



Upload image

Aug 05, 2020

In-silico analysis

avinash.kale¹¹domnic colvin

1

Works for me

dx.doi.org/10.17504/protocols.io.bjdkki4w

UM-DAE Centre for Excellence in Basic Sciences



avinash.kale

DOI

dx.doi.org/10.17504/protocols.io.bjdkki4w

DOCUMENT CITATION

avinash.kale 2020. In-silico analysis. **protocols.io**<https://dx.doi.org/10.17504/protocols.io.bjdkki4w>

LICENSE

This is an open access document distributed under the terms of the [Creative Commons Attribution License](https://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

CREATED

Aug 05, 2020

LAST MODIFIED

Aug 05, 2020

DOCUMENT INTEGER ID

40076

In-silico analysis

The sequences of mosquito larvicidal toxins reported for *B. thuringiensis* like all Crystal (Cry1 to Cry73) proteins and Vegetative insecticidal proteins (VIP-1, VIP-2, VIP-3, VIP-4) in addition to the Binary toxins (Bin-A and Bin-B) and Mosquito-cidal (Mtx-1; Mtx-2; Mtx-3) from *B. sphaericus*, were used as template sequences to search for homologous sequences in the NCBI-BLAST analysis. out against the databases of *Bacillus paramycoides*, *Bacillus australimaris*, *Bacillus cereus*, and *Bacillus tequilensis* and genome by using p-BLAST (<https://blast.ncbi.nlm.nih.gov>) with default search parameters.