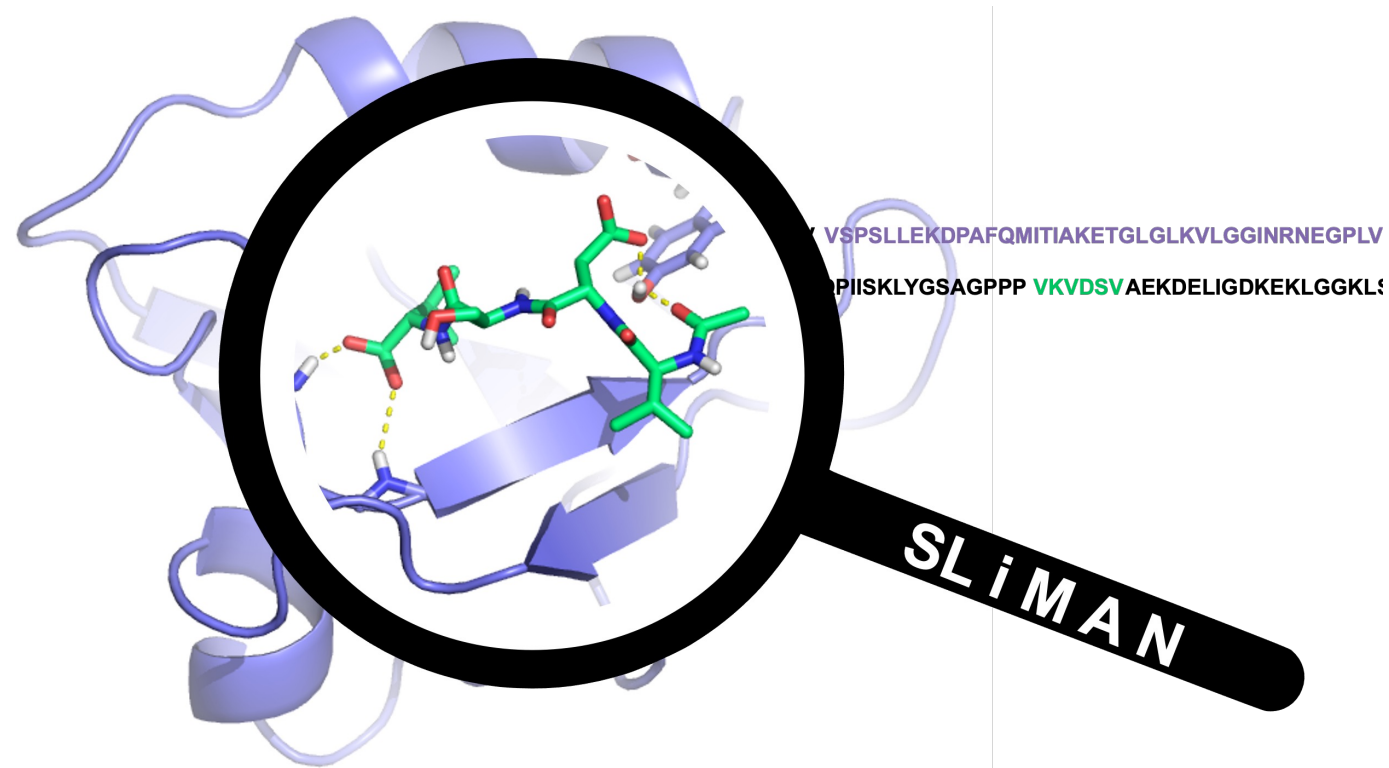


SLiMAN 2

Instruction Manual



Victor Reys
Gilles Labesse

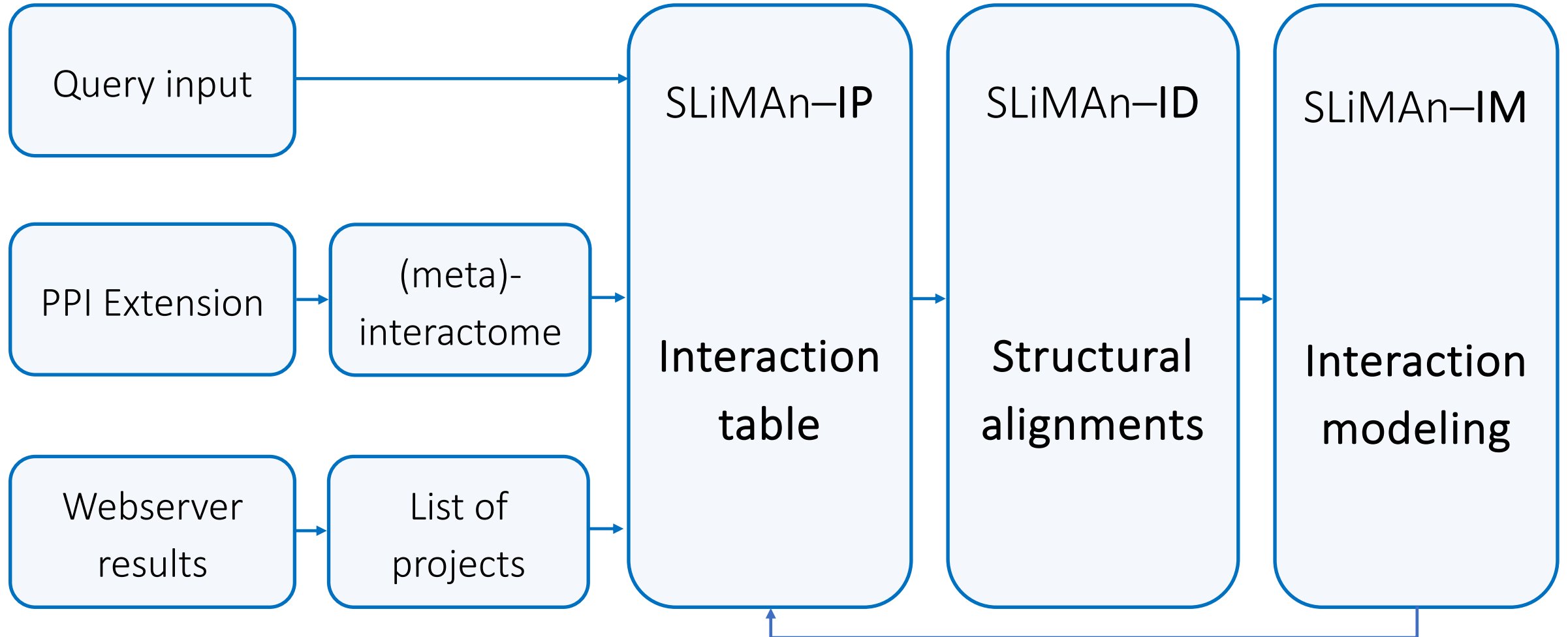
February 2024

web server url

<https://sliman2.cbs.cnrs.fr>

Query entry points scheme

<https://sliman2.cbs.cnrs.fr>



SLiMAN query input

<https://sliman2.cbs.cnrs.fr>

SLiMAN 2.6 Project

Project Name

Uniprot File No file selected.

