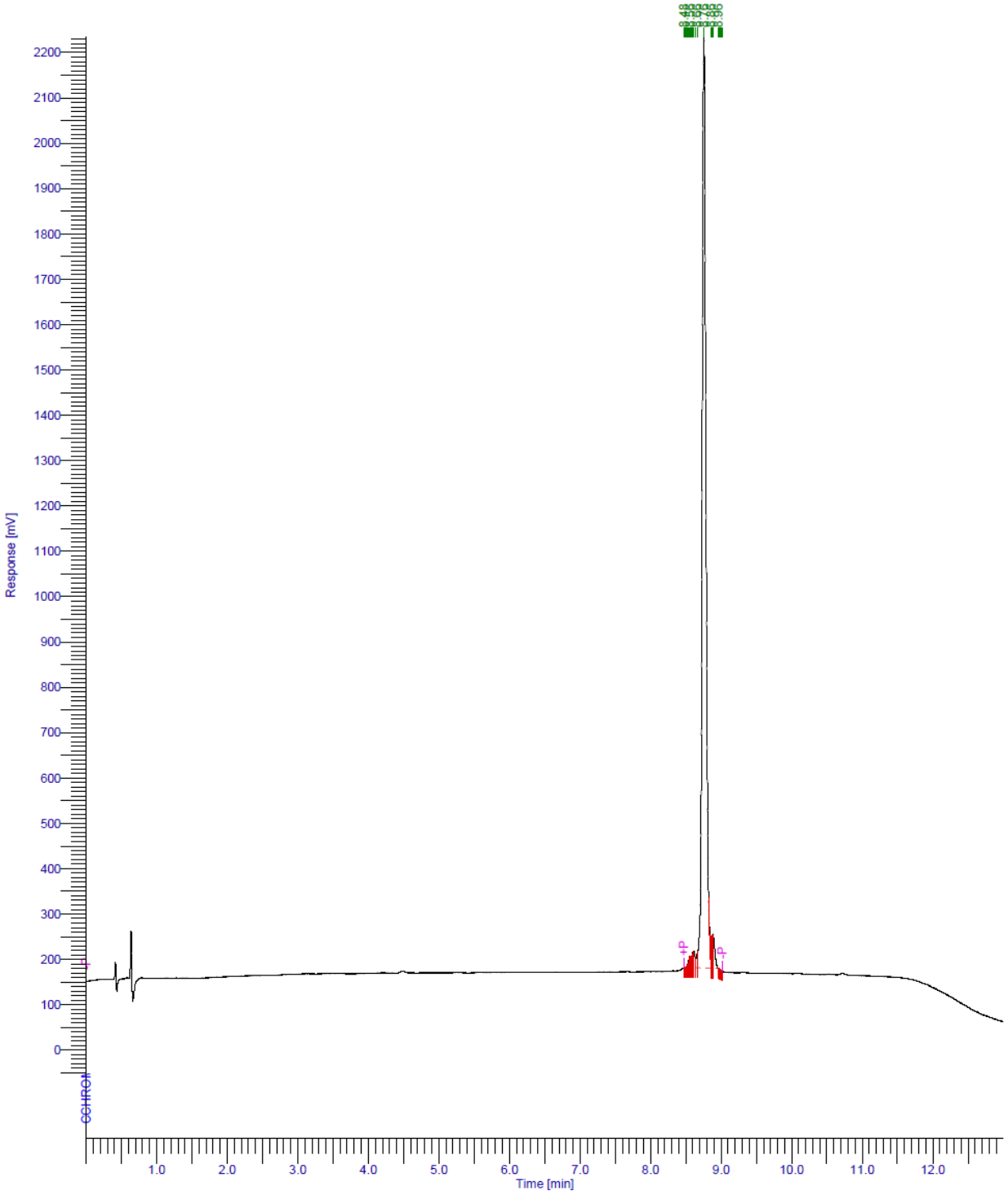

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Peak #	Time [min]	Area [µV·s]	Height [µV]	Area [%]	Norm. Area [%]	BL	Area/Height [s]
-	0.001	0.00	0.00	0.00	0.00		----------
1	8.477	16.06	278.50	0.00	0.00	BB	0.0577
2	8.479	31.83	387.81	0.00	0.00	BB	0.0821
3	8.482	35.38	401.57	0.00	0.00	BV	0.0881
4	8.485	44.93	382.61	0.00	0.00	VV	0.1174
5	8.487	33.96	351.45	0.00	0.00	VB	0.0966
6	8.490	42.92	404.71	0.00	0.00	BV	0.1061
7	8.493	46.59	505.61	0.00	0.00	VV	0.0921
8	8.495	68.36	631.11	0.00	0.00	VV	0.1083
9	8.498	87.27	771.69	0.00	0.00	VV	0.1131
10	8.501	142.81	1074.51	0.00	0.00	VV	0.1329
11	8.503	172.67	1511.97	0.00	0.00	VV	0.1142
12	8.506	275.47	2096.31	0.00	0.00	VV	0.1314
13	8.509	392.05	2721.50	0.00	0.00	VV	0.1441
14	8.511	450.27	3376.96	0.01	0.01	VV	0.1333
15	8.514	645.48	4216.42	0.01	0.01	VV	0.1531
16	8.519	1552.63	5894.62	0.02	0.02	VV	0.2634
17	8.522	1010.98	6789.15	0.01	0.01	VV	0.1489
18	8.525	1162.84	7819.38	0.01	0.01	VV	0.1487
19	8.527	1327.63	8878.12	0.02	0.02	VV	0.1495
20	8.530	1510.31	10089.78	0.02	0.02	VV	0.1497
21	8.552	21521.76	23881.49	0.26	0.26	VV	0.9012
22	8.554	3916.28	25032.12	0.05	0.05	VV	0.1565
23	8.557	4627.25	25713.31	0.06	0.06	VV	0.1800
24	8.559	4379.62	26019.79	0.05	0.05	VV	0.1683
25	8.562	9901.71	25954.16	0.12	0.12	VV	0.3815
26	8.567	8309.68	25070.62	0.10	0.10	VV	0.3315
27	8.572	1915.96	24033.86	0.02	0.02	VV	0.0797
28	8.575	3368.81	23805.12	0.04	0.04	VV	0.1415
29	8.578	3689.36	23908.68	0.04	0.04	VV	0.1543
30	8.581	3922.28	24271.94	0.05	0.05	VV	0.1616
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37	8.610	4935.51	36876.89	0.06	0.06	VV	0.1338
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42	8.663	5225.54	33395.14	0.06	0.06	VV	0.1565
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45	8.671	5802.05	36885.86	0.07	0.07	VV	0.1573
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49	8.863	9991.57	69834.22	0.12	0.12	VV	0.1431
50	8.866	11781.87	70390.71	0.14	0.14	VV	0.1674
51	8.869	9892.04	70958.47	0.12	0.12	VV	0.1394
52	8.871	11412.92	71800.34	0.14	0.14	VV	0.1590
53	8.874	11541.86	72583.86	0.14	0.14	VV	0.1590
54	8.877	12634.93	73338.95	0.15	0.15	VV	0.1723
55	8.879	12356.59	73858.97	0.15	0.15	VV	0.1673
