



VaxiDB: A Database for Potential Antigens of Different Pathogens to Develop Novel Vaccines and Diagnostics

HELP AND GUIDELINES

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1. OVERVIEW

VaxiDB is an innovative online database and tool that facilitates the identification and analysis of potential vaccine protein candidates while also enabling the design of customized vaccine formulations through its unique epitope reshuffling feature, providing users with all possible combinations of the input epitopes.

2. BACKGROUND

Methodology used to train our model:

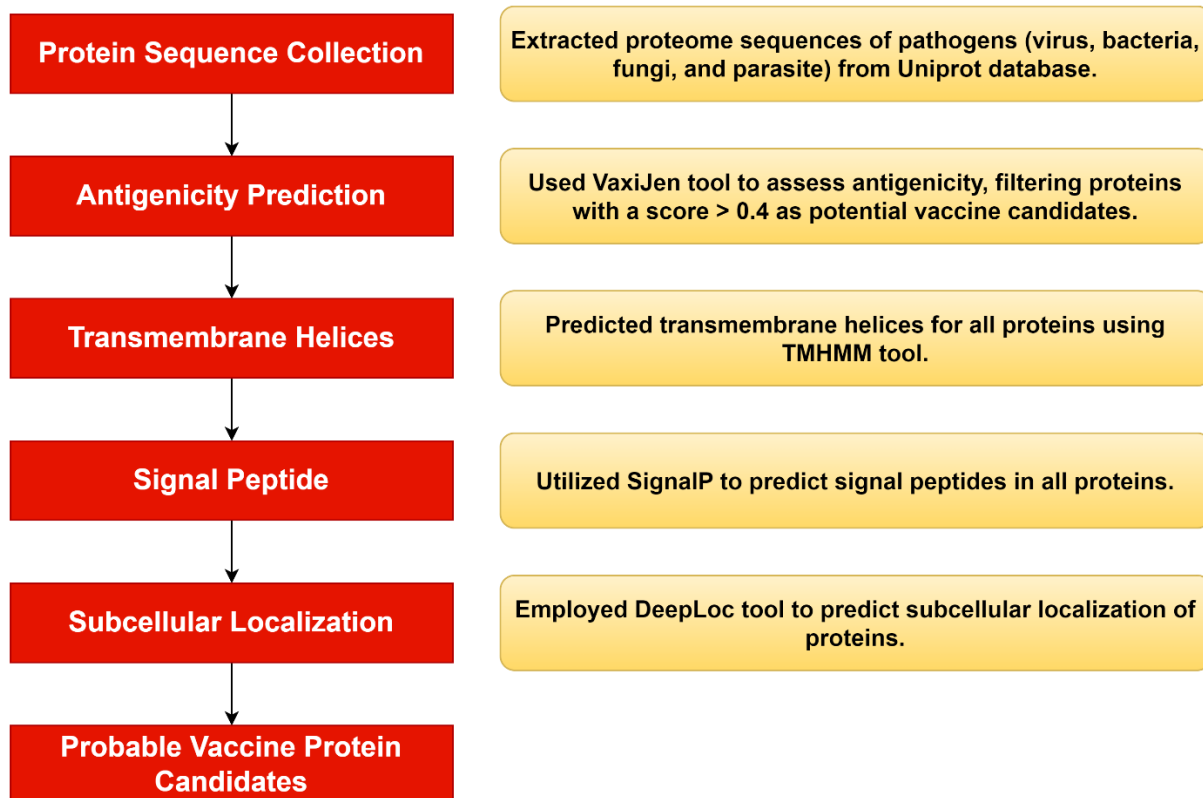
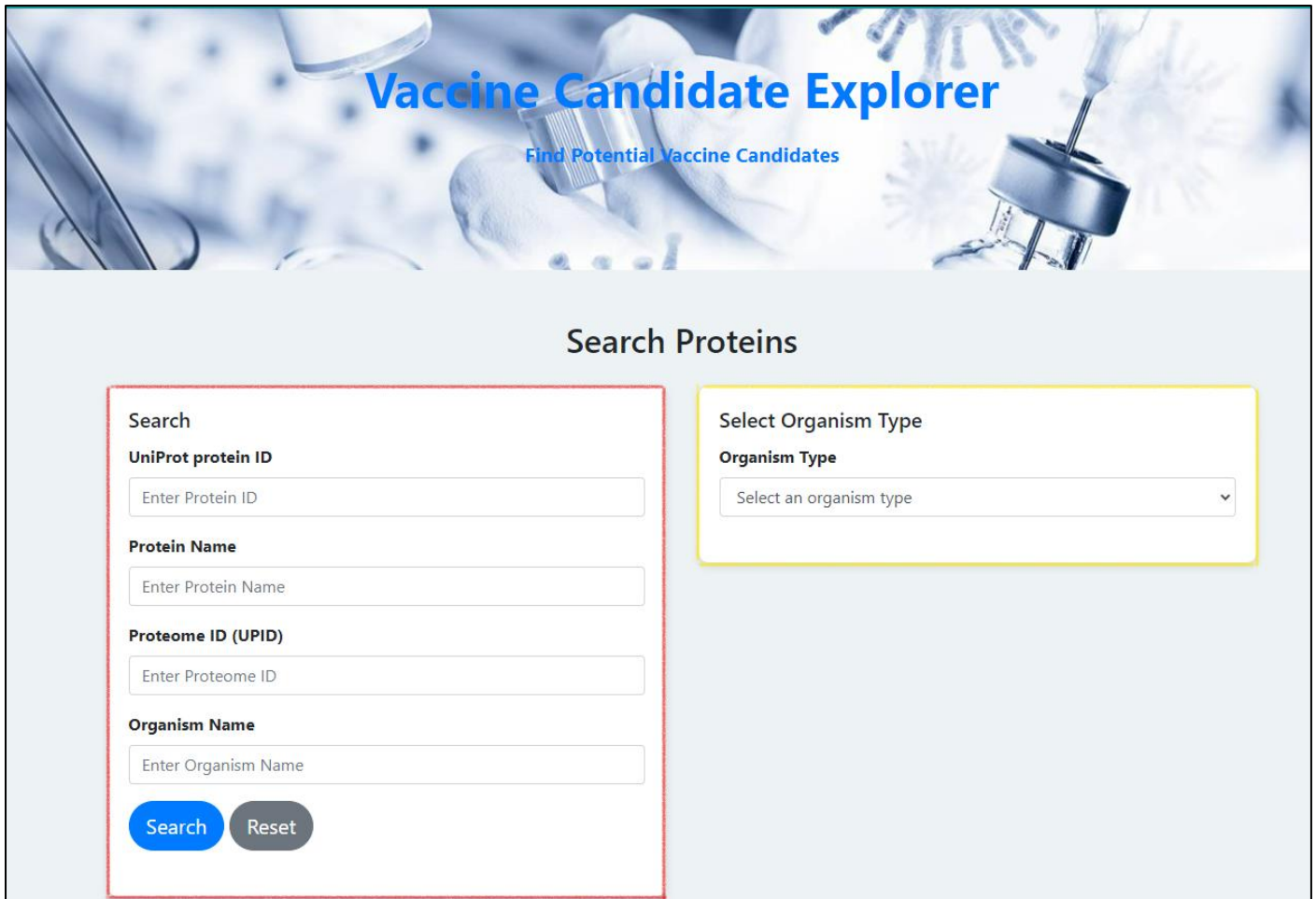


