

Supplementary Information 1 (SI 1):

SI 1. An alignment of amino acid sequences of some identified peptides from protein bands at 50.230 kDa, 61.106 kDa and 93.088 kDa of fraction Rv 50-100 kDa with known extracellular proteins in Gastropoda (taxid:6448) with database UniProtKB/SwissProt, sequences algorithm blastp (protein-protein BLAST), filtered to match records with identity between 50% and 100% (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>).

Peptides from protein band at 93.088 kDa

1) HGDDCCDMDMR

> **RecName: Full=Peroxidase-like protein 2 [Lottia gigantea]**

Sequence ID: B3A0P3.1; Length: 884; Number of Matches: 1; Score = 21.0 bits (42), E value (Expect) **0.14**, Identities 5/5 (100%), Positives 5/5 (100%), Gaps 0/5(0%)

```
Query 2      GDDCC 6
          GDDCC
Sbjct 859    GDDCC 863
```

2) DHGEPPYDDFR

> **RecName: Full=Peroxidase-like protein 2 [Lottia gigantea]**

Sequence ID: B3A0P3.1; Length: 884; Number of Matches: 1; Score = 23.1 bits (47), E value (Expect) **0.024**, Identities 8/11 (73%), Positives 9/11 (81%), Gaps 0/11(0%)

```
Query 1      DHGEPPYDDFR 11
          DHG PPY+ FR
Sbjct 375    DHGVPPYNWFR 385
```

> **RecName: Full=Peroxidase-like protein 3 [Lottia gigantea]**

Sequence ID: B3A0Q8.1; Length: 294; Number of Matches: 2; Score = 21.8 bits(44) , E value (Expect) **0.069**, Identities 7/11(64%); Positives 8/11(72%); Gaps 0/11(0%)

```
Query 1      DHGEPPYDDFR 11
          DHG P Y+ FR
Sbjct 144    DHGLPSYNTFR 154
```

3) LPGAFTGPTFNCIAR

> **RecName: Full=Peroxidase-like protein 3 [Lottia gigantea]**

Sequence ID: B3A0Q8.1; Length: 294; Number of Matches: 1; Score = 29.9 bits(63); E value (Expect) **2e-04**, Identities 11/16(69%); Positives 11/16(68%); Gaps 1/16(6%)

```
Query 1      LPGAFTGPTFNC-IAR 15
          LPG  GPTF C IAR
Sbjct 196    LPGSLLGPTFSCLIAR 211
```

> **RecName: Full=Peroxidase-like protein 2 [Lottia gigantea]**

Sequence ID: B3A0P3.1; Length: 884; Number of Matches: 3; Score = 24.4 bits(50); E value (Expect) **0.017**, Identities 10/16(63%); Positives 10/16(62%); Gaps 1/16(6%)

```
Query 1      LPGAFTGPTFNCI-AR 15
          LPG  G TF CI AR
Sbjct 430    LPGSLLGGETFSCIFAR 445
```

Peptides from protein band at 61.100 kDa

4) MPAQPVAGLFDR

> **RecName: Full=Peroxidase-like protein 2 [Lottia gigantea]**

Sequence ID: B3A0P3.1; Length: 884; Number of Matches: 1; Score = 24.0 bits(49); E value (Expect) **0.014**; Identities 7/7(100%); Positives 7/7(100%); Gaps 0/7(0%)

Query 2 PAQPVAG 8
 PAQPVAG
 Sbjct 138 PAQPVAG 144

5) LDWPVLFNDR

> RecName: Full=L-amino-acid oxidase; Short=LAAO; Short=LAO; AltName: Full=Escapin; Flags: Precursor [Aplysia californica]

Sequence ID: Q6IWZ0.1; Length: 535; Number of Matches: 1; Score 20.6 bits(41); E value (Expect) **0.16**; Identities 7/10(70%); Positives 7/10(70%); Gaps 0/10(0%)

Query 1 LDWPVLFNDR 10
 LDW L NDR
 Sbjct 335 LDWSQLRNDR 344

> RecName: Full=Aplysianin-A; Flags: Precursor [Aplysia kurodai]

Sequence ID: Q17043.1; Length: 556; Number of Matches: 1; Score 18.9 bits(37); E value (Expect) **0.67**; Identities 5/6(83%); Positives 5/6(83%); Gaps 0/6(0%)

Query 1 LDWPVL 6
 LDWP L
 Sbjct 336 LDWPPL 341

6) KLFWHMDWK

RecName: Full=L-amino-acid oxidase; Short=LAAO; Short=LAO; AltName: Full=Escapin; Flags: Precursor [Aplysia californica]