56	8.882	12926.44	74076.95	0.16	0.16	VV	0.1745
57	8.884	137569.02	73814.29	1.66	1.66	VB	1.8637
58	8.958	47.52	258.37	0.00	0.00	BV	0.1839
59	8.962	16.14	314.76	0.00	0.00	VB	0.0513
60	8.964	43.00	243.67	0.00	0.00	BV	0.1764
61	8.967	30.23	408.93	0.00	0.00	VB	0.0739
62	8.970	14.32	207.22	0.00	0.00	BB	0.0691
63	8.975	11.93	226.30	0.00	0.00	BB	0.0527
64	8.978	18.48	265.82	0.00	0.00	BB	0.0695
65	8.980	8.50	159.61	0.00	0.00	BB	0.0533
66	8.983	25.92	318.15	0.00	0.00	BB	0.0815
67	8.985	7.18	168.91	9e-05	9e-05	BV	0.0425
68	8.986	13.73	261.55	0.00	0.00	VB	0.0525
69	8.988	56.86	272.05	0.00	0.00	BV	0.2090
70	8.993	31.48	272.06	0.00	0.00	VB	0.1157
71	8.996	51.16	213.86	0.00	0.00	BV	0.2392
72	8.999	10.67	333.89	0.00	0.00	VB	0.0320
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74	9.006	25.22	193.51	0.00	0.00	BB	0.1303
75	9.009	20.37	176.06	0.00	0.00	BB	0.1157
76	9.012	12.69	261.76	0.00	0.00	BV	0.0485
77	9.012	18.72	330.46	0.00	0.00	VB	0.0567
78	9.015	16.03	188.59	0.00	0.00	*BB	0.0850
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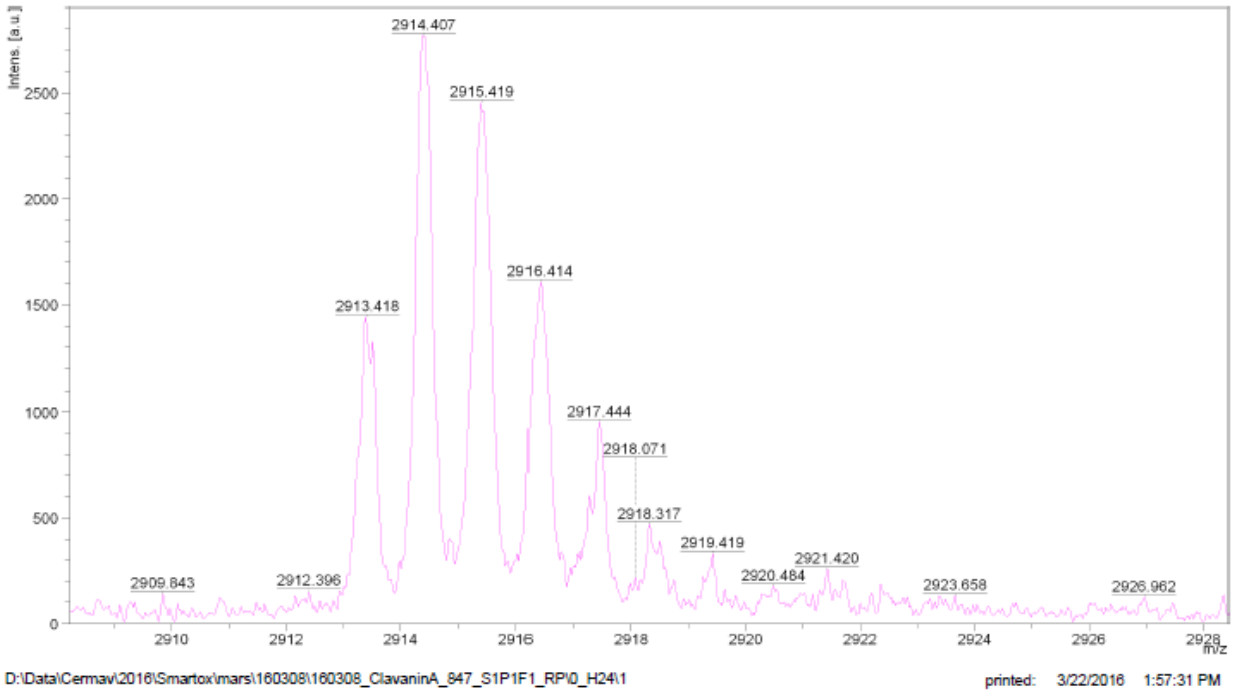

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Certificate of analysis

Date	22/03/2016	Batch	850_s2p1r1
Product name	peptide Contrôle	Catalog #	

Product specifications

AA sequence	C-AEEA-RGEWFWGNLVVSAASFGNHNAGG-OH
Disulfide bond	0
Formula	$C_{119}H_{194}N_{36}O_{34}S$
Appearance	White powder
Theoritical average weight	2681,89 g/mol
CAS number	
Source	Synthetic
Counterion	TFA
Solubility (recommendation)	50 % of Acetonitrile solution 1 mg/mL

Handling & Storage

Storage	Shipped at ambient temperature under lyophilized powder. Store at -20°C (-4°F). Do not freeze-thaw. Aliquot sample if required and store at -80°C (-112°F).
Expiry date	Not defined
Handling and use restriction	Use with caution. Might be toxic. Product intented for research use only, not for use in diagnostic or therapeutic procedures.

Analytical results

Observed purity rate	90,49%	Observed monoisotopic mass [M+H+]+	2681,17 Da
		Theoritical monoisotopic mass	2680,22 Da

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Chromatogram

Sample Name : Sample #: 020 Page 1 of 1
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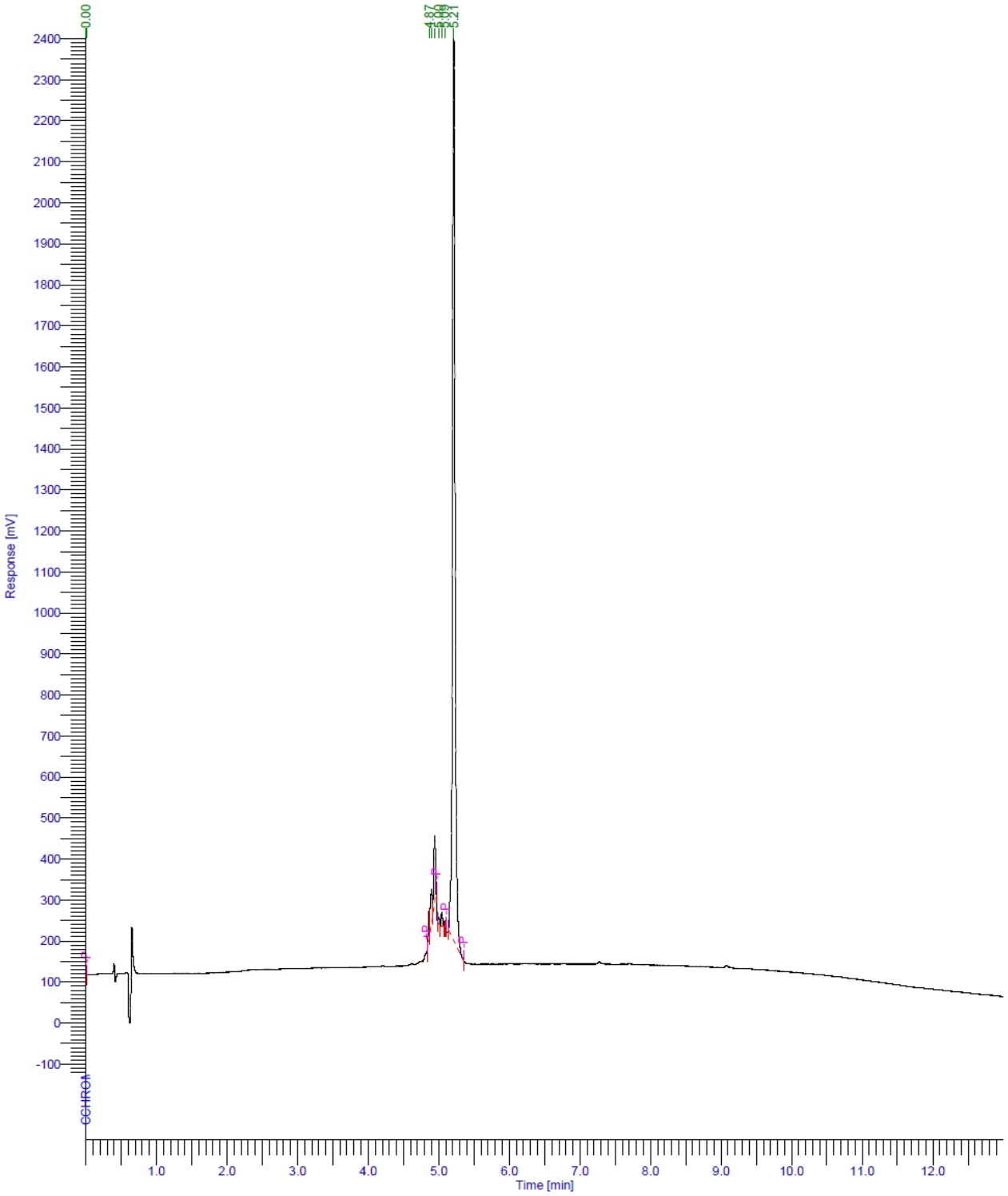

