

Figure S1. Typical 2D JRES spectrum of lyophilized slime from *Helix aspersa* (< 1 kD) in the range from 5.0 to 9.0 ppm, pH=7.35, 298.0 K.

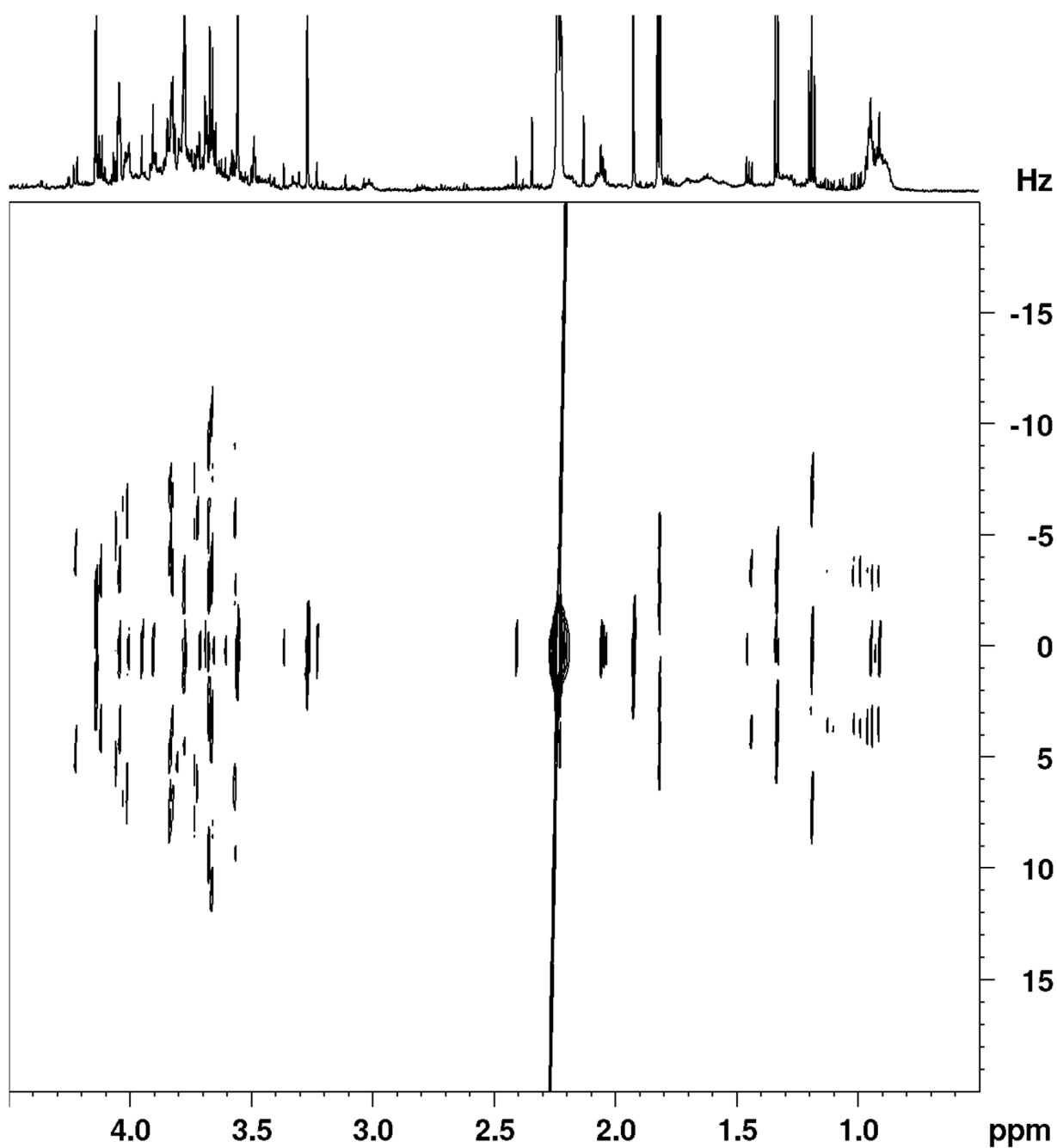


Figure S2. Typical 2D JRES spectrum of lyophilized slime from *Helix aspersa* (< 1 kD) in the range from 4.5 to 0.5 ppm, pH=7.35, 298.0 K.

