# Human microbiome derived synthetic antimicrobial peptides with activity against Gram-negative, Gram-positive, and antibiotic resistant bacteria

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#### **Table of Contents**

Predicted secondary structure and data of peptides	S2
Marfey's Analysis of cyclic peptides	S4
Structures, LC chromatograms, and HRMS spectra of the synthesized peptides	S5
MS/MS fragmentation data of LM6 and its cyclic derivatives LM13a and LM13b	S19

#### Predicted secondary structure and data of peptides



**Figure S1**. A) Helical structure of lactomodulin as predicted by RoseTTA (A1), Quark (A2), and AlphaFold (A3); B) Amino acid sequence of lactomodulin split into five color-coded peptides LM1-LM5 (grey, orange, blue, green, and purple, respectively) and their structural prediction by PEP-FOLD3; C) Sequence of peptides LM6-LM9 obtained based on AMP prediction using CAMPr3 and their structural prediction by PEP-FOLD3.

# Table S1. Novel Lactomodulin derivatives

No.	Sequence	Molecular formula	MW (g/mol)	m/z calcd [M+H] <sup>+</sup>	m/z found [M+H]⁺	Δm (ppm)	Yield (%)	Purity (%)
LM1	MNKLNEVELSKI-NH <sub>2</sub>	$C_{61}H_{109}N_{17}O_{19}S$	1416.78	1416.7879	1416.7736	10.0933	15.1	76
LM2	SGGIGPLVIP-NH <sub>2</sub>	$C_{42}H_{73}N_{11}O_{11}$	908.18	908.5564	908.5530	3.7422	24.0	99
LM3	VAAILGFLAT-NH <sub>2</sub>	$C_{47}H_{79}N_{11}O_{11}$	974.27	974.6033	974.6000	3.3860	29.3	96
LM4	DAWNHADELV-NH <sub>2</sub>	$C_{51}H_{73}N_{15}O_{17}$	1168.28	1168.5382	1168.5320	5.3058	19.7	97
LM5	AGVKQGWERS-NH <sub>2</sub>	$C_{48}H_{77}N_{17}O_{14}$	1116.23	1116.5909	1116.5795	10.2096	19.4	99
LM6	LSKISGGIGPLVIPV-NH <sub>2</sub>	$C_{68}H_{121}N_{17}O_{17}$	1448.92	1448.9199	1448.9039	11.0427	10.8	98
LM7	IGPLVIPVAAIL-NH <sub>2</sub>	$C_{58}H_{103}N_{13}O_{12}$	1174.62	1174.7922	1174.7838	7.1502	19.5	97
LM8	KLNEVELSKISGG-NH <sub>2</sub>	$C_{59}H_{105}N_{17}O_{20}$	1372.67	1372.7774	1372.7755	1.3841	12.5	98
LM9	HADELVAGVKQ-NH <sub>2</sub>	$C_{50}H_{84}N_{16}O_{16}$	1165.38	1165.6324	1165.6274	4.2895	14.4	95
LM10	LSKISGGIGP-NH <sub>2</sub>	$C_{41}H_{74}N_{12}O_{12}$	927.18	927.5622	927.5567	5.9295	31.6	96
LM11	KISGGIGPLV-NH <sub>2</sub>	$C_{43}H_{78}N_{12}O_{11}$	939.24	939.5986	939.5935	5.4278	23.5	97
LM12	LSKISG-NH <sub>2</sub>	$C_{26}H_{50}N_8O_8$	602.77	603.3824	603.3814	1.6573	38.3	95
LM13a	Cyc(LSKISGGIGPLVIPv)	C <sub>68</sub> H <sub>118</sub> N <sub>16</sub> O <sub>17</sub>	1431.79	1431.8934	1431.8863	4.9585	6.1	95
LM13b	Cyc(LSKISGGIGPLVIPV)	C <sub>68</sub> H <sub>118</sub> N <sub>16</sub> O <sub>17</sub>	1431.79	1431.8934	1431.8873	4.2601	1.0	95

## Marfey's Analysis of cyclic peptides



**Figure S2.** Extracted ion chromatogram of Marfey's derivatives (L-/D-FDLA) of L-Val, LM13a and LM13b at 368 Da in negative ion mode.