Figure 1: Flow chart of development of the database.

3. VACCINE CANDIDATE EXPLORER

As its name suggests, the Vaccine Candidate Explorer helps identify potential vaccine candidates through two approaches:

1. Users can manually input data related to the target protein, including any of the following: UniProt Protein ID, Protein Name, Proteome ID (UPID), or Organism Name.
2. Users can select organism types along with their corresponding Proteome ID and Organism Name from a pre-prepared list within the database.



The screenshot displays the 'Vaccine Candidate Explorer' interface. At the top, the title 'Vaccine Candidate Explorer' is prominently displayed in blue, with the subtitle 'Find Potential Vaccine Candidates' below it. The main section is titled 'Search Proteins'. It features two distinct input areas. On the left, a red-bordered box contains four text input fields: 'UniProt protein ID' (with placeholder 'Enter Protein ID'), 'Protein Name' (with placeholder 'Enter Protein Name'), 'Proteome ID (UPID)' (with placeholder 'Enter Proteome ID'), and 'Organism Name' (with placeholder 'Enter Organism Name'). Below these fields are two buttons: a blue 'Search' button and a grey 'Reset' button. On the right, a yellow-bordered box contains a 'Select Organism Type' section with a dropdown menu labeled 'Organism Type' and the placeholder text 'Select an organism type'.

Figure 2: The red box allows for input of either the UniProt Protein ID, Protein Name, Proteome ID (UPID), or Organism Name. The yellow box offers a more streamlined approach, enabling users to choose from predefined options.



Procedure:

To demonstrate how the ‘Vaccine Candidate Explorer’ can be implemented, we will use a classic case from the [UniProt database](#), featuring *Pseudomonas aeruginosa*, the pathogen responsible for lung infections.

3.1. Enter the UniProt Protein ID in the box outlined under “**UniProt protein ID**” and hit the highlighted “**Search**” button

The UniProt Protein ID for a given protein is located after the file icon and before the dot its UniProt page as indicated in the figure below.

The screenshot shows the UniProt protein page for Q9HWS1. The protein name is Q9HWS1 · Q9HWS1_PSEAE. The protein is described as an EF-hand domain-containing protein with 155 amino acids. It is a UniProtKB unreviewed (TrEMBL) entry for Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1). The protein existence is predicted, and the annotation score is 2/5. The page includes navigation links for Entry, Variant viewer, Feature viewer, Genomic coordinates, Publications, and External link.

In this case, “Q9HWS1” has been entered.

The screenshot shows the search interface with four input fields: UniProt protein ID (containing Q9HWS1), Protein Name, Proteome ID (UPID), and Organism Name. A blue arrow points to the Search button.

