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Data Article

Dataset of manually curated peptides against arthropod-borne viruses

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ABSTRACT

Anti-arboviral peptides are biomolecules capable of interfering with key stages of the arboviral lifecycle. We present a dataset compiling 270 peptides composed of standard amino acids with reported activity against arboviruses, along with their lengths, sequences, target specificities, peptide entry mechanisms, and interaction mechanisms. The dataset was structured to support the training of machine learning models designed to identify anti-arboviral peptides. Therefore, it facilitates the development and validation of predictive tools against arboviruses. As a carefully assembled and expert-reviewed resource, this dataset aims to serve as a reference standard for evaluating new prediction models or comparing them with automatically compiled peptide datasets. This resource provides a comprehensive overview of the antiviral mechanisms currently being explored and can serve as a foundation for designing next-generation peptides targeting arboviral infections.

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Specifications Table

Subject	Computer Sciences
Specific subject area	Antiviral peptides against arboviruses: compilation of experimentally and computationally characterized sequences with annotated viral targets and mechanisms of action.
Type of data	Table in XLSX format containing peptide sequences with confirmed antiviral activity and negative controls. Includes separate listings annotated with physicochemical properties, viral targets, and inhibitory mechanisms.
Data collection	We obtained the information contained in this database from scientific articles that investigated the antiviral activity of peptides against arboviruses. We conducted a systematic search of the scientific literature, supplemented by references from previous studies. In addition, we consulted general peptide databases that include peptides with antiviral activity against various viruses and selected those with potential applications against flaviviruses and other arboviruses.
Data source location	Column 10 (J) of the dataset lists the DOI links to the original publications for each peptide, and the reference section ([1–66]) cites the corresponding studies.
Data accessibility	Repository name: Dataset of Anti-arboviral Peptides Data identification number: 10.6084/m9.figshare.29137076 Direct URL to data: https://figshare.com/articles/dataset/Dataset_of_Anti-arboviral_Peptides/29137076?file=54780578
Related research article	None

1. Value of the Data

- This database compiles a curated collection of peptides composed of standard amino acids reported to have activity against arboviruses. It integrates data from literature searches, experimental studies, and computational analyses. The dataset contains information about peptide sequences, viral targets, mechanisms of action, design methodologies, and experimental validation details.
- The dataset can be used to train classification algorithms for predicting peptide sequences with anti-arboviral activity.
- With detailed annotations and standardized parameters, this resource supports interdisciplinary research in bioinformatics, medicinal chemistry, and virology, facilitating the identification of novel antiviral peptide candidates.

2. Background

Diseases caused by arboviruses are of enormous importance today, since they represent a major emerging threat in the areas of human and veterinary health [67,68]. For this reason, access to curated databases of peptides with proven antiviral activity results crucial for the development of therapeutic, diagnostic, and/or preventative strategies.

Our groups have been able to develop peptides, or variants thereof, with proven antiviral activity against viruses, such as Influenza [69]. For this type of study, existing peptides with proven antiviral capacity are often used as a starting point, which can then be improved through rational computational and/or experimental methods.

Given their role in multiple biological processes, proteins and peptides are the subject of study in drug development. In particular, peptide classification algorithms for predicting peptide sequences allow the design of molecules with antiviral activity [70].

Advances in bioinformatics have facilitated the prediction of protein structures, accelerating the design of drugs and peptide-based therapies. In the context of infectious diseases, research on antiviral peptides has revealed new strategies to inhibit viral entry/replication, particularly in high-impact viruses such as arboviruses [71].

The database presented here required an extensive literature review, including both the state-of-the-art and published peptide datasets against arboviruses. Unlike other published databases available at the time of this dataset's release, we carefully curated all entries in our database to confirm that each peptide has documented anti-arboviral activity. In contrast, some previous databases often relied on search algorithms that included peptides lacking actual anti-arboviral activity simply because the referenced articles mentioned an arbovirus, even if the peptides were unrelated to arbovirus studies [1].

Most databases of antimicrobial and antiviral peptides used for training and testing prediction methods contain only peptides composed of standard amino acids. From a computational perspective, this simplifies the use of machine learning approaches. Therefore, most machine learning methods for these problems have used input peptides containing only the 20 standard amino acids [72]. For this reason, the search for anti-arboviral peptides in this study followed the same trend, enabling the collected data to be used directly for training prediction algorithms.

