

Analyze Protein-Protein Interactions with InSyBio Interact

October 2025

Insybio Suite v3.4



InSyBio

Intelligent Systems Biology

User Manual

www.insybio.com

Introduction

Interact is an intracellular interaction analysis tool for the

- analysis of proteins
- analysis of protein interactions
- prediction of proteins' functionality

Proteins are the functional components of many cellular processes and the identification of their physical Protein-Protein Interactions (PPIs) is an area of mature academic research.

InSyBio Interact enables users to combine a variety of sequential, structural, and functional information using a high-performance machine learning technique to predict a confidence and interaction affinity score for each protein pair. These confidence scores indicate the probability of these two proteins interacting and the strength of this interaction. Users are able to tune this confidence score and extract their own datasets as well as obtain only positive or negative interactions. Moreover, InSyBio Suite also provides visualization and meta-analysis of the Protein Interaction Networks. The protein interaction networks are clustered using a novel methodology to extract information about the protein complexes that the proteins form to perform specific tasks. These complexes and the overall PPI networks may be visualized using an interactive visualization module.

With InSyBio Interact you can:

- a) Search Positive/Negative PPIs
- b) Retrieve information about a specific protein
- c) View and download the list of clusters created by the EEMC algorithm
- d) Search proteins and Complexes with a GO Term
- e) Create and Save your own PPI dataset
- f) Create a network from your set of biomarkers (genes, transcripts, proteins)
- g) Perform functional enrichment analysis on your set of biomarkers
- h) Annotate functionally a specific protein using a patent-pending method [Theofilatos, K., Dimitrakopoulos, C., Mavroudi, S., Korfiati, A. and Alexakos, C., Insybio Inc, 2017.

Protein functional and sub-cellular annotation in a proteome. U.S. Patent Application 15/361,461.]

Protein Search

You can extract information about a specific Human protein by providing its UNIPROT identifier.

You can:

- Request the PPIs that are related to the specific protein and download the results;

InSyBio Suite Beta - Protein Search

Uniprot ID of protein: Q9P212

Feature normalization to the interval [0-1]

Export in CSV

Show results

Uniprot Id 1	Uniprot Id 2	Interaction Score	GO Function	GO Component	GO Process	Sequence Similarity	Co-localization	Homology Yeast	Domain Domain Interaction	HPRD	APID_verified	Co-expressions
Q9P212	Q15124	0.2873	0	0	0.03125	0.576036866359447	Not localized on the same cellular compartment	No	0.000133246913580247	No	0	0
Q9P212	Q5NGF3	-0.031725	6.3416091954023e-06	0.00155646153846154	0.0004603125	0.576036866359447	Not localized on the same cellular compartment	No	3.4566049382716e-05	No	0	0
Q9P212	Q6NSJ0	0.017539	0	0	0	0.576036866359447	Not localized on the same cellular compartment	No	0.000191006172839506	No	0	0
Q9P212	Q76KD6	0.15875	0	0	0	0.576036866359447	Not localized on the same cellular compartment	No	0.000229654320987654	No	0	0

First Previous 1 2 Next Last

Show 50 entries

Showing 1 to 50 of 63 entries

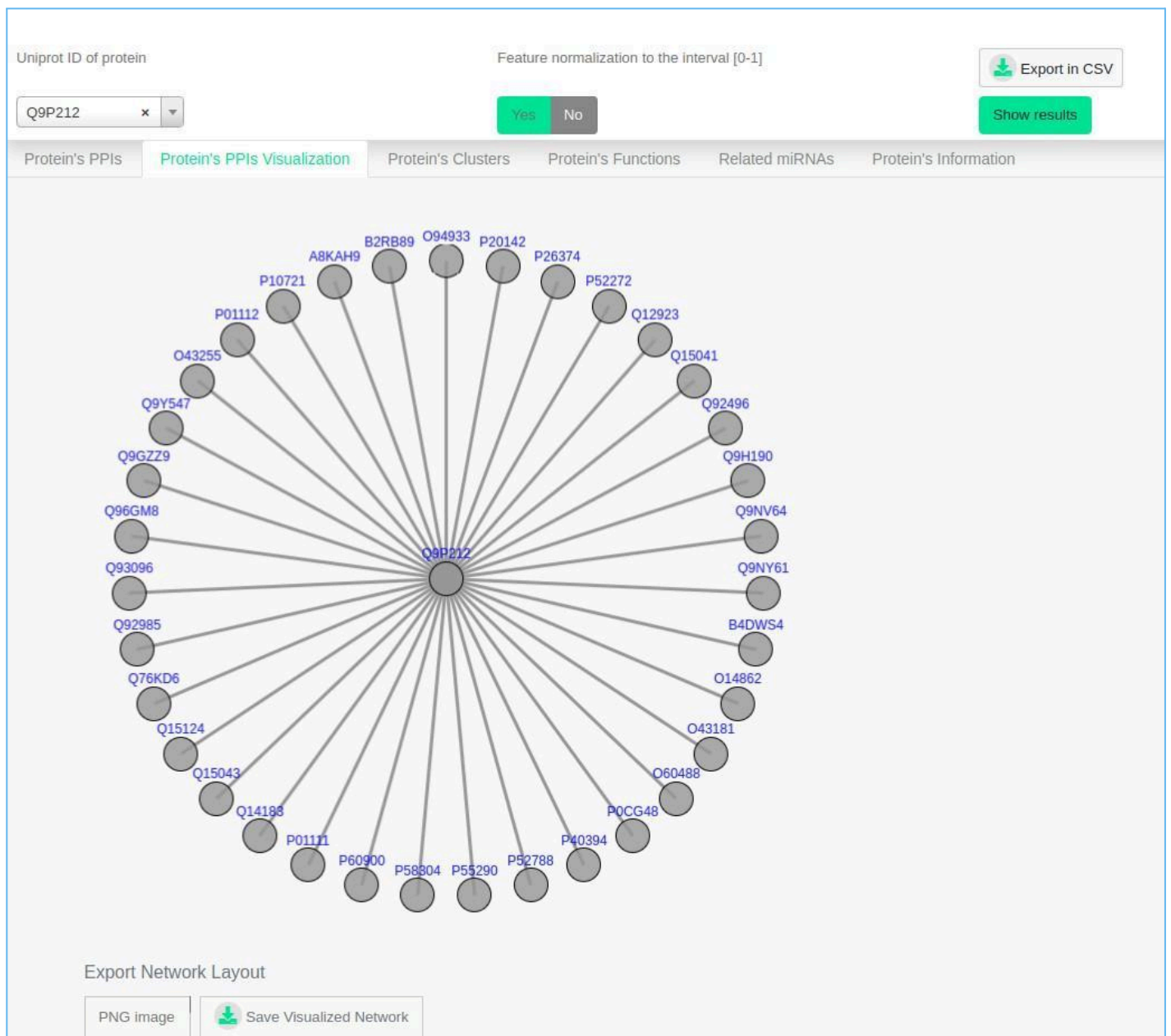
The results are presented on your screen in a browse-able table or you can download them as a TAB delimited CSV file.