Select Organism Type

Organism Type

Select an organism type



Result displayed:

Vaccine Candidate Probability: Close

Experimentally Validated Antigen:

[Download Results](#)

Protein ID	Protein Name	Predicted Antigenic Score	Predicted Antigenic Probability	Predicted Signal Peptide	Number of TMHS	Localizations	Vaccine Candidate Probability	Experimentally Validated Antigen	PMI
Q9HWS1	EF-hand domain-containing protein	1.027	ANTIGEN	Signal peptide (Sec/SPI)	1	Mitochondrion	Highly Probable	NA	NA

You may download the result in .xlsx format by clicking on the “**Download Results**” button.

The screenshot shows an Excel spreadsheet with the following data:

Protein ID	Protein Name	Predicted Antigenic Score	Predicted Antigenic Probability	Predicted Signal Peptide	Number of TMHS	Localizations	Vaccine Candidate Probability	Experimentally Validated Antigen	PMID	Submission ID	DOI
Q9HWS1	EF-hand domain-containing protein	1.027	ANTIGEN	Signal peptide (Sec/SPI)	1	Mitochondrion	Highly Probable	NA	NA	NA	NA

3.2. Enter the name of the protein in the box labeled '**Protein Name.**' A new popup option will appear automatically; **select the organism** you are targeting (as the same protein can be present in different organisms), and then click the highlighted '**Search**' button.

The full name of the protein is displayed below the UniProt Protein ID on the right as indicated in the given figure.

The screenshot shows the UniProt website interface for the protein Q9HWS1. The search results are as follows:

- Protein:** EF-hand domain-containing protein
- Amino acids:** 155 (go to sequence)
- Status:** UniProtKB unreviewed (TrEMBL)
- Protein existence:** Predicted
- Organism:** Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1)
- Annotation score:** 2/5

Navigation options at the bottom include: Entry, Variant viewer, Feature viewer, Genomic coordinates, Publications, External link.

In this example, '**EF-hand domain-containing protein**' has been entered. In the next image, you can see that the organism name or proteome ID option appears automatically.



Search Proteins

Search

UniProt protein ID

Protein Name

Proteome ID and Organism Name

Proteome ID (UPID)

Organism Name

Search Reset

Select Organism Type

Organism Type

The search is specific to the organism **Pseudomonas aeruginosa** (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1).

Search Proteins

Search

UniProt protein ID

Protein Name

Proteome ID and Organism Name

Proteome ID (UPID)

Organism Name

Search Reset

Select Organism Type

Organism Type

Result Displayed:

The search is specific to the organism **Pseudomonas aeruginosa** (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1), which is why the result shows **only one entry**.

Vaccine Candidate Probability:

Experimentally Validated Antigen:

Download Results

Close

Protein ID	Protein Name	Predicted Antigenic Score	Predicted Antigenic Probability	Predicted Signal Peptide	Number of TMHS	Localizations	Vaccine Candidate Probability	Experimentally Validated Antigen	PMID	Submission ID IEDB	DOI
Q9HWS1	EF-hand domain-containing protein	1.027	ANTIGEN	Signal peptide (Sec/SPI)	1	Mitochondrion	Highly Probable	NA	NA	NA	NA



Vaccine Candidate Probability: All Close

Experimentally Validated Antigen: All

[Download Results](#)

Protein ID	Protein Name	Predicted Antigenic Score	Predicted Antigenic Probability	Predicted Signal Peptide	Number of TMHS	Localizations	Vaccine Candidate Probability	Experimentally Validated Antigen
Q9HWS1	EF-hand domain-containing protein	1.027	ANTIGEN	Signal peptide (Sec/SPI)	1	Mitochondrion	Highly Probable	NA
A0A0J5WG44	EF-hand domain-containing protein	0.7111	ANTIGEN	Signal peptide (Sec/SPI)	1	Extracellular	Highly Probable	NA
A0A0J5WX59	EF-hand domain-containing protein	0.5417	ANTIGEN	Signal peptide (Sec/SPI)	0	Extracellular	Highly Probable	NA

The result is not specific to the organism *Pseudomonas aeruginosa* (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1), it represents various organisms consisting of the protein of our interest i.e. **EF-hand domain-containing protein**, hence the data displayed is larger in size.

However, it is possible to filter it by clicking on the drop-down menu next to “**Vaccine Candidate Probability**” and clicking the “**Download Results**” option.

We'll be selecting the “**Highly Probable**” option for this case. This selection rearranges the Protein IDs and their corresponding information in descending order based on their Predicted Antigenic Score, with all scores above 0.5.

Vaccine Candidate Probability: Highly Probable Close

Experimentally Validated Antigen: Highly Probable

[Download Results](#)

Protein ID	Protein Name	Predicted Antigenic Score	Predicted Antigenic Probability	Predicted Signal Peptide	Number of TMHS	Localizations	Vaccine Candidate Probability	Experimentally Validated Antigen
Q9HWS1	EF-hand domain-containing protein	1.027	ANTIGEN	Signal peptide (Sec/SPI)	1	Mitochondrion	Highly Probable	NA
A0A0J5WG44	EF-hand domain-containing protein	0.7111	ANTIGEN	Signal peptide (Sec/SPI)	1	Extracellular	Highly Probable	NA
A0A0J5WX59	EF-hand domain-containing protein	0.5417	ANTIGEN	Signal peptide (Sec/SPI)	0	Extracellular	Highly Probable	NA