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France

Peak #	Time [min]	Area [µV·s]	Height [µV]	Area [%]	Norm. Area [%]	BL	Area/Height [s]
-	0.001	0.00	0.00	0.00	0.00		----------
1	0.002	42.54	245.68	0.00	0.00	BV	0.1732
2	0.007	28.29	356.69	0.00	0.00	VB	0.0793
3	4.869	86010.57	65647.89	1.35	1.35	BV	1.3102
4	4.874	7756.18	59133.80	0.12	0.12	VV	0.1312
5	4.898	154870.24	83562.89	2.43	2.43	VV	1.8533
6	4.944	271621.09	161956.69	4.27	4.27	*VB	1.6771
7	5.002	18420.50	16740.93	0.29	0.29	BB	1.1003
8	5.045	49368.87	34018.14	0.78	0.78	BV	1.4513
9	5.085	8310.72	14378.72	0.13	0.13	VV	0.5780
10	5.086	8566.17	14587.51	0.13	0.13	*VB	0.5872
11	5.215	5755579.60	2.20e+06	90.49	90.49	*BB	2.6139
		6360574.77	2.65e+06	100.00	100.00		

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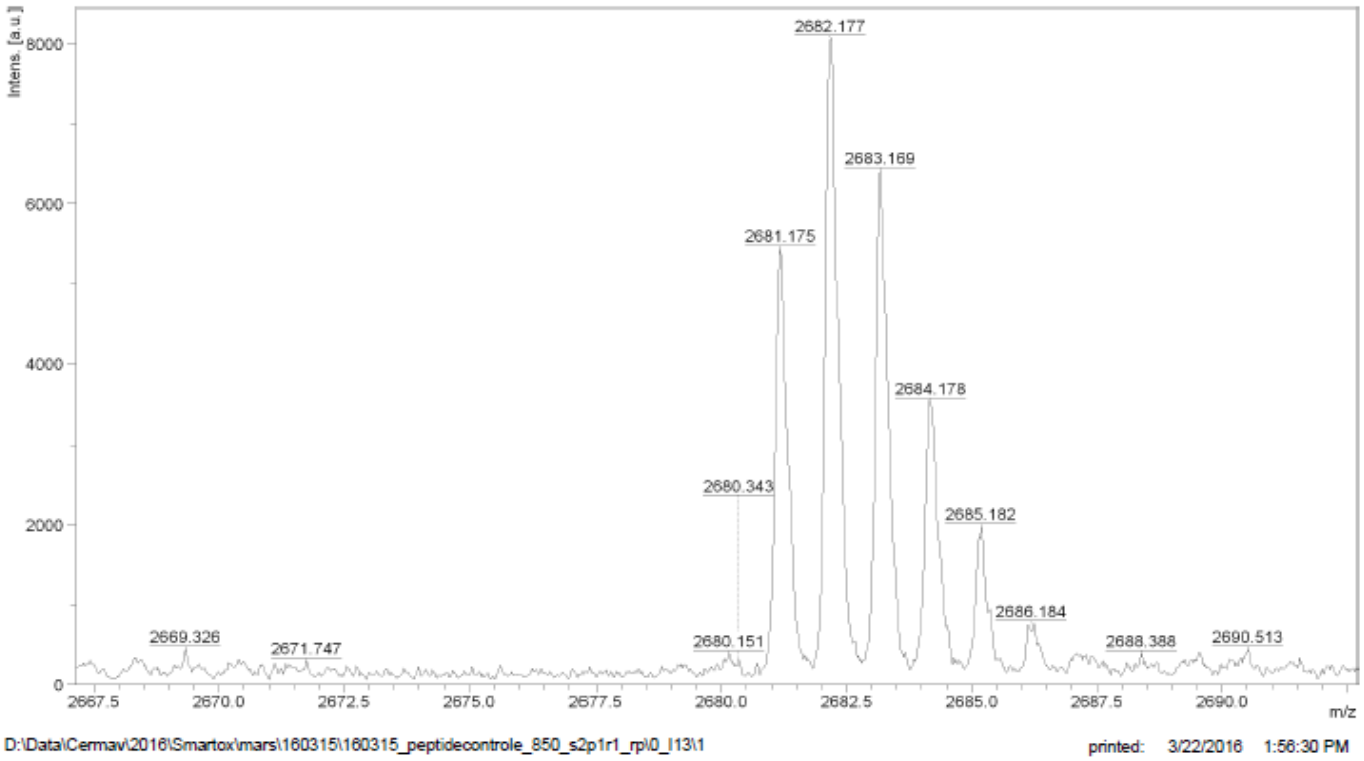
MS Spectra



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Certificate of analysis

Date	21/03/2016	Batch	851_s1p1f1
Product name	Magainin 1-Ccys	Catalog #	

Product specifications

AA sequence	GIGKFLHSAGKFGKAFVGEIMKS-AEEA-C-NH2
Disulfide bond	0
Formula	$C_{121}H_{194}N_{32}O_{31}S_2$
Appearance	White powder
Theoritical average weight	2657,16 g/mol
CAS number	
Source	Synthetic
Counterion	TFA
Solubility (recommendation)	10% acetonrile solution 1 mg/mL

Handling & Storage

Storage	Shipped at ambient temperature under lyophilized powder. Store at -20°C (-4°F). Do not freeze-thaw. Aliquot sample if required and store at -80°C (-112°F).
Expiry date	Not defined
Handling and use restriction	Use with caution. Might be toxic. Product intented for research use only, not for use in diagnostic or therapeutic procedures.