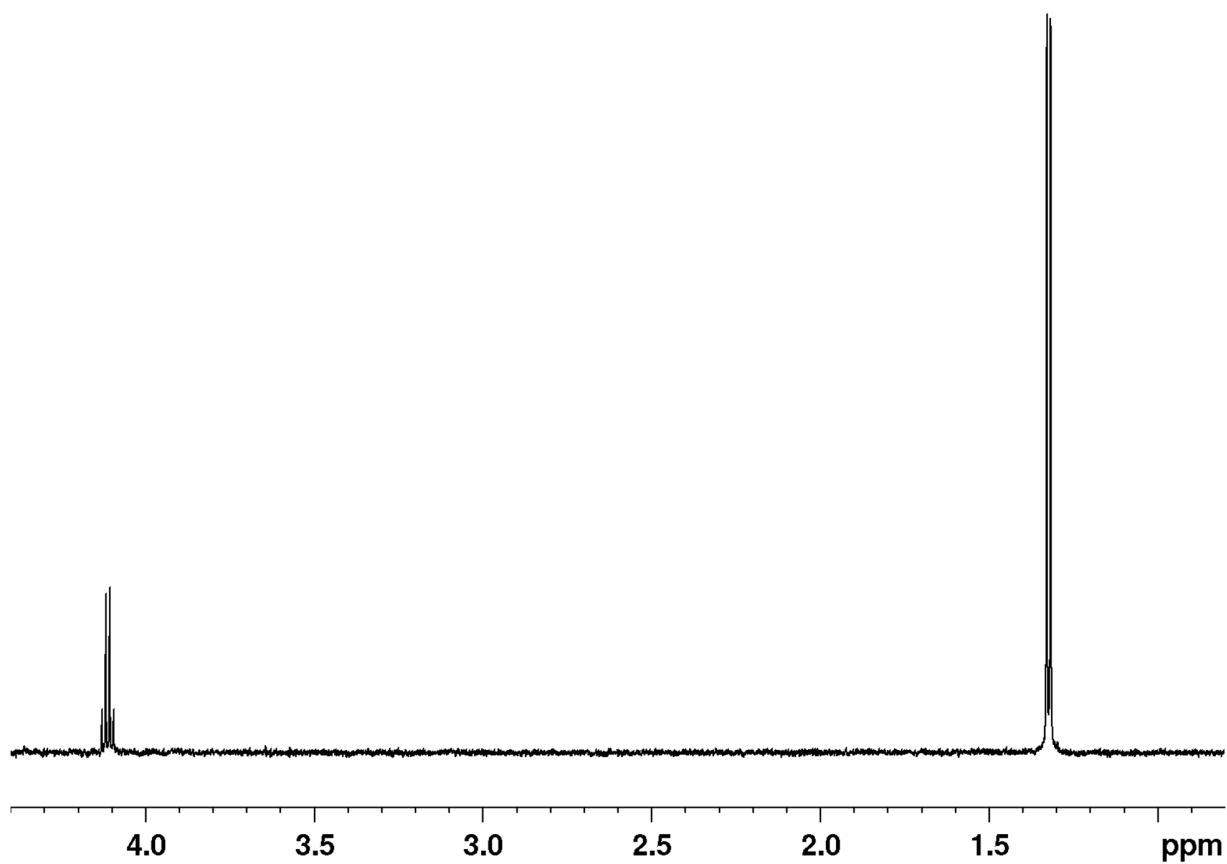


Figure S3. Typical 1D selective TOCSY with water suppression of lyophilized slime from *Helix aspersa* (< 3kD) revealing the metabolite lactic acid (lactate).