For each PPI the following are presented:

- The Uniprot IDs of the two proteins,
- 22 informative sequential, structural and functional features,

- Presence in the APID database,
- The protein-protein interaction score - a confidence score indicating the probability of a protein pair to be an interacting one and the strength of this interaction.

b) Visualize the protein interaction network related to the specific protein and download it in various graph-representation file formats;



The result is an interactive graph displaying the first or the second neighborhood of the protein of interest (after user choice).

Clicking on a node-protein or on an edge-interaction, the respective information is presented.

Right clicking on a node-protein, its first neighborhood is presented.

There are options for decreasing opacity on mouseover and changing layout (force directed, radial, or circle).

The graph can be saved in various formats (PNG image, SVG image, PDF file, XGMML document, GraphML document, or Simple Interaction Format (SIF) document).

c) Find the clusters related to the specific protein;

The screenshot displays the 'InSyBio Suite Beta - Protein Search' web application. The top navigation bar includes a hamburger menu, the application name, and user information ('InSyBio Beta User'). Below the navigation bar, there is a search input field containing 'Q9P212' and a dropdown arrow. To the right of the search field is a 'Feature normalization to the interval [0-1]' toggle with 'Yes' and 'No' buttons. Further right is an 'Export in CSV' button and a 'Show results' button. The main content area has a tabbed interface with the following tabs: 'Protein's PPIs', 'Protein's PPIs Visualization', 'Protein's Clusters' (which is currently selected), 'Protein's Functions', 'Related miRNAs', and 'Protein's Information'. Under the 'Protein's Clusters' tab, there is a section titled 'Cluster 4953' with a right-pointing arrow. This section is divided into two columns: 'Cluster's Proteins' and 'Cluster's Functions'. The 'Cluster's Proteins' column lists two proteins: 'B4DWS4' and 'Q9P212'. The 'Cluster's Functions' column contains a table with three columns: 'GO Term', 'Function Name', and 'Function Namespace'. The table lists six functions related to the cluster.

GO Term	Function Name	Function Namespace
0008513	secondary active organic cation transmembrane transporter activity	molecular_function
0015226	carnitine transmembrane transporter activity	molecular_function
0015293	symporter activity	molecular_function
0015491	cation:cation antiporter activity	molecular_function
0015651	quaternary ammonium group transmembrane transporter activity	molecular_function
0030165	PDZ domain binding	molecular_function

The result is a list of the clusters the protein of interest takes part in.

Clicking on a cluster, the following information is presented:

- The proteins that form the cluster,

- A table of the cluster's functions.

d) List all the functions related to the specific protein;

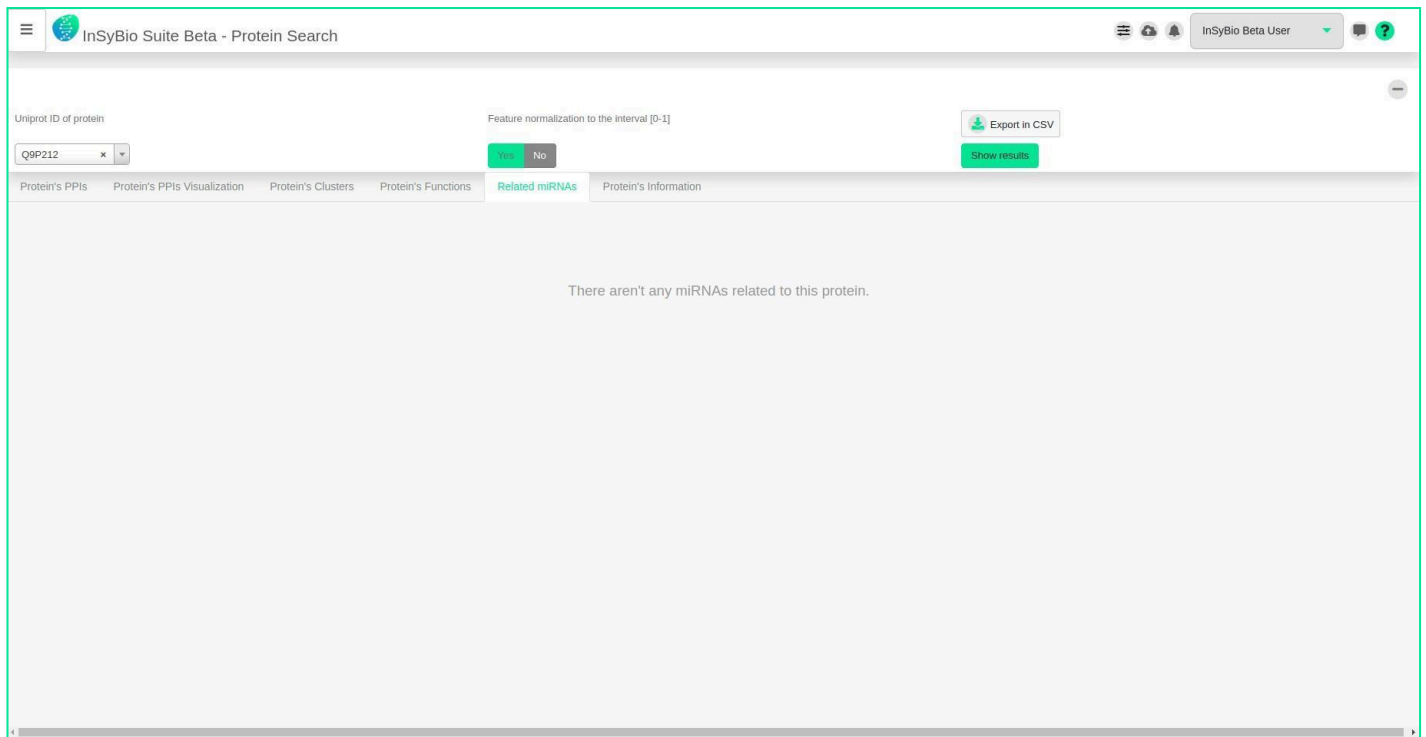
GO Term	Function Name	Function Namespace
0008277	regulation of G-protein coupled receptor protein signaling pathway	biological_process
0008283	cell proliferation	biological_process
0016042	lipid catabolic process	biological_process
0019722	calcium-mediated signaling	biological_process
0043547	positive regulation of GTPase activity	biological_process
0048016	inositol phosphate-mediated signaling	biological_process
0046578	regulation of Ras protein signal transduction	biological_process
0045859	regulation of protein kinase activity	biological_process
0032835	glomerulus development	biological_process
0000187	activation of MAPK activity	biological_process
0001558	regulation of cell growth	biological_process
0043647	inositol phosphate metabolic process	biological_process
0006644	phospholipid metabolic process	biological_process

