



*Sun et al. *Fish Shellfish Immunol.* 2017 Jul;66:487-496.

Figure S1. Amino acid sequence alignments of shrimp Type II crustins: *Litopenaeus vannamei* (LvCrustin P, LvCrustin I, Crustin Lv1, Crustin Lv3, Crustin-like Lv), *Litopenaeus setiferus* (Crustin Ls1, Crustin Ls2, Crustin Ls3), *Farfantepenaeus paulensis* (CrusFpau), *Farfantepenaeus brasiliensis* (CrusFbra), *Farfantepenaeus subtilis* (CrusFsub), *Litopenaeus schmitti* (CrusLsch), *Marsupenaeus japonicus* (Crustin Mj, Crustin-like Mj), *Fenneropenaeus chinensis* (Fc-crus 2, CruFc), *Penaeus monodon* (crustinPm1, crustinPm4, crustinPm5, crustinPm6, crustinPm7), *Fenneropenaeus indicus* (Fi-crustin). The predicted signal peptides are in bold and underlined. Identical amino acid residues are shadowed with black backgrounds. Triangles (▼) indicate the 12 conserved cysteine residues found in crustins. * Sequence obtained from [16] (not deposited in any database).

B

Crustin-like *Lv* gene (Type IIb)

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CAGTCCGTTTCGTCGCAGAGCAAGGAGAAGTATTACAAAGGTGAGGAGGAGAAGCCAACAT 60
TACGAGGCTATGCTTTGAGTTACCAGCTTTGGTTGTCCAAGTGTTCCTTTAAAGTCATAG 120
AAACTCTTACCAATGATCGTGTCAATCACTAGGAGACAAAATGCTGTCCTGTGACAATTC 180
AAAGCTCAAATGTCACCTCCATGATCTTAATTCCGCGTTCGTTTCTTCCTTGTAGATGCTG 240
                                                                 M L
AAGTTTGTAGTATTAGCCGTTGTCGCCGTGGCCGTGGCGCACGCGCAGGATAAAGACAAG 300
K F V V L A V V A V A V A H A Q D K D K
GCCGGCACTCGCTTAGGAGGAGGATTTCGGGGTTCCTGGAGCCGGTGGCGTCTTCCCAGGA 360
A G T R L G G G F G V P G A G G V F P G
GCCGGTGGCGTCCCTGGAGTAGGTGGCGTCTTTCCTGGAGCCGGTGGCGTCTTCCCTGGA 420
A G G V P G V G G V F P G A G G V F P G
GCCGGTGGTATCGGTCTCGGACCCGGCGGCCTCATCCCCGGAGGCGGATTCAACTGCAAT 480
A G G I G P G P G G L I P G G G F N C N
TACTGCAGGACGCCCCGTCGGGTACGTCTGCTGCAAGCCCGGTAGGTGCCCTCCGGTTCGA 540
Y C R T P V G Y V C C K P G R C P P V R
GACGTCTGCCCGTCGACCCGCTTCGGACCCCGGTCTGCCGCCAGGACCTGGACTGCTCC 600
D V C P S T R F G P P V C R Q D L D C S
GGCTCCGACAAGTGCTGCTATGACGTCTGCCTGGAAGACACAGTCTGCAAACCCATCGTG 660
G S D K C C Y D V C L E D T V C K P I V
GCAGGTTCTCAGGATAAGCCTGCATGTGAAACTTATCAAGCCTTCGTTATCAAATAAAT 720
A G S Q G -
GCTATAACTGTTAATTGTAAAT 742
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Figure S2. Genomic nucleotide and deduced amino acid sequences of Type IIa Crustin *Lv* (A) and Type IIb Crustin-like *Lv* (B). The predicted signal peptides are in bold and underlined. The exon and intron sequences are shown in black and grey, respectively. A dash (-) marks the stop codon.