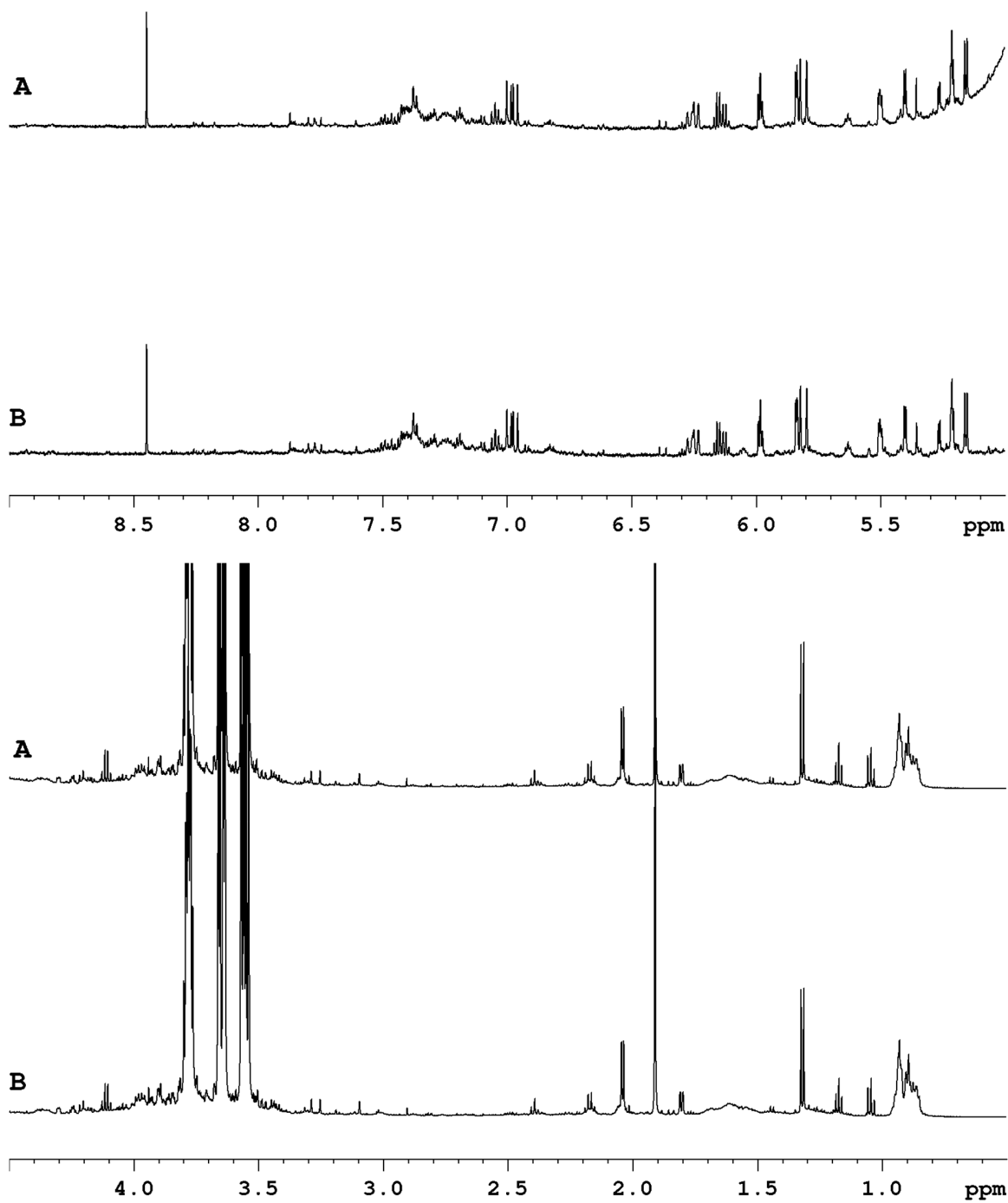


Figure S4. Superposition of $^1\text{H-NMR}$ spectra of lyophilized slime from *Helix aspersa* (< 3kD) **A)** freshly prepared and **B)** after 24 hours at room temperature. There are no visible changes in the spectra.