Download the result in .xlsx format by clicking on the “**Download Results**” button



	A	B	C	D	E	F	G	H	I	J	K	L
1	Protein ID	Protein Name	Predicted pI	Predicted MW	Predicted pI	Number of Signal Peptides	Localization	Vaccine Category	Experiment Type	PMID	Submission Date	DOI
2	Q9HWS1	EF-hand domain	1.027	ANTIGEN	Signal peptide	1	Mitochondrion	Highly Protein	NA	NA	NA	NA
3	A0A0J5WG	EF-hand domain	0.7111	ANTIGEN	Signal peptide	1	Extracellular	Highly Protein	NA	NA	NA	NA
4	A0A0J5WX	EF-hand domain	0.5417	ANTIGEN	Signal peptide	0	Extracellular	Highly Protein	NA	NA	NA	NA
5	A0A1D3CR	EF-hand domain	0.5196	ANTIGEN	Signal peptide	0	Endoplasmic reticulum	Highly Protein	NA	NA	NA	NA
6	A0A6N4B3	EF-hand domain	0.5778	ANTIGEN	Signal peptide	0	Golgi apparatus	Highly Protein	NA	NA	NA	NA
7	A0A6N4AU	EF-hand domain	0.7281	ANTIGEN	Signal peptide	0	Mitochondrion	Highly Protein	NA	NA	NA	NA
8	A0A2H0ZV	EF-hand domain	0.7229	ANTIGEN	Signal peptide	0	Lysosome	Highly Protein	NA	NA	NA	NA
9	A0A6A5CC	EF-hand domain	0.5657	ANTIGEN	Signal peptide	1	Cytoplasm	Highly Protein	NA	NA	NA	NA

As you can see, the data has been filtered, and coincidentally the protein of interest (searched for in the previous step 3.2.).

3.3. Enter the Proteome ID of the protein in the box outlined under “**Proteome ID (UPID)**” and hit the highlighted “**Search**” button

The Proteome ID of a protein can be found below “Proteomes” in the “Names & Taxonomy” section.

UniProt Tools UniProtKB Advanced | List Search Help

Function
Names & Taxonomy
Subcellular Location
Phenotypes & Variants
PTM/Processing
Expression
Interaction

Entry Variant viewer Feature viewer Genomic coordinates Publications Ex

Proteomes¹

Identifier | UP000002438

Component¹ | Chromosome

Organism-specific databases

PseudoCAP | PA4107

In this case, we’ll be entering “UP000002438” as the Proteome ID

Search

UniProt protein ID

Enter Protein ID

Protein Name

Enter Protein Name

Proteome ID (UPID)

UP000002438

Organism Name

Enter Organism Name

Search **Reset**

Select Organism Type

Organism Type

Select an organism type



Result Obtained:

Vaccine Candidate Probability: Close

Experimentally Validated Antigen:

[Download Results](#)

Protein ID	Protein Name	Predicted Antigenic Score	Predicted Antigenic Probability	Predicted Signal Peptide	Number of TMHS	Localizations	Vaccine Candidate Probability	Experimentally Validated Antigen	PMI
Q9HWS1	EF-hand domain-containing protein	1.027	ANTIGEN	Signal peptide (Sec/SPI)	1	Mitochondrion	Highly Probable	NA	NA

3.4. Enter the FULL NAME of the protein in the box outlined under “**Organism Name**” and hit the highlighted “**Search**” button

The full name of the organism is displayed below the “Status” information of the protein on the right as indicated in the figure below.

UniProt Tools UniProtKB Advanced | List Search Help

Q9HWS1 · Q9HWS1_PSEAE

Function

- Names & Taxonomy
- Subcellular Location
- Phenotypes & Variants
- PTM/Processing
- Expression
- Interaction
- Structure

Proteinⁱ | EF-hand domain-containing protein

Statusⁱ | UniProtKB unreviewed (TrEMBL)

Organismⁱ | **Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1)**

Amino acids | 155 (go to sequence)

Protein existenceⁱ | Predicted

Annotation scoreⁱ | 2/5

In our case, we enter “*Pseudomonas aeruginosa* (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1)”.

The result is not specific to the protein **EF-hand domain-containing protein** organism instead it represents various protein in our proteome of interest i.e. *Pseudomonas aeruginosa* (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1), hence the data displayed is larger in size.



However, it is possible to filter it by clicking on the drop-down menu next to “Vaccine Candidate Probability” and clicking the “Download Results” option.

Search

UniProt protein ID

Protein Name

Proteome ID (UPID)

Organism Name

Select Organism Type

Organism Type

Result Displayed:

Vaccine Candidate Probability:

Experimentally Validated Antigen:

Protein ID	Protein Name	Predicted Antigenic Score	Predicted Antigenic Probability	Predicted Signal Peptide	Number of TMHS	Localizations	Vaccine Candidate Probability	Exper Valid: Antig
Q9HWS1	EF-hand domain-containing protein	1.027	ANTIGEN	Signal peptide (Sec/SPI)	1	Mitochondrion	Highly Probable	NA
A0A0J5WG44	EF-hand domain-containing protein	0.7111	ANTIGEN	Signal peptide (Sec/SPI)	1	Extracellular	Highly Probable	NA
A0A0J5WX59	EF-hand domain-containing protein	0.5417	ANTIGEN	Signal peptide (Sec/SPI)	0	Extracellular	Highly Probable	NA



3.6. Selection from Database

3.6.1. Exploring the options when selecting the type of organism, we wish to look into

The screenshot shows a web interface with a section titled "Select Organism Type". Below the title is a label "Organism Type" and a dropdown menu. The dropdown menu is open, showing a list of options: "Select an organism type" (highlighted in blue), "Virus", "Bacteria", "Parasite", and "Fungus".