Analytical results

Observed purity rate	95,61%	Observed monoisotopic mass [M+H+]+	2656,39 Da
		Theoritical monoisotopic mass	2655,40 Da

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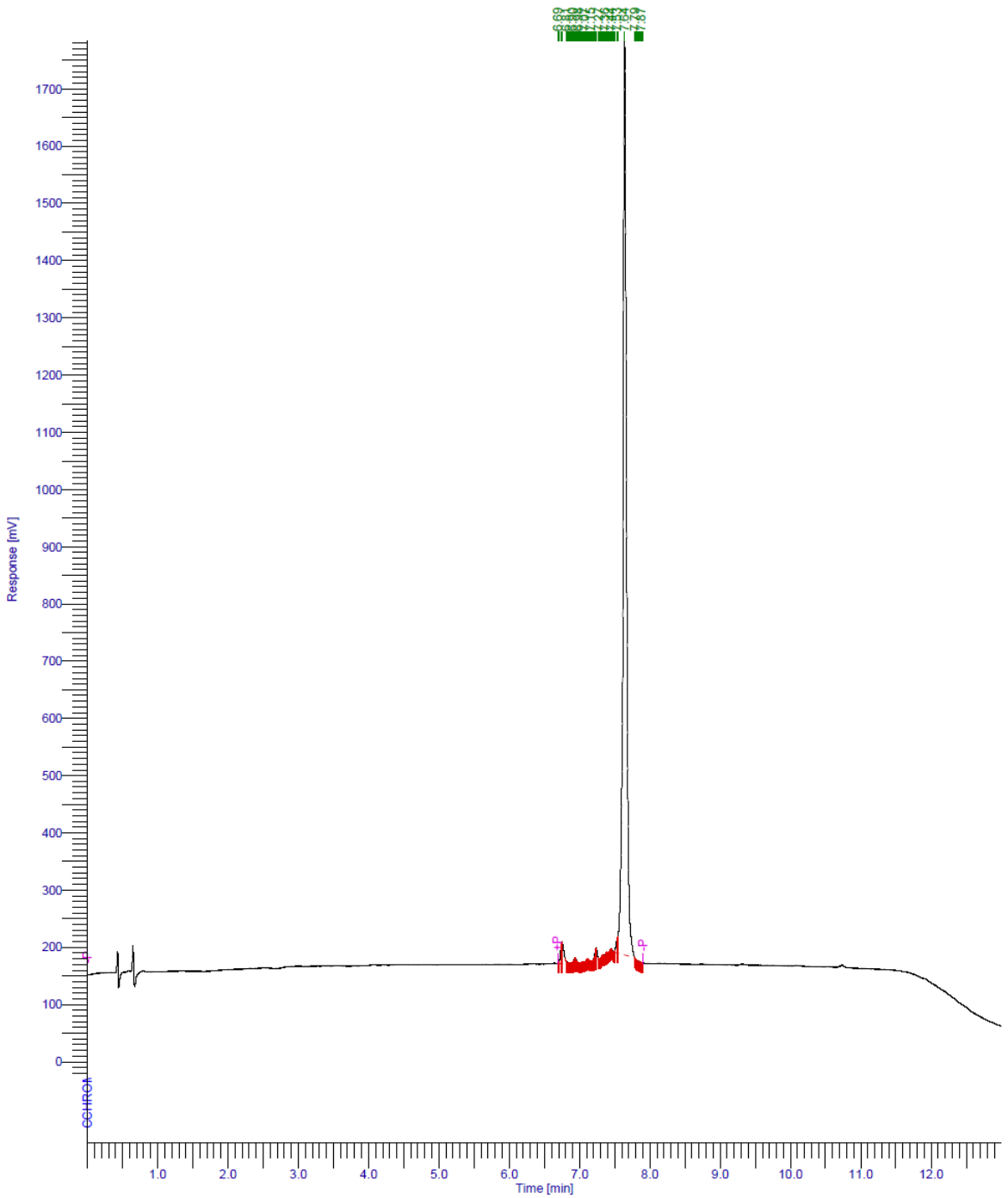
Chromatogram

Sample Name : Sample #: 016 Page 1 of 1
FileName : C:\totalchrom\data\Peptide cea\linjer AEEA fevrier 2016\160303 magainin 1ccys 851s1p1f1.raw
Date : 3/15/2016 9:12:31 AM
Method : cchromolith 5-65 en 10 min.mth Time of Injection: 3/3/2016 9:08:46 PM
Start Time : 0.00 min End Time : 13.00 min Low Point : -28.43 mAU High Point : 1783.45 mAU
Plot Offset: -28.43 mAU Plot Scale: 1811.9 mAU



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Peak #	Time [min]	Area [µV·s]	Height [µV]	Area [%]	Norm. Area [%]	BL	Area/Height [s]
199	7.359	37.65	431.30	0.00	0.00	BV	0.0873
200	7.362	62.26	593.15	0.00	0.00	VV	0.1050
201	7.365	132.78	1181.71	0.00	0.00	VV	0.1124
202	7.367	219.66	1720.05	0.00	0.00	VV	0.1277
203	7.370	322.45	2423.05	0.01	0.01	VV	0.1331
204	7.373	458.22	3113.34	0.01	0.01	VV	0.1472
205	7.375	581.18	3759.34	0.01	0.01	VV	0.1546
206	7.378	628.47	4262.35	0.01	0.01	VV	0.1474
207	7.381	722.46	4530.80	0.01	0.01	VV	0.1595
208	7.383	667.64	4561.89	0.01	0.01	VV	0.1464
209	7.386	774.85	4427.26	0.01	0.01	VV	0.1750
210	7.388	653.02	4062.11	0.01	0.01	VV	0.1608
211	7.391	985.33	3528.49	0.02	0.02	VV	0.2792
212	7.396	476.71	2308.35	0.01	0.01	VV	0.2065
213	7.399	89.65	1576.89	0.00	0.00	VV	0.0569
214	7.401	183.94	1213.24	0.00	0.00	VV	0.1516
215	7.405	88.98	771.10	0.00	0.00	VV	0.1154
216	7.407	47.38	383.29	0.00	0.00	VV	0.1236
217	7.410	27.94	250.60	0.00	0.00	VB	0.1115
218	7.413	22.68	281.60	0.00	0.00	BB	0.0805
219	7.415	16.74	252.52	0.00	0.00	BB	0.0663
220	7.418	20.51	300.09	0.00	0.00	BV	0.0683
221	7.421	48.42	514.08	0.00	0.00	VV	0.0942
222	7.423	97.45	822.22	0.00	0.00	VV	0.1185
223	7.426	122.06	996.43	0.00	0.00	VV	0.1225
224	7.429	189.10	1445.47	0.00	0.00	VV	0.1308
225	7.431	260.02	1923.75	0.00	0.00	VV	0.1352
226	7.434	314.22	2168.52	0.01	0.01	VV	0.1449
227	7.437	380.62	2620.35	0.01	0.01	VV	0.1453
228	7.439	440.35	2809.65	0.01	0.01	VV	0.1567
229	7.442	428.67	2836.71	0.01	0.01	VV	0.1511
230	7.445	441.93	2670.64	0.01	0.01	VV	0.1655
231	7.447	363.58	2458.90	0.01	0.01	VV	0.1479
232	7.449	304.55	2000.89	0.01	0.01	VV	0.1522
233	7.452	108.39	1481.06	0.00	0.00	VV	0.0732
234	7.452	113.68	1357.36	0.00	0.00	VV	0.0838
235	7.454	45.28	776.93	0.00	0.00	VV	0.0583
236	7.455	45.84	672.88	0.00	0.00	VB	0.0681
237	7.458	8.21	151.80	0.00	0.00	BB	0.0541
238	7.460	7.43	151.63	0.00	0.00	BV	0.0490
239	7.460	18.64	318.54	0.00	0.00	VB	0.0585
240	7.482	7.09	184.32	0.00	0.00	BB	0.0384
241	7.484	14.11	191.15	0.00	0.00	BB	0.0738
242	7.487	24.33	286.00	0.00	0.00	BB	0.0851
243	7.490	22.06	315.43	0.00	0.00	BV	0.0699
244	7.493	86.36	687.81	0.00	0.00	VV	0.1256
245	7.495	129.47	1159.81	0.00	0.00	VV	0.1116
246	7.498	199.49	1744.68	0.00	0.00	VV	0.1143
247	7.501	342.53	2635.92	0.01	0.01	VV	0.1299
248	7.504	487.35	3660.54	0.01	0.01	VV	0.1331
249	7.530	20857.84	23066.12	0.36	0.36	VV	0.9043
250	7.538	11995.69	26686.43	0.21	0.21	VV	0.4495
251	7.541	4898.89	27627.31	0.08	0.08	VV	0.1773
252	7.543	3932.89	28745.32	0.07	0.07	VV	0.1368
253	7.641	5583836.78	1.60e+06	95.61	95.61	VB	3.4968
254	7.787	44.38	133.65	0.00	0.00	BB	0.3321
255	7.793	62.63	266.48	0.00	0.00	BB	0.2350
256	7.799	9.21	165.21	0.00	0.00	BB	0.0558
257	7.804	8.21	159.30	0.00	0.00	BB	0.0515
258	7.810	23.68	256.80	0.00	0.00	BB	0.0922
259	7.812	7.74	133.23	0.00	0.00	BB	0.0581
260	7.814	18.66	173.21	0.00	0.00	BB	0.1077
261	7.818	24.98	306.73	0.00	0.00	BV	0.0814
262	7.820	38.38	330.73	0.00	0.00	VB	0.1161
263	7.823	33.27	345.67	0.00	0.00	BV	0.0962
264	7.826	24.46	242.86	0.00	0.00	VB	0.1007
265	7.828	13.35	179.63	0.00	0.00	BB	0.0743
266	7.831	25.25	331.23	0.00	0.00	BB	0.0762
267	7.834	20.37	229.47	0.00	0.00	BB	0.0888
268	7.836	3.72	86.70	6e-05	6e-05	BV	0.0429
269	7.836	7.44	187.96	0.00	0.00	VB	0.0396
270	7.839	29.06	310.31	0.00	0.00	BV	0.0936
271	7.842	23.68	282.79	0.00	0.00	VB	0.0837
272	7.844	27.16	287.98	0.00	0.00	BB	0.0943
273	7.847	34.04	353.19	0.00	0.00	BV	0.0964