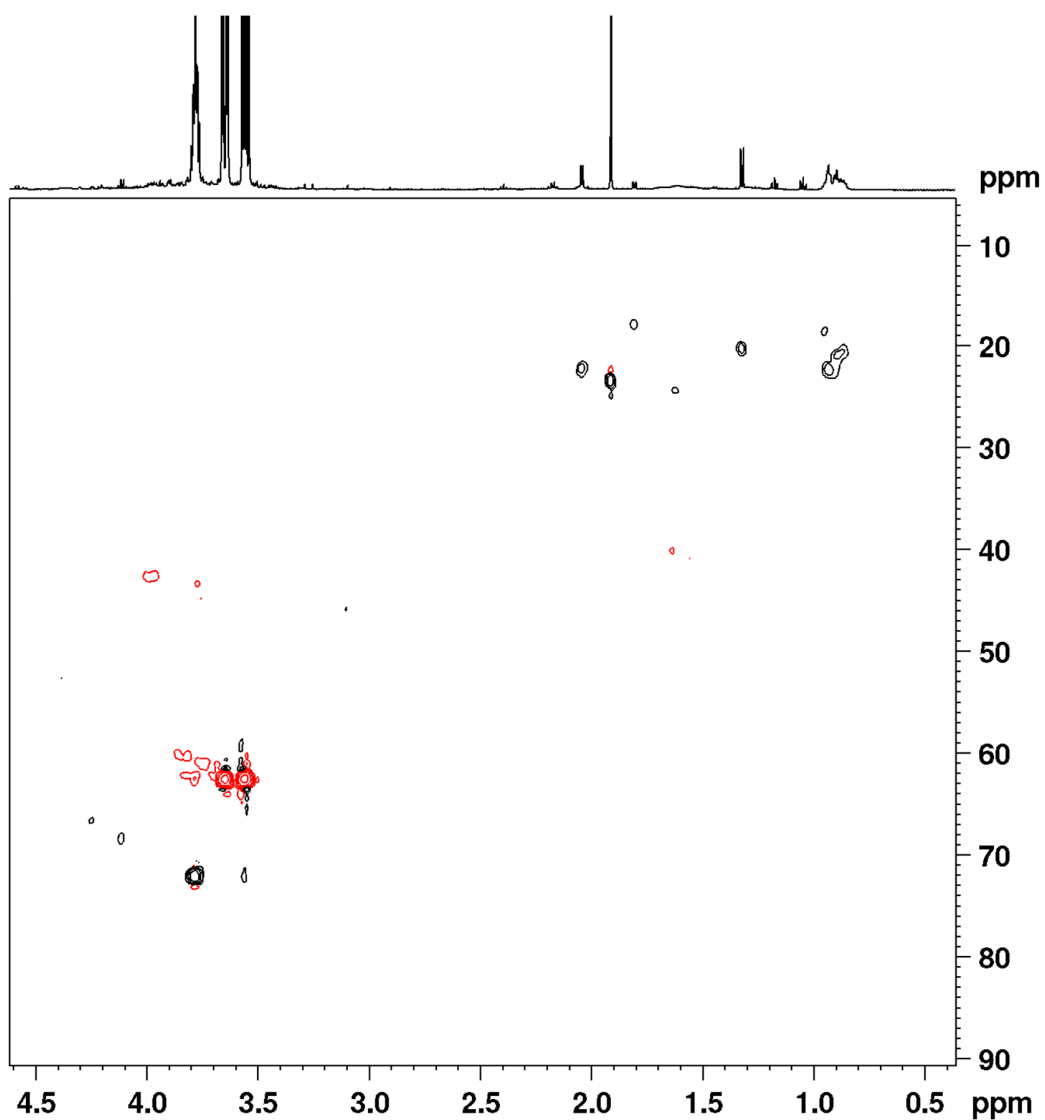


Figure S5. ^1H , ^{13}C HSQC spectrum of lyophilized slime from *Helix aspersa* (< 3kD) (pH 7.35, 298.0 K). The spectral regions devoid of signals have been cut away.