And / Or

Uniprot List (must be separated by comma)

Open Access

Compute PubMed Co-occurrences

0 added

Name of a project

Load an input file (ex : InputFile.txt)

and/or (inputs can be combined)

List of coma separated UniProt Acc/Id*

Make this project visible from the `webserver results` table.

Search for PubMed PPI co-occurrences
(< 50 input proteins)

Build your own ELM class by defining:

- a class name
- a class type
- a motif sequence Regular Expression
- Pfam domain identifiers to which this class can interact with

***Note:** SLiMAN relies on UniProt Accessions (e.g: P06239)
and/or Identifiers (e.g: LCK_HUMAN)

PPI Extension query

<https://sliman2.cbs.cnrs.fr>

PPI Extension

Uniprot File No file selected.

And / Or

Uniprot List (must be separated by comma)

BioGRID

InAct

Load an input file (ex : InputFile.txt)

and/or (inputs can be combined)

List of coma separated protein Acc/Id*

Should BioGRID data be searched

Should IntAct data be searched

Search for (meta-)interactome

***Note:** SLiMAN relies on UniProt Accessions (e.g: P06239) *and/or* Identifiers (LCK_HUMAN)

Access results

<https://sliman2.cbs.cnrs.fr>

Access project results

Project Name

→ Name of a project

Go to Result

→ Access project results

This input section is made for user to access their results from their project name. If you forgot your project name, try to find it in the **`webserver results`** section.

SLiMAn – Create your own RegEx

<https://sliman2.cbs.cnrs.fr>

The screenshot shows a web form titled "New RegEx Builder : Simulate an ELM class". It contains the following fields and a button:

- Motif Class : MOD (dropdown menu)
- Motif Name : USER_MOTIF (text input)
- Motif E-value : 0 (text input with a help icon)
- Regular Expression : (text input)
- Associated PFams : (text input)
- Validate new RegEx importation (button)

Blue arrows point from the text labels on the right to each of these elements in the form.

Define a motif **class**

Define motif **name**

Define motif ***e-value***

Define **Regular Expression**

Define **list of Pfam identifiers** to pair this motif

Finalize the creation of the motif

SLiMAn – Query validation

After starting a new project, you will land on a validation page.
This page holds all the data that was validated / rejected by the server.

SLiMIP

Short Linear Motif Interaction Prediction

Estimated computation time required for your request : 54 seconds
Expected Computation time left : 34 seconds
Your results will be available at this [LINK](#)

Input Notes :

Project Name : **UserManual**
Results Accessibility : Open Access
Computing PubMed co-occurrences
1 new Imported User defined classes :
ClassName : MOD_SerThrTyr_Kinase_UserDef - RegEx : ...[STY]... - PFam(s) : PF00069 - E-value : 0
Results URL : https://sliman2.cbs.cnrs.fr/SLIMAN2/result_request.py?user_id=UserManual
Creation time : 2024-02-26 15:10:18
SLiMIP version : 2.6.08022023

Input Protein list :

XPO1_HUMAN, BUB1_HUMAN, FRAT2_HUMAN, EGFR_HUMAN, RASN_HUMAN, RASK_HUMAN, ERBB2_HUMAN,
CRCM_HUMAN, CTNA1_HUMAN, MLH1_HUMAN, GSK3B_HUMAN, PTN12_HUMAN, ARF_HUMAN, MLH3_HUMAN

Total protein found : 14

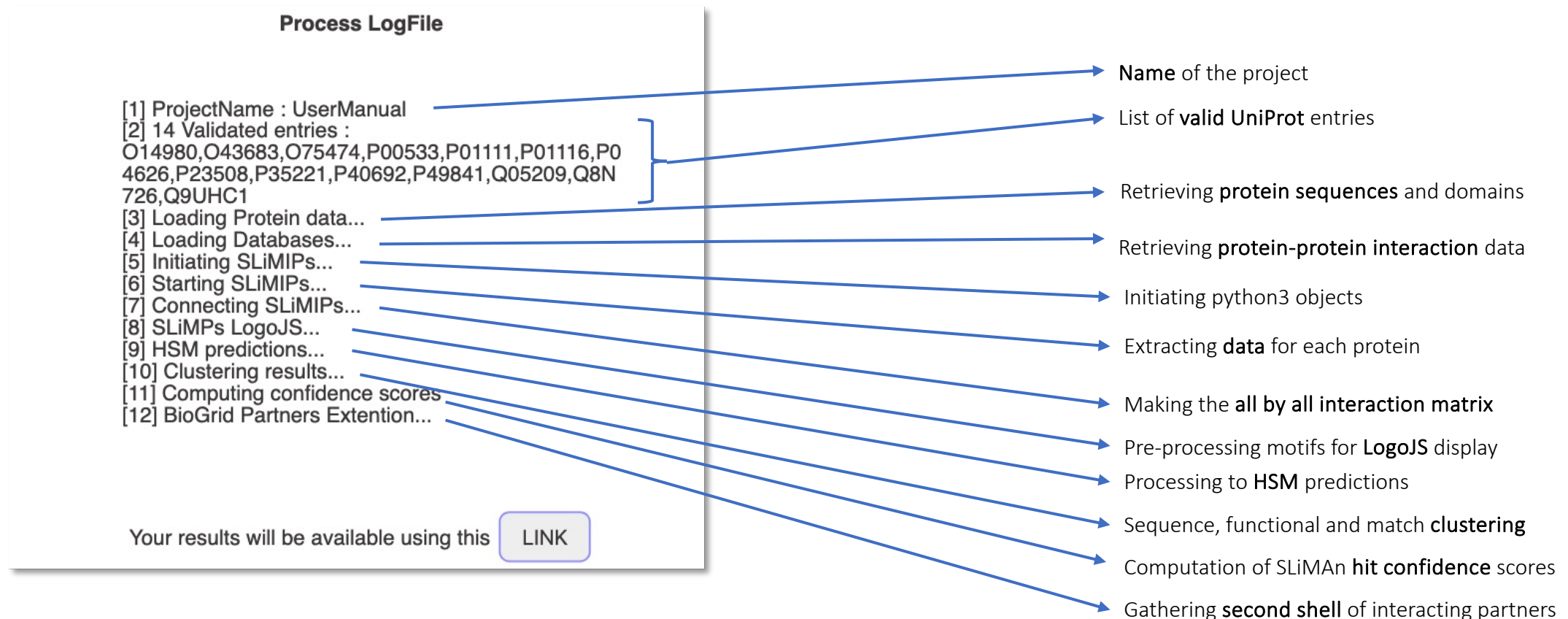
Annotations:

- Time prediction when results will be available
- Button to access the results
- Name of the project
- Accessibility of the project
- Will PubMed co-occurrences be computed?
- List of user defined SLiM classes
- URL of the results
- Date when project was initialized
- SLiMAn version of this project
- List of valid UniProt entries
- Number of validated UniProt entries in the query

SLiMAn – Process Logfile

A SLiMAn query can take from 30 seconds to several minutes.

While waiting for the results to be accessible, you can visualize the process evolution and what kind of computation is going on.



SLiMAN-IP results

SLiMI - Predictions



Query

Project : QL_PPI_GIPC1_HUMAN_B1_L0_H0-IU1_I0_U0
Creation date : 2023-02-19 13h18
SLiMAN version : 2.6.08022023
Accessibility : Open Access
Mode : Read - Write
Input Proteins : 118
Total SLiMIP hits : 43921

Proteins

	In	Out	None
ELM	4	114	0
PFam	4	111	3

Unique Interactions

	In	Out	Sum
ELM	4	238	242
PFam	2	186	188

Total Interactions

	In	Out	Sum
ELM	6	8407	8413
PFam	10	249	259
SLiMIP	33	43888	43921

Download Section

RawInput.txt - InputFile.txt

SLiMIP_Connexions.tsv

SLiMIP_DATA.json

BioGrid_partners.csv - BioGrid_partners.json

IntAct_partners.csv - IntAct_partners.json

AlphaFold InputFiles :

Summary of your
SLiMAN run

Summary tables of
predicted pairings

List of results files to
be downloaded

SLiMAN-IP results

SLiMI - Predictions



Query

Project : QL_PPI_GIPC1_HUMAN_B1_L0_H0-IU1_I0_U0

Creation date : 2023-02-19 13h18

SLiMAN version : 2.6.08022023

Accessibility : Open Access

Mode : Read - Write

Input Proteins : 118

Total SLiMIP hits : 43921

Button to hide/display panel

Name of the project

Date the project was created

SLiMAN **version**

Project **accessibility**

Project mode: *Read-Write* or *Read-only**

Number of input protein**

Number of ELM-Pfam pairings in the interactome

* To switch to read-only, please send us an email

**Click on it to view the list

SLiMAn-IP results

Table containing to protein data

Proteins

	In	Out	None
ELM	4	114	0
PFam	4	111	3

Proteins with Pfam annotations

Proteins with ELM annotations

Table containing to protein data

Unique Interactions

	In	Out	Sum
ELM	4	238	242
PFam	2	186	188

Nb. Pfam domains IDs in interactome

Nb. ELM classes in interactome

Table containing SLiMAn-IP data

Total Interactions

	In	Out	Sum
ELM	6	8407	8413
PFam	10	249	259
SLiMIP	33	43888	43921

Nb. SLiMAn Hits

Nb. Pfam domains IDs in interactome

Nb. ELM classes in interactome

In = Filtered in : Visible



Out = Filtered out : Hidden

Sum = In + Out

None = Unfound



SLiMAn-IP results



Download Section

RawInput.txt  - InputFile.txt 

SLiMIP_Connexions.tsv 

SLiMIP_DATA.json 

BioGrid_partners.csv  - BioGrid_partners.json 

IntAct_partners.csv  - IntAct_partners.json 

AlphaFold InputFiles :

.TXT

.JSON

download the submitted input data

download the SLiMAn input file

download the SLiMAn-IP results as *tsv*


download the SLiMAn-IP results and related data

BioGRID and IntAct files contain all reported PPI for each protein in the input file

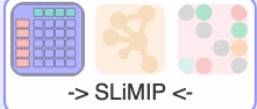
Automatically generate AlphaFold2 input files for the currently displayed *Hits*

SLiMAn-IP – Hit filtering panel

The Hit Filter parameter panel allow the user to fine tune the SLiM-Domain pairings displayed in the table

 Button to hide/display pannel

Hit filters

ELM	Disorder	HSM	PSP+	PPI Db.	SLiMAN	Visual	Settings
<p><i>e-value</i> 0.0012</p> <p>MOD <input checked="" type="checkbox"/> DOC <input checked="" type="checkbox"/></p> <p>LIG <input checked="" type="checkbox"/> DEG <input checked="" type="checkbox"/></p> <p>TRG <input checked="" type="checkbox"/> CLV <input checked="" type="checkbox"/></p> <p>Valid Instances : <input type="checkbox"/></p>	<p>IUpred2A</p> <p>Strict Disorder <input type="checkbox"/></p> <p>Anchor >= 0.5</p> <p>Short >= 0.5</p> <p>Long >= 0.5</p> <p>SDom >= 0.2</p> <p>LDom >= 0</p> <p>AlphaFold</p> <p>pLDDT <= 75</p>	<p>Proba 0.2</p> <p>Appli.Only <input type="checkbox"/></p> <p>BEST(s) :</p> <p>Pair <input type="checkbox"/></p> <p>Domain <input type="checkbox"/></p> <p>Motif <input type="checkbox"/></p>	<p><input type="radio"/> x</p> <p><input type="radio"/> x ∩ o</p> <p><input checked="" type="radio"/> x ∪ (x ∩ o)</p> <p><input type="radio"/> x</p> <p><input type="radio"/> u</p> <p><input type="radio"/> u ∪ x</p> <p><input type="radio"/> u ∪ (x ∩ o)</p> <p><input type="radio"/> u ∪ o</p> <p><input type="radio"/> u ∪ x ∪ o ∪ x</p> <p>Legend:</p> <p>u x o x</p>	<p>BioLow 0</p> <p>BioHigh 0</p> <p>Bio Total 1</p> <p>Or <input checked="" type="radio"/> And</p> <p>IntAct 0</p> <p>HuRI 0</p> <p>IntAct + Huri 1</p> <p>PubMed count 0</p>	<p>Confidence 4</p> <p>Selected <input type="checkbox"/></p> <p>SLiMID templates 0</p> <p>SLiMIM valid models 0</p>	<p>Ordering : Input order</p> <p>PFam query</p> <p>ELM query</p> <p>RenderTimer 1.00 s</p> <p></p> <p>-> SLiMIP <-</p>	<p>Display All</p> <p>Default Settings</p> <p>Save Current State</p>