### **Table S2**: Marfey's analysis of Valine amino acid in LM13a and LM13b

	L-FDLA derivative t <sub>R</sub> (min)	D-FDLA derivative $t_R$ (min)
L-Val	20.5	22.5
1 1 1 2 2	20.5	20.5
	22.5	22.5
LM13b	20.5	22.5

LM13 contains two valine residues. The Marfey's analysis show that the major compound LM13a has both I- and d-Valine residues within its structure, whereas the minor compound LM13b has only I-Valine within its structure. The d-Valine in LM13a is the result of the epimierization of the valine residue at the point of macrocyclization.

# Structures, LC chromatograms, and HRMS spectra of the synthesized peptides A) LM1



**Figure S3: A)** LM1 peptide chemical structure, **B)** LC-UV chromatogram of LM1 at 220nm; tr = 11.81 min; 76% purity, **C)** HRMS-ESI-MS<sup>2</sup> spectrum in the positive mode of LM1 peak

lon	Found	Expected	Δm
MNKLNEVELSKI-NH <sub>2</sub> + H <sup>+</sup>	1416.7736	1416.7879	10.1 ppm
MNKLNEVELSKI-NH <sub>2</sub> + Na <sup>+</sup>	1438.7561	1438.7699	9.6 ppm
MNKLNEVELSKI-NH <sub>2</sub> + 2H <sup>+</sup>	708.8918	708.8976	8.2 ppm
LM1 I-NH <sub>2</sub>	1286.6649	1286.6773	9.6 ppm
LM1 KI-NH <sub>2</sub>	1158.5701	1158.5824	10.6 ppm
LM1 SKI-NH <sub>2</sub>	1071.5406	1071.5503	9.1 ppm

Table S3: MS peaks and MS<sup>2</sup> fragments observed for LM1



Exact Mass: 907.5491



**Figure S4: A)** LM2 peptide chemical structure, **B)** LC-UV chromatogram of LM2 at 220nm;  $t_R = 13.82$  min; 99% purity, **C)** HRMS-ESI-MS<sup>2</sup> spectrum in the positive mode of LM2 peak.

Ion	Found	Expected	Δm
SGGIGPLVIP-NH <sub>2</sub> + H <sup>+</sup>	908.5530	908.5564	3.7 ppm
$(SGGIGPLVIP-NH_2)_2 + H^+$	1816.1020	1816.1055	1.9 ppm
SGGIGPLVIP-NH <sub>2</sub> + 2H <sup>+</sup>	454.7804	454.7819	3.3 ppm
LM2 P-NH <sub>2</sub>	794.4747	794.4771	3.0 ppm
LM2 IP-NH <sub>2</sub>	681.3916	681.3931	2.2 ppm
LM2 VIP-NH <sub>2</sub> H <sub>2</sub> O	564.3135	564.3141	1.1 ppm

Table S4: MS peaks and MS<sup>2</sup> fragments observed for LM2



Chemical Formula: C<sub>47</sub>H<sub>79</sub>N<sub>11</sub>O<sub>11</sub> Exact Mass: 973.5961



**Figure S5: A)** LM3 peptide chemical structure, **B)** LC-UV chromatogram of LM3 at 220nm;  $t_R = 14.90$  min; 96% purity, **C)** HRMS-ESI-MS<sup>2</sup> spectrum in the positive mode of LM3 peak.

lon	Found	Expected	Δm
VAAILGFLAT-NH <sub>2</sub> + H <sup>+</sup>	974.6000	974.6033	3.4 ppm
VAAILGFLAT-NH <sub>2</sub> + Na <sup>+</sup>	996.5820	996.5853	3.3 ppm
(VAAILGFLAT-NH <sub>2</sub> ) <sub>2</sub> + H <sup>+</sup>	1949.1989	1949.2028	2.0 ppm
(VAAILGFLAT-NH <sub>2</sub> ) <sub>2</sub> + Na <sup>+</sup>	1971.1816	1971.1847	1.6 ppm
VAAILGFLAT-NH <sub>2</sub> + 2H <sup>+</sup>	487.8039	487.8053	2.9 ppm
LM3 T-NH <sub>2</sub>	856.5267	856.5291	2.8 ppm
LM3 AT-NH <sub>2</sub>	785.4900	785.4920	2.5 ppm
LM3 LAT-NH <sub>2</sub>	672.4063	672.4080	2.5 ppm

Table S5: MS peaks and MS<sup>2</sup> fragments observed for LM3



 $\begin{array}{l} \mbox{Chemical Formula: } C_{51}H_{73}N_{15}O_{17} \\ \mbox{Exact Mass: } 1167.5309 \end{array}$ 