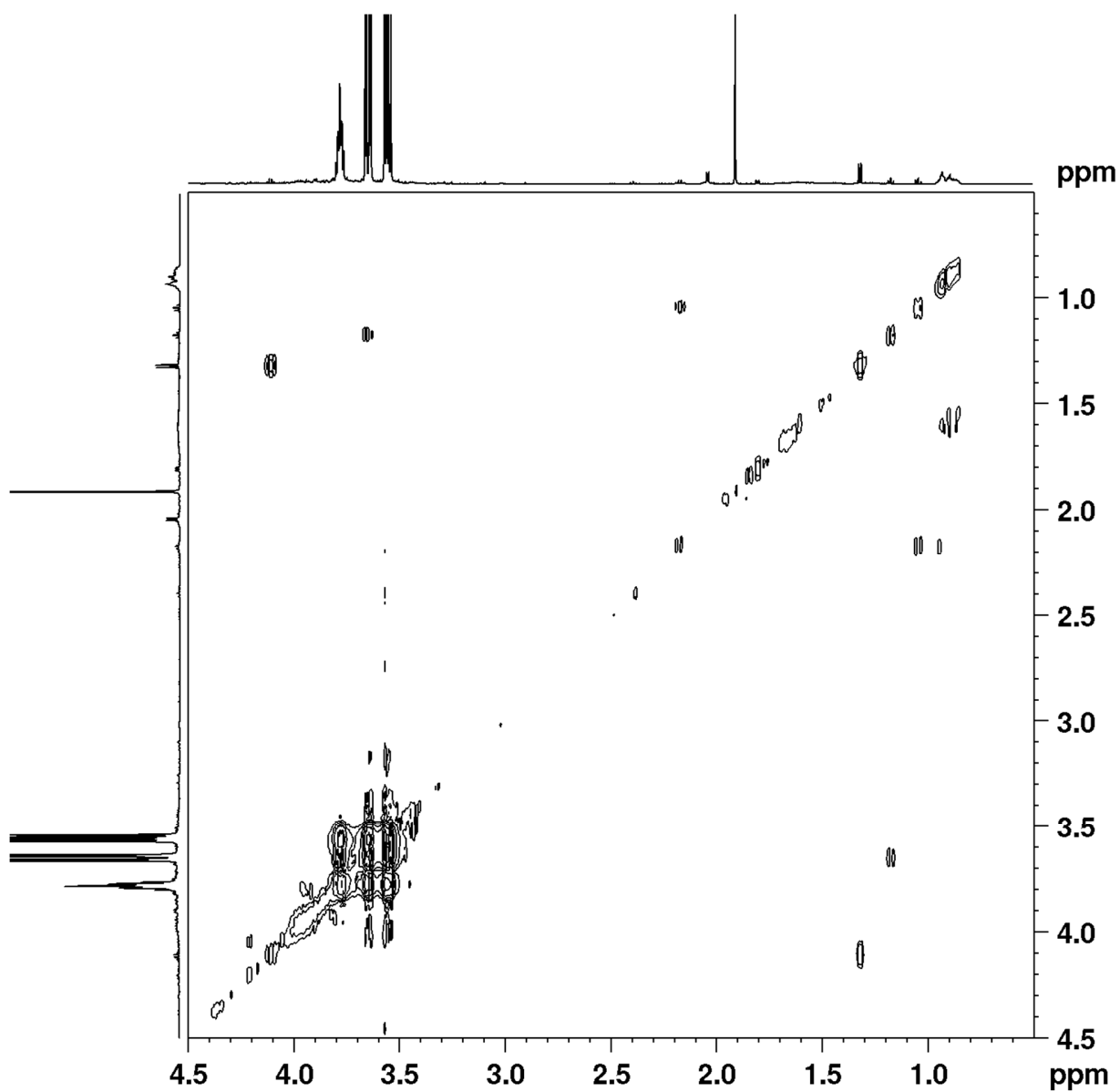


Figure S6. Typical ^1H , ^1H COSY NMR spectrum of lyophilized slime from *Helix aspersa* (< 3kD) (pH 7.35, 298.0 K). The expansion of the 4.5-0.5 ppm region is shown.