ELM related parameters

Motif disorder parameters

HSM perdictions parameters

Post Translational Modifications parameters

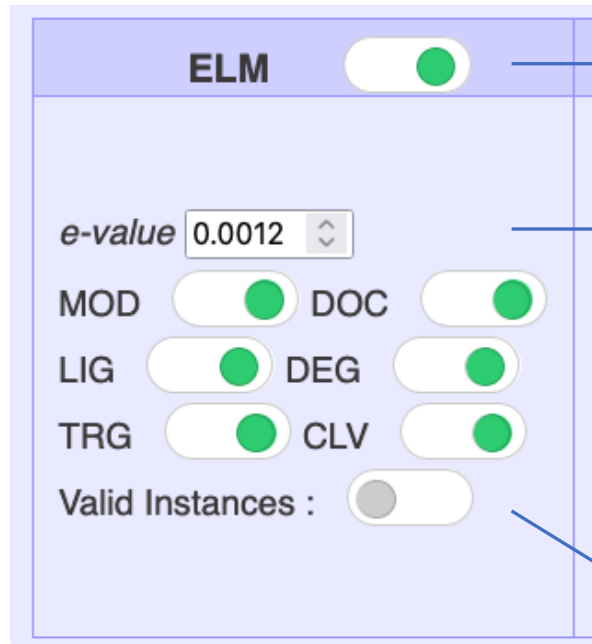
Protein-protein interaction parameters

SLiMAN parameters

Display parameters

Fast global parameter settings

SLiMAn-IP – ELM parameters



Switch Off/On ELM parameters

Set ELM classes *e-value* upper boundary

Switch Off/On certain class **types**

MOD: Post-Translational-modifications sites

DOC: docking site

LIG : Ligand site

DEG: Degradation site

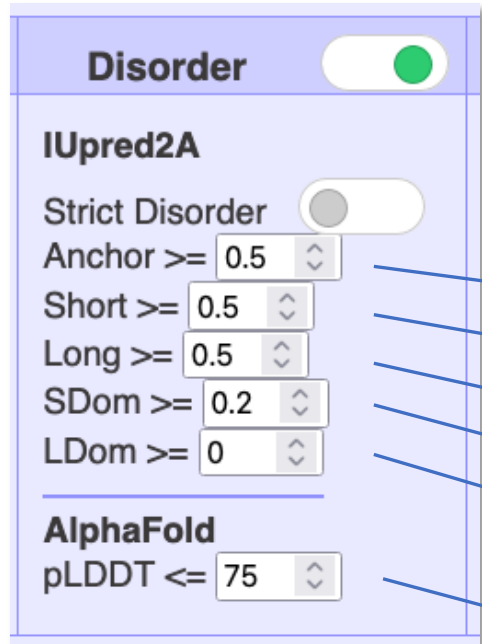
TRG: Targeting site

CLV: Cleavage site

Only show pairings present in ELM instances ¹

¹ Present in this file: http://elm.eu.org/instances.tsv?q=*

SLiMAn-IP – Disorder parameters



The screenshot shows a control panel for disorder parameters. At the top is a 'Disorder' toggle switch, currently turned on (green). Below it is the 'IUpred2A' section, which includes a 'Strict Disorder' toggle switch (currently off, grey) and five numerical input fields: 'Anchor >= 0.5', 'Short >= 0.5', 'Long >= 0.5', 'SDom >= 0.2', and 'LDom >= 0'. Below the IUpred2A section is the 'AlphaFold' section, which includes a 'pLDDT <= 75' input field. Blue arrows point from each of these elements to explanatory text on the right.

Switch Off/On motif disorder parameters

Strict Disorder = (Anchor>0.5 AND Short>0.5. AND Long>0.5)
for all residues in the motif !

IUpred2A **Anchor2** prediction lower boundary

IUpred2A **Short window** prediction lower boundary

IUpred2A **Long window** prediction lower boundary

IUpred2A **Short window Domain** prediction lower boundary

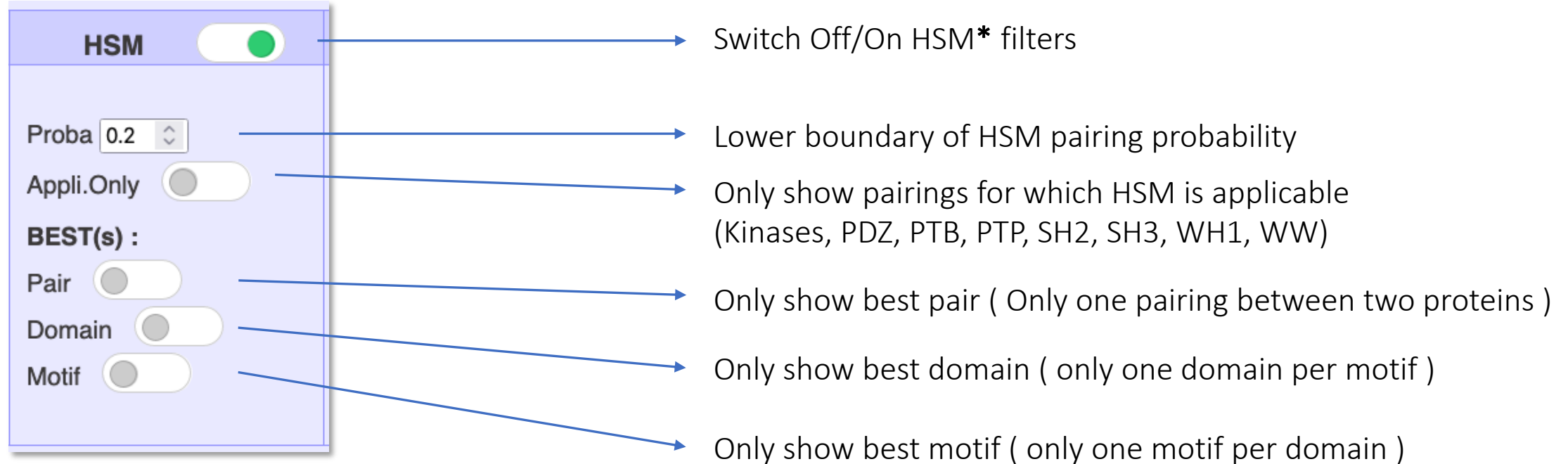
IUpred2A **Long window Domain** prediction lower boundary

