

INTERDICTIONary™

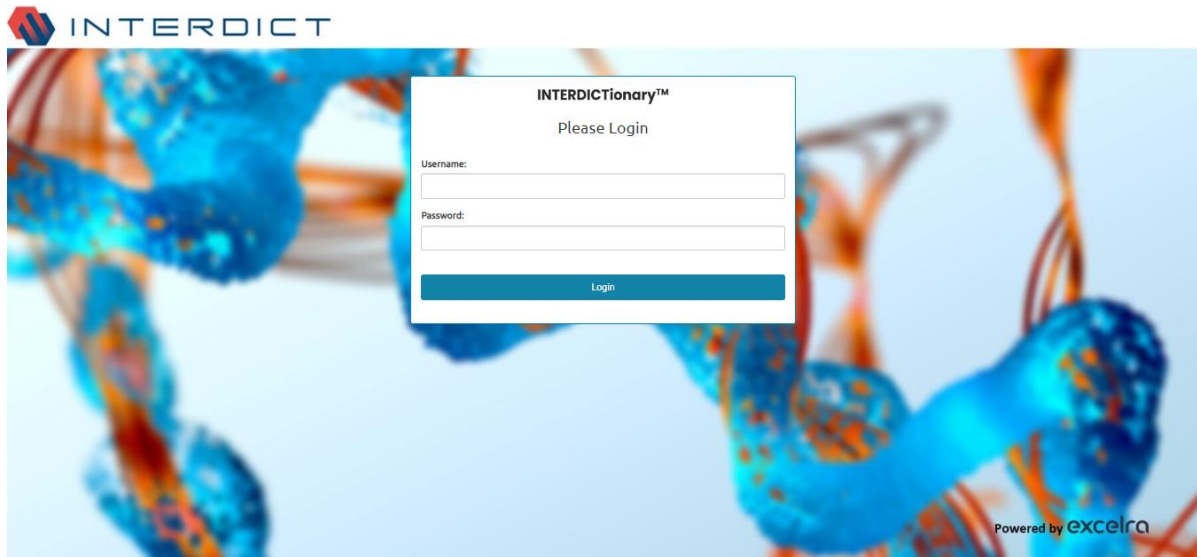
User Manual

Version 1.0

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Accessing the INTERDICTIONary Application



URL: <https://interdictionary.excelra.net/>

Home page after logged in

The screenshot shows the INTERDICTIONary home page after a successful login. The interface is divided into several sections:

- Top Navigation Bar:** Contains buttons for 'Results Summary' (6), 'Selected Data' (7), 'Dashboard' (8), and 'Admin' (9).
- Left Sidebar:** Includes a 'Choose Regex or Normal' section with radio buttons for 'Normal' and 'Regex' (1). Below it is a text input field for 'Enter the sequences' (2) with a note: 'Multiple sequences should be comma separated with no spaces. (E.g. AAAA,AAAT)'. Further down are buttons for 'Filter by Sequence(s)' (3), 'Find overlaps' (4), and a 'UniProt' logo (5).
- Main Content Area:** Features a 'Refine your search' section with an 'Add Filter Condition' button (10). Below this is a table of results showing 1 to 7 of 10 entries. The table has columns: EntryName, Entry, ProteinName, GeneNames, Organism, Length, Sequence, and Position_List. The first three rows of data are visible. To the right of the table is a search bar (12) with a 'Search:' label.
- Bottom Bar:** Contains buttons for 'Column visibility', 'Copy', 'Print', 'Download current page', and 'Download all data' (11).

The image above shows the view post signing-in to the application. The details on the buttons (tagged with numbers) can be referred below:

1. Query

a. Normal

User can enter the n number of sequences with comma separated.

- E.g. AAAA,AANA, AACA

b. Regex

In order to search manually for multiple sequences in a single search, the application also provides an option to perform Regex-based search. Through this, user can obtain results in a single click. The user has to make sure that he is not clubbing multiple different sequences separated by comma.

E.g. **`^PP[G,A,V].T$`**

The above query would search the results for all sequences starting with P, having P at 2nd position, having either G or A or V at 3rd position & ending with T.

2. Input box

The box facilitates the user to enter peptide sequence of interest. He has to make sure that they are either 4/5 amino acids long else warning would be flashed as the application houses only 4/5 length sequences results.

3. Filter by sequence

Once, entering sequences in the input box, user has to click Filter by sequence(s) button to direct the application to show results.

4. Find overlap

User can click on this action button to find the overlapping results (based on Entry) in case he wants to query multiple sequences. This will generate 2 more tables in same page if the overlap exist. "Overlapped Entries for Sequences" show Entries where multiple sequences exist. "Detailed data for Overlapped Entries" will show all the data for multiple overlapping Entries.