You may select one of the following organisms corresponding to the target organism type of your choice:

- Virus
- Bacteria
- Parasite
- Fungus

Upon selecting each of the organism type, the second drop-down option gets affected - we get different dropdowns depending on the organism type we select.

Virus:

The screenshot shows a search interface with two main sections: "Search" and "Select Organism Type".

Search Section:

- UniProt protein ID:** A text input field with the placeholder "Enter Protein ID".
- Protein Name:** A text input field with the placeholder "Enter Protein Name".

Select Organism Type Section:

- Organism Type:** A dropdown menu with "Virus" selected.
- Proteome ID and Organism Name:** A dropdown menu with "Select a proteome ID or organism name" selected. The dropdown is open, showing a list of virus entries with checkboxes and UniProt IDs.

Proteome ID and Organism Name List:

- UP000008448 - Chandipura virus
- UP000002060 - Variola virus (isolate Human/India/Ind3/1967) (VARV) (Smallpox virus) (Isolate Human/India/Ind3/1967)
- UP000002331 - Mumps virus (strain Miyahara vaccine) (MuV)
- UP000002472 - Human respiratory syncytial virus B (strain B1)
- UP000002500 - Dengue virus type 1 (strain Nauru/West Pac/1974)
- UP000002602 - Human herpesvirus 3
- UP000007714 - Human immunodeficiency virus type 1 group N (isolate YBF106) (HIV-1)
- UP000008158 - Influenza B virus (strain B/Lee/1940)
- UP000008165 - Poliovirus type 2 (strain W-2)
- UP000008167 - Human adenovirus C serotype 2 (HAdV-2) (Human adenovirus 2)
- UP000008591 - Hepatitis B virus genotype C subtype ayr (isolate Human/Japan/Okamoto/-) (HBV-C)



Bacteria:

Search

UniProt protein ID

Protein Name

Select Organism Type

Organism Type

Proteome ID and Organism Name

Select a proteome ID or organism name

- UP000000425 - Neisseria meningitidis serogroup B
- UP000000584 - Vibrio cholerae serotype O1 (strain ATCC 39315 / El Tor Inaba N16961)
- UP000000594 - Bacillus anthracis (Ames ancestor)
- UP000000605 - Burkholderia pseudomallei (strain K96243)
- UP000000799 - Campylobacter jejuni subsp. jejuni serotype O:2 (strain ATCC 700819 / NCTC 11168)
- UP000000806 - Mycobacterium leprae (strain TN)
- UP000000811 - Treponema pallidum (strain Nichols)
- UP000000815 - Yersinia pestis (CO-92 / Biovar Orientalis)
- UP000000817 - Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e)
- UP000000818 - Clostridium perfringens (strain 13 / Type A)
- UP000002198 - Corynebacterium diphtheriae (strain ATCC 700971 / NCTC 13129 / Biotype gravis)

Parasite:

Search

UniProt protein ID

Protein Name

Select Organism Type

Organism Type

Proteome ID and Organism Name

Select a proteome ID or organism name

- UP000000643 - Bartonella bacilliformis (strain ATCC 35685 / KC583 / Herrer 020/F12,63)
- UP000002226 - Toxoplasma gondii (strain ATCC 50861 / VEG)
- UP000002316 - Trypanosoma brucei gambiense (strain MHOM/CI/86/DAL972) (MHOM/CI/86/DAL972)
- UP000002437 - Toxoplasma gondii
- UP000008333 - Plasmodium vivax (strain Salvador I)
- UP000008524 - Trypanosoma brucei brucei (strain 927/4 GUTat10.1)
- UP000027744 - Brucella melitensis (C-554)
- UP000028787 - Brucella suis (513UK)
- UP000031513 - Plasmodium knowlesi (strain H)
- UP000053562 - Plasmodium vivax India VII
- UP000078387 - Entamoeba histolytica (HM1:IMSS clone 6)



Fungus:

Search

UniProt protein ID
Enter Protein ID

Protein Name
Enter Protein Name

Proteome ID (UPID)
Enter Proteome ID

Organism Name
Enter Organism Name

Search **Reset**

Select Organism Type

Organism Type
Fungus

Proteome ID and Organism Name
Select a proteome ID or organism name
Select a proteome ID or organism name
UP000230249 - Candida auris (Yeast) (B8441)

Here, in our case upon selecting “Bacteria” as the organism type and “UP000002438 - Pseudomonas aeruginosa” option in the Proteome ID and Organism Name section.