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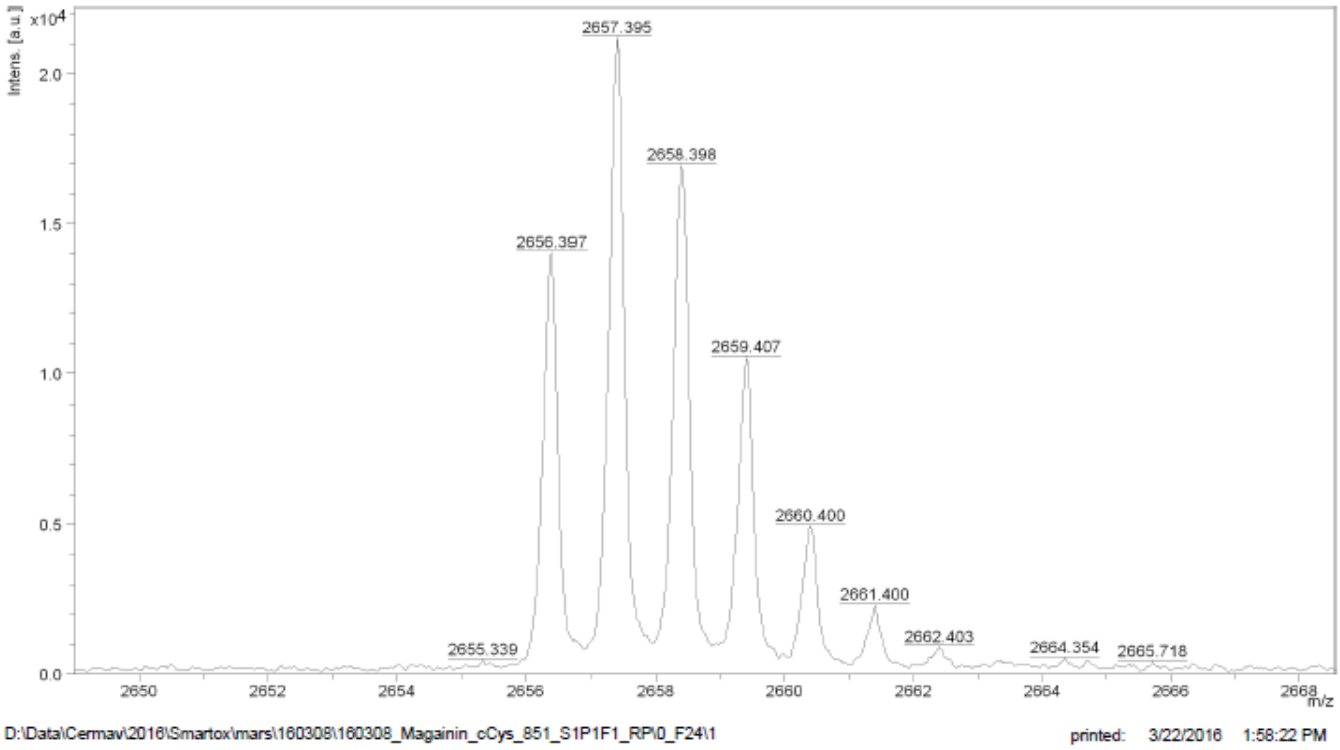

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Certificate of analysis

Date	21/03/2016	Batch	852_s1p1f2
Product name	peptide PGQ	Catalog #	

Product specifications

AA sequence	GVLSNVIGYLKKLGTGALNAVLKQ-AEEA-C-NH2
Disulfide bond	0
Formula	$C_{121}H_{211}N_{33}O_{34}S$
Appearance	White powder
Theoritical average weight	2704,23 g/mol
CAS number	
Source	Synthetic
Counterion	TFA
Solubility (recommendation)	Water 1 mg/mL

Handling & Storage

Storage	Shipped at ambient temperature under lyophilized powder. Store at -20°C (-4°F). Do not freeze-thaw. Aliquot sample if required and store at -80°C (-112°F).
Expiry date	Not defined
Handling and use restriction	Use with caution. Might be toxic. Product intented for research use only, not for use in diagnostic or therapeutic procedures.

Analytical results

Observed purity rate	97,92%	Observed monoisotopic mass [M+H+]+	2703,59 Da
		Theoritical monoisotopic mass	2702,55 Da