AlphaFold motif pLDDT upper boundary

- Low pLDDT = low confidence prediction ~ disordered
- High pLDDT = high confidence prediction ~ ordered

***Note:** All disorder scores are averaged over the SLiM residues

SLiMAn-IP – HSM parameters



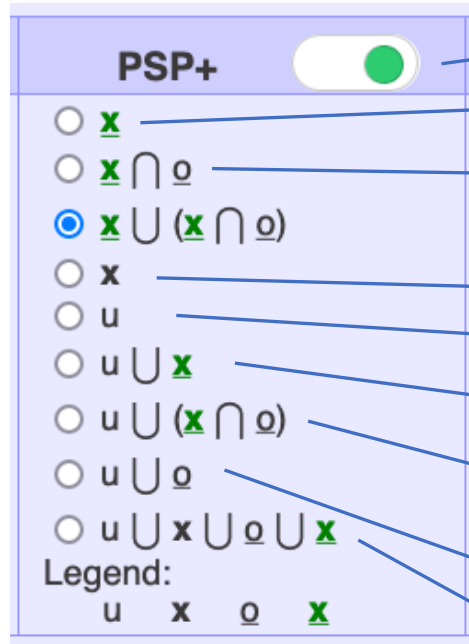
The image shows a control panel for HSM parameters. At the top, there is a toggle switch labeled 'HSM' which is currently turned on (green). Below this, there is a 'Proba' field with a value of 0.2 and a dropdown arrow. Further down, there are four more toggle switches: 'Appli.Only', 'Pair', 'Domain', and 'Motif', all of which are currently turned off (grey).

- Switch Off/On HSM* filters
- Lower boundary of HSM pairing probability
- Only show pairings for which HSM is applicable (Kinases, PDZ, PTB, PTP, SH2, SH3, WH1, WW)
- Only show best pair (Only one pairing between two proteins)
- Only show best domain (only one domain per motif)
- Only show best motif (only one motif per domain)



*J. M. Cunningham, G. Koytiger, P. K. Sorger, and M. AlQuraishi, **Biophysical prediction of protein-peptide interactions and signaling networks using machine learning**, *Nat Methods*, vol. 17, pp. 175–183, Feb 2020.

SLiMAn-IP – PTM parameters



u = Unannotated motifs
 x = unsatisfied ELM PTM
 o = Experimental PTM
x = Satisfied ELM PTM

Switch Off/On PTM filters

Motifs with only one Satisfied ELM + Experimental PTM

Motifs with Satisfied ELM + Experimental PTM
AND an extra experimental PTM elsewhere

Motifs with only one Unsatisfied ELM PTM

Unannotated motifs

Unannotated motifs AND Motifs with only one Satisfied ELM +
Experimental PTM

Unannotated motifs AND (Motifs with Satisfied ELM +
Experimental PTM AND an extra experimental PTM elsewhere)

Unannotated motifs with an extra experimental PTM elsewhere

All motifs

SLiMAn-IP – PPI parameters

PPI Db.

BioLow 0

BioHigh 0

Bio Total 1

Or And

IntAct 0

HuRI 0

IntAct + Huri 1

PubMed count 0

Switch Off/On protein-protein interaction filters

Set lower boundary of BioGRID **low** throughput experiment count between two proteins

Set lower boundary of BioGRID **high** throughput experiment count between two proteins

Set lower boundary of BioGRID **low + high** throughput experiment count between two proteins

And / Or **Logical operator** between the BioGRID and IntAct parameters

Set lower boundary of IntAct experiment count between two proteins

Set lower boundary of HuRI Y2H count between two proteins

Set lower boundary of IntAct + HuRI experiment count

Set lower boundary protein names co-occurrences in research articles from PubMed

SLiMAN-IP – SLiMAN parameters

SLiMAN

Confidence 4

Selected

SLiMID templates 0

SLiMIM valid models 0

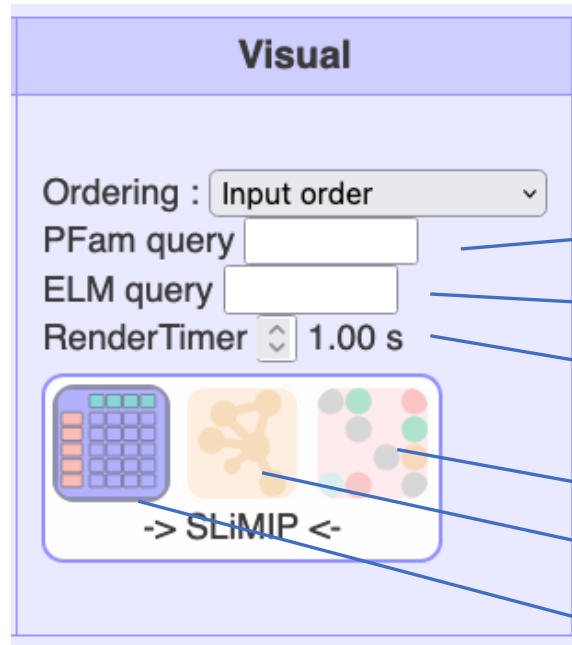
Lower boundary of SLiMAN Hit Confidence scores

Filters in only **selected** hits

Set the lower boundary of available template for a corresponding ELM-Pfam pairing

Set the lower boundary of validated SLiMAN-IM validated homology models (usefull to retrieve all generated models)

SLiMAn-IP – Display parameters



Set **order of the proteins** in the table

Filters **domains** based on text (usefull to search for specific domain or protein)
! CASE SENSITIVE !