The result is a table with the functions that the protein of interest has.

For each function, the following information is presented:

- The function's GO term,
- The function's name, and
- The function's namespace.

e) List all the miRNAs related to the specific protein;



The result is a table with the miRNAs that regulate the expression of the protein of interest.

For each miRNA, the following information is presented:

- The miRNA's accession number, and
- The miRNA's id.

f) Find the protein's information;

Uniprot ID of protein: B2R789

Feature normalization to the interval [0-1]: Yes No

Export in CSV Show results

Uniprot ID	Official Gene Symbol	Protein Name	Sequence
B2R789	STARD13	START domain containing 13, isoform CRA_b	MKLDVNFQRKKGDSDEEDLCISNWKTFQRTSRNRSVDDLYTLPRGDRNGSPGGTGMRMTSSSESVLTDLSEPEVCSIHSESSGGSRSQPGQCCT DNPVNLADPLVSSSLPQPPDVLNHPFHFKNEKPTRAKSFLKRMETLRGKGAHGHKSGSGRTGGLVISGPMLOQEPESFKAMQCIQIPNGDLQNSPP PACRKGPCSGKSSGESSPEHSSGVSTPCLKERKCHEANKRGMYLEDLVLAGTALPDAGDSRMHEFHSQENLVVHIPKDHKPGTFPKALSIESL SPTDSSNGVMNRGSGISLGRQVPGAREPRLMASCHRASRSVSDYDNPVPSHLYASTGDLLEKDDLFPHLDDTLQHVNGLOEVVDWSDVLPLOTH DTLLGEPGLSTFPSPNQITLDFEGNSVSEGRTPSDVERDVTSLNESEPPGVDRDRSGVGASLTPNRRLRWNSFOLSHQPRPAPASHISSQTASQL SLLQKPSLLRLTAIMEKSHSNKNGWTSVPKFWKRVDPVDKDAVGVPLTVHVRGTGGLPOSTQOALRYLSKCLDQVGLPKSGVSKRSHALBQ MNEFNPENWNYEDOSAYDVMKQFFRDLPEPLFTNKLSETFLHIZVYVSKERLQAVQAAITLLADENREVLOTLLCFMDVNLVEENORTPMMLA VCLAPSLFHLNLLKKESSPRVIOKKYATGKPDQKDLNENLAAAGLAHIMECDRLFVPHLVAQSRNSVVAEIHVPTLEELGTQLEESGATFHTYL NHLIOGLQKEAKEFKGQVTCSTNDTLAFKKVGDGNPLKWKASVEVEAPPVVLNRVLREHLWDEDFVQKVVTETLDRQTEIYYVLSNMAPHP5 RDFVVLRTNKTDLPGKQCTLYSLSVHEEEAQLLGGVRAVVMDSQYLIEPCGSGKSRLLTHICRIDLKGHPWYSKGFHGLCAAEVARIRMSFQPLIAEG PETKI


The result is a table containing information about the protein of interest.


For each protein, the following information is presented:

- The UniProt ID,
- The official gene symbol
- The protein name, and
- The protein's sequence.

Computationally Predicted Protein Complexes

You can view a list of all the clusters computed from the algorithm EEMC. EEMC (Evolutionary Enhanced Markov Clustering) is a novel fully unsupervised methodology that InSyBio team has proposed for the prediction of protein complexes from weighted PPI graphs. It is a hybrid combination of an adaptive evolutionary algorithm and a state-of-the-art clustering algorithm named Enhanced Markov Clustering. When applied to new human datasets EEMC's performance was encouraging in the prediction of protein complexes which consist of proteins with high functional similarity. From EEMC analysis, we suggest new potentially true Human protein complexes which should be further validated using experimental techniques.


InSyBio Suite - Computationally Predicted Protein Complexes

InSyBio Beta User


Cluster 1 ▶

Cluster 2 ▶

Cluster 3 ▶

Cluster 4 ▶

Cluster 5 ▶

Cluster 6 ▶

Cluster's Proteins

A0AVK6
Q8NFC6

Cluster's Functions

GO Term	Function Name	Function Namespace
0001047	core promoter binding	molecular_function
0003714	transcription corepressor activity	molecular_function

Export EEMC Clusters in .TXT

The result is a list of the clusters calculated using the EEMC algorithm.

Clicking on a cluster, the user can be informed about the proteins that form the cluster and the cluster’s functions.