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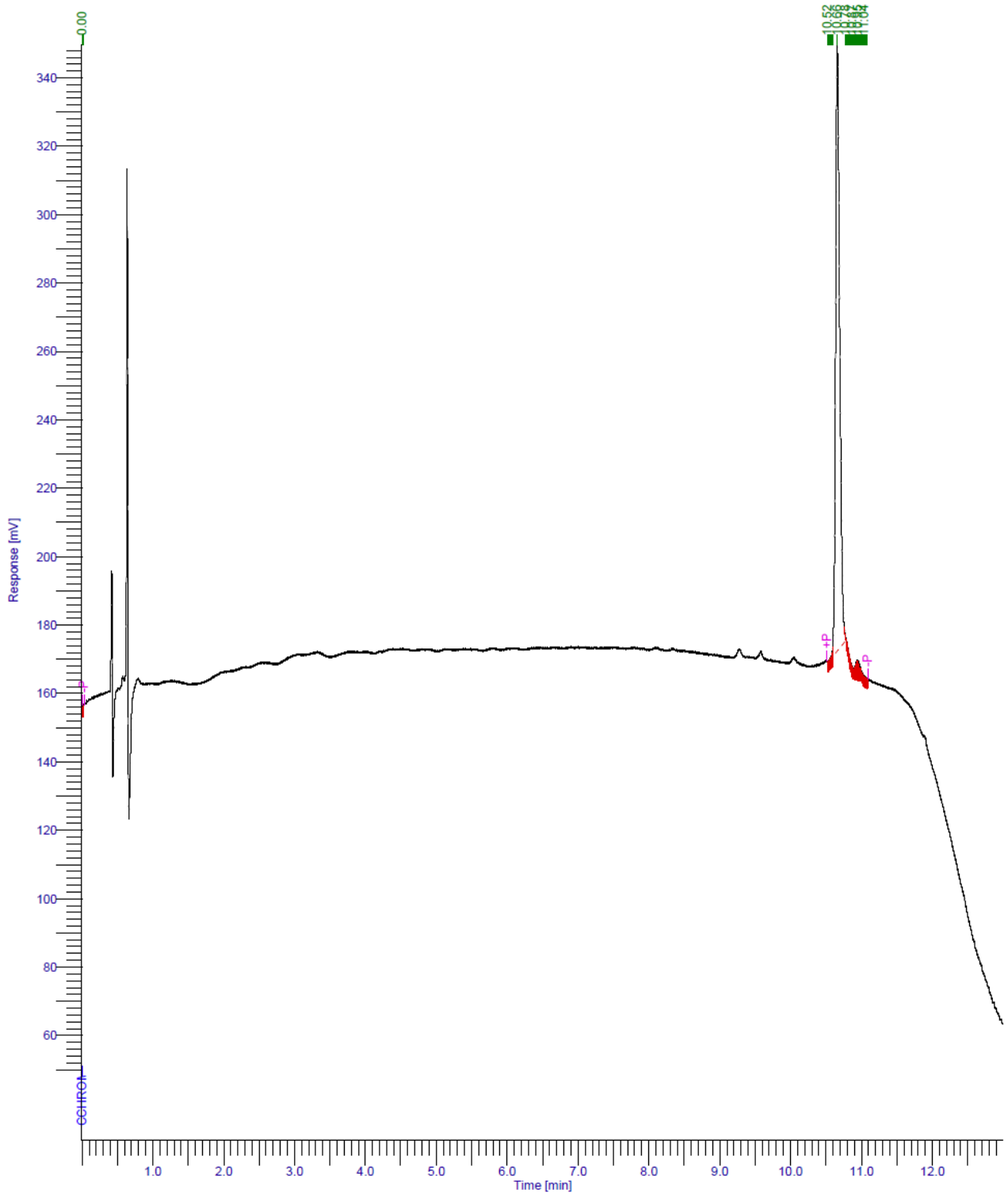
Chromatogram

Sample Name : Sample #: 026 Page 1 of 1
FileName : C:\totalchrom\data\Peptide cea\linjer AEEA fevrier 2016\160304 pgq 852s1p1f2.raw
Date : 3/22/2016 9:26:22 AM
Method : cchromolith 5-65 en 10 min.mth Time of Injection: 3/4/2016 11:22:27 PM
Start Time : 0.00 min End Time : 13.00 min Low Point : 48.26 mAU High Point : 349.56 mAU
Plot Offset: 48.26 mAU Plot Scale: 301.3 mAU



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Peak #	Time [min]	Area [µV·s]	Height [µV]	Area [%]	Norm. Area [%]	BL	Area/Height [s]
-	0.001	0.00	0.00	0.00	0.00		----------
1	0.003	26.52	301.71	0.00	0.00	BV	0.0879
2	0.005	29.05	300.47	0.00	0.00	VB	0.0967
3	0.008	24.28	289.71	0.00	0.00	BV	0.0838
4	0.011	22.94	211.76	0.00	0.00	VB	0.1083
5	0.014	28.98	347.00	0.00	0.00	BV	0.0835
6	0.016	22.64	288.75	0.00	0.00	VB	0.0784
7	0.019	21.52	304.84	0.00	0.00	BB	0.0706
8	0.022	22.65	211.65	0.00	0.00	BV	0.1070
9	0.024	16.55	272.74	0.00	0.00	VV	0.0607
10	0.027	18.71	212.36	0.00	0.00	VB	0.0881
11	10.520	19.13	255.53	0.00	0.00	BB	0.0749
12	10.522	23.27	169.37	0.00	0.00	BV	0.1374
13	10.526	15.88	243.23	0.00	0.00	VB	0.0653
14	10.528	25.54	305.91	0.00	0.00	BB	0.0835
15	10.531	16.48	263.72	0.00	0.00	BV	0.0625
16	10.534	22.87	232.41	0.00	0.00	VV	0.0984
17	10.536	26.20	281.86	0.00	0.00	VV	0.0929
18	10.538	23.62	159.49	0.00	0.00	VB	0.1481
19	10.542	26.52	341.29	0.00	0.00	BV	0.0777
20	10.544	31.06	340.05	0.00	0.00	VV	0.0913
21	10.547	29.26	292.68	0.00	0.00	VV	0.1000
22	10.550	42.07	413.02	0.01	0.01	VV	0.1019
23	10.552	38.50	376.56	0.01	0.01	VV	0.1022
24	10.555	62.27	409.42	0.01	0.01	VV	0.1521
25	10.558	32.11	364.78	0.00	0.00	VV	0.0880
26	10.560	41.41	404.20	0.01	0.01	VV	0.1024
27	10.563	36.64	364.94	0.01	0.01	VV	0.1004
28	10.566	37.36	416.20	0.01	0.01	VV	0.0898
29	10.568	44.15	421.07	0.01	0.01	VV	0.1048
30	10.571	54.39	527.65	0.01	0.01	VV	0.1031
31	10.574	67.34	543.85	0.01	0.01	VV	0.1238
32	10.576	61.73	545.19	0.01	0.01	VV	0.1132
33	10.578	72.76	450.51	0.01	0.01	VV	0.1615
34	10.582	96.41	772.89	0.01	0.01	VV	0.1247
35	10.584	140.43	1023.12	0.02	0.02	VV	0.1373
36	10.587	169.01	1280.76	0.02	0.02	VV	0.1320
37	10.590	226.00	1697.16	0.03	0.03	VV	0.1332
38	10.593	269.07	2109.73	0.04	0.04	VV	0.1275
39	10.595	385.55	2803.13	0.05	0.05	VV	0.1375
40	10.659	713376.20	177068.23	97.92	97.92	VE	4.0288
41	10.778	480.16	541.27	0.07	0.07	EV	0.8871
42	10.784	52.68	487.43	0.01	0.01	VB	0.1081
43	10.789	72.49	350.17	0.01	0.01	BV	0.2070
44	10.795	126.34	335.42	0.02	0.02	VB	0.3767
45	10.805	92.42	355.28	0.01	0.01	BB	0.2601
46	10.813	25.22	318.08	0.00	0.00	BB	0.0793
47	10.816	34.37	379.36	0.00	0.00	BB	0.0906
48	10.819	91.53	314.50	0.01	0.01	BB	0.2910
49	10.829	24.04	263.16	0.00	0.00	BV	0.0914
50	10.832	26.03	335.05	0.00	0.00	VB	0.0777
51	10.837	24.58	307.76	0.00	0.00	BV	0.0799
52	10.840	30.64	345.61	0.00	0.00	VB	0.0886
53	10.843	9.97	170.24	0.00	0.00	BV	0.0586
54	10.846	29.15	328.11	0.00	0.00	VB	0.0888
55	10.848	136.69	337.24	0.02	0.02	BV	0.4053
56	10.867	26.36	285.40	0.00	0.00	VB	0.0923
57	10.870	34.13	304.59	0.00	0.00	BV	0.1120
58	10.872	20.12	300.86	0.00	0.00	VB	0.0669
59	10.875	52.51	312.16	0.01	0.01	BV	0.1682
60	10.880	22.81	265.18	0.00	0.00	VB	0.0860
61	10.883	17.27	225.33	0.00	0.00	BB	0.0767
62	10.885	25.49	158.79	0.00	0.00	BV	0.1606
63	10.887	21.14	160.78	0.00	0.00	VV	0.1315
64	10.891	30.08	353.87	0.00	0.00	VB	0.0850
65	10.894	37.96	366.72	0.01	0.01	BV	0.1035
66	10.896	106.50	405.85	0.01	0.01	VV	0.2624
67	10.902	78.88	641.81	0.01	0.01	VV	0.1229
68	10.904	90.73	712.83	0.01	0.01	VV	0.1273
69	10.907	123.82	952.87	0.02	0.02	VV	0.1299
70	10.910	156.64	1079.11	0.02	0.02	VV	0.1452
71	10.912	181.51	1279.32	0.02	0.02	VV	0.1419
72	10.915	204.72	1426.92	0.03	0.03	VV	0.1435
73	10.917	235.91	1479.75	0.03	0.03	VV	0.1594
74	10.920	273.92	1858.63	0.04	0.04	VV	0.1474
75	10.922	281.59	1868.97	0.04	0.04	VV	0.1507
76	10.926	352.73	2232.73	0.05	0.05	VV	0.1580
77	10.928	317.93	2428.64	0.04	0.04	VV	0.1309
78	10.931	567.64	2526.52	0.08	0.08	VV	0.2247
79	10.934	310.00	2632.88	0.04	0.04	VV	0.1177
80	10.936	390.51	2838.37	0.05	0.05	VV	0.1376
81	10.939	408.08	2942.89	0.06	0.06	VV	0.1387
82	10.942	560.08	3054.82	0.08	0.08	VV	0.1833
83	10.944	448.63	3033.79	0.06	0.06	VV	0.1479
84	10.947	474.21	3067.70	0.07	0.07	VV	0.1546
85	10.950	409.57	3020.90	0.06	0.06	VV	0.1356
86	10.952	425.28	2909.80	0.06	0.06	VV	0.1462
87	10.954	1651.34	2754.66	0.23	0.23	VV	0.5995
88	10.965	324.40	2294.14	0.04	0.04	VV	0.1414
89	10.968	1416.51	2199.07	0.19	0.19	VV	0.6441
90	10.981	200.95	1192.57	0.03	0.03	VV	0.1685
91	10.984	457.77	1108.28	0.06	0.06	VB	0.4130
92	10.998	77.21	366.21	0.01	0.01	BB	0.2108
93	11.003	33.23	397.56	0.00	0.00	BV	0.0836
94	11.006	124.41	388.92	0.02	0.02	VB	0.3199
95	11.019	31.35	261.11	0.00	0.00	BV	0.1201
96	11.024	44.46	289.73	0.01	0.01	VB	0.1535
97	11.030	54.36	333.48	0.01	0.01	BV	0.1630
98	11.035	18.22	232.92	0.00	0.00	VB	0.0782
99	11.038	33.54	335.20	0.00	0.00	BV	0.1000
100	11.040	30.71	345.51	0.00	0.00	VB	0.0889
101	11.043	21.65	279.85	0.00	0.00	BV	0.0774
102	11.045	33.30	347.73	0.00	0.00	VB	0.0958
103	11.051	29.02	369.13	0.00	0.00	BB	0.0786
104	11.054	28.70	373.50	0.00	0.00	BV	0.0768
105	11.056	31.06	291.98	0.00	0.00	VV	0.1064
106	11.059	25.19	342.14	0.00	0.00	VB	0.0736
107	11.062	43.11	273.54	0.01	0.01	BB	0.1576
108	11.067	10.15	148.59	0.00	0.00	BV	0.0683
109	11.070	13.56	249.56	0.00	0.00	VB	0.0543
110	11.071	17.04	146.92	0.00	0.00	BB	0.1160
111	11.074	16.24	122.07	0.00	0.00	BB	0.1330
112	11.077	14.82	176.29	0.00	0.00	BB	0.0841
113	11.083	25.45	308.59	0.00	0.00	BV	0.0825
114	11.086	15.50	173.15	0.00	0.00	*VB	0.0895
		728513.35	264018.78	100.00	100.00		