Filters **motifs** based on text (usefull to search for specific classes or protein)
! CASE SENSITIVE !

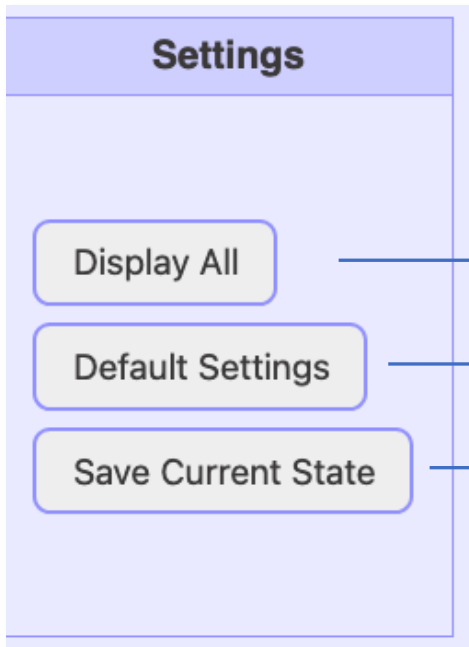
Set **time before rendering a new table**. This allows you to modify multiple parameters before the table is updated.

PPI matrix view (experimental)

Cytoscape network view

SLiMAn-IP result table view

SLiMAn-IP – Global parameters



Display All

Put all **parameters** to their **least stringent values**

Default Settings

Set **default values** for all parameters

Save Current State

Save **current parameters AND hit selection**.
This can be usefull to save your selection and keep it for the next time you connect.

SLiMAn-IP – Result table

Color code of the Hit confidence levels
(the higher the more confident)

Confidence Levels					I	II	III	IV	V	VI	VII	VIII
ELM Analysis					GSK3B_HUMAN			STRN4_Q9N				
Protein	ELM_class	RegEx	Motif	Location	P49841 PF00069 Kinase	PF00400 WD40 1	PF00400 WD40 2					
GSK3B_HUMAN P49841	MOD_PKB_1	R.R..((ST)) [*P]..	RPRTISFAE	4-12	<input checked="" type="checkbox"/> Hit Align(29) Model							
HECW2_HUMAN Q9P2P5	MOD_PK_1	[RK]..(S)[VI]..	RSNSIQQ	849-855	<input checked="" type="checkbox"/> Hit Align(25) Model							
	MOD_PKB_1	[RK]..(S)[VI]..	RYQSIRR	862-868	<input type="checkbox"/> Hit Align(25) Model							
PKHA4_HUMAN Q9H4M7	DEG_SCF_FBW7_1	[LIVMP]_{0,2} (T)P..((ST))	LLTPSP	209-215	<input type="checkbox"/> Hit Align(3) Model	<input type="checkbox"/> Hit Align(3) Model	<input type="checkbox"/> Hit Align(3) Model					
	DEG_SCF_FBW7_1	[LIVMP]_{0,2} (T)P..((ST))	LTPSP	210-215	<input type="checkbox"/> Hit Align(3) Model	<input type="checkbox"/> Hit Align(3) Model	<input type="checkbox"/> Hit Align(3) Model					
	MOD_DYRK1A_RPxSP_1	R[PSVA]. ((ST))P	RARS	226-230	<input type="checkbox"/> Hit Align(1) Model							
	MOD_DYRK1A_RPxSP_1	R[PSVA]. ((ST))P	RPPSP	238-242	<input type="checkbox"/> Hit Align(1) Model							
	MOD_DYRK1A_RPxSP_1	R[PSVA]. ((ST))P	RPHTP	268-272	<input type="checkbox"/> Hit Align(1) Model							
	MOD_DYRK1A_RPxSP_1	R[PSVA]. ((ST))P	RPPTP	293-297	<input type="checkbox"/> Hit Align(1) Model							
	MOD_DYRK1A_RPxSP_1	R[PSVA]. ((ST))P	RPTSP	610-614	<input type="checkbox"/> Hit Align(1) Model							
MYC_HUMAN P01106	MOD_PK_1	[RK]..(S)[VI]..	KLDSVRV	326-332	<input type="checkbox"/> Hit Align(25) Model							

In **rows** are presented the various protein **motifs**.
For each protein, their corresponding motifs are shown with their:

- UniProt Identifier and Accession (links)
- ELM Class name (link)
- Regular Expression used to parse the sequence
- The motif sequence
 - X = unmodified/unannotated residue
 - X = modified residue PSP+ (link)
 - **X** = **unsatisfied ELM modification**
 - X = satisfied ELM + PSP+ modification (link)
- Start and End location of the motif on the sequence

In columns are presented the various protein domains.

A SLiMAn-IP Hit box, pairing a motif and a structured domain.

LogoJS

Logo of the consensus motif for the MOD_DYRK1A_RPxSP_1 class observed with current parameters

SLiMAn Confidence Score

SLiMAn-IP Hits are color coded according to the SLiMAn confidence score.

Confidence Levels	I	II	III	IV	V	VI	VII	VIII

The confidence score is an **heuristic** function computed by **summing terms** based on the various predictors available in SLiMAn. It is computed as follow:

Confidence score = 1

ELM experimental evidence: +7

IUpredAnchor ≥ 0.7 : +1

IUpred StrictDisorder: +2

Motif AlphaFold2 pLDDT ≤ 65 : +1

HSM prediction ≥ 0.7 : +1

HSM prediction ≤ 0.1 : -1

ELM expected PTM satisfied by PSP+ annotation: +1

ELM expected PTM satisfied by PSP+ annotation & Paired domain is also supposed catalyzing protein-kinase: +2

BioGRID low throughput ≥ 1 : +1

BioGRID high throughput ≥ 3 : +1

BioGRID low + high ≥ 10 : +1

IntAct ≥ 2 : +1

HuRI ≥ 1 : +1

PubMed co-occurrences ≥ 7 : +1

SLiMAn-IP Hit box

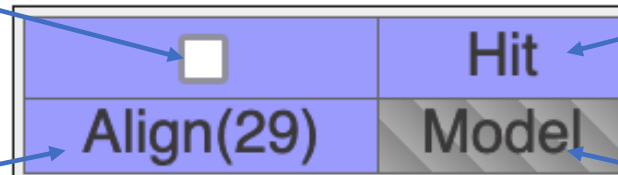
Each SLiM-domain pairing is presented as a SLiMAn-IP **Hit box**, composed of 4 areas.