Sequence ID: Q6IWZ0.1; Length: 535; Number of Matches: 1; Score 17.6 bits(34); E value (Expect) **1.6**; Identities 5/8(63%); Positives 6/8(75%); Gaps 1/8(12%)

Query 2 LFWHM-DW 8
 LF +M DW
 Sbjct 384 LFSQMYDW 391

7) MFHFDELLDLPR

> RecName: Full=L-amino-acid oxidase; Short=LAAO; Short=LAO; AltName: Full=Escapin; Flags: Precursor [Aplysia californica]

Sequence ID: Q6IWZ0.1; Length: 535; Number of Matches: 2; Score 20.6 bits(41); E value (Expect) **0.24**; Identities 6/7(86%); Positives 6/7(85%); Gaps 0/7(0%)

Query 4 FDELLDL 10
 FDE LDL
 Sbjct 200 FDEALDL 206

> RecName: Full=Aplysianin-A; Flags: Precursor [Aplysia kurodai]

Sequence ID: Q17043.1; Length: 556; Number of Matches: 2; Score 20.6 bits(41); E value (Expect) **0.24**; Identities 6/7(86%); Positives 6/7(85%); Gaps 0/7(0%)

Query 4 FDELLDL 10
 FDE LDL
 Sbjct 201 FDEALDL 207

8) DYHFDELLDLMR

> RecName: Full=Aplysianin-A; Flags: Precursor [Aplysia kurodai]

Sequence ID: Q17043.1; Length: 556; Number of Matches: 3; Score 22.3 bits(45); E value (Expect) **0.059**; Identities 6/11(55%); Positives 8/11(72%); Gaps 0/11(0%)

Query 2 YHFDELLDLMR 12
 YHFD+ + MR
 Sbjct 489 YHFDDVMSTMR 499

>RecName: Full=L-amino-acid oxidase; Short=LAAO; Short=LAO; AltName: Full=Escapin; Flags: Precursor [Aplysia californica]

Sequence ID: Q6IWZ0.1; Length: 535; Number of Matches: 2; Score 21.4 bits(43); E value (Expect) **0.12**; Identities 6/11(55%); Positives 7/11(63%); Gaps 0/11(0%)

```
Query   2      YHFDELLDLMR   12
          YHFD+      MR
Sbjct   485    YHFDDVISTMR   495
```

9) YDRWDVPEPEFVVL

>RecName: Full=Aplysianin-A; Flags: Precursor [Aplysia kurodai]

Sequence ID: Q17043.1; Length: 556; Number of Matches: 2; Score 16.8 bits(32); E value (Expect) **9.6**; Identities 5/8(63%); Positives 6/8(75%); Gaps 0/8(0%)

```
Query   2      DRWDVPEP    9
          DR   +PEP
Sbjct   458    DRSTIPEP   465
```

10) TFAGFVLSGIGTSA

>RecName: Full=Hemocyanin type 2 unit e; AltName: Full=RtH2-e [Rapana venosa]

Sequence ID: P83040.1; Length: 413; Number of Matches: 1; Score 29.1 bits(61); E value(Expect) **2e-05**; Identities 11/13(85%); Positives 11/13(84%); Gaps 0/13(0%)

```
Query   2      FAGFVLSGIGTSA   14
          FAGF L GIGTSA
Sbjct   317    FAGFLLEGIGTSA   329
```

>RecName: Full=Hemocyanin 2; AltName: Full=Keyhole limpet hemocyanin B; Short=KLH-B; Flags: Precursor [Megathura crenulata]

Sequence ID: Q10584.2; Length: 3421; Number of Matches: 9; Score 32.5 bits(69); E value (Expect) **2e-05**; Identities 12/13(92%); Positives 12/13(92%); Gaps 0/13(0%)

```
Query   2      FAGFVLSGIGTSA   14
          FAGFVLSGI TSA
Sbjct   3225    FAGFVLSGIYTSA   3237
```

Sequence ID: Q10584.2; Length: 3421; Number of Matches: 9; Score 29.9 bits(63); E value (Expect) **4e-04**; Identities 12/14(86%); Positives = 12/14(85%); Gaps = 0/14(0%)

```
Query   1      TFAGFVLSGIGTSA   14
          TFAGF LS IG TSA
Sbjct   748    TFAGFFLSYIGTSA   761
```

Sequence ID: Q10584.2; Length: 3421; Number of Matches: 9; Score 28.6 bits(60); E value (Expect) **5e-04**; Identities 10/14(71%); Positives = 11/14(78%); Gaps = 0/14(0%)

```
Query   1      TFAGFVLSGIGTSA   14
          TFA F+LSG G SA
Sbjct   324    TFASFILSGFGGSA   337
```

