

Supplementary Information:

SI S1. An alignment of amino acid sequences of some identified peptides from *C. aspersum* mucus with known antimicrobial peptides with data base AMPs by CAMPSing, Matrix: BLOSUM 80 (<http://www.campsign.bicnirrh.res.in/blast.php>, accessed on 24 March 2024) and with proteins by BLAST (<https://blast.ncbi.nlm.nih.gov>, accessed on 24 March 2024).

PEPTIDE 1. LLPFKEPDL

> DBAASP_4424|4774|Indolicidin
Length=13, Score = 18.5 bits (34), Expect = 2.4
Identities = 6/9 (67%), Positives = 7/9 (78%), Gaps = 0/9 (0%)

```
Query 1  ILPFKEPDL 9
        ILP K+P L
Sbjct 1  ILPWKKPKL 9
```

PEPTIDE 3. LNLGGNGANGLVGG

>UniProtKb_253|Q8K4I4|BPIA1_RAT; **BPI fold-containing family A member 1**; Lipid-binding protein which plays a role in the innate immune responses of the upper airways.
Length=270, Score = 22.4 bits (43), Expect = 0.66
Identities = 8/11 (73%), Positives = 9/11 (82%), Gaps = 0/11 (0%)

```
Query 4      GGNGANGLVGG 14
              GG +NGLVGG
Sbjct 97     GGGSSNGLVGG 107
```

>UniProtKb_251|P97361;Q7TQJ2|BPIA1_MOUSE; **BPI fold-containing family A member 1**;
Lipid-binding protein which plays a role in the innate immune responses of the upper airways.
Length=278, Score = 22.4 bits (43), Expect = 0.67
Identities = 8/11 (73%), Positives = 9/11 (82%), Gaps = 0/11 (0%)

```
Query 4      GGNGANGLVGG 14
              GG +NGLVGG
Sbjct 105    GGGNSNGLVGG 115
```

PEPTIDE 4. AGVGGAAGNPSTYVG

>CAMPSQ2894; **Enterocin E-760**; **AMP Family: Bacteriocin**; Source: Bacteria *Enterococcus durans*; Activity: Gram+ve, Gram-ve
Length=62, Score = 20.2 bits (38), Expect = 2.5
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

```
Query 2      GVGGAAG 8
              GVGGAAG
Sbjct 11     GVGGAAG 17
```

PEPTIDE 6. MLGGGVNSLRPPK

>CAMPSQ2582; **Hyastatin**; Source: *Hyas araneus* [Great spider crab] Activity: Antibacterial, Antifungal; Gram+ve, Gram-ve
Length=131, Score = 21.5 bits (41), Expect = 1.1
Identities = 7/10 (70%), Positives = 8/10 (80%), Gaps = 0/10 (0%)

```
Query 2      LGGGVNSLRP 11
              LGGG+ S RP
Sbjct 79     LGGGIGSTRP 88
```

PEPTIDE 7. CVGGAGGHHGDSKAKGT

>APD_2350|AP02350|**Microcin B**; AMP Family: Bacteriocin; Activity: Antimicrobial

Length=42, Score = 20.6 bits (39), Expect = 1.6
Identities = 7/10 (70%), Positives = 7/10 (70%), Gaps = 0/10 (0%)

Query 3 GGAGGHGDSC 12
GG GG G SC
Sbjct 6 GGGGGGGGSC 15

> CAMPSQ1503 **Bacteriocin microcin B17**; AMP Family: Bacteriocin; Source: *Escherichia coli*; Activity: Antimicrobial

Length=43, Score = 20.6 bits (39), Expect = 1.6
Identities = 7/10 (70%), Positives = 7/10 (70%), Gaps = 0/10 (0%)

Query 3 GGAGGHGDSC 12
GG GG G SC
Sbjct 6 GGGGGGGGSC 15

> LAMP_Experimental_1801|L06AT00084|Q5Z434_ORYSJ

Length=45, Score = 20.6 bits (39), Expect = 1.7
Identities = 7/10 (70%), Positives = 8/10 (80%), Gaps = 0/10 (0%)

Query 5 AGGHGDSCAK 14
AGG D+CAK
Sbjct 19 AGGSRDTCAK 28

PEPTIDE 8. GGGGYHTWGE G G K F

> UniProtKb_1144|Q8RYE7;Q6ZZS3|DF196_ARATH: **Defensin-like protein 196**; Organism *Arabidopsis thaliana*

Length=97, Score = 22.4 bits (43), Expect = 0.53
Identities = 8/11 (73%), Positives = 8/11 (73%), Gaps = 0/11 (0%)

Query 3 GGYHTWGE G G K 13
GG WGE G G K
Sbjct 67 G G K C L W G E G G K 77

> Yadamp_463|1414|**Glycine-rich protein GWK isoform 3**

Length=34, Score = 20.6 bits (39), Expect = 1.1
Identities = 8/13 (62%), Positives = 9/13 (69%), Gaps = 0/13 (0%)

Query 1 GGGGYHTWGE G G K 13
GGGG+ G G G K
Sbjct 20 GGGGWKGGGGGGGK 32

> Yadamp_508|1455|**Glycine-rich protein GWK isoform 2**

Length=35, Score = 20.6 bits (39), Expect = 1.1
Identities = 8/13 (62%), Positives = 9/13 (69%), Gaps = 0/13 (0%)

Query 1 GGGGYHTWGE G G K 13
GGGG+ G G G K
Sbjct 20 GGGGWKGGGGGGGK 32

> CAMPSQ3973 **Glycine-rich protein GWK**; Source: *Cucumis melo* [Muskmelon]; Activity: Antifungal

Length=36, Score = 20.6 bits (39), Expect = 1.1
Identities = 8/13 (62%), Positives = 9/13 (69%), Gaps = 0/13 (0%)

Query 1 GGGGYHTWGE G G K 13
GGGG+ G G G K
Sbjct 20 GGGGWKGGGGGGGK 32

PEPTIDE 10. NLVGGSGGGGRGGANPLG

> APD_1398|AP02256|**Procambarin**, Activity: Antibacterial

Length=155, Score = 28.4 bits (57), Expect = 0.008
Identities = 10/15 (67%), Positives = 11/15 (73%), Gaps = 0/15 (0%)

Query 4 GGSGGGGRGGANPLG 18
GG GGGG GG P+G
Sbjct 26 GGFGGGGLGGGKPIG 40

> CAMPSQ322; **Holotricin-3**; Source: *Holotrichia diomphalia* Activity: Antibacterial, Antifungal

Length=84; Score = 26.7 bits (53), Expect = 0.022
Identities=9/10 (90%), Positives=9/10 (90%), Gaps=0/10 (0%)

Query 4 GGSGGGGRGG 13
GG GGGGRGG
Sbjct 41 GGHGGGRGG 50

> APD_2350|AP02350|Microcin B; AMP Family: Bacteriocin; Activity: Antimicrobial

Length=42; Score = 24.5 bits (48), Expect = 0.060
Identities = 8/12 (67%), Positives = 10/12 (83%), Gaps = 0/12 (0%)

Query 3 VGGSGGGGRGGA 14
+GG GGGG GG+
Sbjct 3 IGGGGGGGGGS 14

PEPTIDE 11. GTMSPAGGEMGPVTAGVG

> UniProtKb_2464|A1XQR6|ROM01_PIG; Reactive oxygen species modulator 1; It has antibacterial activity against a variety of bacteria including *S.aureus*, *P.aeruginosa* and *M.tuberculosis*. Acts by inducing bacterial membrane breakage (By similarity).