3. Data Description

The creation of a database of peptides with anti-arboviral activity is a crucial resource for identifying and analyzing new therapeutic candidates. We obtained the information contained in this database from scientific articles that study the antiviral activity of peptides against arboviruses. The database of 270 peptides is displayed in an Excel .xlsx file. Table 1

The following describes the columns of the dataset:

- #: Position of the peptide entry in the table.
- ID: Code or name of the peptide.
- Sequence: Amino acid sequence of the peptide.
- Virus: Name of the virus in which the peptide has demonstrated activity.
- Target(s): Viral component or region where the peptide exerts its activity.
- Mechanism(s) of Action: Describes the peptide's mechanism of action, specifying the stage of the viral life cycle at which it exhibits inhibitory effects.
- Year: Year of publication of the study reporting the peptide.
- Design Method: Indicates whether the study was experimental or computational.
- Experimental test: Specifies whether the experimental study was conducted *in vivo* or *in vitro*. For computational studies, it details the type of simulation performed.
- Reference (link): Provides the URL or DOI of the study reporting the peptide and its activity.
- Original Reference (link): Provides the URL or DOI of the first study that initially reported the peptide and its activity.
- Inhibitory Concentration: Indicates the documented inhibitory concentration of the peptide, as reported in the reference study.

Table 1 presents some examples of sequences that meet the mentioned description.

Fig. 1(A) illustrates the data presentation for some peptide examples. This figure also displays the relative frequency of each standard amino acid (B) and a histogram of the peptide length distribution (C).

Based on the currently collected data, we conducted a series of statistical analyses to characterize the anti-arboviral peptides in the dataset. These analyses include parameters such as

Table 1
Some examples of attribute-value entries in the dataset.

Attribute	Value
DN59	
#	168
Sequence	MAILGDTAWDFGSLGGVFTSIGKALHQVFGAIY
Virus	DENV-2
Target(s)	Viral envelope protein (E)
Mechanism	Inhibition of viral membrane fusion
Year	2005
Design Method	Experimental
Experimental Test	*In vitro*
Reference	https://doi.org/10.1038/s41598–024–63064–1
Original Reference	https://doi.org/10.1186/1743–422X-2–49
Inhibitory Concentration	IC50 (μM): 10
WN82	
#	210
Sequence	VVDRGWGNGAGLFGKGSID
Virus	WNV
Target(s)	Viral envelope protein (E)
Mechanism	Inhibition of viral membrane fusion
Year	2005
Design Method	Experimental
Experimental Test	*In vitro*
Reference	https://doi.org/10.1186/1743–422X-2–49
Original Reference	https://doi.org/10.1186/1743–422X-2–49
Inhibitory Concentration	-
Aprotinin	
#	226
Sequence	RPDFCLEPPYTGPCKARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCMRTCGGA
Virus	DENV3
Target(s)	Viral protease complex (NS2B-NS3)
Mechanism	Inhibition of viral replication
Year	2017
Design Method	Experimental
Experimental Test	*In vitro*
Reference	https://doi.org/10.7150/ijms.21875
Original Reference	https://doi.org/10.1128/jvi.06225–11
Inhibitory Concentration	-

Table 2
Notable characteristics of the anti-arboviral peptide dataset.

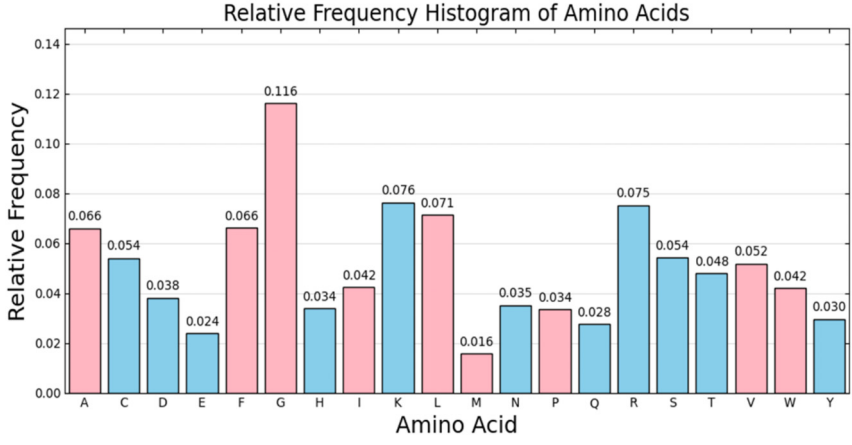
Category	Quantity
Total number of peptides with only standard amino acids and with activity against arbovirus in the dataset	270
Peptides identified solely by experimental methods	190
Peptides identified solely by computational methods	57
Peptides obtained through combined studies	23
Peptides active against viral envelope proteins	165
Peptides inhibiting the arbovirus replication	62
Peptides with other mechanisms of action	43
Average length of the peptide chain	16.80
Standard deviation of the chain length	13.26
The most frequent amino acid	G (526)
The least frequent amino acid	M (71)
Total amount of cysteines (C)	245
Total amount of histidines (H)	153