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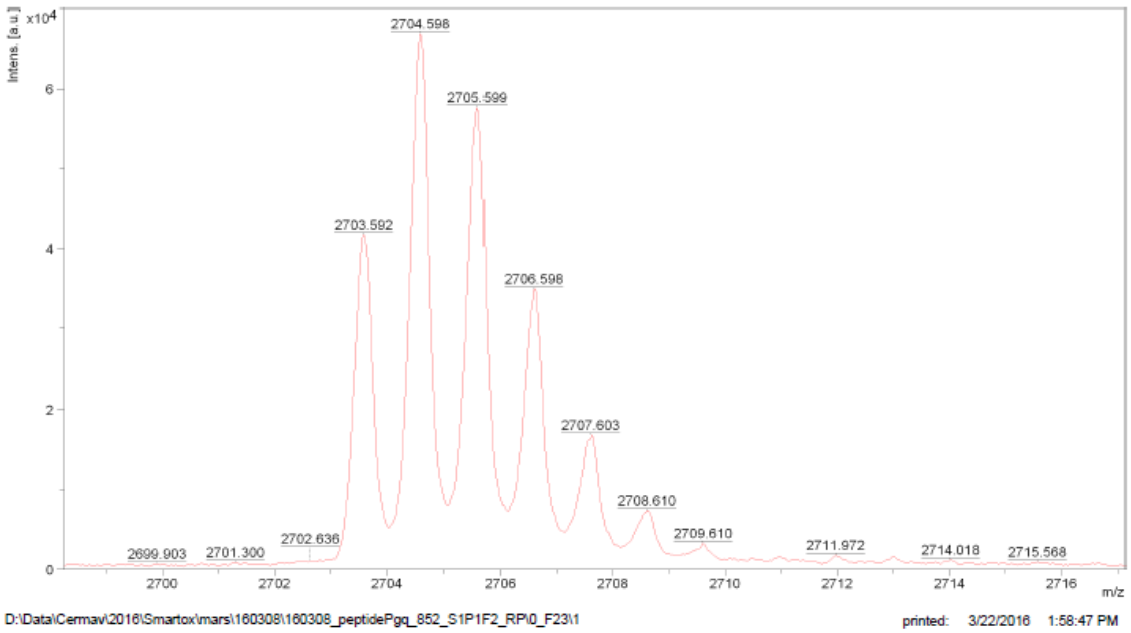
MS Spectra



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Certificate of analysis

Date	22/03/2016	Batch	853_s1p1r2
Product name	Leucocin A 24	Catalog #	

Product specifications

AA sequence	C-AEEA-SVNWGEAFSAGVHRLANGGNGFW-OH
Disulfide bond	0
Formula	$C_{119}H_{170}N_{36}O_{34}S$
Appearance	White powder
Theoritical average weight	2681,89 g/mol
CAS number	
Source	Synthetic
Counterion	TFA
Solubility (recommendation)	50% of Acetonitrile solution 1 mg/mL

Handling & Storage

Storage	Shipped at ambient temperature under lyophilized powder. Store at -20°C (-4°F). Do not freeze-thaw. Aliquot sample if required and store at -80°C (-112°F).
Expiry date	Not defined
Handling and use restriction	Use with caution. Might be toxic. Product intented for research use only, not for use in diagnostic or therapeutic procedures.

