

# LC-MS/MS-BASED PROTEOMIC ANALYSIS OF ANISAKIDAE L3 LARVAE

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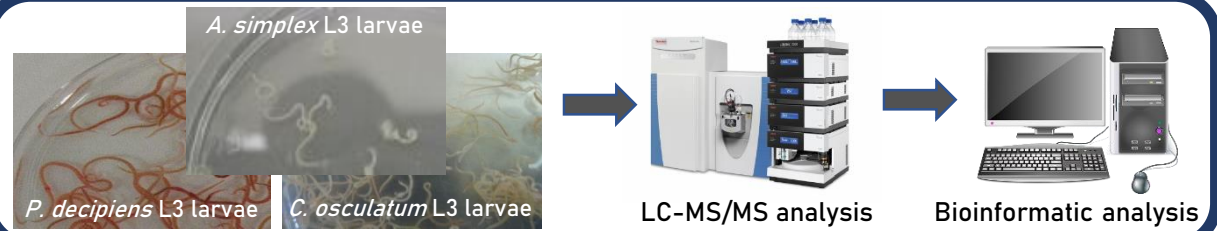
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## Aim

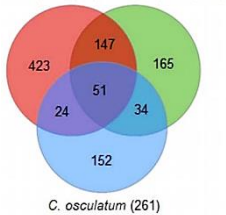
We aimed to provide more insight into Anisakidae proteomes by comparative investigation of *A. simplex*, *P. decipiens*, and *C. osculatum* L3 larvae using LC-MS/MS technology.

## Materials and Methods



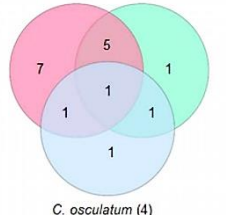
## Results

*A. simplex* (645) *P. decipiens* (397)



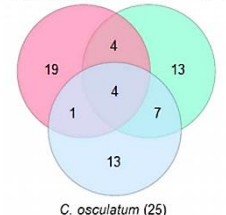
No. of all identified proteins

*A. simplex* (14) *P. decipiens* (8)