The entire set of clusters can be downloaded in a txt file with the following format:

```
cluster_id,proteins,go_terms
1,A0AV96 Q9C0H2,0005254
2,Q8NFC6 A0AVK6,0001047 0003714
3,A0AVT1 Q7Z6D5,0019780 0016874
...
```

Positive/Negative PPI Search

You can search positive and negative Human Protein-Protein Interaction Data by specifying threshold referring to the PPI classification confidence score and the affinity of the interaction.

Classification threshold value

Regression threshold value

Define positive/ negative results
☒ Positive ☐ Negative

Feature normalization to the interval [0-1]

486448 Records

You can search by choosing:

- A classification confidence threshold value
- A regression (affinity) threshold value
- Positive (interacting) or Negative (non-interacting) PPIs
- Normalization to the [0,1] interval or not

And you get a table view of the selected PPIs along with their informative features:

General View of the Table

Uniprot ID 1	Uniprot ID 2	RefSeq ID 1	RefSeq ID 2	Sequence 1	Sequence 2
<input type="text" value="Search Uniprot ID 1"/>	<input type="text" value="Search Uniprot ID 2"/>	<input type="text" value="Search RefSeq ID 1"/>	<input type="text" value="Search RefSeq ID 2"/>	<input type="text" value="Search Sequence 1"/>	<input type="text" value="Search Sequence 2"/>
A0A024R1R8	P35354	NP_001382942	NP_000954	MSSHEGGKKKALKQPKKQAKEMDEEKAFAKQKQEEQKLEVLKAKVVGKGLATGGIKKSGKK	MLRALLLCAVLASHTANPCSCSHPCQNRGVCHSVGFDDQYKDCCTRGTGYGE LKPTPNTVHYILTHFGFMVNNIPFLRNAISYVLTSLRSLIDSPPTYN YYTRALPPVPDCCPTPLGVKGGKQLPOSNEIVEKLLRRKFIPOGSMNMF DHRIGPAFTNGLGHGVDLNIHYGETLARQKRLFKDGKQKYQIIDGENHYPP VPEHLRFVAGQEVFGLVPLMMYATINLREHNRVCDVLKDEHPENGEQLFO IEDYVQHLSGYHFKLPDELLFNKQFQYQNRJAEFNTLYHNPPLPOTFO NSILLEHGITOPVESFTROJAGRIVAGRNVPAAVKVQASIDQSRQNKYQS SFEELTGKEMSAELEALYGDIDAVELYALLVEKPRPDATFGETMVEVGAP AYWNPSTFGGEGVFOINTASIQSLICNNKGCPTFSVPDPelikTVITIN VLLKERSTEL
A0A024R1R8	P04629	NP_001382942	NP_002520	MSSHEGGKKKALKQPKKQAKEMDEEKAFAKQKQEEQKLEVLKAKVVGKGLATGGIKKSGKK	MLRGGRRGQGMHSAAGPGLLAWLILASAGAACPACCPHCSSGLRCTR NLTELYENQOHLQHLRLGLGELRNLTIVKSGLRFAVPAHFHTPRLS KTVQGLSLQELVLSGNPLHSCALRWLRWEEGLGVPEQKLOCHGQGLA QVPNASVDGDDVLLRCQVEGRGLEQAGWILTELEQATVMKSGGLPSLGLT CWAENDVGRAEVSQVNVFPASVOLHTAVENHMCIPFSVDGQAPAPSLRWL EFLEPAANETVRHGLRLNQPHTVNNQNTLLAANPFGQASASIMAAFNPN PVDNTSGDPVEKDETPFGVSVAVLAVFACFLSTLLLVNKKGRNKF AMSLHFMTLGGSSLSPTGKSGSLGQHIENPOYFSDACVHMKRROIVLKW CHILLPEQDKMLVAVKAKEASEARQDFOREAELLTHLQHQHIVRFVGVCT GDLNRLRSHGPDAKLLAGGEDVAPGLGLGQLLAVASQVAGMVLVAGLHF GLVYKIGDFGMSADISYDYYRVGRTHLPIRMHPESILYKFTTESDWS PWYQLSNTAIDCITQRELERPRACCPPEVATNRGQWREPQRHSIKDVI NUIZ




First Previous 1 2 3 4 5 ... 9919 Next Last

Show 50 entries

Showing 1 to 50 of 495,943 entries

Feature Groups with Pop-Up features

Hover cursor over features for more info

iRefIndex Check	RNA Co-Expression	Gene Co-Expression	AA Difference	Molecular Weight Difference	Aromaticity Index Difference	Instability Index Difference	Amino Acid Fraction Difference
		176466.314		0.031	8.294		 96100

The results are presented on your screen in a browsable table, or you can download them as a TAB-delimited CSV file.

- For each PPI, the following are presented:
- The UniProt IDs, RefSeq IDs, and Sequences of the two proteins
- 75 total informative sequential, structural, and functional features
- Presence in other databases (iRefIndex, Mint, APID, BIOGRID, DIP)
- Two protein-protein interaction scores - the classifier's probability score and affinity predictions for each interaction.

For every protein pair, 75 informative features are calculated and provided, including sequential, structural, and functional features:

- **PPI descriptive features** (6 features): UniProt IDs, RefSeq IDs, and Sequences of the two proteins.
- **Disorder Check** (3 features): Checks the intrinsic disorder of the two proteins. If one of the two proteins has disorder >0.5, the rest of the features aren't calculated for that pair.
- **Interaction Scores** (2 features): Classifier Confidence and Affinity Prediction.
- **Domain- Domain Interaction** (1 feature): Presence of known domain interactions extracted from Pfam Database, a database of protein families and domains, each represented by multiple sequence alignments and hidden Markov models (HMMs). Interactions between Pfam IDs are derived from the 3did DB.
- **Sequence Similarity** (1 feature): The E-value of the sequence similarity
- **Co-Localization** (1 feature): Subcellular co-localization of the two proteins in the pair. The database used for extracting information about protein localizations in the eukaryotic cell is eSLDB.
- **GO term similarity** (GO Process, GO Function, GO Component – 3 features): The similarity of the proteins in the pair based on the similarity of their respective GO terms. The GO terms are filtered, keeping only those that are indicative of a biological process, of a molecular function, and of a cellular component. Similarity is measured using the Lin method.
- **Orthology in other organisms** (Orthology Mouse, Drosophila, Yeast, Ecoli – 4 features): Existence of a corresponding orthologous protein in other organisms. PPIs from the other organisms are derived from the DIP database, and the mapping of homologous proteins was done via NCBI- HomoloGene Dataset.
- **Existence in other Databases** (Exists in DIP, in APID, in BIOGRID, in Mint – 4 features): These columns indicate if each PPI is recorded in the DIP, APID, BIOGRID, and Mint databases as

well.