**Figure S6: A)** LM4 peptide chemical structure, **B)** LC-UV chromatogram of LM4 at 220nm;  $t_R = 15.95$  min; 97% purity, **C)** HRMS-ESI-MS<sup>2</sup> spectrum in the positive mode of LM4 peak.

lon	Found	Expected	Δm	
DAWNHADELV-NH <sub>2</sub> + H <sup>+</sup>	1168.5320	1168.5382	5.3 ppm	
DAWNHADELV-NH <sub>2</sub> + Na <sup>+</sup>	1190.5161	1190.5202	3.4 ppm	
DAWNHADELV-NH <sub>2</sub> + 2H <sup>+</sup>	584.7705	584.7727	3.8 ppm	
LM4 V-NH <sub>2</sub>	1052.4380	1052.4432	4.9 ppm	
LM4 LV-NH <sub>2</sub>	939.3547	939.3592	4.8 ppm	
LM4 ELV-NH <sub>2</sub>	810.3134	810.3166	3.9 ppm	
LM4 DELV-NH <sub>2</sub>	695.2872	695.2896	3.5 ppm	
LM4 ADELV-NH <sub>2</sub>	624.2506	624.2525	3.0 ppm	

Table S6: MS peaks and MS<sup>2</sup> fragments observed for LM4





**Figure S7: A)** LM5 peptide chemical structure, **B)** LC-UV chromatogram of LM5 at 220nm;  $t_R = 6.41$  min; 99% purity, **C)** HRMS-ESI-MS<sup>2</sup> spectrum in the positive mode of LM5 peak.

lon	Found	Expected	Δm
AGVKQGWERS-NH <sub>2</sub> + H <sup>+</sup>	1116.5795	1116.5909	10.2 ppm
AGVKQGWERS-NH <sub>2</sub> + 2H <sup>+</sup>	558.7941	558.7991	8.9 ppm
LM5 S-NH <sub>2</sub>	1012.5203	1012.5323	11.9 ppm
LM5 AGV + H <sup>+</sup>	889.4544	889.4639	10.7 ppm
LM5 AGVK + H <sup>+</sup>	761.3609	761.3690	10.6 ppm
LM5 AGVKQGW + H <sup>+</sup>	390.2058	390.2096	9.7 ppm

Table S7: MS peaks and MS<sup>2</sup> fragments observed for LM5

A) LM6



Exact Mass: 1448.8967



**Figure S8: A)** LM6 peptide chemical structure, **B)** LC-UV chromatogram of LM6 at 220nm;  $t_R = 14.51$  min; 98% purity, **C)** HRMS-ESI-MS<sup>2</sup> spectrum in the positive mode of LM6 peak.

lon	Found	Expected	Δm
LSKISGGIGPLVIPV-NH <sub>2</sub> + H <sup>+</sup>	1448.9039	1448.9199	11.0 ppm
LSKISGGIGPLVIPV-NH <sub>2</sub> + Na <sup>+</sup>	1470.8867	1470.9019	10.3 ppm
LSKISGGIGPLVIPV-NH <sub>2</sub> + 2H <sup>+</sup>	724.9565	724.9636	9.8 ppm
LM6 CO-NH <sub>2</sub>	1403.8853	1403.8985	9.4 ppm
LM6 V-NH <sub>2</sub>	1332.8122	1332.8250	9.6 ppm
LM6 PV-NH <sub>2</sub>	1235.7593	1235.7722	10.4 ppm
LM6 IPV-NH <sub>2</sub>	1122.6756	1122.6882	11.2 ppm
LM6 IGPLVIPV-NH <sub>2</sub>	643.3703	643.3774	11.0 ppm



 $\begin{array}{c} \mbox{Chemical Formula: } C_{58}H_{103}N_{13}O_{12} \\ \mbox{Exact Mass: } 1173.7849 \end{array}$ 



**Figure S9: A)** LM7 peptide chemical structure, **B)** LC-UV chromatogram of LM7 at 220nm; tR = 15.83 min; 97% purity, **C)** HRMS-ESI-MS<sup>2</sup> spectrum in the positive mode of LM7 peak.