Search

UniProt protein ID
Enter Protein ID

Protein Name
Enter Protein Name

Proteome ID (UPID)
Enter Proteome ID

Organism Name
Pseudomonas

Search

Select Organism Type

Organism Type
Bacteria

Proteome ID and Organism Name
Select a proteome ID or organism name

- UP000000018 - Clostridium perfringens (strain 13 / Type A)
- UP000002198 - Corynebacterium diphtheriae (strain ATCC 700971 / NCTC 13129 / Biotype gravis)
- UP000002438 - Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1)
- UP000002671 - Coxiella burnetii (strain RSA 493 / Nine Mile phase I)
- UP000007841 - Klebsiella pneumoniae subsp. pneumoniae (strain HS11286) (HS11286)
- UP000008816 - Staphylococcus aureus (strain NCTC 8325 / PS 47)
- UP000036338 - Burkholderia cepacia (Pseudomonas cepacia) (LK29)
- UP000049127 - Paenibacillus sordellii (Clostridium sordellii) (R28058)
- UP000192091 - Vibrio vulnificus (VN-0101)
- UP000000429 - Helicobacter pylori (strain ATCC 700392 / 26695)



Results obtained via Selection from Database – same as in steps 3.1. and 3.3.:

Vaccine Candidate Probability: Close

Experimentally Validated Antigen:

[Download Results](#)

Protein ID	Protein Name	Predicted Antigenic Score	Predicted Antigenic Probability	Predicted Signal Peptide	Number of TMHS	Localizations	Vaccine Candidate Probability	Experimentally Validated Antigen	PMI
Q9HWS1	EF-hand domain-containing protein	1.027	ANTIGEN	Signal peptide (Sec/SPI)	1	Mitochondrion	Highly Probable	NA	NA

Please Note: We can filter data based on whether the antigen has been experimentally validated.

Vaccine Candidate Probability: Close

Experimentally Validated Antigen:

[Download Results](#)

The database authors perform necessary updates on a weekly basis, incorporating the latest research findings.

Experimentally Validated Antigen:

[Download Results](#)

Protein ID	Protein Name	Predicted Antigenic Score	Predicted Antigenic Probability	Predicted Signal Peptide	Number of TMHS	Localizations	Vaccine Candidate Probability	Experimentally Validated Antigen	PMID	Submission ID IEDB	DOI
Q9CC67	Secreted p60-family protein	0.5652	ANTIGEN	Signal peptide (Sec/SPI)	1	Extracellular	Highly Probable	YES	23283462	NA	NA
P46842	Alanine and proline-rich secreted protein Apa	0.4885	ANTIGEN	Signal peptide (Sec/SPI)	1	Extracellular	Highly Probable	YES	23283462	NA	NA
Q05868	MPT51 antigen	0.4657	ANTIGEN	Signal peptide (Sec/SPI)	1	Extracellular Endoplasmic reticulum	Highly Probable	YES	16339528	NA	NA
Q9CD80	Putative phthiocerol dimycocerosate transporter LppX	0.6513	ANTIGEN	Signal peptide (Sec/SPI)	0	Extracellular	Highly Probable	YES	7525488	NA	NA
Q49738	D-ribose-binding protein	0.5408	ANTIGEN	Signal peptide (Sec/SPI)	1	Extracellular	Highly Probable	YES	16339528	NA	NA
Q9CBI7	beta-lactamase	0.5531	ANTIGEN	Signal peptide (Sec/SPI)	0	Extracellular	Highly Probable	YES	NA	1000638	NA

Users can download only experimentally validated and highly probable data.

