# SPR-BASED FRAGMENT SCREENING ROUTE TO POTENTIAL BINDERS OF MOSQUITO'S SALIVA LIPS-2 PROTEIN

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Over the last decades the spread of tiger mosquito Aedes albopictus has enormously increased worldwide[1] as vector responsible for the transmission of several arboviral diseases like Zika, yellow fever and dengue. Given the lack of specific antiviral treatments or effective vaccines, the development of new strategies for their control is an urgent need. In this scenario, a salivary protein, named labrum-interacting protein of the saliva 2 (LIPS-2), has been identified from tiger mosquito Aedes albopictus. LIPS-2 plays a key role as secondary messenger for blood feeding process. Therefore, the probing mechanism may be disrupted by interfering with these signals, thus decreasing the female mosquito ability to acquire a blood meal and then reproduce. This ultimately could lead to the decline of arboviral disease transmission to humans.[2] Aided by the knowledge of LIPS-2 X-ray crystal structure along with the availability of optimized protein expression and purification techniques, a fragment-based drug-design (FBDD) approach was envisaged. Our goal was represented by the discovery of LIPS-2 potential binders able to modulate the activity of these proteins. A small library of molecular fragments was designed and, subsequently, submitted to biophysical screening through surface plasmon resonance (SPR) experiments to identify potential LIPS-2 ligands as displayed in **Figure 1**. False positive removal and kinetics analysis returned a potential binder ($K_D$ = 733 mM, LE = 0.24, patent pending), with promising activities also in *in vivo* assays.

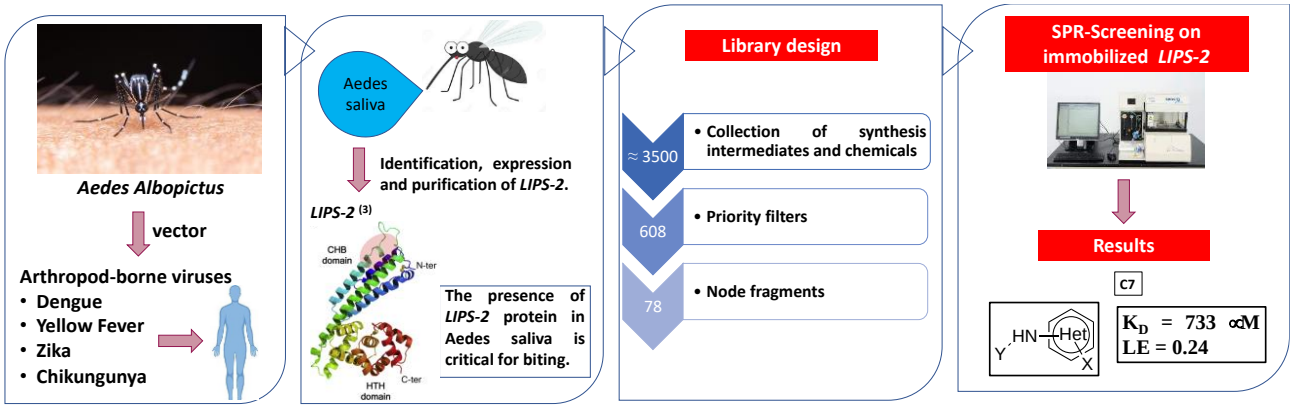


**Figure 1.** Fragment-based approach workflow**.**

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***References***

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2. Arnoldi, I., Mancini, G., Fumagalli, M. *et al*. Current Biology, (2022), 32, 16, 3493-3504.