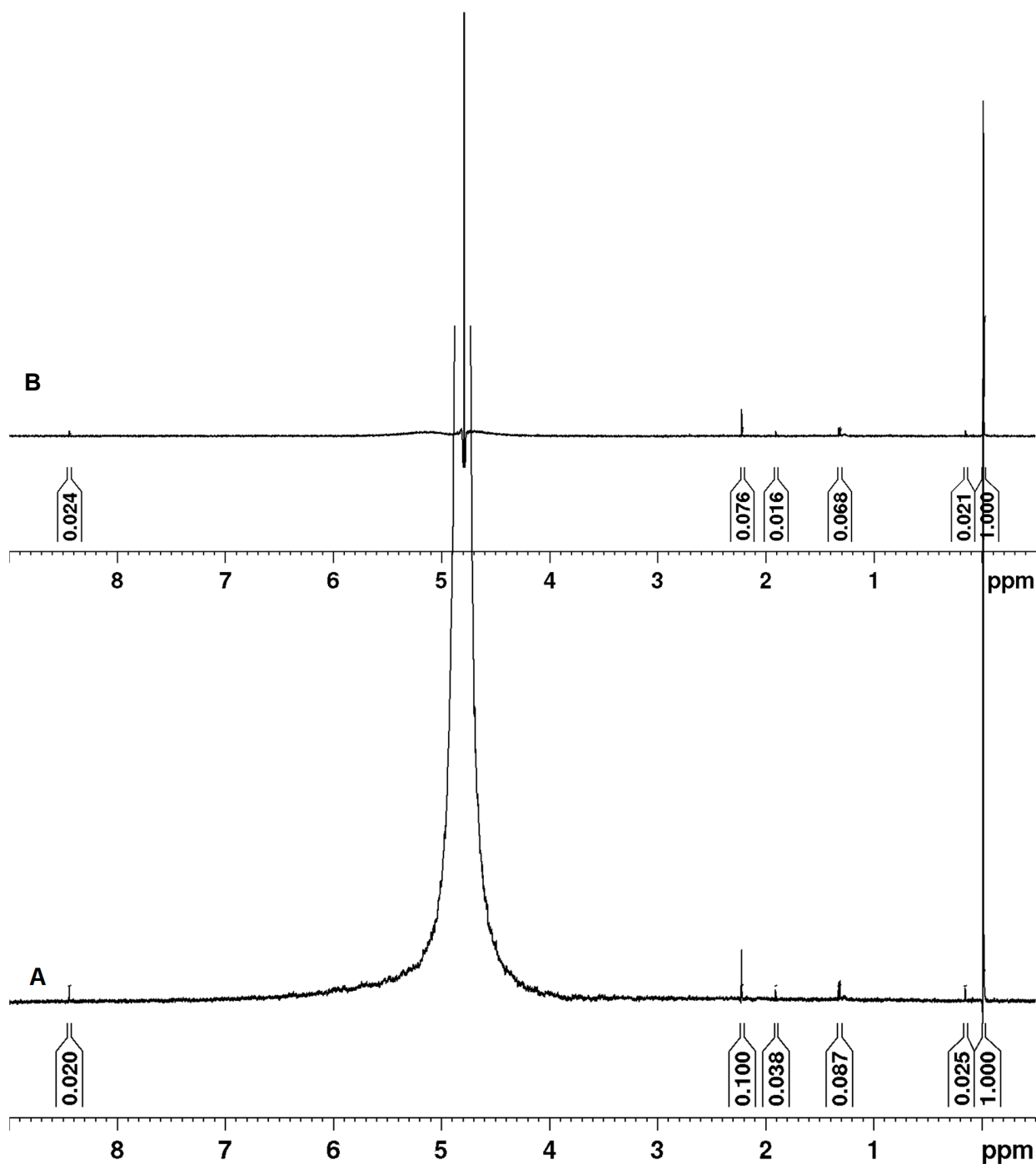


Figure S7. Typical ^1H NMR spectrum of a buffer sample prepared under identical conditions but lacking snail mucus (pH 7.35, 298.0 K). The concentrations of contaminants (In this case: lactic acid at 1.32 ppm – 0.05 mM; acetic acid at 1.91 ppm – 0.03 mM; acetone at 2.22 ppm – 0.03 mM and formic acid/formate at 8.44 ppm – 0.03 mM) are usually at least an order of magnitude lower than the determined concentrations in the actual samples. **A:** 1D NOESY (noesygppld.2); **B:** 1D sequence (zgesgpe) with water suppression using excitation sculpting with gradients using perfect echo.