lon	Found	Expected	Δm
IGPLVIPVAAIL-NH <sub>2</sub> + H <sup>+</sup>	1174.7838	1174.7922	7.2 ppm
IGPLVIPVAAIL-NH <sub>2</sub> + Na <sup>+</sup>	1196.7665	1196.7742	6.4 ppm
IGPLVIPVAAIL-NH <sub>2</sub> + K <sup>+</sup>	1212.7397	1212.7481	6.9 ppm
(IGPLVIPVAAIL-NH <sub>2</sub> ) <sub>3</sub> + 2H <sup>+</sup>	1762.1749	1762.1864	6.5 ppm
(IGPLVIPVAAIL-NH <sub>2</sub> ) <sub>2</sub> + H <sup>+</sup>	2349.5687	2349.5805	5.0 ppm
IGPLVIPVAAIL-NH <sub>2</sub> + 2H <sup>+</sup>	587.8960	587.8998	6.5 ppm
LM7 L-NH <sub>2</sub>	1044.6744	1044.6816	6.9 ppm
LM7 IL-NH <sub>2</sub>	931.5912	931.5976	6.9 ppm
LM7 AIL-NH <sub>2</sub>	860.5550	860.5605	6.4 ppm
LM7 AAIL-NH <sub>2</sub>	789.5181	789.5233	6.6 ppm

Table S9: MS peaks and MS<sup>2</sup> fragments observed for LM7



**Figure S10: A)** LM8 peptide chemical structure, **B)** LC-UV chromatogram of LM8 at 220nm;  $t_R = 14.98$  min; 98% purity, **C)** HRMS-ESI-MS<sup>2</sup> spectrum in the positive mode of LM8 peak.

I	0		
lon	Found	Expected	Δm
KLNEVELSKISGG-NH <sub>2</sub> + H <sup>+</sup>	1372.7774	1372.7795	1.5 ppm
KLNEVELSKISGG-NH <sub>2</sub> + Na <sup>+</sup>	1394.7594	1394.7614	1.4 ppm
KLNEVELSKISGG-NH <sub>2</sub> + K <sup>+</sup>	1410.7302	1410.7354	3.7 ppm
LM8 GG-NH <sub>2</sub>	1241.7084	1241.7100	1.3 ppm
LM8 ISGG-NH <sub>2</sub>	1041.5924	1041.5939	1.4 ppm
LM8 KISGG-NH <sub>2</sub>	913.4970	913.4990	2.2 ppm
LM8 SKISGG-NH <sub>2</sub>	826.4655	826.4669	1.7 ppm

Table S10: MS peaks and MS<sup>2</sup> fragments observed for LM8



Exact Mass: 1164.6251



**Figure S11: A)** LM9 peptide chemical structure, **B)** LC-UV chromatogram of LM9 at 220nm;  $t_R = 9.41$  min; 95% purity, **C)** HRMS-ESI-MS<sup>2</sup> spectrum in the positive mode of LM9 peak.

Table S11: MS peak	ks and MS <sup>2</sup> fragments o	bserved for LM9

lon	Found	Expected	Δm
HADELVAGVKQ-NH <sub>2</sub> + H <sup>+</sup>	1165.6274	1165.6324	4.3 ppm
HADELVAGVKQ-NH <sub>2</sub> + 2H <sup>+</sup>	583.3180	583.3199	3.3 ppm
LM9 Q-NH <sub>2</sub>	1020.5430	1020.5473	4.2 ppm
LM9 KQ-NH <sub>2</sub>	892.4489	892.4524	3.9 ppm
LM9 VKQ-NH <sub>2</sub>	793.3813	793.3839	3.3 ppm
LM9 GVKQ-NH <sub>2</sub>	736.3600	736.3625	3.4 ppm
LM9 AGVKQ-NH <sub>2</sub>	665.3227	665.3254	4.1 ppm
LM9 VAGVKQ-NH <sub>2</sub>	566.2552	566.2570	3.2 ppm
LM9 LVAGVKQ-NH <sub>2</sub>	453.1715	453.1729	3.1 ppm
LM9 HADEL + H <sup>+</sup>	600.3805	600.3828	3.8 ppm
LM9 HADELV + H <sup>+</sup>	501.3124	501.3144	4.0 ppm
LM9 HADELVA + H <sup>+</sup>	430.2755	430.2773	4.2 ppm





Figure S12: A) LM10 peptide chemical structure, B) LC-UV chromatogram of LM10 at 220nm; tR = 13.63 min; 96% purity, **C)** HRMS-ESI-MS<sup>2</sup> spectrum in the positive mode of LM10 peak.