Length=79, Score = 20.2 bits (38), Expect = 3.2
Identities = 9/18 (50%), Positives = 11/18 (61%), Gaps = 1/18 (6%)

Query 2 TMSPAGGEMGPVTA-GVG 18
TM +GG GP A G+G
Sbjct 59 TMMQSGGTFGPFMAIGMG 76

PEPTIDE 12. GTKGCGPGSCPPGDTVAGVG

> CAMPSQ2192; **Crustin-like antimicrobial peptide**; Source: *Fenneropenaeus indicus* Activity: Antimicrobial

Length=117, Score = 25.0 bits (49), Expect = 0.11
Identities = 9/16 (56%), Positives = 10/16 (63%), Gaps = 1/16 (6%)

Query 5 CGPGSCPP-GDTVAGV 19
C PG CPP DT G+
Sbjct 63 CKPGRCPPVRDTCPIG 78

> CAMPSQ3075 **Gallinacin 8**; Source: *Gallus gallus* [Chicken]; Activity: Antimicrobial

Length=41, Score = 23.7 bits (46), Expect = 0.14
Identities = 7/14 (50%), Positives = 10/14 (71%), Gaps = 0/14 (0%)

Query 5 CGPGSCPPGDTVAG 18
C G+CPP T++G
Sbjct 12 CRAGACPPTFTISG 25

> APD_166|AP01147|**Gallinacin 8**, Activity: Antimicrobial

Length=41, Score = 23.7 bits (46), Expect = 0.14
Identities = 7/14 (50%), Positives = 10/14 (71%), Gaps = 0/14 (0%)

Query 5 CGPGSCPPGDTVAG 18
C G+CPP T++G
Sbjct 12 CRAGACPPTFTISG 25

> CAMPSQ1841 Gallinacin-10; Source: *Gallus gallus*; Activity: Antibacterial
Length=43, Score = 23.7 bits (46), Expect = 0.15
Identities = 7/14 (50%), Positives = 10/14 (71%), Gaps = 0/14 (0%)

Query 5 CGPGSCPPGDTVAG 18
C G+CPP T++G
Sbjct 14 CRAGACPPTFTISG 27

> UniProtKb_877|Q2V433|DEF52_ARATH; **Putative defensin-like protein 52;
Arabidopsis thaliana (Mouse-ear cress)**
Length=81, Score = 24.1 bits (47), Expect = 0.18
Identities = 10/19 (53%), Positives = 11/19 (58%), Gaps = 0/19 (0%)

Query 2 TKGCGPGSCPPGDTVAGVG 20
T+G GSC PG T A G
Sbjct 47 TEGYDDGSCVPGPTTAKCG 65

> UniProtKb_1513|Q6QLQ9|GLL10_CHICK; Gallinacin 10
Length=68, Score = 23.7 bits (46), Expect = 0.23
Identities = 7/14 (50%), Positives = 10/14 (71%), Gaps = 0/14 (0%)

Query 5 CGPGSCPPGDTVAG 18
C G+CPP T++G
Sbjct 39 CRAGACPPTFTISG 52

> CAMPSQ1080 Gallinacin-4; Source: *Gallus gallus*; Activity: Antibacterial
Length=38, Score = 22.8 bits (44), Expect = 0.28
Identities = 7/15 (47%), Positives = 9/15 (60%), Gaps = 0/15 (0%)

Query 5 CGPGSCPPGDTVAGV 19
C PG CP G+ G+
Sbjct 13 CTPGKCPHGNYLGL 27

> CAMPSQ2874 Chicken AvBD4; Activity: Antibacterial; Gram-ve
Length=38, Score = 22.4 bits (43), Expect = 0.42
Identities = 7/15 (47%), Positives = 9/15 (60%), Gaps = 0/15 (0%)

Query 5 CGPGSCPPGDTVAGV 19
C PG CP G+ G+
Sbjct 13 CTPGKCPYGNAYLGL 27

> CAMPSQ4487 Basic endochitinase B; Activity: Antifungal
Length=255, Score = 22.8 bits (44), Expect = 0.62
Identities = 7/11 (64%), Positives = 7/11 (64%), Gaps = 0/11 (0%)

Query 5 CGPGSCPPGDT 15
C PG PPG T
Sbjct 40 CTPGGTPPGPT 50

> UniProtKb_483|P19171;Q9S7J5;Q9S838;Q9SXJ2;Q9SXJ3;Q9SXJ4|CHIB_ARATH
Length=335, Score = 22.8 bits (44), Expect = 0.63
Identities = 7/11 (64%), Positives = 7/11 (64%), Gaps = 0/11 (0%)

Query 5 CGPGSCPPGDT 15
C PG PPG T
Sbjct 73 CTPGGTPPGPT 83

PEPTIDE 13. ACSLLLGGGGVGGGKGGGGHAG

> CAMPSQ3913, Ctenidin-1 from *Cupiennius salei* [Wandering spider], Activity: Antimicrobial
Length=119, Score = 37.0 bits (77), Expect = 9e-006, Identities = 12/16 (75%), Positives = 15/16 (94%), Gaps = 0/16 (0%)

```
P 9      7      GGGGVGGGKGGGGHAG  22
          GGGG+GGG+GGGG+ G
Sbjct  88      GGGGLGGGRGGGGYGG  103
```

> CAMPSQ3914, Ctenidin-3 from *Cupiennius salei* [Wandering spider], Activity: Antimicrobial
Length=120, Score = 37.0 bits (77), Expect = 1e-005, Identities = 12/16 (75%), Positives = 15/16 (94%), Gaps = 0/16 (0%)

```
P 9      7      GGGGVGGGKGGGGHAG  22
          GGGG+GGG+GGGG+ G
Sbjct  90      GGGGLGGGRGGGGYGG  105
```

> DBAASP_2873|3113|Acanthoscurrin-2 from *Acanthoscurria gomesiana* [Tarantula spider], Activity: Antibacterial (Gram-), Antifungal, Target: *E.coli* SBS363, *C.albicans*
Length=130, Score = 33.1 bits (68), Expect = 2e-004, Identities = 13/20 (65%), Positives = 16/20 (80%), Gaps = 3/20 (15%)

```
P 9      6      LGGGGVGGGK---GGGGHAG  22
          LGGGG+GGG+   GGGG+ G
Sbjct  99      LGGGGLGGGRGGYGGGGYGG  118
```

> CAMPSQ1508, Acanthoscurrin-1 from *Acanthoscurria gomesiana* [Tarantula spider], Activity: Antibacterial (Gram-), Antifungal, Target: *E.coli* SBS363, *C.albicans*
Length=132, Score = 32.7 bits (67), Expect = 3e-004, Identities = 14/19 (74%), Positives = 15/19 (79%), Gaps = 2/19 (11%)

```
P 9      6      LGGGGVGGGK--GGGGHAG  22
          LGGGG+GGGK   GGGG  G
Sbjct  31      LGGGGLGGGKGLGGGGLGG  49
```

PEPTIDE 14. LLLDGFGGGLLVEHDPGS

> CAMPSQ3509 Prolixicin Source: *Rhodnius prolixus* [Triatomid bug]; Activity: Antibacterial; Gram+ve, Gram-ve
Length=77, Score = 19.8 bits (37), Expect = 4.5
Identities = 5/9 (56%), Positives = 8/9 (89%), Gaps = 0/9 (0%)

```
Query  6      FGGGLLVEH  14
          +GGG+ +EH
Sbjct  65      YGGGMRIEH  73
```

> APD_888|AP01798|Prolixicin
Length=77, Score = 19.8 bits (37), Expect = 4.5
Identities = 5/9 (56%), Positives = 8/9 (89%), Gaps = 0/9 (0%)

```
Query  6      FGGGLLVEH  14
          +GGG+ +EH
Sbjct  65      YGGGMRIEH  73
```

PEPTIDE 15. MGGWGGLGGGHNGGWMPK

> CAMPSQ959; Shepherin II; Source: *Capsella bursa-pastoris* [Shepherd purse]; Activity: Antibacterial, Antifungal; Gram+ve, Gram-ve
Length=38, Score = 28.0 bits (56), Expect = 0.003
Identities = 10/13 (77%), Positives = 11/13 (85%), Gaps = 0/13 (0%)

```
Query  2      GGWGGLGGGHNGG  14
          GG GG GGG+NGG
Sbjct  4      GGHGGHGGGYNGG  16
```

> APD_1790|AP00512|Shepherin II
Length=38, Score = 28.0 bits (56), Expect = 0.003
Identities = 10/13 (77%), Positives = 11/13 (85%), Gaps = 0/13 (0%)

Query 2 GGWGGGLGGGHNGG 14
GG GG GGG+NGG
Sbjct 4 GGHGGHGGGYNGG 16

> AMSDb_802|SHEP_CAPBU|ANTIMICROBIAL PEPTIDE SHEP-GRP. SHEPHERIN-1;
Length=120 Score = 28.0 bits (56), Expect = 0.010
Identities = 10/13 (77%), Positives = 11/13 (85%), Gaps = 0/13 (0%)

Query 2 GGWGGGLGGGHNGG 14
GG GG GGG+NGG
Sbjct 75 GGHGGHGGGYNGG 87

PEPTIDE 16. ACLTPVDHFFAGMPCGGGP

> CAMPSQ5060, **Cyclotide 2a** from *Viola baoshanensis*, Activity: Antimicrobial
Length=113, Score = 20.2 bits (38), Expect = 3.6, Identities = 8/16 (50%), Positives = 10/16 (63%), Gaps = 0/16 (0%)