- **iRefindex Check** (3 features): These columns indicate if each PPI is recorded in the iRefIndex database, which was originally used for training and testing the classification models. For each PPI also appearing in iRefindex, the experimental method of detection (Detection Method) and the PMID of the citation (PMID of Interaction) are also referenced.
- **RNA Co-Expression** (2 features): These features calculate the similarity between each protein in the pair, in terms of their RNA expression profiles. The RNA expression datasets used were GSE227375 and GSE228702 from the NCBI Gene Expression Omnibus. Spearman correlation is used for calculating the expression similarity of each PPI pair.
- **Gene Co- Expression** (15 features): These features represent the similarity of the two proteins in terms of their Gene Expression among fifteen NCBI Gene Expression Omnibus datasets (GDS531, GDS534, GDS596, GDS651, GDS806, GDS807, GDS843, GDS987, GDS1085, GDS2855, GDS1402, GDS181, GDS1088, GDS841, GDS3257). Spearman correlation is used for calculating the expression similarity of each PPI pair.
- **AA Difference** (20 features): The difference in the percentage of every amino acid in the PPI proteins' sequences.
- **Molecular Weight Difference** (1 feature): The difference in molecular weight between the PPI proteins.
- **Aromaticity Index Difference** (1 feature): The difference in aromaticity index between the PPI proteins.
- **Instability Index Difference** (1 feature): The difference in instability index between the PPI proteins.
- **Amino Acid Fraction Difference** (3 features): The difference in fraction of total amino acids that are contained in the helix (Helix Difference), in the turn (Turn Difference), and in the sheet (Sheet Difference)
- **Molar Extinction Coefficient Difference** (2 features): The difference in molar extinction coefficient (MEC) when it is calculated assuming cysteines reduced (MEC Reduced Difference), and assuming cysteine residues (MEC Residues Difference).
- **GRAVY Index Difference** (1 feature): The difference in GRAVY (Grand Average of Hydropathy) between the PPI proteins.
- **Protein Charge Difference** (1 feature): The difference in protein charge at pH=7 between the PPI proteins.

PPI Datasets

You can create your own datasets by using a simple form to choose the number of positive and negative examples.

InSyBio Suite - PPI Dataset Creation Tool

Number of positive interactions: All positive PPIs in HPRD: ☒ Yes ☐ No [Export in CSV](#)

Number of negative interactions: Feature normalization to the interval [0-1]: ☒ Yes ☐ No [Show results](#)

Uniprot ID 1	Uniprot ID 2	RefSeq ID 1	RefSeq ID 2	Sequence 1
Q32M84	Q81YJ2	NP_001305118	NP_001352791	MIMSNTHKARLERRVTGSTRWRLLPKQFSGDLLSLQMCXKALSTDFEALRNPRCLCSQIQKFFFNFKNKDITQSGEADVTLECLGFKMELHQFQLFQSETLAKLYLKALAQGTHPLRELEELLRAQSPKCKTEKSPAKRIIISLKINDPLVTKVAFATALKNLYNSEV
Q8H468	Q9Y2E8	NP_857595	NP_001247420	MGCDGRVSGLLRRNLQPTLTYSVFFSFGLCIAFLGPTLLDLRCQTHSSLPQISWVFSSQQLCLLLGSALGGVFKRTLQASLWALFTSSLAISLVFAVIFPCRDVKVLASVHAGLAGMGICIDTVAMQQLVRMYQKDSAVFLQVLHFVFGGALLSPLTADPFLSEANCLPA
P30613	P50548	NP_000289	NP_001287964	MSIQENISSQLRSWVSKSQRDIAKSLITGAPGGPAGYLRASVAQLTQELGTAFFQQQLPAAMADTFLEHLCLLDIDSEPVAARSTSIATIGPASRSVERLKEMIKAGWITARLNFSGHSHEYHAEIAMVREAVESFAGSPLSYRPAIALDTKGPETRTGILQGGPE
Q8NGZ4	Q9NMY5	NP_001001914	NP_058640	MGLGNESSLNDFILLGFSOHPRLEAVLFVFLFYLLTVGNFTIIISYLDPPHPTMYFFLSNLSLDLCFTTSLAPQTLVNLQRPKKTITYGGCVAQLYISLALGSTECILLADMALDRYIACVKPLHYVYIMNPRLCQQLASISWLSGLASSLIHATFTLQLPLCGNH

There are options for:

- All positive PPIs being in HPRD or not,
- The application of normalization to the features to the interval [0-1].

The results are presented on your screen in a browse-able table or you can download them as a TAB delimited CSV file.