Table S12: MS peaks and MS	<sup>2</sup> fragments observed for LM10
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lon	Found	Expected	Δm
LSKISGGIGP-NH <sub>2</sub> + H <sup>+</sup>	927.5567	927.5622	5.9 ppm
LSKISGGIGP-NH <sub>2</sub> + Na <sup>+</sup>	949.5391	949.5442	5.4 ppm
$(LSKISGGIGP-NH_2)_3 + 2H^+$	1391.3347	1391.3414	4.8 ppm
$(LSKISGGIGP-NH_2)_2 + H^+$	1854.1102	1854.1172	3.8 ppm
LSKISGGIGP-NH <sub>2</sub> + 2H <sup>+</sup>	464.2824	464.2848	5.2 ppm
LM10 P-NH <sub>2</sub>	813.4781	813.4829	5.9 ppm
LM10 GP-NH <sub>2</sub>	756.4573	756.4615	5.6 ppm
LM10 IGP-NH <sub>2</sub>	643.3743	643.3774	4.8 ppm
LM10 GGIGP-NH <sub>2</sub>	529.3322	529.3345	4.3 ppm



Exact Mass: 938.5913



**Figure S13: A)** LM11 peptide chemical structure, **B)** LC-UV chromatogram of LM11 at 220nm;  $t_R = 17.32 \text{ min}$ ; 97% purity, **C)** HRMS-ESI-MS<sup>2</sup> spectrum in the positive mode of LM11 peak.

lon	Found	Expected	Δm
KISGGIGPLV-NH <sub>2</sub> + H <sup>+</sup>	939.5935	939.5986	5.4 ppm
KISGGIGPLV-NH <sub>2</sub> + Na <sup>+</sup>	961.5761	961.5806	4.7 ppm
(KISGGIGPLV-NH <sub>2</sub> ) <sub>2</sub> + H <sup>+</sup>	1878.1840	1878.1899	3.1 ppm
KISGGIGPLV-NH <sub>2</sub> + 2H <sup>+</sup>	470.3007	470.3030	4.9 ppm
LM11 V-NH <sub>2</sub>	823.5037	823.4989	5.8 ppm
LM11 LV-NH <sub>2</sub>	710.4158	710.4196	5.3 ppm
LM11 PLV-NH <sub>2</sub>	613.3636	613.3668	5.2 ppm
LM11 GPLV-NH <sub>2</sub>	556.3430	556.3454	4.3 ppm

A) LM12



NL: 1.58E5 UV\_VIS\_1 UV MD016\_T2 \_TC

2000

Figure S14: A) LM12 peptide chemical structure, B) LC-UV chromatogram of LM12 at 220nm; tR = 9.94 min; 95% purity, **C)** HRMS-ESI-MS<sup>2</sup> spectrum in the positive mode of LM12 peak.

Table S14: MS peaks and MS	<sup>2</sup> fragments observed for LM12
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lon	Found	Expected	Δm
LSKISG-NH <sub>2</sub> + H <sup>+</sup>	603.3814	603.3824	1.7 ppm
LSKISG-NH <sub>2</sub> + Na <sup>+</sup>	625.3637	625.3644	1.1 ppm
LSKISG-NH <sub>2</sub> + K <sup>+</sup>	641.3373	641.3384	1.7 ppm
$(LSKISG-NH_2)_2 + H^+$	1205.7542	1205.7576	2.8 ppm
LM12 NH <sub>2</sub>	586.3549	586.3559	1.7 ppm
LM12 G-NH <sub>2</sub>	529.3336	529.3345	1.7 ppm
LM12 SG-NH <sub>2</sub>	442.3017	442.3024	1.6 ppm
LM12 L + H <sup>+</sup>	490.2972	490.2984	2.4 ppm



Chemical Formula: C<sub>68</sub>H<sub>118</sub>N<sub>16</sub>O<sub>17</sub> Exact Mass: 1430.88609



**Figure S15: A)** LM13a peptide chemical structure, **B)** LC-UV chromatogram of LM13a at 220nm;  $t_R = 17.76 \text{ min}$ ; 95% purity, **C)** HRMS-ESI-MS<sup>2</sup> spectrum in the positive mode of LM13a peak.

lon	Found	Expected	Δm
Cyc(LSKISGGIGPLVIPv) + H <sup>+</sup>	1431.8863	1431.8934	5.0 ppm
Cyc(LSKISGGIGPLVIPv) + Na <sup>+</sup>	1453.8704	1453.8753	3.4 ppm
Cyc(LSKISGGIGPLVIPv) + 2H <sup>+</sup>	716.4477	716.4503	3.6 ppm