P 10 1 ACLTPVDHFFAGMPCG 16
A L +DH G+PCG
Sbjct 69 ALLKNLDHGRNGVPCG 84

PEPTIDE 17. NGLFGGLGGGGHGGGKGPGE GGG

> CAMPSQ322, **Holotricin-3** from *Holotrichia diomphalia* [Korean black chafer], Activity: Antibacterial, Antifungal
Length=84, Score = 39.2 bits (82), Expect = 1e-006, Identities = 16/23 (70%), Positives = 17/23 (74%), Gaps = 0/23 (0%)

P 11 2 GLFGGLGGGGHGGGKGPGE GGG 24
G FGG GGGHGGGG+G G GG
Sbjct 33 GGFGGGHGGGHGGGGRGGGSSG 55

> CAMPSQ3914, **Ctenidin-3** from *Cupiennius salei* [Wandering spider], Activity: Antimicrobial
Length=120, Score = 38.8 bits (81), Expect = 3e-006, Identities = 15/20 (75%), Positives = 16/20 (80%), Gaps = 0/20 (0%)

P 11 5 GGLGGGGHGGGGKGPGE GGG 24
GG GGGG+GGGG G G GGG
Sbjct 11 GGYGGGGYGGGGGGYGGGGG 30

> CAMPSQ3913 **Ctenidin-1** from *Cupiennius salei* [Wandering spider], Activity: Antimicrobial
Length=119, Score = 37.9 bits (79), Expect = 5e-006, Identities = 15/20 (75%), Positives = 16/20 (80%), Gaps = 0/20 (0%)

P 11 5 GGLGGGGHGGGGKGPGE GGG 24
GGLGGG GGGG G G+GGG
Sbjct 70 GGLGGGQGGGGGLGGGQGGG 89

> CAMPSQ1508, **Acanthoscurrin-1** from *Acanthoscurria gomesiana* [Tarantula spider] Activity: Antibacterial (Gram-), Antifungal, Target: *E.coli* SBS363, *C.albicans*
Length=132, Score = 37.5 bits (78), Expect = 8e-006, Identities = 15/19 (79%), Positives = 15/19 (79%), Gaps = 0/19 (0%)

P 11 6 GLGGGGHGGGGKGPGE GGG 24
GLGGGG GGGG G G GGG
Sbjct 93 GLGGGGLGGGGLGGGRGGG 111

PEPTIDE 18. LLLDNKGGGLVGGLLGGGGKGGG

> CAMPSQ3894 **Leptoglycin**; Source: *Leptodactylus pentadactylus* [Smokey jungle frog] Activity: Antibacterial; Gram-ve
Length=22, Score = 33.1 bits (68), Expect = 5e-005
Identities = 13/16 (81%), Positives = 14/16 (88%), Gaps = 0/16 (0%)

Query 8 GGLVGGLLGGGGKGGG 23
GGL+G LLGGGG GGG
Sbjct 4 GLLGPLLGGGGGGGG 19

> DBAASP_2873|3113|Acanthoscurrin-2; Source: *Acanthoscurria gomesiana* [Tarantula spider]
 Activity: Antibacterial, Antifungal; Gram-ve
 Length=130, Score = 33.6 bits (69), Expect = 2e-004
 Identities = 14/17 (82%), Positives = 14/17 (82%), Gaps = 0/17 (0%)

Query 7 GGGLVGGLLGGGGKGGG 23
 GGGL GG LGGGG GGG
 Sbjct 23 GGGLGGGGLGGGGLGGG 39

> CAMPSQ1508 Acanthoscurrin-1; Source: *Acanthoscurria gomesiana* [Tarantula spider] Activity:
 Antibacterial, Antifungal; Gram-ve
 Length=132 Score = 33.6 bits (69), Expect = 2e-004
 Identities = 14/17 (82%), Positives = 14/17 (82%), Gaps = 0/17 (0%)

Query 7 GGGLVGGLLGGGGKGGG 23
 GGGL GG LGGGG GGG
 Sbjct 23 GGGLGGGGLGGGGLGGG 39

PEPTIDE 19. GMVLLHCSPALDFHKTPAV

> CAMPSQ4289; Hepcidin; Source: *Crocodylus siamensis* [Siamese crocodile];
 Activity: Antibacterial; Gram+ve, Gram-ve
 Length=99, Score = 19.3 bits (36), Expect = 7.0
 Identities = 7/9 (78%), Positives = 8/9 (89%), Gaps = 0/9 (0%)

Query 2 MVLLHCSPA 10
 +VLLH SPA
 Sbjct 13 LVLLHGSPA 21

PEPTIDE 20. LPFLLGVGGLLGGSVGGGGGGGAPL

> CAMPSQ3894 Leptoglycin; Source: *Leptodactylus pentadactylus* [Smokey jungle frog] Activity:
 Antibacterial; Gram-ve
 Length=22, Score = 34.4 bits (71), Expect = 2e-005
 Identities = 14/20 (70%), Positives = 16/20 (80%), Gaps = 0/20 (0%)

Query 7 VGGLLGGSVGGGGGGGAPL 26
 +GGLLG +GGGGGGG L
 Sbjct 3 LGGLLGPLLGGGGGGGGLL 22
 Sbjct 3 LGGLLGPLLGGGGGGGGLL 22

> DBAASP_2873|3113|Acanthoscurrin-2 Source: *Acanthoscurria gomesiana* [Tarantula spider],
 Activity: Antibacterial (Gram-), Antifungal, Target: *E.coli* SBS363, *C.albicans*
 Length=130, Score = 33.1 bits (68), Expect = 3e-004
 Identities = 14/19 (74%), Positives = 15/19 (79%), Gaps = 0/19 (0%)

Query 5 LGVGGLLGGSVGGGGGGG 23
 LG GGL GG +GGGG GGG
 Sbjct 42 LGGGGLGGGGLGGGGLGGG 60

> CAMPSQ1508 Acanthoscurrin-1 Source: *Acanthoscurria gomesiana* [Tarantula spider], Activity:
 Antibacterial (Gram-), Antifungal, Target: *E.coli* SBS363, *C.albicans*
 Length=132 Score = 33.1 bits (68), Expect = 3e-004
 Identities = 14/19 (74%), Positives = 15/19 (79%), Gaps = 0/19 (0%)

Query 5 LGVGGLLGGSVGGGGGGG 23
 LG GGL GG +GGGG GGG
 Sbjct 42 LGGGGLGGGGLGGGGLGGG 60

PEPTIDE 21. MVLDGKGGGGLLGGVLGGGKDAHLGG

> DBAASP_2873|3113|Acanthoscurrin-2; Source: *Acanthoscurria gomesiana* [Tarantula spider],
 Activity: Antibacterial (Gram-), Antifungal, Target: *E. coli* SBS363, *C. albicans*
 Length=130, Score = 32.7 bits (67), Expect = 4e-004
 Identities = 14/22 (64%), Positives = 16/22 (73%), Gaps = 0/22 (0%)

Query 5 GKGGGGLLGGVLGGGKDAHLGG 26
 G GGGGL GG LGGG+ + GG
 Sbjct 93 GLGGGGLGGGGLGGGRGGYGGG 114

PEPTIDE 22. LLKDNGVGGLLGGGGAGGGGLVGGNLGGGAG

> DBAASP_2873|3113|Acanthoscurrin-2 (> CAMPSQ1805) Source: *Acanthoscurria gomesiana* [Tarantula spider], Activity: Antibacterial (Gram-), Antifungal, Target: E. coli SBS363, C. albicans
Length=130, Score = 45.2 bits (96), Expect = 2e-008
Identities = 19/24 (79%), Positives = 19/24 (79%), Gaps = 0/24 (0%)

```
Query 8  GGLLGGGGAGGGGLVGGNLGGGAG 31
        GG LGGGG GGGGL GG LGGG G
Sbjct 44 GGGGLGGGGLGGGGLGGGGLGGGKG 67
```

> CAMPSQ1508; Acanthoscurrin-1; Source: *Acanthoscurria gomesiana* [Tarantula spider],
Activity: Antibacterial (Gram-), Antifungal, Target: E. coli SBS363, C. albicans
Length=132; Score = 31.4 bits (64), Expect = 0.001
Identities = 16/22 (73%), Positives = 16/22 (73%), Gaps = 2/22 (9%)

```
Query 5  GKGGGGLLGGVLGGGKDAHLGG 26
        G GGGGL GG LGGGK LGG
Sbjct 25 GLGGGGLGGGGLGGGKG--LGG 44
```

PEPTIDE 23. KTSKLMVYLAGGGGGLLGGVGGGGGAGGGGPGL

> CAMPSQ3913; Ctenidin-1; Source: *Cupiennius salei* [Wandering spider]; Activity: Antimicrobial
Length=119, Score = 45.7 bits (97), Expect = 2e-008
Identities = 19/24 (79%), Positives = 19/24 (79%), Gaps = 0/24 (0%)

```
Query 11 GGGGGLLGGVGGGGGAGGGGPGL 34
        GGGGGL GG GGGG G GGGG GG
Sbjct 87 GGGGGLGGGRGGGGYGGGGGYGG 110
```