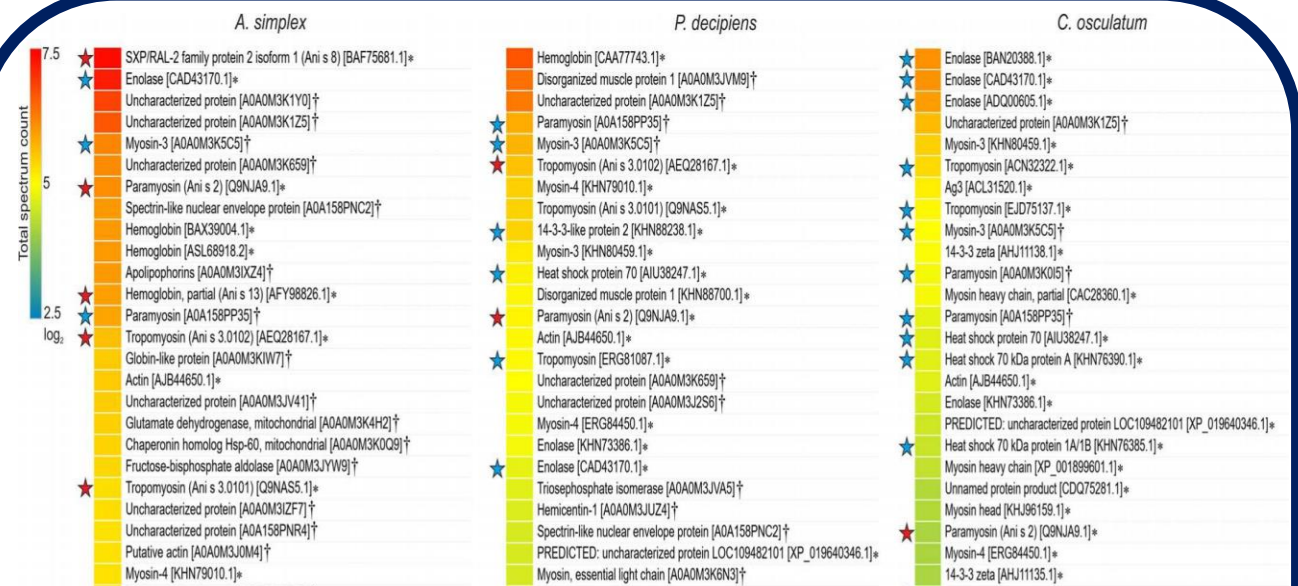


No. of identified allergens

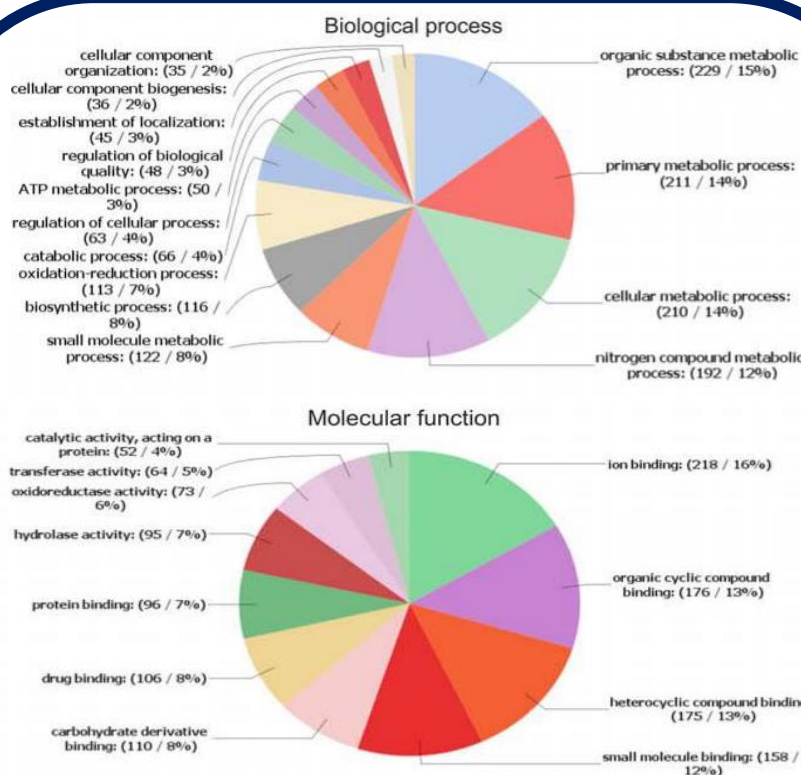
*A. simplex* (28) *P. decipiens* (28)



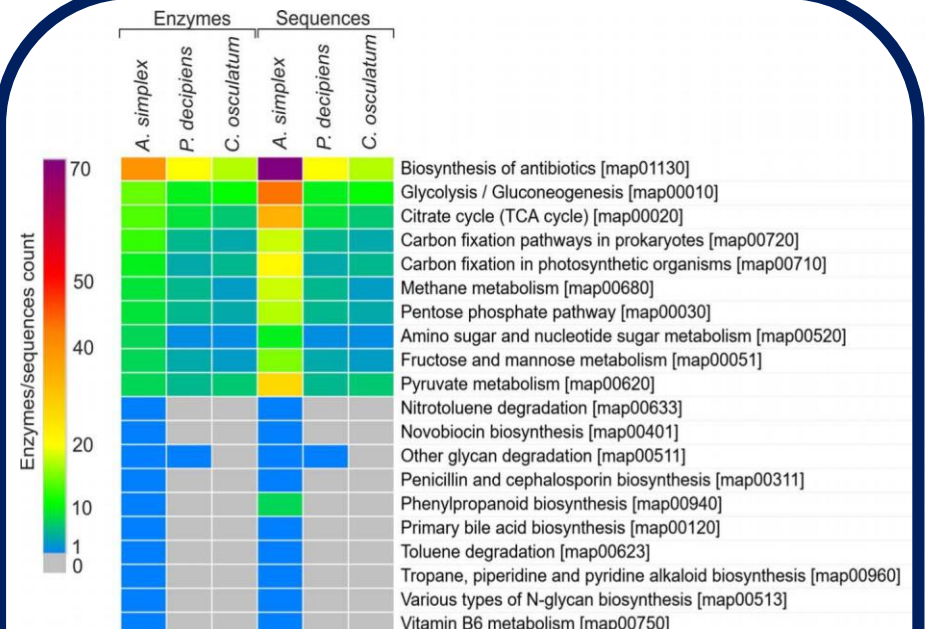
No. of possible allergens



Heat map of top 25 most abundant proteins of *A. simplex*, *P. decipiens*, and *C. osculatum* determined by label-free quantification mass spectrometry. Proteins identified as allergens and possible allergens are additionally marked in the heat map. Accession nos. of proteins were obtained from NCBI-nr protein database or UniProtKB (\*).



Gene Ontology (GO) pie charts of *A. simplex* L3 larvae proteins assigned using Blast2GO. The identified GO terms at level 3 with the corresponding number of identified proteins and percentage distribution of sequences among GO categories are presented. The structures of GO terms among the 3 proteomes were similar.



Heat map of top 20 most abundant of Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways identified in *A. simplex*, *P. decipiens*, and *C. osculatum* L3 larvae.

## Conclusion

In addition to *A. simplex*, *P. decipiens* and *C. osculatum* should also be considered as potential sources of allergens that could lead to IgE-mediated hypersensitivity.