A)

Information on peptides designed for arboviruses

#	ID	Sequence	Virus	Target(s)	Mechanism(s) of Action	Year	Design Method	Experimental Test	Reference (link)	Original Reference (Link)	Inhibitory Concentration	Comments	Article Name
1	V28S	MAILGDTAWD	DENV	Viral envelope pr	Inhibition of viral membrane fusion	2024	Computational	Molecular dynamics	https://doi.org	-	-	In silico modific	In silico design of p
2	V28K	MAILGDTAWD	DENV	Viral envelope pr	Inhibition of viral membrane fusion	2024	Computational	Molecular dynamics	https://doi.org	-	-	In silico modific	In silico design of p
3	L14H	MAILGDTAWD	DENV	Viral envelope protein (E)	Inhibition of viral membrane fusion	2024	Computational	Molecular dynamics	https://doi.org	-	-	In silico modific	In silico design of p
4	I21Q	MAILGDTAWD	DENV	Viral envelope protein (E)	Inhibition of viral membrane fusion	2024	Computational	Molecular dynamics	https://doi.org	-	-	In silico modific	In silico design of p
5	Peptide 1	ELLVTFKNAHA	DENV1/DENV4	Viral envelope protein (E)	Inhibition of viral membrane fusion	2023	Experimental	In vitro	https://doi.org	https://doi.	-	Efficient for DEI	Development of no
6	-	-	-	-	-	-	-	-	-	-	-	-	-
7	-	-	-	-	-	-	-	-	-	-	-	-	-

B)



C)

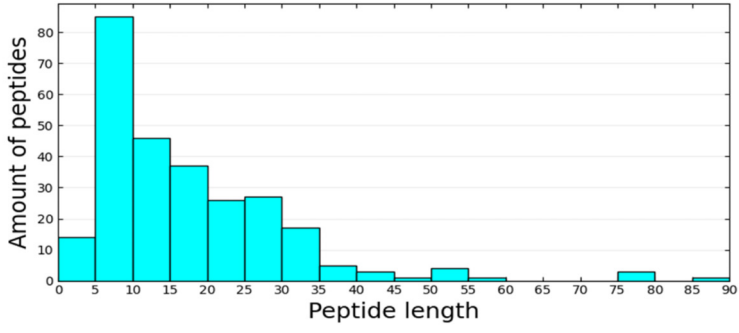


Fig. 1. Properties of peptides with anti-arboviral activity in the dataset: A) Distribution of peptide data in the dataset. B) Relative frequency of amino acids: polar amino acid frequencies are depicted in blue, non-polar in red. C) Histogram of peptide length distribution.

amino acid composition, target distribution, design method, and mechanism of action. Table 2 summarizes the most relevant features derived from this review.

4. Experimental Design, Materials and Methods

Peptide data were obtained from scientific publications between 2005 and 2025. The search was conducted across PubMed, Scopus, and Google Scholar from November 2024 to March

2026. The following query strings were used: ("antiviral peptide" OR "antiviral peptides") AND ("dengue" OR "zika" OR "chikungunya" OR "arbovirus" OR "flavivirus"), as well as ("dengue peptide inhibitor" OR "arboviral peptide sequence"). The searches were complemented by manual screening of references.

The inclusion criteria focused on peptides with reported antiviral activity against arboviruses, with sequences composed exclusively of the 20 standard amino acids. Experimental (*in vitro* or *in vivo*) and computational studies were considered. The dataset includes annotations for each entry regarding viral target, mechanism of action, experimental test, year, reference DOI, and, when available, inhibitory activity. On the other hand, the exclusion criteria included peptides containing non-standard amino acids or chemical modifications, glycans, proteins, or non-peptide molecules, duplicated sequences, and peptides not directly related to arboviral activity.

All selected entries were manually curated. Each peptide and its corresponding publication were independently reviewed, and inconsistencies were resolved through discussion among the authors.

As mentioned previously, in addition to a systematic review of the literature, databases of antimicrobial peptides such as dbAMP 3.0 [73], DBAASP 3.0 [74], and DRAMP 4.0 [75], as well as the DRAVP 2.0 [76] with antiviral peptides, were reviewed in March 2026. We selected the peptides composed solely of standard amino acids, with literature reference, and with target/description regarding arboviruses with the terms: ("Dengue" OR "DENV"), ("Chikungunya" OR "CHIKV"), ("West Nile Virus" OR "WNV"), ("Yellow Fever" OR "YFV"), ("Zika" OR "ZIKV"), ("Japanese Encephalitis Virus" OR "JEV"), ("Rift Valley Fever" OR "RVFV"), ("Vesicular Stomatitis" OR "VSV").