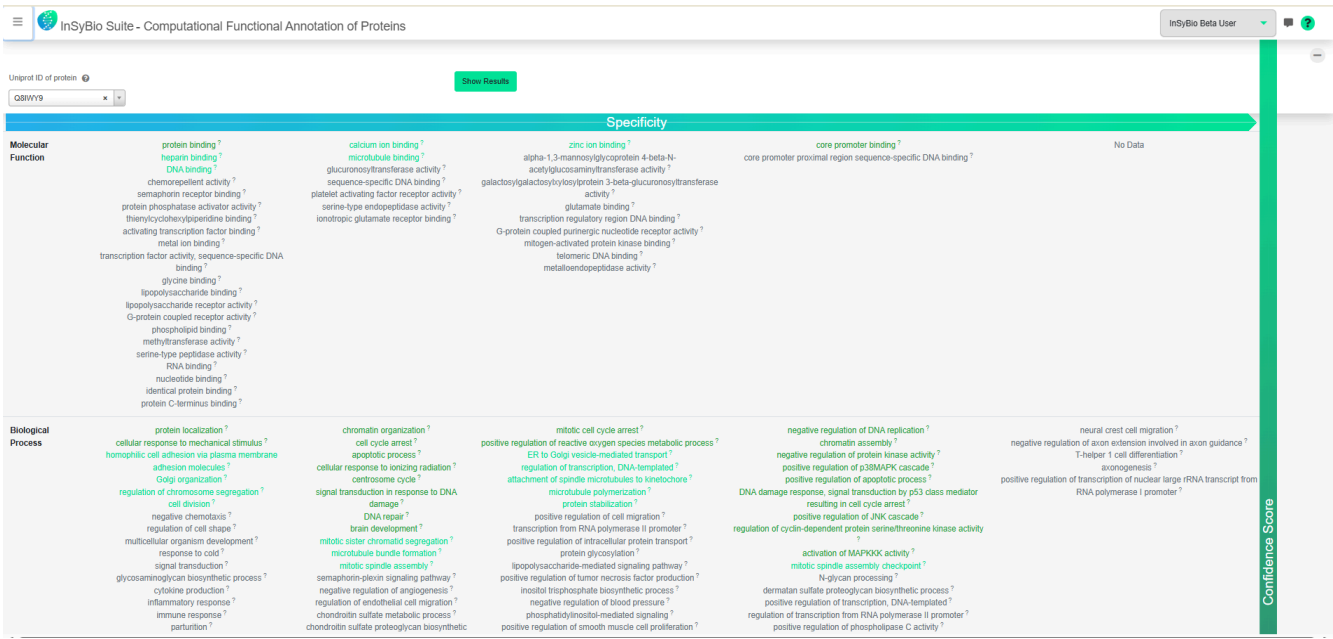
For each PPI the following are presented:

- The Uniprot IDs of the two proteins,

- 22 informative sequential, structural and functional features,
- Presence in the APID database,
- The protein-protein interaction score - a confidence score indicating the probability of a protein pair to be an interacting one and the strength of this interaction.

Computational Functional Annotation of Proteins

You can view the confirmed and predicted functional annotation of a given protein, from our database.



You can provide the Uniprot ID of your protein of interest, and the results of our Functional Annotation Patented method will appear. The associated GO terms with the protein are separated into 3 rows, one for each major term group (molecular function, biological process and cellular component terms). Going from left to right, the specificity of the term increases. Each term's position in a cell represents its predicted confidence score in descending order, dark green are confirmed associations (score 1), light green high confidence and gray medium confidence predicted associations (with score near 0.5).

GO Functional Annotation

You can derive the details of your function of interest by providing its GO-term.

For each function, the following information is presented:

- The function's GO term,
- The function's name, and
- The function's namespace.

Selecting the respective tab, you can also view the related:

a) Complexes;

InSyBio Suite - GO Functional Annotation

GO Term (7-digit code) Show Results

Complexes | Proteins

GO term: **0000987**

Function Name: core promoter proximal region sequence-specific DNA binding

Function Namespace: molecular_function

Complexes List

Cluster: 468

Cluster's Proteins: F8WA75, Q96CQ1

Cluster's Functions

GO Term	Function Name	Function Namespace
0000977	RNA polymerase II regulatory region sequence-specific DNA binding	molecular_function
0000987	core promoter proximal region sequence-specific DNA binding	molecular_function
0001046	core promoter sequence-specific DNA binding	molecular_function
0001077	transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding	molecular_function
0003705	transcription factor activity, RNA polymerase II distal enhancer sequence-specific binding	molecular_function
0042826	histone deacetylase binding	molecular_function
0046983	protein dimerization activity	molecular_function
0071837	HMG box domain binding	molecular_function

The result is a list of the complexes having the function of interest.

Clicking on a cluster, the following information is presented:

- The proteins that form the cluster,
and
- A table of the cluster's functions.

b) Proteins;

The screenshot displays the InSyBio Suite - GO Functional Annotation web application. The interface includes a header with the InSyBio logo and a user profile dropdown showing 'InSyBio Beta User'. Below the header, a search bar contains the GO term '0000987' and a 'Show Results' button. The main content area is divided into two panels. The left panel, titled 'Complexes', shows the selected GO term '0000987' and its associated function: 'core promoter proximal region sequence-specific DNA binding'. The right panel, titled 'Proteins List', displays a list of protein IDs: F8W7V7, Q43474, P05549, P15173, P23771, P84022, Q02447, Q02962, Q13351, Q13485, Q92793, Q9Y5R6, and Q8IXT2.

GO term	Proteins List
0000987	F8W7V7
	Q43474
	P05549
	P15173
	P23771
	P84022
	Q02447
	Q02962
	Q13351
	Q13485
	Q92793
	Q9Y5R6
	Q8IXT2

The result is a list of the proteins having the function of interest. Clicking on a protein the user will be guided to the protein's page.

Enrichment Analysis Functionality

You can perform enrichment analysis with hypergeometric distribution on a given list of proteins, genes or transcripts and produce a list of GO terms associated with the list, with their term specificity and score in the distribution. You can also provide your custom annotation, term, term type and functional annotation of molecules files, that will be appended to the default files to perform the enrichment.

In the tab New Enrichment Analysis you can:

InSyBio Suite Beta - Enrichment Analysis

Perform Enrichment Analysis

Performed Enrichment Analyses **New Enrichment Analysis** Running and Pending Enrichment Analyses Errors at Enrichment Analyses

Perform Enrichment Analysis

GO term Enrichment Analysis from your set of biomarkers based on the protein-go term correlation knowledge base of InSyBio Interact.

input mode

☒ Type or Copy-Paste biomarkers ☐ Upload a file with biomarkers ☐ Upload custom input files

Use any known identifier for denoting your biomarkers: Uniprot IDs, gene symbols, RefSeq_id and so on. Mixed identifiers are not supported!

Pvalue threshold *: 0.05

New enrichment analysis title : Title...

List of symbols *: ATM,TP53,BRCA1,...