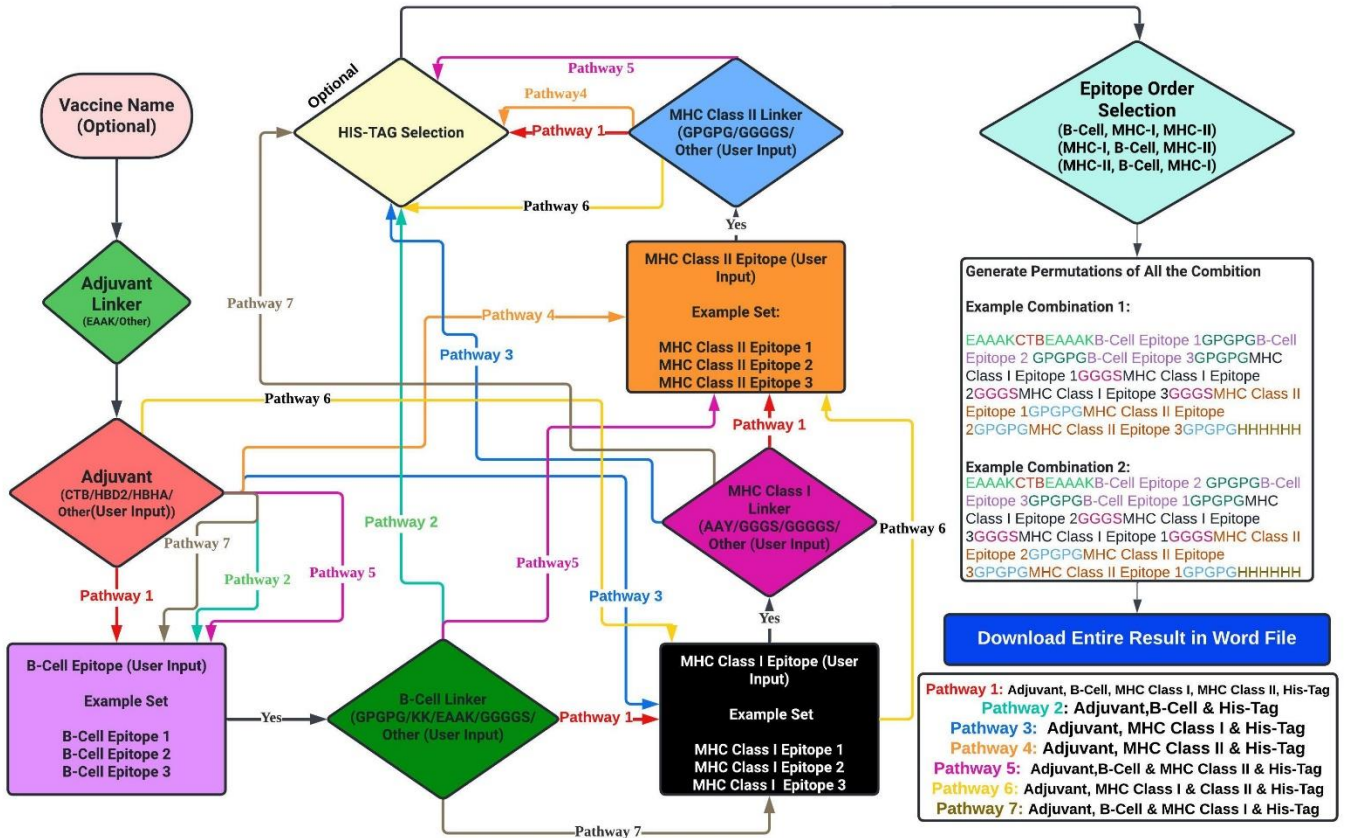
Additionally, they can apply any filters based on their preferences when downloading.



4. VACCINE DESIGNING

The vaccine designing tool is a comprehensive selection for customising and subsequently designing a vaccine.

Guide to Vaccine Design Workflow



Homepage:

Vaccine Designing
Select Your Preferred Options

Vaccine Name (Optional)
Enter Your Vaccine Name
Select Options

Adjuvant Linker
Select an option

Adjuvant
Select an option

Select Options

B Cell Epitope
Enter B Cell Epitopes, each on a new line



Procedure:

4.6. Vaccine Name (Optional)

Vaccine Name (Optional)

4.7. Configuring Adjuvant Options

4.7.1. Adjuvant Linker

The sequence that connects the adjuvant to the rest of the vaccine construct. Linkers in vaccine design ensure flexibility and proper spacing between the adjuvant and the antigenic epitopes to avoid steric hindrance, which could interfere with epitope presentation and immune recognition. These linkers are typically short peptide sequences. We have provided all the options that are already reported in various research studies. However, we also included an '**Others**' option in all the scenarios, allowing you to input your own if needed.

Select Options

Adjuvant Linker

Select an option

Select an option

EAAAK

Other

4.7.2. Adjuvant

An adjuvant is a substance used in vaccines to enhance the immune response to an antigen. In a multi-epitope vaccine, the adjuvant can help improve the immunogenicity of the otherwise small epitopes, ensuring a stronger and longer-lasting immune response. Common adjuvants include molecules like toll-like receptor agonists or cytokines. The role of the adjuvant in the construct is to help stimulate the immune system more efficiently.

Adjuvant

Select an option

Select an option

Cholera toxin subunit B (CTB)

Human β -defensin 2 (HBD2)

Heparin-binding hemagglutinin (HBHA)

Other

LVATAFEGRAIVRRVF

Select Options

Adjuvant Linker

EAAAK

Adjuvant

Human β -defensin 2 (HBD2)



4.8. B Cell

4.8.1. B Cell Epitope

It is the specific part of an antigen that is recognized by B cells and their antibodies. In a vaccine, B cell epitopes are included to elicit a humoral immune response (production of antibodies). The goal is for B cells to recognize these epitopes and produce neutralizing antibodies against the pathogen or its toxin.

Select Options

B Cell Epitope

Enter B Cell Epitopes, each on a new line

4.8.2. B Cell Linker

It connects individual B cell epitopes or links the B cell epitope to other components of the vaccine (such as MHC epitopes or adjuvants). These linkers ensure that the epitopes are presented in an accessible and flexible manner, maximizing their ability to interact with B cells and elicit an antibody response.

B Cell Linker

Select an option

Select an option

- GPGPG
- KK
- EAAAK
- GGGGS
- Other

Select Options

B Cell Epitope

TDAYNQKLSERRAN
NATAEGRAINRRVE

B Cell Linker

GGGGS

4.9. MHC Class I

4.9.1. MHC Class I Epitope

It is a short peptide (usually 8-10 amino acids) that is presented by MHC Class I molecules on the surface of antigen-presenting cells (APCs). These epitopes are recognized by CD8⁺ cytotoxic T cells, which are responsible for killing infected or cancerous cells. MHC Class I epitopes are crucial for inducing a cellular immune response against intracellular pathogens, like viruses.