> CAMPSQ3914; Ctenidin-3; Source: *Cupiennius salei* [Wandering spider]; Activity: Antimicrobial
Length=120, Score = 45.7 bits (97), Expect = 2e-008
Identities = 19/24 (79%), Positives = 19/24 (79%), Gaps = 0/24 (0%)

```
Query 11 GGGGGLLGGVGGGGGAGGGGPGL 34
        GGGGGL GG GGGG G GGGG GG
Sbjct 89 GGGGGLGGGRGGGGYGGGGGYGG 112
```

> Yadamp_463|1414|Glycine-rich protein GWK isoform 3
Length=34; Score = 43.5 bits (92), Expect = 2e-008
Identities = 19/26 (73%), Positives = 19/26 (73%), Gaps = 2/26 (8%)

```
Query 11 GGGGGLLGGVGGGG--GAGGGGPGL 34
        GGGGG GG GGGGG G GGGG GG
Sbjct 9  GGGGGWKGGGGGGGWKGGGGGKGG 34
```

> Yadamp_508|1455|Glycine-rich protein GWK isoform 2
Length=35; Score = 43.5 bits (92), Expect = 2e-008
Identities = 19/26 (73%), Positives = 19/26 (73%), Gaps = 2/26 (8%)

```
Query 11 GGGGGLLGGVGGGG--GAGGGGPGL 34
        GGGGG GG GGGGG G GGGG GG
Sbjct 9  GGGGGWKGGGGGGGWKGGGGGKGG 34
```

> CAMPSQ1805; Acanthoscurrin-2; Source: *Acanthoscurria gomesiana* [Tarantula spider],
Activity: Antibacterial (Gram-), Antifungal, Target: E. coli SBS363, C. albicans
Length=131; Score = 42.6 bits (90), Expect = 2e-007
Identities = 18/23 (78%), Positives = 18/23 (78%), Gaps = 0/23 (0%)

```
Query 12 GGGGLLGGVGGGGGAGGGGPGL 34
        GGGGL GG G GGGG GGGG GG
Sbjct 32 GGGGLGGGKGLGGGGLGGGGLGG 54
```

> CAMPSQ1508; Acanthoscurrin-1; Source: *Acanthoscurria gomesiana* [Tarantula spider],
Activity: Antibacterial (Gram-), Antifungal, Target: E. coli SBS363, C. albicans
Length=132; Score = 42.6 bits (90), Expect = 2e-007

Identities = 18/23 (78%), Positives = 18/23 (78%), Gaps = 0/23 (0%)

```
Query 12 GGGGLLGGVGGGGGGAGGGPGG 34
      GGGGL GG G GGGG GGGG GG
Sbjct 32 GGGGLGGGKGLGGGGLGGGGLGG 54
```

Supplementary Information S2 (SI S2):

SI S2. An alignment of amino acid sequences of some identified peptides from protein bands of mucus fraction with MW>20 kDa with known proteins in Gastropoda (taxid:6448), Mollusca (taxid: 6447) and land snails (taxid: 6527) with database Non-redundant protein sequences (nr) and UniProtKB/Swiss-Prot, sequences algorithm blastp (protein-protein BLAST), filtered to match records with percent identity between 50% and 100% (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>, accessed on 12 April 2024).

TAAFTEDTSVVTGR

> mucus protein [Cornu aspersum] [land snail, non-redundant protein sequences (nr)]

Sequence ID: QEG59314.1, Length: 159, Number of Matches: 1, Score 35.8, bits(77), E value (Expect) 8e-05, Identities 12/14(86%), Positives 12/14(85%), Gaps 0/14(0%)

```
Query 1 TAAFTEDTSVVTGR 14
      TAAFTEDTSV GR
Sbjct 28 TAAFTEDTSVAEGR 41
```

FTAAFTEDTSVAEGR

> mucus protein [Cornu aspersum] [land snail, non-redundant protein sequences (nr)]

Sequence ID: QEG59314.1, Length: 159, Number of Matches: 1, Score 49.0, bits(108), E value (Expect) 2e-09, Identities 15/15(100%), Positives 15/15(100%), Gaps 0/15(0%)

```
Query 1 FTAAFTEDTSVAEGR 15
      FTAAFTEDTSVAEGR
Sbjct 27 FTAAFTEDTSVAEGR 41
```

GNVAF TAAFTEDTSVAEGR

> mucus protein [Cornu aspersum] [land snail, non-redundant protein sequences (nr)]

Sequence ID: QEG59314.1, Length: 159, Number of Matches: 1, Score 60.4, bits(135), E value (Expect) 4e-13, Identities 19/19(100%), Positives 19/19(100%), Gaps 0/19(0%)

```
Query 1 GNVAF TAAFTEDTSVAEGR 19
      GNVAF TAAFTEDTSVAEGR
Sbjct 23 GNVAF TAAFTEDTSVAEGR 41
```

GALNGNVAF TAAFTEDTSVAEGR

> mucus protein [Cornu aspersum] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: QEG59314.1, Length: 159, Number of Matches: 1, Score 60.4, bits(135), E value (Expect) 2e-11, Identities 19/19(100%), Positives 19/19(100%), Gaps 0/19(0%)

```
Query 5 GNVAF TAAFTEDTSVAEGR 23
      GNVAF TAAFTEDTSVAEGR
Sbjct 23 GNVAF TAAFTEDTSVAEGR 41
```

GSCNWPM TILMLES LR

RecName: Full=NADH-ubiquinone oxidoreductase chain 6; AltName: Full=NADH dehydrogenase subunit 6 [Albinaria caerulea]

Sequence ID: P48922.1, Length: 155, Number of Matches: 4; Score 22.7 bits(46), E value (Expect) 0.005, Identities 7/9(78%), Positives 7/9(77%), Gaps 1/9(11%)

```
Query 7 MT-ILMLES 14
      MT ILM ES
Sbjct 144 MTSILMVES 152
```

QYLQITWPSR

> H-type lectin domain-containing protein [Biomphalaria glabrata] [gastropoda, non reduntant protein]

Sequence ID: KAI8776186.1, Length: 683, Number of Matches: 1, Score 31.6, bits(67), E value (Expect) 0.041, Identities 8/8(100%), Positives 8/8(100%), Gaps 0/8(0%)

```
Query 2 YLQITWPS 9
      YLQITWPS
Sbjct 430 YLQITWPS 437
```

VP SDDPGR

> Chain A, Helix aspersa agglutinin (HAA) [Cornu aspersum] [land snail, non-redundant protein sequences (nr)]

Sequence ID: 4Q56_A, Length: 101, Number of Matches: 1, Score 28.2, bits(59), E value (Expect) 0.003, Identities 8/8(100%), Positives 8/8(100%), Gaps 0/8(0%)

```
Query 1 VPSDDPGR 8
      VPSDDPGR
Sbjct 19 VPSDDPGR 26
```

DITFASPYCR

> Chain A, Helix aspersa agglutinin (HAA) [Cornu aspersum] [land snail, non-redundant protein sequences (nr)]

Sequence ID: 4Q56_A, Length: 101, Number of Matches: 1, Score 34.6, bits(74), E value (Expect) 1e-04, Identities 9/10(90%), Positives 10/10(100%), Gaps 0/10(0%)

```
Query 1 DITFASPYCR 10
      +ITFASPYCR
Sbjct 35 NITFASPYCR 44
```

NGGLVHPGPR

> uncharacterized protein LOC112554950 [Pomacea canaliculata] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: XP_025078819.1, Length: 229, Number of Matches: 1, Score 25.7, bits(53), E value (Expect) 4.5, Identities 8/9(89%), Positives 8/9(88%), Gaps 0/9(0%)

```
Query 2 GGLVHPGPR 10
      GGLV PGPR
Sbjct 30 GGLVYPGPR 38
```

DWTLYVNTPLAPAR

> unnamed protein product, partial [Candidula unifasciata] [land snail, non-redundant protein sequences (nr)]

Sequence ID: CAG5130849.1, Length: 1003, Number of Matches: 2, Score 25.7, bits(53), E value (Expect) 0.33, Identities 7/9(78%), Positives 7/9(77%), Gaps 0/9(0%)

```
Query 2 WTLVNTPL 10
      W LY NTPL
Sbjct 61 WILYGNTPL 69
```