5. UniProt

User can click on this UniProt logo, it redirects to UniProt website
<https://www.uniprot.org/id-mapping>

Tab description

In this application there are 4-tab panels

6. Results Summary

Shows the filtered data which is generated using query. The rows are clickable & allows the user to see detailed results in the *Selected Data* Tab.

Query to filter data

Filtered data

EntryName	Entry	ProteinName	GeneNames	Organism	Length	Sequence	Position_List	Count
RIPP1_HUMAN	Q02K10-2	Protein ripp1	RIPPL1	Homo sapiens (Human)	104	AACA	4	1
RIPP2_HUMAN	Q5TAB7	Protein ripp2	RIPPL2 C6orf159	Homo sapiens (Human)	128	AACA	15	1
RIPP1_HUMAN	Q02K10-3	Protein ripp1	RIPPL1	Homo sapiens (Human)	151	AACA	4	1
CL16A_HUMAN	Q2KH73-3	Protein CLEC16A (C-type lectin domain family 16 member A)	CLEC16A KIAA0350	Homo sapiens (Human)	140	AACA	129	1
CR027_HUMAN	Q96H53	Putative uncharacterized protein encoded by LOC00167 (PRD10-07 divergent transcript)	PRD10-07 CL10F07 LOC00167 NCRNA00267	Homo sapiens (Human)	147	AACA	69	1

7. Selected Data

- Shows the selected rows which are selected from **Results Summary**, for this user must click on the **Extract Data**

Selected two rows

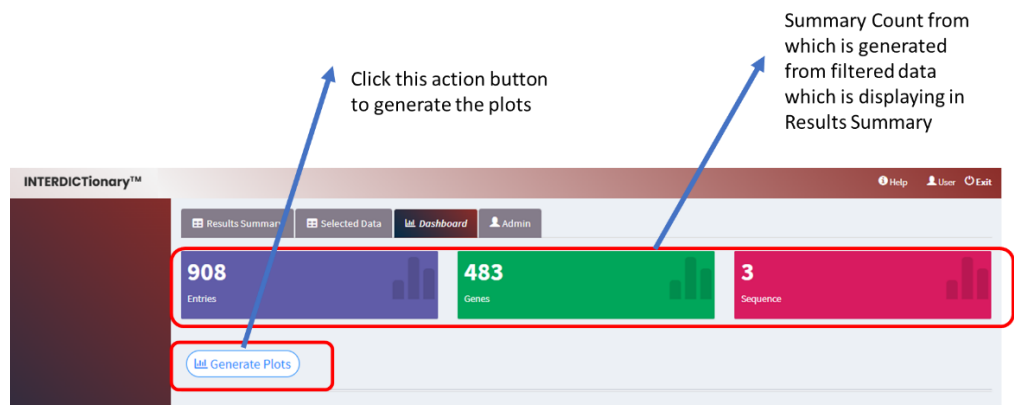
EntryName	Entry	ProteinName	GeneNames	Organism	Length	Sequence	Position_List	Count
RIPP2_HUMAN	Q5TAB7	Protein ripp2	RIPPL2 C6orf159	Homo sapiens (Human)	128	AACA	15	1
CL16A_HUMAN	Q2KH73-3	Protein CLEC16A (C-type lectin domain family 16 member A)	CLEC16A KIAA0350	Homo sapiens (Human)	140	AACA	129	1

- Go to **Selected Data** tab-panel and click on **Extract Data** button then user can see the data like below

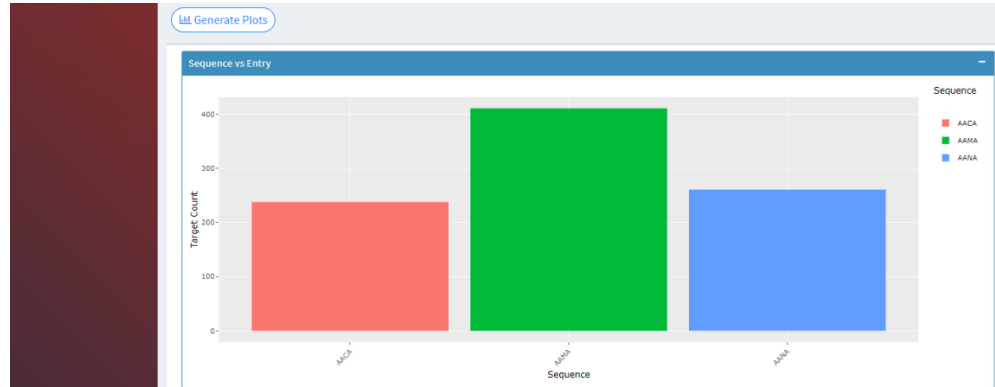
EntryName	Entry	ProteinName	GeneNames	Organism	Length	Sequence	Position_List	Count
RIPP2_HUMAN	Q5TAB7	Protein ripp2	RIPPL2 C6orf159	Homo sapiens (Human)	128	AACA	15	1
CL16A_HUMAN	Q2KH73-3	Protein CLEC16A (C-type lectin domain family 16 member A)	CLEC16A KIAA0350	Homo sapiens (Human)	140	AACA	129	1