Table S15: MS peaks observed for LM13a



Exact Mass: 1430.88609



**Figure S16: A)** LM13b peptide chemical structure, **B)** LC-UV chromatogram of LM13b at 220nm; tR = 18.35 min; 95% purity, **C)** HRMS-ESI-MS<sup>2</sup> spectrum in the positive mode of LM13b peak.

lon	Found	Expected	Δm
Cyc(LSKISGGIGPLVIPV) + H <sup>+</sup>	1431.8873	1431.8934	4.3 ppm
Cyc(LSKISGGIGPLVIPV) + Na <sup>+</sup>	1453.8715	1453.8753	2.6 ppm
Cyc(LSKISGGIGPLVIPV) + 2H <sup>+</sup>	716.4480	716.4503	3.2 ppm

Table S16: MS peaks observed for LM13a

# MS/MS fragmentation data of LM6 and its cyclic derivatives LM13a and LM13b



Figure S17: MS<sup>2</sup> fragmentation pattern and MS<sup>2</sup> spectrum of linear peptide LM6.

Ion	Observed m/z	lon	Observed m/z
b13	1235.7515	a8	728.4599
b12	1122.6769	b7	643.3734
b11	1023.6040	b5	529.3349
a11	995.6180	b4	442.3050
b9	813.4699	у3	327.2381
a9	785.4830	y2	214.1551
b8	756.4548	y1	117.1025

 Table S17: MS<sup>2</sup> fragments observed for LM6 (LSKISGGIGPLVIPV)

#### LM13a

MD016\_CyclicPurePk2\_B #2399 RT: 17.86 AV: 1 NL: 6.37E5 F: FTMS + p ESI d Full ms2 1431.8934@hcd30.00 [196.3333-2945.0000]



Figure S18: MS	S <sup>2</sup> fragmentation	pattern of cyclic	peptide LM13a.
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lon	Additional	Observed m/z	lon	Observed m/z
LM13a	-CO	1403.8964	LM13a -IVLPGI	839.5005
LM13a -I / -L		1318.8057	LM13a -KSLVPI	794.4776
LM13a -I / -L	-CO	1290.8112	LM13a -IVLPGIGG	725.4554
LM13a -VL / -IV / -LV		1219.7365	LM13a -IVLPGIGGS	638.4217
LM13a -VL -IV / -LV	-CO	1191.7389	LM13a -GGSIKSLVP	593.4095
LM13a -VLP / -PIV / -LVP		1122.6906	LM13a -IVLPGIGGSI	525.3398
LM13a -VLPG		1065.6654	LM13a -IGGSIKSLVP	480.3174
LM13a -LVPI / -IVLP		1009.6015	LM13a -IGGSIKSLVPI	367.2330
LM13a -IVLPG / -VLPGI		952.5800	PVL / PLV / LVI / VIP	310.2119
LM13a -IVLPG / -VLPGI	-CO	924.5857	IP / PL	211.1430
LM13a -KSLVP		907.5642		

#### LM13b



1432.8793

Figure S19:	MS <sup>2</sup> fragmentation	pattern of cycli	c peptide LM13b.
0			

lon	Additional	Observed m/z	lon	Additional	Observed m/z
LM13a -I / -L		1318.7905	LM13a -IVLPGIGGS	-H <sub>2</sub> O	620.4110
LM13a -VL / -IV / -LV		1219.7368	LM13a -IVLPGIGGSI		525.3386
LM13a -VLP / -PIV / -LVP		1122.6755	LM13a -IGGSIKSLVP		480.3187
LM13a -LVPI / -IVLP		1009.5878	IPVL / LVIP / PLVI		423.2933
LM13a -IVLPG / -VLPGI		952.5773	PVLS		397.2423
LM13a -IVLPG / -VLPGI	-CO	924.5790	LSK / SKI / KIS		329.2177
LM13a -IVLPGI		839.4883	PVL/PLV/LVI/VIP		310.2123
LM13a -IKSLVP	-H <sub>2</sub> O	776.4604	GPL / IGP		268.1648
LM13a -IVLPGIGG		725.4523	IP / PL		211.1430
LM13a -IKSLVPI		681.3889	PV		197.1282
LM13a -IVLPGIGGS		638.4219	PV	-CO	169.1338
			К		129.1021