>RecName: Full=Hemocyanin 1; AltName: Full=Keyhole limpet hemocyanin A; Short=KLH-A; Flags: Precursor [Megathura crenulata]

Sequence ID: Q10583.2; Length: 3414; Number of Matches: 9; Score 32.0 bits(68); E value (Expect) **3e-05**; Identities 11/13(85%); Positives 11/13(84%); Gaps 0/13(0%)

```
Query   2      FAGFVLSGIGTSA   14
          FAGFVLSGI T A
Sbjct   3217    FAGFVLSGIRTTA   3229
```

Sequence ID: Q10583.2; Length: 3414; Score 28.6 bits(60); E value (Expect) **5e-04**; Identities 10/13(77%); Positives 10/13(76%); Gaps 0/13(0%)

```
Query   2      FAGFVLSGIGTSA   14
          FAGF L G GTSA
Sbjct   1990   FAGFLLEGFGTSA   2002
```

Sequence ID: Q10583.2; Length: 3414; Score 28.2 bits(59); E value (Expect) **7e-04**; Identities 10/13(77%); Positives 10/13(76%); Gaps 0/13(0%)

```
Query   2      FAGFVLSGIGTSA   14
          FAGF L  IGTTSA
Sbjct   1566   FAGFLLHNIGTSA   1578
```

>RecName: Full=Hemocyanin type 2 unit a; AltName: Full=Hemocyanin RHSS2 subunit; AltName: Full=Hemocyanin Rta; AltName: Full=Hemocyanin heavy structural subunit; AltName: Full=RtH2-a [Rapana venosa]

Sequence ID: P80960.2; Length: 407; Number of Matches: 2; Score 30.3 bits(64); E value (Expect) **1e-04**; Identities 10/13(77%); Positives 10/13(76%); Gaps 0/13(0%)

```
Query   2      FAGFVLSGIGTSA   14
          FAGF L GIG SA
Sbjct   300   FAGFLLRGIGSSA   312
```

11) EYRYYWDWQER

>RecName: Full=Hemocyanin 2; AltName: Full=Keyhole limpet hemocyanin B; Short=KLH-B; Flags: Precursor [Megathura crenulata]

Sequence ID: Q10584.2; Length: 3421; Number of Matches: 9; Score 23.1 bits(47); E value (Expect) **0.024**; Identities 5/6(83%); Positives = 5/6(83%); Gaps = 0/6(0%)

```
Query   5      YWDWQE    10
          YWDW  E
Sbjct   1362   YWDWTE    1367
```

>RecName: Full=Hemocyanin 1; AltName: Full=Keyhole limpet hemocyanin A; Short=KLH-A; Flags: Precursor [Megathura crenulata]

Sequence ID: Q10583.2; Length: 3414; Number of Matches: 8; Score 23.1 bits(47); Expect **0.024**; Identities 5/6(83%); Positives 5/6(83%); Gaps =0/6(0%)

```
Query   5      YWDWQE    10
          YWDW  E
Sbjct   107   YWDWTE    112
```

Peptides from protein band at 50.230 kDa

12) GHKKRIRK

>RecName: Full=Hemocyanin type 2 unit a; AltName: Full=Hemocyanin RHSS2 subunit; AltName: Full=Hemocyanin Rta; AltName: Full=Hemocyanin heavy structural subunit; AltName: Full=RtH2-a [Rapana venosa]

Sequence ID: P80960.2; Length: 407; Number of Matches: 1; Score 20.6 bits(41); E value (Expect) **0.10**; Identities 6/8(75%); Positives 6/8(75%); Gaps 0/8(0%)

```
Query   1      GHKKRIRK    8
          GH K IRK
Sbjct   3      GHSKKIRK    10
```

13) IWATWQTLQK

RecName: Full=Hemocyanin 2; AltName: Full=Keyhole limpet hemocyanin B; Short=KLH-B; Flags: Precursor [Megathura crenulata]

Sequence ID: Q10584.2; Length: 3421; Number of Matches: 8; Score 31.6 bits(67); E value (Expect) **2e-05**;
Identities 8/10(80%); Positives 8/10(80%); Gaps 0/10(0%)

```
Query 1      IWATWQTLQK  10
          IWA WQ LQK
Sbjct 2728   IWAIWQALQK  2737
```

RecName: Full=Hemocyanin 1; AltName: Full=Keyhole limpet hemocyanin A; Short=KLH-A; Flags: Precursor [Megathura crenulata]