Start Enrichment Analysis

- Either Type or Copy-Paste biomarkers or

InSyBio Suite - Enrichment Analysis

InSyBio Beta User

Perform Enrichment Analysis

Performed Enrichment AnalysesNew Enrichment AnalysisRunning and Pending Enrichment AnalysesErrors at Enrichment Analyses

Perform Enrichment Analysis

GO term Enrichment Analysis from your set of biomarkers based on the protein-go term correlation knowledge base of InSyBio Interact.

Input mode

Type or Copy-Paste biomarkers

Upload a file with biomarkers

Upload custom input files

Use any known identifier for denoting your biomarkers: Uniprot IDs, gene symbols, RefSeq_id and so on. Mixed identifiers are not supported!

Pvalue threshold ? :

0.05

New enrichment analysis title :

Title...

Select File Biomarker Input ? :

Drop file here to upload or Click to select file

Start Enrichment Analysis

- Upload a file with biomarkers or

InSyBio Suite - Enrichment Analysis

Perform Enrichment Analysis

Performed Enrichment Analyses | **New Enrichment Analysis** | Running and Pending Enrichment Analyses | Errors at Enrichment Analyses

Perform Enrichment Analysis

GO term Enrichment Analysis from your set of biomarkers based on the protein-go term correlation knowledge base of InSyBio Interact.

Input mode

☐ Type or Copy-Paste biomarkers ☐ Upload a file with biomarkers ☒ Upload custom input files

Use any known identifier for denoting your biomarkers: Uniprot IDs, gene symbols, RefSeq_id and so on. **Mixed identifiers are not supported!**

Pvalue threshold ? : 0.05

New enrichment analysis title : Title...

Select File Biomarker Input ? :

Drop file here to upload or Click to select file

Custom Enrichment Files

Select file (Go Terms) ? :

Drop file here to upload or Click to select file

Select file (Annotations) ? :

Drop file here to upload or Click to select file

Select file (Go Terms Full) ? :

Drop file here to upload or Click to select file

Select file (Go Types) ? :

Drop file here to upload or Click to select file

Select file (Goa Pruned) ? :

Drop file here to upload or Click to select file

Start Enrichment Analysis

- Upload a file with biomarkers and other custom annotation, term, term type and functional annotation of molecules files

You can use any known identifier for denoting your biomarkers: Uniprot IDs, gene symbols, RefSeq_id and so on. Mixed identifiers are not supported! Note that each symbol should be in one line or separated by comma.

You can also define a pvalue threshold for the biomarker to GO terms association output.

After the enrichment analysis, the job will appear in the Performed Enrichment Analyses tab.

InSyBio Suite - Enrichment Analysis

Perform Enrichment Analysis

Performed Enrichment Analyses | New Enrichment Analysis | Running and Pending Enrichment Analyses | Errors at Enrichment Analyses

List of Performed Enrichment Analyses

ID	Title	Biomarkers	Symbols DB	Submitted	Start Processing	End Processing	Action
28	test_symbols_enrichment	ATM, TP53, BRCA1, ...	GENESYMBOLS	11/13/19 12:09 PM	11/13/19 12:10 PM	11/13/19 12:10 PM	View Results
25	enrichment_test	ATM, TP53, BRCA1...	GENESYMBOLS	10/11/19 1:32 PM	10/11/19 1:32 PM	10/11/19 1:32 PM	View Results
22	1_test	ATM, TP53...	GENESYMBOLS	10/4/19 2:23 PM	10/8/19 6:54 AM	10/8/19 6:54 AM	View Results
21	1_test	ATM, TP53...	GENESYMBOLS	10/4/19 2:23 PM	10/8/19 6:54 AM	10/8/19 6:54 AM	View Results

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Show 10 entries

By clicking View Results you will be redirected to the Enrichment Analysis Results window, where you can view the results and download them in a tab delimited file. The results are a list of GO terms, terms type and name, specificity, enrichment score, associated Uniprot ids and input ids.

InSyBio Suite - Enrichment Analysis Results						
<div> <div>Dashboard</div> <div> <div>Job Status</div> <div>Job ID</div> <div>Submission Date</div> <div>Execution Time</div> <div>Input Data and Parameters</div> </div> </div> <div> <div>COMPLETED</div> <div>28</div> <div>Nov 13, 2019 12:09:28 PM</div> <div>00 hours, 00 minutes, 01 seconds</div> <div></div> </div> <div>Export Results</div>						
GO Term	GO Term's Type	GO Term's Name	GO Term's Specificity	Enrichment Score	Associated UniProt ids	Associated Input Ids
GO:000122	biological:process	negative regulation of transcription from RNA polymerase II promoter		9	0.0352905428365	P04637 TP53
GO:000729	biological:process	DNA double-strand break processing		8	0.00584764660219	P38398, Q13315 BRCA1, ATM
GO:000731	biological:process	DNA synthesis involved in DNA repair		7	0.030471091652	P38398, Q13315 BRCA1, ATM
GO:000732	biological:process	strand displacement		6	0.0188080869079	P38398, Q13315 BRCA1, ATM
GO:0002331	biological:process	pre-B cell allelic exclusion		13	0.0249351691907	Q13315 ATM
GO:0003677	molecular:function	DNA binding		5	0.0291025373332	P04637, P38398, Q13315 TP53, BRCA1, ATM
GO:0003700	molecular:function	transcription factor activity, sequence-specific DNA binding		3	0.0284145684002	P04637 TP53
GO:0004677	molecular:function	DNA-dependent protein kinase activity		8	0.032967327857	Q13315 ATM
GO:0005515	molecular:function	protein binding		3	3.47534911816e-18	P04637, P38398, Q13315 TP53, BRCA1, ATM
GO:0005524	molecular:function	ATP binding		6	0.00218574886077	P04637, Q13315 TP53, ATM