Although the primary focus of our review is peptides with anti-arboviral activity, our dataset includes a separate section containing 21 peptides that have not demonstrated activity against one or more arboviruses in the experimental tests (*in vitro*/*in vivo*) reported in the literature studies reviewed during the search process. Peptides that demonstrated low activity in the experiments (<50 % at tested concentrations) were considered inactive and included in this section. Given the problem of the lack of annotation of negative cases and the importance of the negative selection method for the classification of antimicrobial peptides [77], these peptides could serve as negative examples for machine learning models designed for the respective arboviruses tested.

Also, two databases focused on anti-arboviral peptides were analyzed: AVPdb [2] and ADPDB [1]. For AVPdb, all selected peptides (in January 2025) with anti-arboviral activity were composed solely of standard amino acids. On the other hand, after a careful visual inspection of the sequences in ADPDB (in August 2025), we found particular cases worth mentioning. Since this dataset contains 606 peptides with anti-dengue activity, we have reviewed each of their sequences in detail:

- First, we identified 34 peptides with "not available" sequences (e.g., ADPBD4 or #4).
- Of the remaining peptides (572), we found 82 repeated sequences (e.g., peptide DN59 appears in #13, #62, #132, #182, #187, and #204).
- Of the remaining peptides (490), we manually reviewed each sequence and its respective references to select peptides composed solely of standard amino acids. Some points to highlight are as follows:
  - Cases that did not correspond to peptides, but to glycans (e.g., #6 and #11).
  - Appearance of non-standard amino acids (e.g., #36, #101, and #537) and D-amino acids (e.g., #14 and #233).
  - Chemical modifications at the terminals, such as benzoyl (e.g., #41 and #156), phenylacetyl (e.g., #32 and #157), and aldehyde (e.g., #107 and #138), among others.
  - Hybrid peptides (e.g., #103 and #141).
  - Peptides with the sequence field written differently but referring to the same amino acid sequence (e.g., #98-#210 and #274-#275).
  - Cases corresponding to proteins (e.g., #232, #342, and #429).

- Peptides that were not actually anti-dengue, but instead analyzed parts of the virus (e.g., #244, #329, and #419), endogenous peptides from the transmitting mosquito (e.g., #430, #431, and #432), drug delivery peptides (e.g., #272 and #273), peptides with activity against other viruses (e.g., #1, #7, #8, and #443), or antimicrobial peptides (e.g., #2, #3, #5, and #164).
- Peptides with no or very low effect against dengue (e.g., #203, #242, #276, and #277).

• After considering these cases, the final number of anti-dengue peptides composed only of standard amino acids is 147 in this ADPDB.

The database we are now presenting here, after a systematic review of the literature and all related databases, compiled a total number of 270 anti-arboviral peptides.

Since the sequences in our dataset and those listed above (dbAMP, DBAASP, DRAMP, and DRAVP) have the same format (one letter per amino acid), we performed a direct search for sequences in our dataset within each of the other datasets for a coverage analysis. The results are as follows:

- dbAMP: 35,518 peptides in total, with 105 peptides in common with our dataset (105/270 = 38.89 % coverage).
- DBAASP: 24,748 peptides in total, with 42 peptides in common with our dataset (15.56 % coverage).
- DRAMP: 30,260 peptides in total, with 72 peptides in common with our dataset (26.67 % coverage).
- DRAVP: 5688 peptides in total, with 104 peptides in common with our dataset (38.52 % coverage).

A key point is that the number of anti-arboviral peptides in our dataset found in any of these four peptide sets is 140 (out of 270). This means that nearly half of the peptides compiled in this study are not included in any of the analyzed databases. Therefore, it can be concluded that this database contains specific information on anti-arboviral peptides that is not present in known databases for antimicrobial or antiviral peptides.

Limitations

Two main limitations should be acknowledged when utilizing this dataset. First, peptides containing non-standard amino acids have not been included. Second, peptides with chemical modifications (particularly at the terminal ends) have not been included.

Ethics Statement

Not applicable.

Credit Author Statement

Victor Martínez: Data curation, Writing, Original draft preparation, Investigation. **Víctor Hermosilla-Mechetti**: Dataset and bibliographic review. **Helena Gomez-Adorno**: Dataset and bibliographic review. **Diego P. Pinto-Roa**: Dataset and bibliographic review. **Christian Schaerer**: Dataset and bibliographic review. **Santiago Di Lella**: Dataset and bibliographic review. **José Colbes:** Conceptualization, Methodology, Data curation, Supervision.

Data Availability

Dataset of Anti-arboviral Peptides (Reference data) (Figshare).

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Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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