Sequence ID: Q10583.2Length: 3414Number of Matches: 8; Score 31.6 bits(67); E value (Expect) **2e-05**;
Identities 8/10(80%); Positives 8/10(80%); Gaps 0/10(0%)

```
Query 1      IWATWQTLQK  10
          IWA WQ LQK
Sbjct 1068   IWAIWQALQK  1077
```

RecName: Full=Hemocyanin 2-c chain; AltName: Full=KLH2-c [Megathura crenulata]

Sequence ID: P81732.1; Length: 420Number of Matches: 1; Score 28.2 bits(59); E value (Expect) **3e-04**;
Identities 7/9(78%); Positives 7/9(77%); Gaps 0/9(0%)

```
Query 2      WATWQTLQK  10
          WA WQ LQK
Sbjct 223    WAIWQALQK  231
```

RecName: Full=Hemocyanin type 2 unit a; AltName: Full=Hemocyanin RHSS2 subunit; AltName: Full=Hemocyanin Rta; AltName: Full=Hemocyanin heavy structural subunit; AltName: Full=RtH2-a [Rapana venosa]

Sequence ID: P80960.2; Length: 407; Number of Matches: 1; Score 26.1 bits(54); E value (Expect) **3e-04**;
Identities 7/9(78%); Positives 7/9(77%); Gaps 0/9(0%)

```
Query 2      WATWQTLQK  10
          WA WQ LQK
Sbjct 209    WAIWQELQK  217
```

14) DEVVPNPFVR

>RecName: Full=Hemocyanin 1; AltName: Full=Keyhole limpet hemocyanin A; Short=KLH-A; Flags: Precursor [Megathura crenulata]

Sequence ID: Q10583.2Length: 3414Number of Matches: 2; Score 22.3 bits(45); E value (Expect) **0.039**;
Identities 6/8(75%); Positives 6/8(75%), Gaps 0/8(0%)

```
Query 3      VVPNPFVR  10
          V PNPFR
Sbjct 2215   VMPNPFAR  2222
```

>RecName: Full=Hemocyanin type 2 unit a; AltName: Full=Hemocyanin RHSS2 subunit; AltName: Full=Hemocyanin Rta; AltName: Full=Hemocyanin heavy structural subunit; AltName: Full=RtH2-a [Rapana venosa]

Sequence ID: P80960.2; Length: 407; Number of Matches: 1; Score 20.2 bits(40); E value (Expect) **0.23**;
Identities 5/5(100%);Positives 5/5(100%), Gaps 0/5(0%)

```
Query 6      NPFVR  10
          NPFVR
Sbjct 114    NPFVR  118
```

>RecName: Full=Hemocyanin 2; AltName: Full=Keyhole limpet hemocyanin B; Short=KLH-B; Flags: Precursor [Megathura crenulata]

Sequence ID: Q10584.2; Length: 3421; Number of Matches: 4; Score 19.7 bits(39); E value (Expect) **0.33**;
Identities 6/8(75%); Positives 6/8(75%); Gaps 0/8(0%)

```
Query 1      DEVVPNPF 8
          D VV NPF
Sbjct 2218   DAVVNNPF 2225
```

15) VEITKALHKLGLR

>RecName: Full=Hemocyanin 2; AltName: Full=Keyhole limpet hemocyanin B; Short=KLH-B; Flags: Precursor [Megathura crenulata]

Sequence ID: Q10584.2; Length: 3421; Number of Matches: 9; Score 26.5 bits(55); E value (Expect) **0.002**;
Identities 8/10(80%); Positives 9/10(90%); Gaps 0/10 (0%)

```
Query 2      EITKALHKLGL 11
          +IT ALHKLGL
Sbjct 1626   DITSALHKLGL 1635
```

>RecName: Full=Hemocyanin 2-c chain; AltName: Full=KLH2-c [Megathura crenulata]

Sequence ID: P81732.1; Length: 420; Number of Matches: 1; Score 21.0 bits(42); E value (Expect) **0.20**;
Identities 7/11(64%); Positives 7/11(63%); Gaps 0/10 (0%)

```
Query 2      EITKALHKLGL 12
          EI ALH L L
Sbjct 369    EISQALHDLDL 379
```

16) YHRQEHRRWWKD

RecName: Full=Hemocyanin 1; AltName: Full=Keyhole limpet hemocyanin A; Short=KLH-A; Flags: Precursor [Megathura crenulata]

Sequence ID: Q10583.2; Length: 3414; Number of Matches: 1; Score 19.3 bits(38); E value (Expect) **0.58**;
Identities 5/6(83%); Positives 5/6(83%); Gaps 0/6(0%)

```
Query 3      RQEHRR 8
          RQEH R
Sbjct 1983   RQEHSR 1988
```