> mucin 18b [Plakobranhus ocellatus] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: GFO09821.1, Length: 124, Number of Matches: 7, Score 24.4, bits(50), E value (Expect) 27, Identities 6/8(75%), Positives 6/8(75%), Gaps 0/8(0%)

```
Query 1 DWTLYVNT 8
      DWTLY T
Sbjct 24 DWTLYLST 31
```

FCPNAQRTR

> glutathione S-transferase omega-1-like [Pomacea canaliculata] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: XP_025114871.1, Length: 274, Number of Matches: 1, Score 28.6, bits(60), E value (Expect) 0.31, Identities 8/9(89%), Positives 8/9(88%), Gaps 0/9(0%)

```
Query 1 FCPNAQRTR 9
      FCP AQRTR
Sbjct 34 FCPYAQRTR 42
```

> glutathione S-transferase omega-1 [Elysia marginata] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: GFR70608.1, Length: 410, Number of Matches: 1, Score 28.6, bits(60), E value (Expect) 0.31, Identities 8/9(89%), Positives 8/9(88%), Gaps 0/9(0%)

```
Query 1 FCPNAQRTR 9
      FCP AQRTR
```

```
Sbjct 192 FCPYAQRTR 200
```

> Glutathione S-transferase omega-1 [Bulinus truncatus] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: KAH9494607.1, Length: 287, Number of Matches: 1, Score 28.6, bits(60), E value (Expect) 0.31, Identities 8/9(89%), Positives 8/9(88%), Gaps 0/9(0%)

```
Query 1 FCPNAQRTR 9
      FCP AQRTR
```

Sbjct 74 FCPYAQRTR 82

NPVGSVPVLELDGK

> glutathione S-transferase omega-1-like [Pomacea canaliculata] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: XP_025099831.1, Length: 241, Number of Matches: 1, Score 33.7, bits(72), E value (Expect) 0.013, Identities 12/14(86%), Positives 12/14(85%), Gaps 0/14(0%)

Query 1 NPVGSVPVLELDGK 14

NP GSVPVLE DGK

Sbjct 64 NPSGSVPVLEKDGK 77

> glutathione S-transferase omega-1-like [Biomphalaria glabrata] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: KAI8762368.1, Length: 240, Number of Matches: 1, Score 32.9, bits(70), E value (Expect) 0.026, Identities 11/14(79%), Positives 11/14(78%), Gaps 0/14(0%)

Query 1 NPVGSVPVLELDGK 14

NP G VPVLELD K

Sbjct 63 NPNGTVPVLELDNK 76

GPCFTPHTYTNWSWLR

> unnamed protein product, partial [Candidula unifasciata] [land snail, non-redundant protein sequences (nr)]

Sequence ID: CAG5121511.1, Length: 301, Number of Matches: 1, Score 34.1, bits(73), E value (Expect) 4e-04, Identities 10/16(63%), Positives 11/16(68%), Gaps 4/16(25%)

Query 4 FTPHTY----TNWSWL 15

FTP+TY T WSWL

Sbjct 35 FTPQTYKRWMTTWSWL 50

DFLPPASLPDFAPSPRVAER

> unnamed protein product, partial [Candidula unifasciata] [land snail, non-redundant protein sequences (nr)]

Sequence ID: CAG5136685.1, Length: 401, Number of Matches: 1, Score 26.9, bits(56), E value (Expect) 0.34, Identities 10/19(53%), Positives 12/19(63%), Gaps 5/19(26%)

Query 1 DFLPPASLPDFAPSPRVA 19

++LP A LPDF RVA

Sbjct 69 EYLPVAGLPDF-----RVA 82

AGYLQITWPSPR

> mucus protein [Cornu aspersum] [land snail, non-redundant protein sequences (nr)]

Sequence ID: QEG59312.1, Length: 340, Number of Matches: 1, Score 40.1, bits(87), E value (Expect) 1e-08, Identities 11/11(100%), Positives 11/11(100%), Gaps 0/11(0%)

Query 1 AGYLQITWPSP 11

AGYLQITWPSP

Sbjct 103 AGYLQITWPSP 113

>H-type lectin domain-containing protein [Biomphalaria glabrata]

Sequence ID: KAI8776186.1Length: 683, Number of Matches: 1, Score 31.6 bits(67), E value (Expect) E=0.055, Identities 8/8(100%), Positives 8/8(100%), Gaps 0/8(0%)

Query 3 YLQITWPS 10

YLQITWPS

Sbjct 430 YLQITWPS 437

H-type lectin domain-containing protein [Biomphalaria glabrata]

Sequence ID: KAK6961697.1Length: 364Number of Matches: 1 Number of Matches: 1, Score 31.6 bits(67), E value (Expect) E=0.055, Identities 8/8(100%), Positives 8/8(100%), Gaps 0/8(0%)

Query 3 YLQITWPS 10

YLQITWPS

Sbjct 111 YLQITWPS 118

VGSNGAR

> mucus protein [Cornu aspersum] [land snail, non-redundant protein sequences (nr)]

Sequence ID: QEG59312.1, Length: 340, Number of Matches: 1, Score 23.1, bits(47), E value (Expect) E=0.004, Identities 7/7(100%), Positives 7/7(100%), Gaps 0/7(0%)

Query 1 VGSNGAR 7

VGSNGAR
Sbjct 188 VGSNGAR 194

ASVTGDLSNK

> mucus protein [Cornu aspersum] [land snail, non-redundant protein sequences (nr)]

Sequence ID: QEG59312.1, Length: 340, Number of Matches: 1, Score 32.0, bits(68), E value (Expect) 8e-04, Identities 10/10(100%), Positives 10/10(100%), Gaps 0/10(0%)

Query 1 ASVTGDLSNK 10
ASVTGDLSNK
Sbjct 93 ASVTGDLSNK 102

ELLGNYRAAFTEDTSVAEGR

> mucus protein [Cornu aspersum] [land snail, non-redundant protein sequences (nr)]

Sequence ID: QEG59314.1, Length: 159, Number of Matches: 1, Score 46.9, bits(103), E value (Expect) 3e-08, Identities 17/22(77%), Positives 18/22(81%), Gaps 1/22(4%)

Query 1 ELLGNV-YRAAFTEDTSVAEGR 21
E GNV + AAFTEDETSVAEGR
Sbjct 20 EFIGNVAFTAFTEDTSVAEGR 41

ANVTFDLSEK

> von Willebrand factor A domain-containing protein 3B-like isoform X1 [Biomphalaria glabrata] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: XP_013069929.2, Length: 1663, Number of Matches: 1, Score 28.2, bits(59), E value (Expect) 0.59, Identities 8/8(100%), Positives 8/8(100%), Gaps 0/8(0%)

Query 3 VTFDLSEK 10
VTFDLSEK
Sbjct 23 VTFDLSEK 30

> von Willebrand factor A domain-containing protein 3B-like isoform X2 [Biomphalaria glabrata] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: XP_013069930.2, Length: 1656, Number of Matches: 1, Score 28.2, bits(59), E value (Expect) 0.59, Identities 8/8(100%), Positives 8/8(100%), Gaps 0/8(0%)

Query 3 VTFDLSEK 10
VTFDLSEK
Sbjct 23 VTFDLSEK 30

LFSTASGGR

> Collagen alpha-6(VI) chain, partial [Biomphalaria pfeifferi] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: KAI8767740.1, Length: 799, Number of Matches: 1, Score 26.5 bits(55), E value (Expect) 1.9, Identities 8/9(89%), Positives 9/9(100%), Gaps 0/9(0%)

Query 1 LFSTASGGR 9
+FSTASGGR
Sbjct 708 MFSTASGGR 716

> Collagen alpha-6(VI) chain, partial [Biomphalaria pfeifferi]

Sequence ID: KAK0040452.1, Length: 518, Number of Matches: 1, Score 26.5 bits(55), E value (Expect) 1.9, Identities 8/9(89%), Positives 9/9(100%), Gaps 0/9(0%)

Query 1 LFSTASGGR 9
+FSTASGGR
Sbjct 427 MFSTASGGR 435

LPLYEDPKLDVSSLR

> uncharacterized protein LOC101853718 [Aplysia californica] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: XP_012941625.1, Length: 327, Number of Matches: 2, Score 30.3, bits(64), E value (Expect) 0.27, Identities 10/12(83%), Positives 10/12(83%), Gaps 0/12(0%)

Query 4 YEDPKLDVSSLR 15
YE PKLDV SLR
Sbjct 235 YELPKLDVASLR 246

FDANPFFSGR

> RecName: Full=Hemocyanin, beta-C chain unit D [Helix pomatia] [land snail, UniProtKB/Swiss-Prot]