Information S8: Information on the similarity of amino acid sequences of some identified peptides from *H. aspersa* mucus (Table 2):

A) An alignment with known AMPs database by CAMPSing
(<http://www.campsign.bicnirrh.res.in/blast.php>):

Peptide P4: LGLGNGGAGGGLVGG

> CAMPSQ3913| Ctenidin-1 (from *Cupiennius salei* [Wandering spider], UniProt P86798)
Length 119, Identities = 11/15 (73%), Positives = 12/15 (80%), Gaps = 0/15 (0%)
Sequences producing significant alignment: Score = 28.0 bits (56), E -Value = 0.008

```
P4      1    LGLGNGGAGGGLVGG  15
          +GLG GG GGGL GG
Sbjct  61    VGLGGGGYGGGLGGG  75
```

Identities = 11/15 (73%), Positives = 11/15 (73%), Gaps = 1/15 (7%)
Sequences producing significant alignment: Score = 23.7 bits (46), E -Value = 0.23

```
P4      2    GLGNG-GAGGGLVGG  15
          GLG G G GGGL GG
Sbjct  71    GLGGGQGGGGGLGGG  85
```

> CAMPSQ3914| Ctenidin-3 (from *Cupiennius salei* [Wandering spider])
Length 120, Identities = 11/14 (79%), Positives = 11/14 (79%), Gaps = 0/14 (0%)
Sequences producing significant alignment: Score = 28.0 bits (56), E -Value = 0.008

```
P4      2    GLGNG-GAGGGLVGG  15
          GLG G G GGGL GG
Sbjct  71    GLGGGQGGGGGLGGG  85
```

Identities = 11/15 (73%), Positives = 11/15 (73%), Gaps = 1/15 (7%)
Sequences producing significant alignment: Score = 23.7 bits (46), E- Value = 0.23

```
P4      2    GLGNG-GAGGGLVGG  15
          GLG G G GGGL GG
Sbjct  83    GLGGGQGGGGGLGGG  97
```

Peptide P7: AAGLAGAGNGGG

> CAMPSQ5393| Cecropin TY1 (from *Tabanus yao* [Horsefly]), Antibacterial activity
Length=63, Identities = 8/10 (80%), Positives = 9/10 (90%), Gaps = 0/10 (0%)
Sequences producing significant alignment: Score = 21.5 bits (41), E - Value = 0.75

```
P7      1    AAGLAGAGNG  10
          AAG+AGA NG
Sbjct  54    AAGVAGALNG  63
```


B) An alignment with protein data base by BLAST (<https://blast.ncbi.nlm.nih.gov>):

Peptide P4: LGLGNGGAGGGLVGG

RecName: Full=Glycine-rich cell wall structural protein; **Flags:** Precursor [*Arabidopsis thaliana*]

Sequence ID: [P27483.2](#), **Length:** 349, **Number of Matches:** 55

Range 1: 92 to 104 [GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
28.2 bits(59)	0.74	12/14(86%)	12/14(85%)	1/14(7%)

```
P4      2      GLGNGGAGGGLVGG  15
          GLG GGAGGGL GG
Sbjct   92      GLG-GGAGGGLGGG  104
```

https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastp&PAGE_TYPE=BlastSearch&LINK_LOC=blasthome

RecName: putative protein LI1785 [*Littorina littorea*]

Sequence ID: [MBX96353.1](#), **Length:** 791, **Number of Matches:** 6

Range 1: 424 to 436 [GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
30.3 bits(64)	0.90	11/13(85%)	11/13(84%)	0/13(0%)

```
P4      2      GLGNGGAGGGLVGG  14
          GLG GGAGGGL G
Sbjct  424      GLGGGAGGGLMG  436
```

Peptide P7: AAGLAGAGNNGG

RecName: Full=Voltage-dependent calcium channel gamma-8 subunit; **AltName:**

Full=Neuronal voltage-gated calcium channel gamma-8 subunit; **AltName:**

Full=Transmembrane AMPAR regulatory protein gamma-8; **Short=TARP gamma-8 [Homo sapiens]**

Sequence ID: [Q8WXS5.3](#), **Length:** 425, **Number of Matches:** 5

Range 1: 319 to 330 [GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
30.3 bits(64)	0.075	11/12(92%)	11/12(91%)	0/12(0%)

```
P7      1      AAGLAGAGNNGG  12
          AAGLAGAG GGG
Sbjct  319      AAGLAGAGGGGG  330
```