

INTERDICTIONary

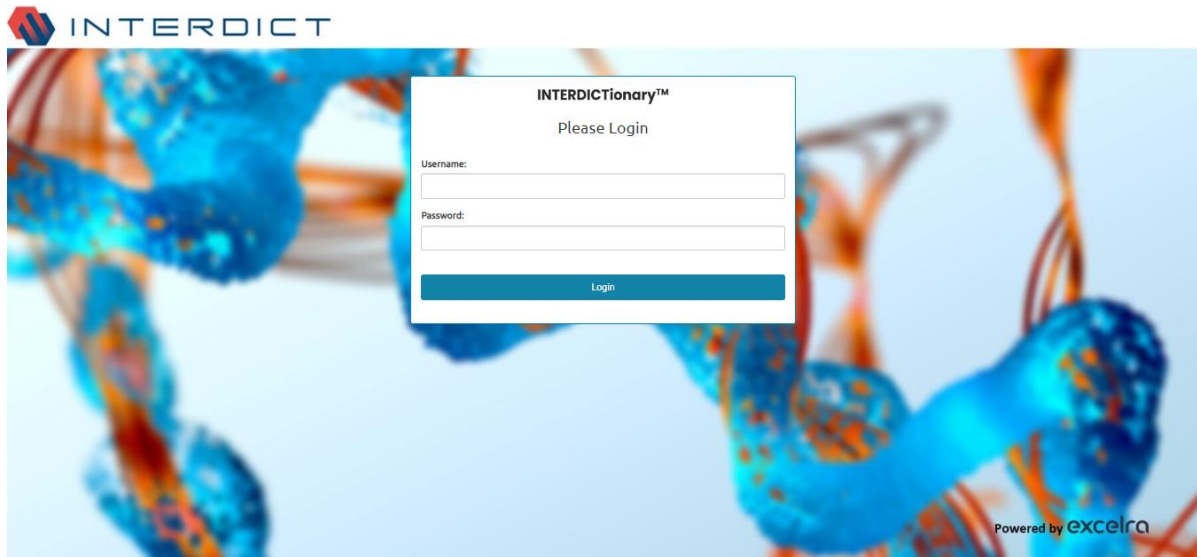
User Manual

Version 1.0

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Accessing the INTERDICTIONary Application



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

Home page after logged in

EntryName	Entry	ProteinName	GeneNames	Organism	Length	Sequence	Position_List
HXA13_HUMAN	P31271	Homeobox protein Hox-A13 (Homeobox protein Hox-1J)	HOXA13 HOX1J	Homo sapiens (Human)	388	AAAAA	38,39,40,41,42,43,44,45,46,47,62,73,74,75,76,77,78,79,80,116,117,118,119,120,121,122,123,
SOX21_HUMAN	Q9Y651	Transcription factor SOX-21 (SOX-A)	SOX21 SOX25 SOXA	Homo sapiens (Human)	276	AAAAA	137,138,139,140,141,142,154,155,156,157,158,159,160,161,162,208,209,210,211,212,213,21
PHOX2B_HUMAN	Q99453	Paired mesoderm homeobox protein 2B (Neuroblastoma Phox, NBPhox) (PHOX2B homeodomain)	PHOX2B PMX2B	Homo sapiens (Human)	314	AAAAA	159,160,161,162,163,241,242,243,244,245,246,247,248,249,250,251,252,253,254,255,256

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.

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. ResultsSummary

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	GeneName	Organism	Length	Sequence	Position	Count
RIPF2_HUMAN	Q02KX3-2	Protein ripply2	RIPF2	Homo sapiens (Human)	104	AKCA	4	1
RIPF2_HUMAN	Q5T8B7	Protein ripply2	RIPF2 Clorf139	Homo sapiens (Human)	128	AKCA	15	1
RIPF2_HUMAN	Q02KX3	Protein ripply2	RIPF2	Homo sapiens (Human)	151	AKCA	4	1
CLB4_HUMAN	Q29HT3-3	Protein CLB4 (C-type lectin domain family 16 member A)	CLB4 KIAA0390	Homo sapiens (Human)	140	AKCA	129	1
ORF113_HUMAN	Q9H933	Putative uncharacterized protein encoded by LOC10187 (PRDM12-OT divergent transcript)	PRDM12-OT C11orf127 LOC10187 HCRNA00187	Homo sapiens (Human)	147	AKCA	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

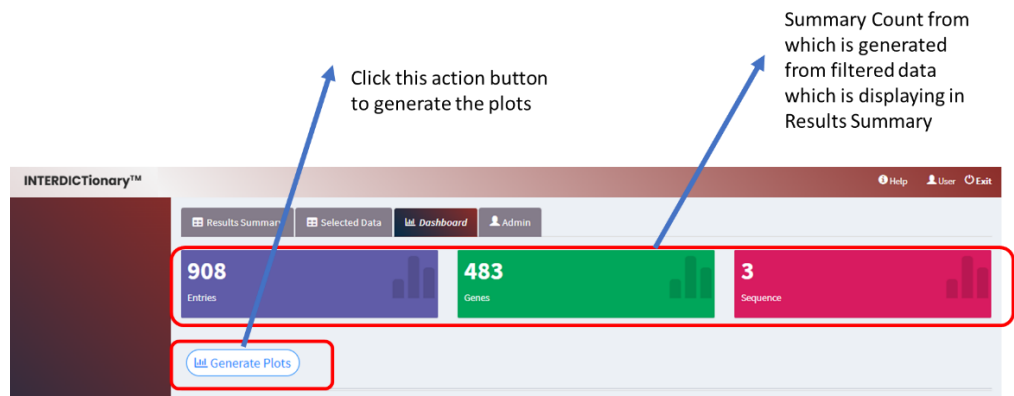
EntryName	Entry	ProteinName	GeneNames	Organism	Length	Sequence	Position_List	Count
RIPP2_HUMAN	Q5TAB7	Protein ripp2	RIPPL2	Homo sapiens (Human)	128	AACA	15	1
CL16A_HUMAN	Q2KH73-3	Protein CLEC16A (C-type lectin domain family 16 member A)	CLEC16A KIAA0350	Homo sapiens (Human)	140	AACA	129	1