Sequence ID: P12031.2, Length: 410, Number of Matches: 2, Score 29.1, bits(61), E value (Expect) 9e-06, Identities 8/9(89%), Positives 8/9 (88%), Gaps 0/9(0%)

```
Query 1      FDANPFFSG 9
          FD NPFSSG
Sbjct 120    FDPNPFFSG 128
```

HGSPIGVPYWDWTR

> hemocyanin alphaN [Cornu aspersum] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: AYO86684.1, Length: 3432, Number of Matches: 8, Score 52.8, bits(117), E value (Expect) 2e-09, Identities 14/14(100%), Positives 14/14 (100%), Gaps 0/14(0%)

```
Query 1      HGSPIGVPYWDWTR 14
          HGSPIGVPYWDWTR
Sbjct 1784    HGSPIGVPYWDWTR 1797
```

LISEATYFNSR

> hemocyanin beta [Cornu aspersum] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: AYO86685.1, Length: 3433, Number of Matches: 1, Score 38.4 bits(83), E value (Expect) 2e-04, Identities 11/11(100%), Positives 11/11(100%), Gaps 0/11(0%)

```
Query 1      LISEATYFNSR 11
          LISEATYFNSR
Sbjct 1388    LISEATYFNSR 1398
```

> RecName: Full=Hemocyanin, beta-C chain unit D [Helix pomatia] [land snail, UniProtKB/Swiss-Prot]

Sequence ID: P12031.2, Length: 410, Number of Matches: 1, Score 30.3 bits(64), E value (Expect) 6e-05, Identities 9/11(82%), Positives 10/11(90%), Gaps 0/11(0%)

```
Query 1      LISEATYFNSR 11
          LIS ATY+NSR
Sbjct 106     LISKATYYNSR 116
```

FDPNPFFSGR

> RecName: Full=Hemocyanin, beta-C chain unit D [Helix pomatia] [land snail, UniProtKB/Swiss-Prot]

Sequence ID: P12031.2, Length: 410, Number of Matches: 1, Score 33.3, bits(71), E value (Expect) 3e-07, Identities 9/9(100%), Positives 9/9 (100%), Gaps 0/9(0%)

```
Query 1      FDPNPFFSG 9
          FDPNPFFSG
Sbjct 120     FDPNPFFSG 128
```

EVFEQVEHALLAR

Hemocyanin beta [Cornu aspersum] [gastropods, non-redundant protein sequences (nr)]

Sequence ID: AYO86685.1, Length: 3433, Number of Matches: 5, Score 34.6 bits(74), E value (Expect) 0.006, Identities 10/10(100%), Positives 10/10(100%), Gaps 0/10(0%)

```
Query 4      EQVEHALLAR 13
          EQVEHALLAR
Sbjct 1358    EQVEHALLAR 1367
```

RecName: Full=Hemocyanin, beta-C chain unit D [Helix pomatia] [gastropods, UniProtKB/Swiss-Prot]

Sequence ID: P12031.2, Length: 410, Number of Matches: 3, Score 22.7 bits(46), E value (Expect) 0.050, Identities 7/8(88%), Positives 7/8(87%), Gaps 0/8(0%)

```
Query 4      EQVEHALL 11
          EQVE ALL
Sbjct 76      EQVEEALL 83
```

QYLQITWSPPR

> fibrinogen-like protein A isoform X1 [Biomphalaria glabrata] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: XP_055864456.1, Length: 383, Number of Matches: 1, Score 24.4, bits(57), E value (Expect) 1.4, Identities 7/9(78%), Positives 7/9 (77%), Gaps 0/9(0%)

```
Query 2      YLQITWSP 10
          YLQITW P
Sbjct 105     YLQITWTHP 113
```

TDVTSALLGARCNEGNTNTHSPLR

> unnamed protein product, partial [Candidula unifasciata] [gastropoda, non-redundant protein sequences (nr)]
Sequence ID: CAG5131631.1, Length: 449, Number of Matches: 1, Score 36.7, bits(79), E value (Expect) 0.006,
Identities 14/20(70%), Positives 14/20 (70%), Gaps 0/20(0%)

```
Query 1 TDVTSALLGARCNEGGTNTH 20
      TDVT LLGA GGTNTH
Sbjct 328 TDVTTSLLGAPYLGGGTNTH 347
```

> unnamed protein product [Candidula unifasciata] [gastropoda, non-redundant protein sequences (nr)]
Sequence ID: CAG5131621.1, Length: 584, Number of Matches: 2, Score 32.0, bits(68), E value (Expect) 0.26,
Identities 12/19(63%), Positives 13/19 (68%), Gaps 0/19(0%)

```
Query 2 DVTSALLGARCNEGGTNTH 20
      D+ S L GA EGGTNTH
Sbjct 462 DIASSLIGAEYEGGTNTH 480
```

LTQHFNVSNGAR

> mucus protein [Cornu aspersum] [gastropoda, non-redundant protein sequences (nr)]
Sequence ID: QEG59312.1, Length: 340, Number of Matches: 1, Score 36.7 bits(79), E value (Expect) 0.001,
Identities 11/12(92%), Positives 11/12(91%), Gaps 0/12(0%)

```
Query 2 TQHFNVGSNGAR 13
      TQHF VGSNGAR
Sbjct 183 TQHFKVGSNGAR 194
```

> unnamed protein product [Candidula unifasciata]
Sequence ID: CAG5131621.1, Length: 584, Number of Matches: 3, Score 31.2 bits(66), E value (Expect) 0.094,
Identities 10/13(77%), Positives 11/13(84%), Gaps 0/13(0%)

```
Query 1 LTQHFNVSNGAR 13
      LT+HFNVG GAR
Sbjct 426 LTEHFNVG YKGAR 438
```

> unnamed protein product, partial [Candidula unifasciata]
Sequence ID: CAG5131631.1, Length: 449, Number of Matches: 2, Score 29.5 bits(62), E value (Expect) 0.38,
Identities 9/12(75%), Positives 10/12(83%), Gaps 0/12(0%)

```
Query 1 LTQHFNVSNGA 12
      LT+HF VG NGA
Sbjct 293 LTHHFTVGPNGA 304
```

MPDYDCGCCNGSNGSYGSGGGGGGGGR

> unnamed protein product, partial [Candidula unifasciata] [gastropoda, non-redundant protein sequences (nr)]
Sequence ID: CAG5126455.1, Length: 305, Number of Matches: 8, Score 32.5, bits(69), E value (Expect) 0.23,
Identities 12/15(80%), Positives 12/15 (80%), Gaps 0/15(0%)

```
Query 11 GSNGSYGSGGGGGGG 25
      G GSYGS GGGGGG
Sbjct 83 GGGGSYGSSGGGGGG 97
```

> unnamed protein product [Candidula unifasciata] [gastropoda, non-redundant protein sequences (nr)]
Sequence ID: CAG5131834.1, Length: 354, Number of Matches: 8, Score 32.5, bits(69), E value (Expect) 0.24,
Identities 15/24(63%), Positives 15/24 (62%), Gaps 9/24(37%)

```
Query 11 GSNGSYG-----SGGGGG-GG 25
      GSNGSYG SGGGGG GG
Sbjct 254 GSNGSYGGGYGGSAYSGGGGGYGG 277
```

DGMSAAPQAENAFALK

> RecName: Full=Achacin; Flags: Precursor [Lissachatina fulica] [gastropoda, UniProtKB/Swiss-Prot]
Sequence ID: P35903.1, Length: 531, Number of Matches: 3, Score 29.5, bits(62), E value (Expect) 3e-04, Identities
12/17(71%), Positives 13/17 (76%), Gaps 2/17(11%)

```
Query 1 DGMSAAPQA-ENAFALK 16
      DGMSA PQA +AF LK
Sbjct 251 DGMSALPQALADAF-LK 266
```

> RecName: Full=L-amino-acid oxidase; AltName: Full=Escapin; Flags: Precursor [Aplysia californica]
[gastropoda, UniProtKB/Swiss-Prot]

Sequence ID: Q6IWZ0.1, Length: 535, Number of Matches: 1, Score 19.7, bits(39), E value (Expect) 0.95, Identities
5/8(63%), Positives 6/8 (75%), Gaps 0/8(0%)

```
Query 1 DGMSAAPQ 8
      +GMS PQ
```

Sbjct 254 EGMSSVPQ 261

SGFPTTSKDR

> RecName: Full=L-amino-acid oxidase; AltName: Full=Escapin; Flags: Precursor [Aplysia californica] [gastropoda, UniProtKB/Swiss-Prot]

