Identified in this peptide Drom highlighted in yellow. The region of Tal indicate similar amino acid residues. In this figure the SMART identified PDH domain is respectively).

PDH (Daphnia magna)

Alignment of Eurydice pulchra PDH (Ep-PDH; Accession no. GQ380440) with the T. saltator PDH-I and PDH-II (Tal-PDH-I and Tal-PDH-II) deduced from the Trinity de novo transcriptome assembly, together with the top two Tal-PDH-I tblastn species homologue sequences Marsupenaeus japonicus PDH-II (Marja-PDH-II; Accession No. AB073368), Daphnia magna PDH (Dapma-PDH; Accession No. HQ843173) and the Euphausia crystallorophias sequences PDH-La, PDH-Lbl, and PDH-LblII (Eupcr-PDH-La, Eupcr-PDH-Lbl, and Eupcr-PDH-LblII respectively). '*' indicates identical amino acid residues in the two peptides, '.' and ':' indicate similar amino acid residues. In this figure the SMART identified PDH domain is highlighted in yellow. The region of Tal-PDH-II that corresponds to the PDH regions of Drome-PDF and Tal-PDH-I is highlighted in blue, though no PDH domain per se was identified in this peptide using SMART.

Figure S18. Putative Talitrus saltator PIGMENT DISPERSING HORMONE (PDH) peptides