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Show 10 entries

Showing 1 to 10 of 55 entries

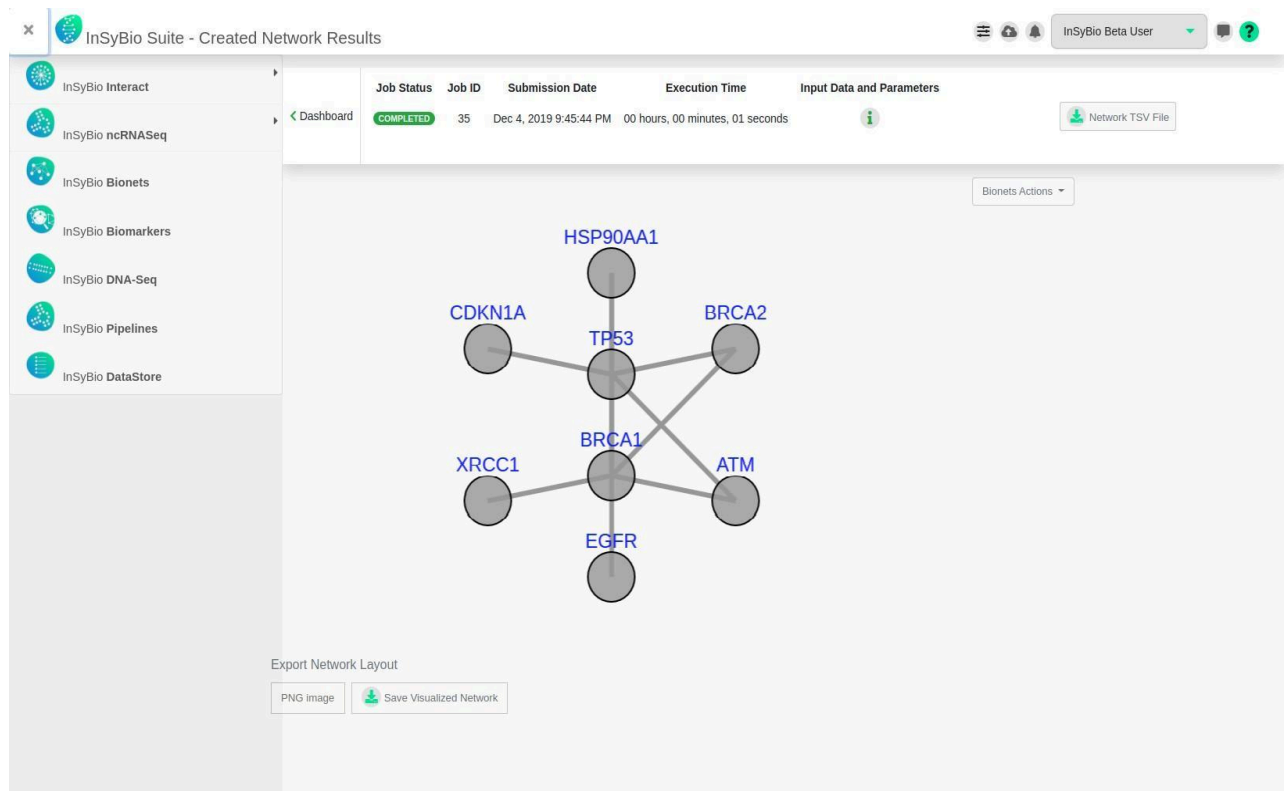
Network Creation

You can create and view biological networks from your set of biomarkers based on the protein-protein interactions knowledge base of InSyBio Interact.

In the tab New Network Creation you can either Type or Copy-Paste the biomarkers or Upload a file with biomarkers. You can use any known identifier for denoting your biomarkers: UniProt IDs, gene symbols, RefSeq_id and so on. Mixed identifiers are not supported! Note that each symbol should be in one line or separated by comma (without extra spaces or symbols between the commas).

The screenshot shows the 'InSyBio Suite Beta - Network Creation' web interface. At the top, there is a navigation bar with a hamburger menu, the InSyBio logo, and the text 'InSyBio Suite Beta - Network Creation'. On the right side of the navigation bar, there are icons for a menu, a user profile, and a help icon, along with the text 'InSyBio Beta User'. Below the navigation bar, the main heading is 'Create Network'. Underneath, a sub-heading reads 'Creation of biological networks from your set of biomarkers based on the protein-protein interactions knowledge base of InSyBio Interact.' There are four tabs: 'Created Networks', 'New Network Creation' (which is active), 'Running and Pending Processes', and 'Errors'. Below the tabs, a instruction says 'Create a new network from a list of biomarkers'. A green bar labeled 'Input mode' contains two radio buttons: 'Type or Copy-Paste biomarkers' (selected) and 'Upload a file with biomarkers'. Below this, there is a form with two main sections. The first section is 'New network's title:' with a text input field containing 'Title...'. The second section is 'List of symbols' with a large text area containing 'ATM,TP53,BRCA1...'. At the bottom left of the form, there is a green button labeled 'Start Network Creation'.

After the network creation, the job will appear in the Created Networks tab. By clicking View Results a new page is opened.



Networks' visualization provides an interactive graphical interface. Users can retrieve information about clicked nodes and edges, export the image in different formats (a PNG, SVG, PDF, XGMML, GraphML or SIF document), decrease opacity on mouseover and view the network using different visualization layouts (force-directed, circle or radial).

You can download the network in a TSV format and perform a list of supported actions in InSyBio BioNets tool.

Cloud computing Infrastructurer and Security Certifications

InSyBio Suite and all its tools are running over the cloud computing as a service infrastructure of Vultr (<https://www.vultr.com>), at the Amsterdam (Netherlands) facilities, offering the following security attestations and certifications (SOC 2+ (HIPAA), PCI (Merchant), CSA Star Level 1, ISO/IEC 20000-1:2018, ISO/IEC 27001:2022, ISO/IEC 27017:2015, ISO/IEC 27018:2019).

How to get InSyBio Interact

To request a free one month license of InSyBio Suite please email us at info@insybio.com.

To purchase InSyBio Interact commercial version 3.3 please contact us at sales@insybio.com.

About Us

InSyBio Inc is a bioinformatics pioneer company (www.insybio.com) in personalized healthcare, that focuses on developing computational frameworks and tools for the analysis of complex life-science and biological data in order to develop predictive integrated biomarkers (biomarkers of various categories) with increased prognostic and diagnostic aspects for the personalized Healthcare Industry.

InSyBio Suite consists of tools for providing integrated biological information from various sources, while at the same time it is empowered with robust, user-friendly and installation-free bioinformatics tools based on intelligent algorithms and methods.

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