Sequence ID: Q6IWZ0.1, Length: 535, Number of Matches: 1, Score 21.4, bits(43), E value (Expect) 0.080, Identities 6/6(100%), Positives 6/6 (100%), Gaps 0/6(0%)

```
Query 4 PTTSKD 9
      PTTSKD
Sbjct 299 PTTSKD 304
```

VGGGPSGVELDEFEARVELK

> RecName: Full=Achacin; Flags: Precursor [Lissachatina fulica] [gastropoda, UniProtKB/Swiss-Prot]

Sequence ID: P35903.1, Length: 531, Number of Matches: 1, Score 21.4, bits(43), E value (Expect) 0.40, Identities 11/27(41%), Positives 11/27 (40%), Gaps 15/27(55%)

```
Query 1 VGGGPSG-----VELDEFE 14
      VG GPSG VEL FE
Sbjct 43 VGAGPSGTYSAYKLNRKQTVEL--FE 67
```

AELKGDMQYTYADSEKVR

> fibrillin-3, partial [Biomphalaria pfeifferi] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: KAK0048148.1, Length: 391, Number of Matches: 1, Score 31.2, bits(66), E value (Expect) 0.22, Identities 12/25(48%), Positives 14/25 (56%), Gaps 10/25(40%)

```
Query 4 KGDM--QYTY-----ADSEKVR 18
      KGDM QY Y A+SEK+R
Sbjct 157 KGDMNWQYDYWMPPIVVGYANSEKIR 181
```

> fibrillin-3, partial [Biomphalaria glabrata] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: KAK6970092.1, Length: 5172, Number of Matches: 2, Score 31.2, bits(66), E value (Expect) 0.22, Identities 12/25(48%), Positives 14/25 (56%), Gaps 10/25(40%)

```
Query 4 KGDM--QYTY-----ADSEKVR 18
      KGDM QY Y A+SEK+R
Sbjct 3269 KGDMSWQYDYWMPPIVVGYANSEKIR 3293
```

AKVQVIGVPDDRLLLR

> acyl-CoA synthetase family member 2, mitochondrial-like, partial [Pomacea canaliculata] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: XP_025086706.1, Length: 514, Number of Matches: 1, Score 35.4, bits(76), E value (Expect) 0.005, Identities 10/11(91%), Positives 11/11 (100%), Gaps 0/11(0%)

```
Query 3 VQVIGVPDDR 13
      VQVIGVPD+RL
Sbjct 431 VQVIGVPDERL 441
```

> unnamed protein product, partial [Candidula unifasciata] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: CAG5136482.1, Length: 571, Number of Matches: 1, Score 35.4, bits(76), E value (Expect) 0.005, Identities 10/11(91%), Positives 11/11 (100%), Gaps 0/11(0%)

```
Query 3 VQVIGVPDDR 13
      VQVIGVPD+RL
Sbjct 491 VQVIGVPDERL 501
```

YVLEDLSAADLELSR

> RecName: Full=FMRamide-activated amiloride-sensitive sodium channel; AltName: Full=FANACH [Cornu aspersum] [land snail, UniProtKB/Swiss-Prot]

Sequence ID: Q25011.1, Length: 625, Number of Matches: 3, Score 18.5, bits(36), E value (Expect) 0.14, Identities 5/5(100%), Positives 5/5 (100%), Gaps 0/5(0%)

```
Query 3 LEDLS 7
      LEDLS
Sbjct 511 LEDLS 515
```

GSSVSLCVWDWAVLPR

> RecName: Full=FMRamide-activated amiloride-sensitive sodium channel; AltName: Full=FANACH [Cornu aspersum] [land snail UniProtKB/Swiss-Prot]

Sequence ID: Q25011.1, Length: 625, Number of Matches: 2, Score 15.5, bits(29), E value (Expect) 1.9, Identities 5/7(71%), Positives 5/7 (71%), Gaps 0/7(0%)

```
Query   3      SVSLCVW   9
          SVSL   W
Sbjct  420  SVLSYW   426
```

MVTSLYPGEDWAMLPR

> mucin-5AC-like, partial [Haliotis rufescens] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: XP_048239711.1, Length: 740, Number of Matches: 1, Score 31.2, bits(66), E value (Expect) 0.15, Identities 9/16(56%), Positives 11/16 (68%), Gaps 3/16(18%)

```
Query   1  MVTSLYPGEDWAMLPR  16
          M+T LYP +   MLPR
Sbjct   1  MITNLYPAQ---MLPR  13
```

ETVSPGYSEGEECTCASITQK

> mucin-5B-like isoform X4 [Haliotis rubra] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: XP_046552239.1, Length: 790, Number of Matches: 4, Score 27.4, bits(57), E value (Expect) 6.7, Identities 13/21(62%), Positives 14/21 (66%), Gaps 3/21(14%)

```
Query   2      TV--SPGYSEGEECTCASITQK  20
          TV  SPG S+G  T A ITQK
Sbjct  261  TVTWSPG-SQGSSTSAPITQK  280
```

HGGGGGGFGGGGFGSR

> uncharacterized protein LOC124113905 [Haliotis rufescens] [molluscs, non-redundant protein sequences (nr)]

Sequence ID: XP_046330350.2, Length: 1175, Number of Matches: 4, Score 38.8, bits(84), E value (Expect) 9e-04, Identities 13/13(100%), Positives 13/13 (100%), Gaps 0/13(0%)

```
Query   2      GGGGGGFGGGGFG  14
          GGGGGGFGGGGFG
Sbjct  322  GGGGGGFGGGGFG  334
```

> fibroin heavy chain isoform X1 [Aplysia californica] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: XP_012943828.1, Length: 1169, Number of Matches: 28, Score 33.7, bits(72), E value (Expect) 0.018, Identities 13/16(81%), Positives 13/16 (81%), Gaps 3/16(18%)

```
Query   2      GGGGGGFGGG---GFG  14
          GGGGGGFGGG   GFG
Sbjct  608  GGGGGGFGGGPGSGFG  623
```

> elastin-like [Ostrea edulis] [molluscs, non-redundant protein sequences (nr)]

Sequence ID: XP_056017499.1, Length: 757, Number of Matches: 46, Score 34.1, bits(73), E value (Expect) 0.038, Identities 13/15(87%), Positives 13/15 (86%), Gaps 2/15(13%)

```
Query   2      GGGGGGF--GGGGFG  14
          GGGGGGF  GGGGFG
Sbjct  115  GGGGGGFAGGGGFG  129
```

> RecName: Full=Glycine, alanine and asparagine-rich protein; Flags: Precursor [Haliotis asinina] [molluscs, UniProtKB/Swiss-Prot]

Sequence ID: P86732.1, Length: 507, Number of Matches: 47, Score 26.5, bits(55), E value (Expect) 0.004, Identities 11/17(65%), Positives 11/17 (64%), Gaps 4/17(23%)

```
Query   2      GGGGGGFGGG---GFG  14
          G  GG GFGGG   GFG
Sbjct  99   GSGGSGFGGSGSGSGFG  115
```

VFADFELHNIGASADVR

> hemocyanin beta [Cornu aspersum] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: AYO86685.1, Length: 3433, Number of Matches: 6, Score 56.6, bits(126), E value (Expect) 2e-10, Identities 17/17(100%), Positives 17/17 (100%), Gaps 0/17(0%)

```
Query   1      VFADFELHNIGASADVR  17
          VFADFELHNIGASADVR
Sbjct  327  VFADFELHNIGASADVR  343
```

CQVSLPYWDWAVPLR

> RecName: Full=Hemocyanin, beta-C chain unit G [Helix pomatia] [land snail, UniProtKB/Swiss-Prot]

Sequence ID: P56823.1, Length: 404, Number of Matches: 2, Score 25.2, bits(52), E value (Expect) 5e-04, Identities 5/5(100%), Positives 5/5 (100%), Gaps 0/5(0%)

```
Query   6      PYWDW   10
          PYWDW
Sbjct   98      PYWDW   102
```

LSGYDVSKVNEILK

> hemocyanin beta [Cornu aspersum] [land snail, non-redundant protein sequences (nr)]

Sequence ID: AYO86685.1, Length: 3433, Number of Matches: 3, Score 35.8, bits(77), E value (Expect) 8e-05, Identities 11/13(85%), Positives 11/13 (84%), Gaps 0/13(0%)

```
Query   2      SGYDVSKVNEILK   14
          SGYDV  VNEILK
Sbjct  3216      SGYDVGQVNEILK   3228
```

HLWLLHCFEHDNLNGYEYDNL

> hemocyanin beta [Cornu aspersum] [land snail, non-redundant protein sequences (nr)]