Hit selection checkbox:

- Click on it to validated/select a hit
- Remember to save your selection using the "Save Current State" button

Hit details:

- Click on it to open a pop-up window holding all the information related to this motif



Hit alignment link:

- Click on it to reach the SLiMAn-ID data for this hit and perform the paired alignment to pre-extracted PDB structures present in the SLiMAnDB.
- The number in parenthesis corresponds to the number of available templates for the modeling

Hit models link:

- Click on it to reach the SLiMAn-IM models that you already generated.
- If in grey, you should first generated models from the SLiMAn-ID page.

SLiMAn-IP Validated hit box

In this example, the Hit was selected, and it is highlighted by a pink circle around the hit box

Hit selection checkbox:

- Click on it to unvalidated/unselect a hit



<input checked="" type="checkbox"/>	Hit
Align(29)	Model

SLiMAN-IP Hit data

SLiMAN-IP Hit index

Motif protein data

Domain protein data

Motif sequence

Switch between PTM and Disorder motif representation

ELM data related to the motif

IUpred2A data related to the motif

Number of BioGRID PPI data

Number of IntAct PPI data

Number of HuRI PPI data

Switch button to validate/select this particular hit

SLiMAN Hit confidence level (and color)

Close this window

Fast access to PubMed search engine: All protein alternative names are combined in a single click

Value of HSM predictions

Motif AlphaFold pLDDT score

Switch opening table holding all retrieved experimental data

Button to twinned sequence alignment to SLiMANDB templates in SLiMAN-ID (e.g: 13 templates are available)

Button to access generated models in SLiMAN-IM

SLiMIP Hit '447'
||
✕

Motif protein : FRAT2_HUMAN (O75474) - TRG_NES_CRM1_1

Domain protein : XPO1_HUMAN (O14980) - PF08389 - Xpo1 (123 - 268)

Motif : DRLVAQIGETLQLD (PSP, ELM, ELM+PSP)

IUpred ELM + PSP

Motif Data

ELM	IUpred2	AlphaFold	HSM
Class Name = TRG_NES_CRM1_1 Class E-Value = 0.000762613786385 Motif Boundaries = 41 - 54 Verified Instance = No	Short Avg_score = 0.42 Long Avg_score = 0.55 Short Domain Average Score = 1 Long Domain Average Score = 1 Anchor2 Average Score = 0.81 Strict Disordered Part = No	PLDDT=83	Not Applicable

BioGrid Data : Total interactions = 1

LowThroughput interactions = 0
HighThroughput interactions = 1

Toggle details:

IntAct Data : Total interactions = 0

FRAT2_HUMAN -> XPO1_HUMAN = 0
XPO1_HUMAN -> FRAT2_HUMAN = 0

Toggle details:

HuRI Data : Total interactions = 0

FRAT2_HUMAN -> XPO1_HUMAN = 0
XPO1_HUMAN -> FRAT2_HUMAN = 0

Toggle details:

PubMed queries ⓘ

- FRAT2 (26)
- XPO1 (1399)
- FRAT2 + XPO1 (0)

SLiM-IP
 Selected

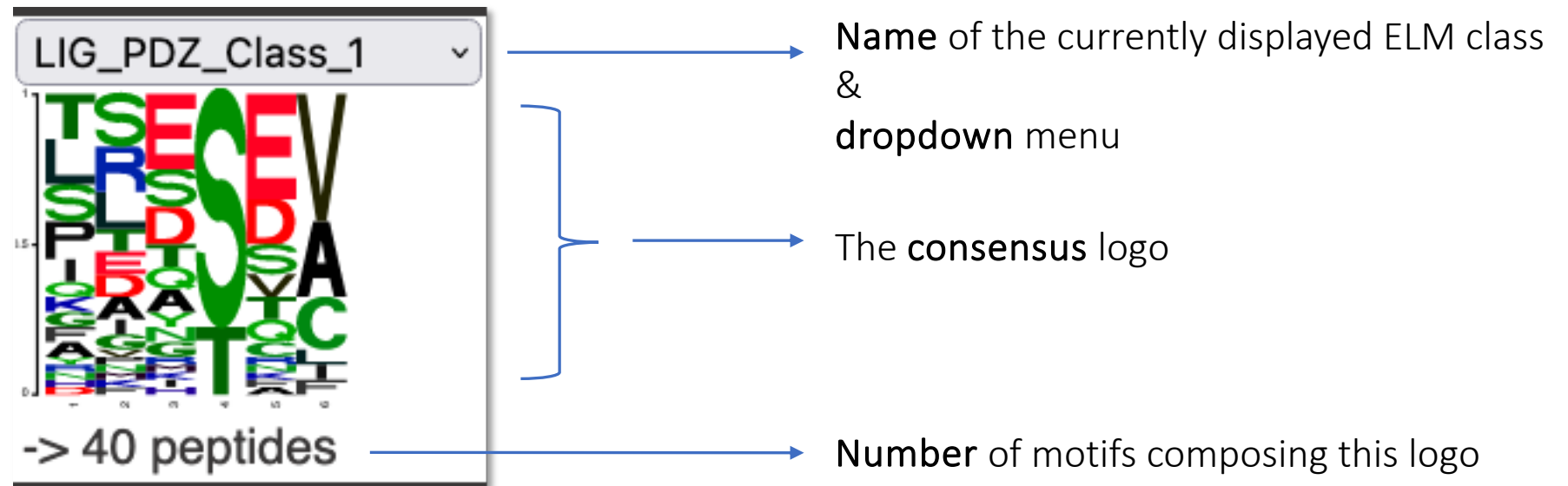
SLiM-ID
 Alignments
 (13 templates)

SLiM-IM
 Models (2 validated)

SLiMAn-IP Consensus logo

At the bottom of the SLiMAn-IP table, consensus logos are displayed.

- Logos are generated by the *LogoJS** library
- Logos are computed on a **per-ELM class basis**
- Because multiple classes could pair the same domain, you can change class using the **dropdown menu**
- Logos are computed based on **currently displayed motifs** (modify the parameters will update them)



*H. Pratt and Z. Weng, LogoJS: a Javascript package for creating sequence logos and embedding them in web applications, *Bioinformatics*, vol. 36, pp. 3573–3575, Jun 2020.