Select Options

MHC Class I Epitope

Enter MHC Class I Epitopes, each on a new line



4.9.2. MHC Class I Linker

It connects multiple MHC Class I epitopes or links an MHC Class I epitope to other elements of the vaccine. The linker ensures that each epitope remains accessible for proper binding to MHC Class I molecules without interference from nearby sequences.

MHC Class I Linker

Select an option

Select an option

AAY

GGGS

GGGGS

Other

Select Options

MHC Class I Epitope

MAGE-1

MHC Class I Linker

AAY

4.10. MHC Class II

4.10.1. MHC Class II Epitope

A longer peptide (usually 13-18 amino acids) presented by MHC Class II molecules on the surface of APCs. These are recognized by CD4+ helper T cells, which assist in coordinating the overall immune response, including the activation of B cells and cytotoxic T cells. MHC Class II epitopes help stimulate a helper T cell response, promoting a stronger immune system coordination.

Select Options

MHC Class II Epitope

Enter MHC Class II Epitopes, each on a new line

4.10.2. MHC Class II Linker

A sequence used to connect different MHC Class II epitopes or link them to other components in the vaccine construct. These linkers provide flexibility and proper spacing to prevent structural constraints that could interfere with epitope presentation on MHC Class II molecules and recognition by helper T cells.

MHC Class II Linker

Select an option

Select an option

GPGPG

GGGGS

Other

Select Options

MHC Class II Epitope

HLA-DOB

MHC Class II Linker

GPGPG



4.11. HIS-TAG and Epitope Order

4.11.1. HIS-TAG

A sequence of histidine residues (usually 6) added to the protein construct for purification purposes. His-tags bind to nickel ions in a purification column, allowing the tagged protein to be easily isolated from other cellular proteins during the production process. His-tags are not typically part of the final vaccine product that is administered to patients, but they are crucial during vaccine development and purification stages.

Select Options

HIS-TAG

Select an option

- Select an option
- Penta His-Tag
- 6 His-Tag
- 7 His-Tag
- 8 His-Tag
- 9 His-Tag
- 10 His-Tag
- Other

4.11.2. Epitope Order

The sequential arrangement of B cell, MHC Class I, and MHC Class II epitopes within the multi-epitope vaccine construct. The correct ordering of epitopes is critical to ensure proper folding, epitope accessibility, and an effective immune response. The arrangement may affect how well the immune system processes and presents these epitopes, ultimately determining the strength and breadth of the immune response.

Epitope Order

B Cell, MHC I, MHC II

B Cell, MHC I, MHC II

MHC I, B Cell, MHC II

MHC I, MHC II, B Cell

Select Options

HIS-TAG

8 His-Tag

Epitope Order

MHC I, B Cell, MHC II

Submit



4.12. Result:

You may now download the results of the permutations of the combinations of your vaccine design and view it in doc file.

Results:

Download All Combinations as Word Document

Combination 1 For My Vaccine

EAAAKGIGDPVTCLKSGAICHVPFCPRRYKQIGTCGLPGTK
 CCKKPEAAAKMAGE-1AAYTDAYNQKLSERRANGGGGSNA
 TAEGRAINRRVEGGGSHLA-DOBGPGPGHHHHHHHH

Copy to Clipboard

Combination 2 For My Vaccine

EAAAKGIGDPVTCLKSGAICHVPFCPRRYKQIGTCGLPGTK
 CCKKPEAAAKMAGE-1AAYNATAEGRAINRRVEGGGSTD
 AYNQKLSERRANGGGGSHLA-DOBGPGPGHHHHHHHH

Copy to Clipboard

Results:

Download All Combinations as Word Document

Combination 1 For My Vaccine

EAAAKGIGDPVTCLKSGAICHVPFCPRRYKQIGTCGLPGTK
 CCKKPEAAAKMAGE-1AAYTDAYNQKLSERRANGGGGSNA
 TAEGRAINRRVEGGGSHLA-DOBGPGPGHHHHHHHH

Copy to Clipboard

Combination 2 For My Vaccine

EAAAKGIGDPVTCLKSGAICHVPFCPRRYKQIGTCGLPGTK
 CCKKPEAAAKMAGE-1AAYNATAEGRAINRRVEGGGSTD
 AYNQKLSERRANGGGGSHLA-DOBGPGPGHHHHHHHH

Copy to Clipboard

My Vaccine_results.docx (Protected View) - Word

File Home Insert Draw Design Layout References Mailings Review View Help Tell me

Combination 1 For My Vaccine

EAAAKGIGDPVTCLKSGAICHVPFCPRRYKQIGTCGLPGTKCCKKPEAAAKMAGE-
 1AAYTDAYNQKLSERRANGGGGSNATAEGRAINRRVEGGGSHLA-DOBGPGPGHHHHHHHH

Combination 2 For My Vaccine

EAAAKGIGDPVTCLKSGAICHVPFCPRRYKQIGTCGLPGTKCCKKPEAAAKMAGE-
 1AAYNATAEGRAINRRVEGGGSTDAYNQKLSERRANGGGGSHLA-DOBGPGPGHHHHHHHH