Sequence ID: AYO86685.1, Length: 3433, Number of Matches: 16, Score 40.1, bits(87), E value (Expect) 8e-06, Identities 13/15(87%), Positives 13/15 (86%), Gaps 2/15(13%)

```
Query   8      FEHDLN-GYEYDNL  21
          FEHD N GYEYDNL
Sbjct  3201      FEHD-NLGYEYDNL  3214
```

ANNARLTDASHDNPFSYTLR

> hemocyanin beta [Cornu aspersum] [land snail, non-redundant protein sequences (nr)]

Sequence ID: AYO86685.1, Length: 3433, Number of Matches: 6, Score 50.7, bits(112), E value (Expect) 1e-09, Identities 15/16(94%), Positives 15/16 (93%), Gaps 0/16(0%)

```
Query   6      LTDASHDNPFSYTLR   21
          LTDASHDNPFSYT R
Sbjct  3046      LTDASHDNPFSYTIR   3061
```

VGRIESES YVVKKSK

> zinc finger protein 502-like [Biomphalaria glabrata] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: XP_055863608.1, Length: 967, Number of Matches: 1, Score 31.2, bits(66), E value (Expect) 0.12, Identities 10/13(77%), Positives 11/13 (84%), Gaps 0/13(0%)

```
Query   3      RIESES YVVKKSK   15
          RI SES+VVKK K
Sbjct  283      RISSESFVVKKRK   295
```

> zinc finger protein 184 [Biomphalaria glabrata] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: KAI8795828.1, Length: 967, Number of Matches: 1, Score 31.2, bits(66), E value (Expect) 0.12, Identities 10/13(77%), Positives 11/13 (84%), Gaps 0/13(0%)

```
Query   3      RIESES YVVKKSK   15
          RI SES+VVKK K
Sbjct  283      RISSESFVVKKRK   295
```

VLTFYQSCDCVVDHCHR

> zinc finger protein 664-like [Patella vulgata] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: XP_050401404.1, Length: 400, Number of Matches: 1, Score 28.6, bits(60), E value (Expect) 1.5, Identities 9/12(75%), Positives 9/12 (75%), Gaps 3/12(25%)

```
Query   1      VLTFYQSCDCV   12
          VLTFYQ  CVV
Sbjct   6      VLTFYQ---CVV   14
```

GEPGSTGPPGLK

> collagen alpha-1(IV) chain-like, partial [Pomacea canaliculata] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: XP_025114158.1, Length: 339, Number of Matches: 4, Score 38.4, bits(83), E value (Expect) 2e-04, Identities 12/12(100%), Positives 12/12 (100%), Gaps 0/12(0%)

Query 1 GEPGSTGPPGLK 12
GEPGSTGPPGLK
Sbjct 167 GEPGSTGPPGLK 178

NGPSGVELDEFEARVELK

> collagen alpha-1(XIII) chain-like isoform X7 [Haliotis rubra] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: XP_046573418.1, Length: 327, Number of Matches: 1, Score 28.2, bits(59), E value (Expect) 2.5, Identities 10/17(59%), Positives 12/17 (70%), Gaps 1/17(5%)

Query 3 PSGVELDEFEAR-VELK 18
P G ELDE+ R +ELK
Sbjct 186 PAGLELDEYQRIIELK 202

FVDMMDGMFSSAAGGRPEAR

> collagen alpha-4(VI) chain-like isoform X2 [Physella acuta] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: XP_059154404.1, Length: 273, Number of Matches: 1, Score 35.0, bits(75), E value (Expect) 0.012, Identities 11/14(79%), Positives 12/14 (85%), Gaps 0/14(0%)

Query 5 DGMFSSAAGGRPEA 18
D MFSSA GGRP+A
Sbjct 180 DKMFSSASGGRPDA 193

> collagen alpha-1(XII) chain-like [Physella acuta] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: XP_059163536.1, Length: 692, Number of Matches: 3, Score 31.2, bits(66), E value (Expect) 0.26, Identities 9/12(75%), Positives 10/12 (83%), Gaps 0/12(0%)

Query 7 MFSSAAGGRPEA 18
MF AAGGRP+A
Sbjct 596 MFGTAAGGRPDA 607

RAYTDGMFSSAAGGRPEAR

> collagen alpha-4(VI) chain-like isoform X2 [Physella acuta] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: XP_059154404.1, Length: 273, Number of Matches: 1, Score 35.0, bits(75), E value (Expect) 0.012, Identities 11/14(79%), Positives 12/14 (85%), Gaps 0/14(0%)

Query 5 DGMFSSAAGGRPEA 18
D MFSSA GGRP+A
Sbjct 180 DKMFSSASGGRPDA 193

> collagen alpha-4(VI) chain-like isoform X1 [Physella acuta] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: XP_059154396.1, Length: 278, Number of Matches: 1, Score 35.0, bits(75), E value (Expect) 0.012, Identities 11/14(79%), Positives 12/14 (85%), Gaps 0/14(0%)

Query 5 DGMFSSAAGGRPEA 18
D MFSSA GGRP+A
Sbjct 185 DKMFSSASGGRPDA 198

CNEGGTNTHSPLR

> collagen alpha-6(VI) chain-like [Physella acuta] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: XP_059164377.1, Length: 1896, Number of Matches: 2, Score 26.1, bits(54), E value (Expect) 6.2, Identities 8/9(89%), Positives 8/9 (88%), Gaps 0/9(0%)

Query 4 GGTNTHSPL 12
GGTNTHS L
Sbjct 1085 GGTNTHSAL 1093

NPGYLVSKVNEILK

> mucin-2-like [Physella acuta] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: XP_059140993.1, Length: 984, Number of Matches: 1, Score 28.6, bits(60), E value (Expect) 0.84, Identities 10/14(71%), Positives 11/14 (78%), Gaps 0/14(0%)

Query 1 NPGYLVSKVNEILK 14
NP LVSK+ EILK
Sbjct 799 NPTALVSKIKEILK 812

> serine/arginine repetitive matrix protein 2 [Biomphalaria glabrata] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: KAI8735946.1, Length: 1477, Number of Matches: 1, Score 28.6, bits(60), E value (Expect) 0.84, Identities 10/14(71%), Positives 11/14 (78%), Gaps 0/14(0%)

```
Query 1      NPGYLVSKVNEILK 14
           NP  LVSK+ EILK
Sbjct 1307  NPTALVSKIKEILK 1320
```

DCRVRVGGPLFAPSPYLFER

> mucin-17-like [Haliotis rubra] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: XP_046554219.1, Length: 1822, Number of Matches: 2, Score 29.9, bits(63), E value (Expect) 0.78, Identities 13/25(52%), Positives 14/25 (56%), Gaps 10/25(40%)

```
Query 3      RVRVGGPLF-----APSPYLFE 19
           RVRVG  LF          A SPYLF+
Sbjct 1559  RVRVG--LFDKTKMGGQACSPYLFQ 1581
```

FNFLPLSADALESLR

> E3 ubiquitin-protein ligase HERC2-like isoform X2 [Biomphalaria glabrata] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: XP_055894969.1, Length: 4995, Number of Matches: 5, Score 29.5, bits(62), E value (Expect) 0.45, Identities 10/12(83%), Positives 10/12 (83%), Gaps 0/12(0%)

```
Query 4      LPLSADALESLR 15
           LPLS DAL SLR
Sbjct 4137  LPLSCDALASLR 4148
```

ASSGSCDFSSTAANR

> mucin-5AC-like isoform X2 [Haliotis rufescens] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: XP_048252836.1, Length: 621, Number of Matches: 3, Score 29.9, bits(63), E value (Expect) 0.45, Identities 11/13(85%), Positives 11/13 (84%), Gaps 0/13(0%)

```
Query 2      SSGSCDFSSTAA 14
           SSGS  FSSSTAA
Sbjct 252  SSGSSSFSSSTAA 264
```

> mucin-5AC-like isoform X1 [Haliotis rufescens] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: XP_048252834.1, Length: 702, Number of Matches: 3, Score 29.9, bits(63), E value (Expect) 0.45, Identities 11/13(85%), Positives 11/13 (84%), Gaps 0/13(0%)

```
Query 2      SSGSCDFSSTAA 14
           SSGS  FSSSTAA
Sbjct 333  SSGSSSFSSSTAA 345
```

GCAGCPQAGSK

> fibrillin-1-like [Biomphalaria glabrata] [gastropoda, non-redundant protein sequences (nr)]

Sequence ID: XP_055888733.1, Length: 2868, Number of Matches: 3, Score 26.5, bits(55), E value (Expect) 3.0, Identities 8/9(89%), Positives 8/9 (88%), Gaps 0/9(0%)

```
Query 2      CAGCPQAGS 10
           CAGCPQ GS
Sbjct 960  CAGCPQIGS 968
```