8. Dashboard

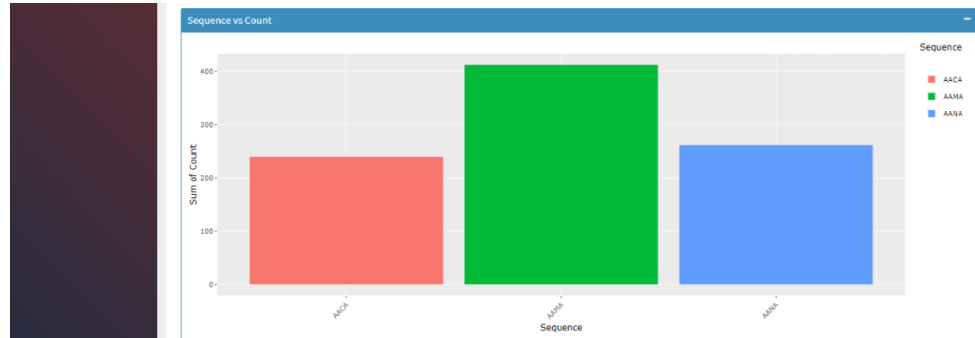
- Dashboard shows list of top 100 maximum occurring sequences
- It also shows list of top 100 least occurring sequences.
- Dashboard will generate the plots and summary counts based on filtered data
 - Summary counts will be displayed automatically
 - To generate the plots user must click on the Generate Plots button
- Dashboard will be changed dynamically after changed the query in Results Summary



Sequence vs Entry (In how many Entries the queried sequence is present)



Sequence vs Count (frequency of sequence occurring)

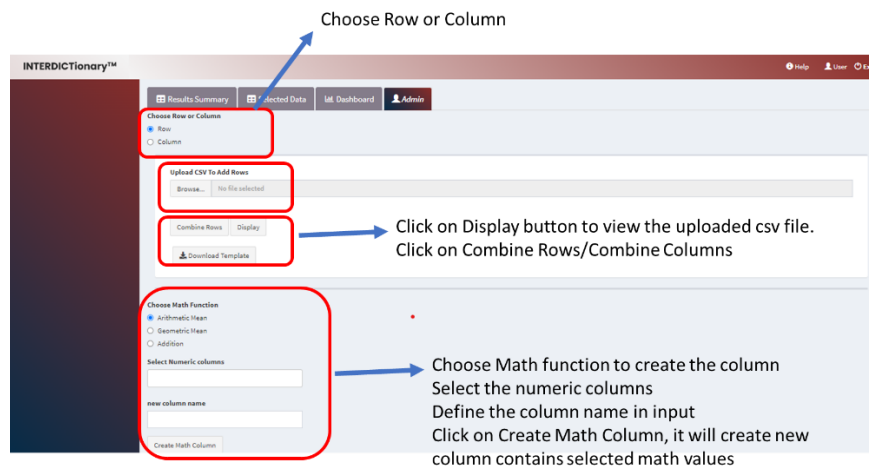


Sequence vs Gene Count (How many Genes, queried sequence is present)



9. Admin

- Admin tab-panel will be accessible only by admin
- Admin panel will contain multiple options to manipulate the data which is presented in *Selected Data* tab-panel



i. Add Row

1. Download the template and add data to be appended to the template and upload it by clicking on the Combine Rows button
2. Results will be displayed in the *Selected Data* tab-panel

ii. Add Column

1. Download the template and add newer data to the template and upload it by clicking on the Combine Column button
2. Results will be displayed in the *Selected Data* tab-panel

iii. Add Match Column

1. Choose Math Function
 - a. Arithmetic Mean
 - i. Will calculate Arithmetic Mean of two or more columns and creates the new column
 - b. Geometric Mean
 - i. Will calculate Geometric Mean of two or more columns and creates the new column
 - c. Addition
 - i. Will calculate summation of two or more columns and creates the new column
2. New column name should be mentioned in the input box by the user.
3. Manipulated data will be displayed in the *Selected Data* tab-panel