# Two Odorant Binding Proteins from Malaria-vector *Anopheles gambiae* and their interaction with natural insect repellents: a calorimetric and thermodynamic study

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Parasites and viruses can be transmitted to humans through the bites of infected mosquitoes causing several diseases such as malaria, dengue fever, West Nile virus, and other vector-borne afflictions.

In this context, *Anopheles gambiae* is considered the primary mosquito vector responsible for the transmission of the malaria parasite *Plasmodium falciparum*, causing more than 1 million deaths each year. Unfortunately, no effective vaccines against malaria are currently available, and besides few prophylactic drugs, repellents against mosquitoes and other blood-sucking arthropods represent a valuable personal protection measure against insect bites. Over the last decade, there has been an incremental interest in eco-friendly natural plant-derived repellents to overcome safety concerns regarding the potential mammalian toxicity and carcinogenicity related to the commonly used repellents [1,2] as well as the development of resistance in mosquitoes [3].

Like other insects, female mosquitoes rely on their olfactory system to find mates and blood meals; therefore, novel strategies targeting the mosquito olfactory system are considered promising tools to control their host-seeking behaviour.

The Odorant-Binding Proteins (OBPs) constitute a class of proteins that play a key role in the mosquitoes' olfactory apparatus. In this frame, we present a calorimetric and thermodynamic study of two *Anopheles gambiae* OBP-targets. In particular, based on a preliminary screening through a crystallographic approach, a nanoDSC investigation was performed for these OBPs at pH 8.0 in their *apo*- form and the presence of potential ligands [4,5], namely the plant monoterpenoid phenols carvacrol and thymol, the aromatic compounds methyl eugenol and n-butyl cinnamate, and the monoterpenoid PMD (p-menthane-3,8-diol), which is the active ingredient of the commercial repellent Citridiol. The application of thermodynamic models [6] to the calorimetric data allowed us to gain information on the stability of the protein thermodynamic domains through the recognition of the thermal denaturation mechanisms and to highlight the specific ligand binding properties and peculiarities.

## Bibliography

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