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

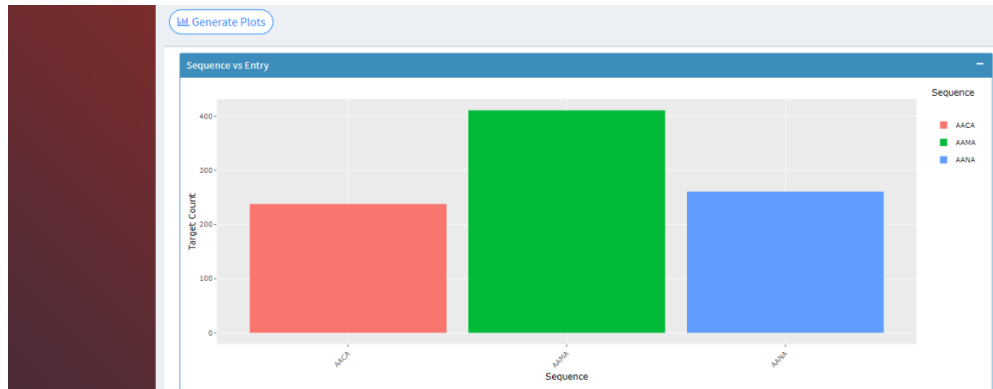
EntryName	Entry	ProteinName	GeneNames	Organism	Length	Sequence	Position	Count
RIPP2_HUMAN	Q5TAB7	Protein ripp2	RIPPL2 CBorf159	Homo sapiens (Human)	128	AACA	15	1
CL16A_HUMAN	Q2KH73-3	Protein CLEC16A (C-type lectin domain family 16 member A)	CLEC16A KIAA0350	Homo sapiens (Human)	140	AACA	129	1

8. Dashboard

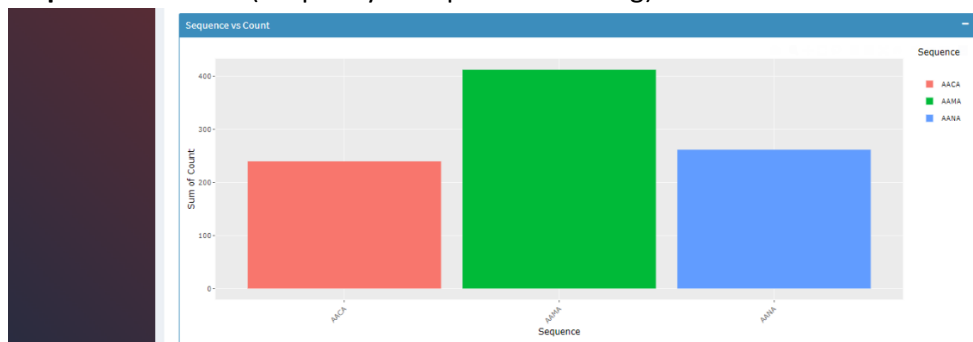
- Dashboard will generate the plots and summary counts based on filtered data
 - Summary counts will be displayed automatically
 - To generate the plots user must click on the Generate Plots button
- Dashboard will be changed dynamically after changed the query in Results Summary



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



Sequence vs Count (frequency of sequence occurring)

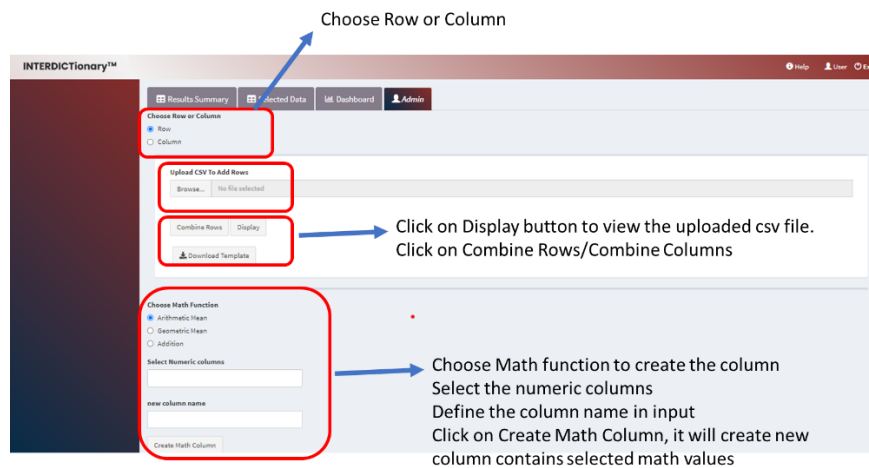


Sequence vs Gene Count (How many Genes, queried sequence is present)



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