

Gene set enrichment analysis of neuroendocrine system of the silkworm *Bombyx mori*

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Silkworm *Bombyx mori* represents a model organism for studying the neuroendocrine system in invertebrates. This system of nervous organs and endocrine glands regulates large number of life functions including movement, ecdysis, courting and mating. We have analysed strand-specific Illumina RNA-seq data from *B. mori* samples originated from different endocrine glands of both sexes and several developmental stages. Reads were mapped to the *B. mori* transcriptome using the *Bowtie 2* aligner. Since the silkworm genome is abundant in repetitive sequences (Mita *et al.*, 2004), the mapping allowing unlimited multi-mappings (required by *eXpress*) was extremely computing demanding. Transcript level RNA-seq quantification was performed using the *eXpress*

tool based on an online expectation-maximization algorithm. Obtained data were consequently analysed in several gene set enrichment packages, including *topGO* and *gplots* (both *R* packages), where highly expressed genes were clustered and visualised, according to the functional GO enrichment analysis, and clustered by gene expression level.

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References

Mita K *et al.* (2004) The genome sequence of silkworm, *Bombyx mori*. *DNA Res.* **11**(1), 27-35. <http://dx.doi.org/10.1093/dnares/11.1.27>