Analytical results

Observed purity rate	90,34%	Observed monoisotopic mass [M+H+]+	2681,12 Da
		Theoritical monoisotopic mass	2680,22 Da

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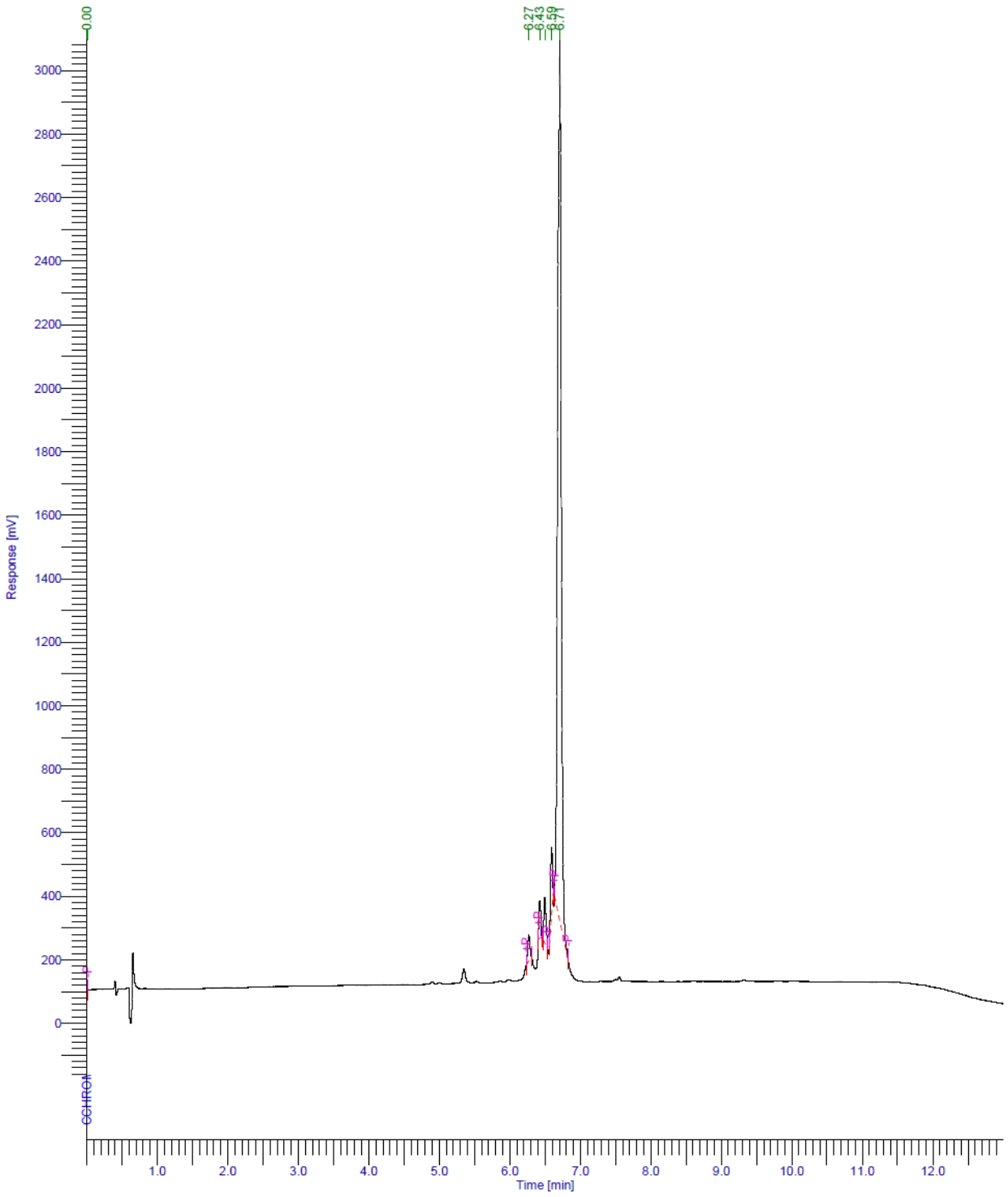
Chromatogram

Sample Name : Sample #: 027 Page 1 of 1
FileName : C:\totalchrom\data\Peptide cea\linjer AEEA fevrier 2016\160314 leucocin a24 aeea 853 s1p1r2.raw
Date : 3/21/2016 2:59:05 PM
Method : cchromolith 5-95 en 10 min.mth Time of Injection: 3/15/2016 1:53:49 AM
Start Time : 0.00 min End Time : 13.00 min Low Point : -162.95 mAU High Point : 3096.09 mAU
Plot Offset: -162.95 mAU Plot Scale: 3259.0 mAU



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Peak #	Time [min]	Area [µV·s]	Height [µV]	Area [%]	Norm. Area [%]	BL	Area/Height [s]
-	0.001	0.00	0.00	0.00	0.00		----------
1	0.002	13.20	202.92	0.00	0.00	BB	0.0650
2	0.004	24.09	271.87	0.00	0.00	BV	0.0886
3	0.007	26.34	302.68	0.00	0.00	VB	0.0870
4	0.010	17.32	234.24	0.00	0.00	*BB	0.0739
5	6.270	170379.05	81098.26	1.60	1.60	*BB	2.1009
6	6.426	195125.07	117045.40	1.84	1.84	*BB	1.6671
7	6.498	304319.96	145871.10	2.87	2.87	*BB	2.0862
8	6.594	355984.87	202441.13	3.35	3.35	*BB	1.7585
9	6.708	9591283.16	2.79e+06	90.34	90.34	*BB	3.4412
		10617173.06	3.33e+06	100.00	100.00		

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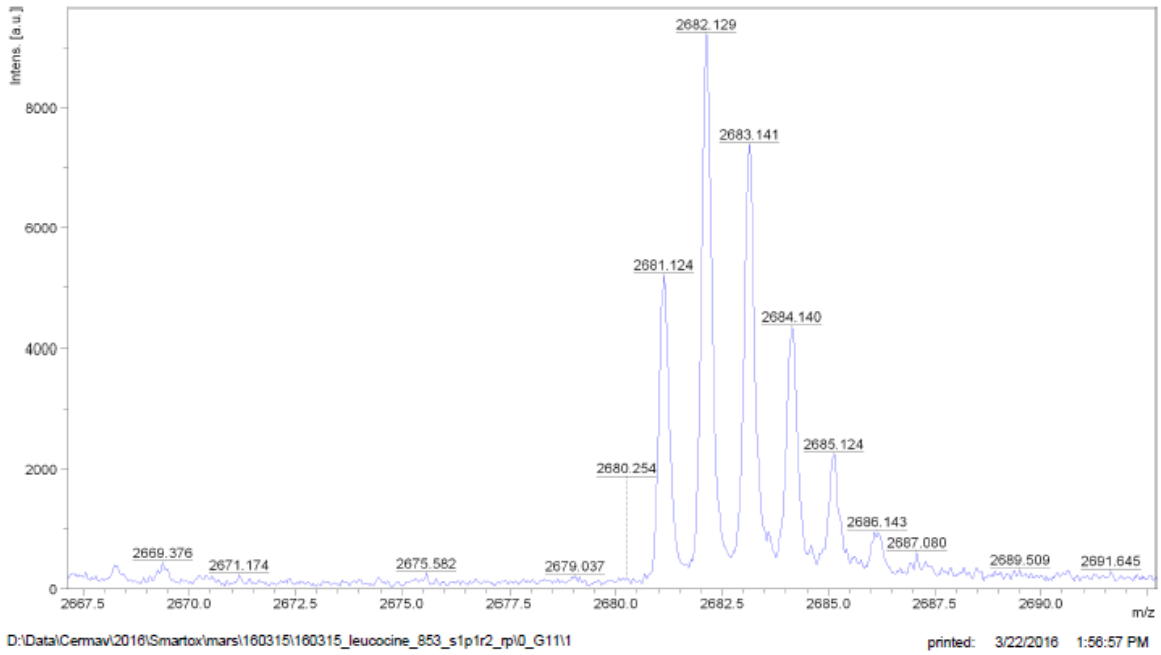

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