SLiMAn-ID Sequences

At the top of the SLiMAn-ID page, extracted motif and domain sequences are **highlighted** on the full protein canonical sequences.

Segmentation boundaries can be manually tuned by the user and subsequent alignments updated.

Template alignments

ELM match : FRAT2_HUMAN (O75474) - TRG_NES_CRM1_1

- Parsing Regex : (([DEQ].[0,1]{[LM]}.(2,3){[LIVMF][^P]}(2,3){[LMVF].[LMIV]}.(0,3){DE}))*([DE].[0,1]{[LM]}.(2,3){[LIVMF][^P]}(2,3){[LMVF].[LMIV]}.(0,3){DEQ})
- Class E-value : 0.000762613786385

MPCRRREEEEAGEEAEAGEEEEDDSFLLQQSVTLGSSGEVDRLVAQIGETLQLDAQDSPASPCAPPVPLRAPGLAAAVPADKARPPAVPLLLPPASAEITVGPAPSGALRCALGDRGRVGRAPYCVAEVAAGPSALPGPCRRGWLRDAVTSRRLQQRRTQAGARAGDDPHRLQLQVLVSGNLIKEAVRRLQ
RAVAAVAATGPASAPGPGGGRSGPDRIALQPSGSL

User defined motif segmentation : from 42 to 54
ELM RegEx segmentation : from 40 to 54

Motif Segmentation : From To

[Update alignments with current segmentation](#)

PFam match : XPO1_HUMAN (O14980) - PF08389 - Xpo1

MPAINTMLADHAARQLLDFSQKLDINLLDNVNCLYHGEGAQQRMAQEVLTSLKEHPDAWTRVDTILEFSQNMNTKYYGLQILENVIKTRWKILPRNQCEGIKKYVVGIIKTSSDPTCVEKEKVIIGKLNMLVQILKQEWPKHWPTFISDIVGASRTSESLCQNNMVIKLLSEEVDFSSGQITQVKSJKLSDS
MCNEFSQIFQLCQFVMSNQAPLVHATLETLLRFLNWIPLGYIFETKLISTLIYKFLNVPMFRNVSLKCLTEIAGVSVSQYEEQVTLFTLTMMLKQMLPLNTNIRLAYSNGKDDQNFQNLFLCTFLKEHDQIEKRLNLRRETLMEALHYMLLVSEVEETEIFKICLEYWNHLAAELYRESPPSTASPLL
SGSQHFVPPRRQLYLPLFKVRLLMVSRMAKPEEVLVENDQGEVVFVRFMKDTSINLYKNMRETIVYLTHLDYVDTERTIMEKLNQVNGTEWSKNLNTLCWAIIGSISGAMHEEDEKRFVTVIKDLLGLCEQKRGKDNKAIASNIMYIVGQYPRFLRAHKKFLKTVVVKLFEFEMHETHDGVQDMACDTFIKI
AQKCRRHFEVQVQVGEVMPFIDEILNNINIIICDLQPQQVHTFYEAAGVYMIQAQTDQIVQEHLEIKYMLLPNQVWDSIIQAQTKNVDILKDPETVKQLGSIILKTNVCRACKAVGHPEVFIQLGRIYLDMLNVYKCLSENIISAAIQANGEMVTKQPLIRSMRTVKRETLLKLSGIVSRSDNPQVAENFVPLLDVAVLIDY
QRNVPAAREPEVLSMAIIVNKLGGHITAEIPQIFDAVFECTLNMINKDFEYEPHRTNFFLLQAVNSHCFPAFLAIPPTQFKLVLDSIIWAFKHTMRNVADTGLQILFTLLQNVAQEEAAAQSFYQYFCDILQHFISVVTDTSHTAGLTMHASILAYMFNIVEEGKISTSLNFGNPNVNNQIFLQEVVANLLKSA
FPHLQDAQVKLFVFTGLFSLNQDIAPFKEHLRDLVQIKFEPAGEDTSDLFLEEREIALRQADEEKHRQMSVPGIFNPHEIPEEMCD

User defined segmentation : from 520 to 620
PFam Domain segmentation : from 123 to 268

Modify Domain Segmentation : From To

Motif protein name

ELM class data

Motif protein sequence

Motif extraction boundaries

Button to **update alignments**

Domain protein name

Domain protein sequence

Domain extraction boundaries

SLiMAn-ID twinned alignments table

At the bottom of the SLiMAn-ID page, twinned alignments (motif & domain) to PDB templates are shown.

Automated fast selection tools:

- None: Unselect all
- Top 5: Select top 5 models from table
- No Double: Select all templates without duplicating PDBids
- All: Select all available models

Query Peptide Motif(s) : RLVAQIGETLQLD
 Query Pfam Sequence : VIKDLLGLCEQKRGKDNKAIASNIMYIVGQYPRFLRAHWKFLKTVVNLKLFEMHETHDGVQDMACDTFIKIAQKRRHFVQVQVGEVMPFIDEILNNT
 Selected Templates :

- 6X2V_C_complex_peptide_8_20_D.pdb
- 6X2S_C_complex_peptide_6_19_D.pdb
- 6X2P_C_complex_peptide_7_20_D.pdb
- 6CIT_C_complex_peptide_80_93_D.pdb
- 6A38_C_complex_peptide_80_93_D.pdb

Launch Modeling !

List of selected templates

Launch homology modeling on selected templates

Each row in the table corresponds to a template

Selectors	PDB ID	Entry	Reso	Motif	ChainID	%Ident	%QueryCov	Nb Contacts	Aligned Sequences
None			Å	Domain			%TemplCov	(%)	
<input checked="" type="checkbox"/>	6X2V	6X2V_C_cPep_8_20_D.pdb	2.82	ELM	D	23.1	92.3	33	RLVAQIGETLQLD--- -ELAKLAGLDIDE--
				Pfam	C	75.8	100.0	73	VIKDLLGLCEQKRGKDNKAIASNIMYIVGQYPRFLRAHWKFLKTVVNLKLFEMHETHDGVQDMACDTFIKIAQKRRHFVQVQVGEVMPFIDEILNNT VIKDLLGLCEQKRGKDNKAVVASDIMYVVGQYPRFLKAHWNFLRTVILKLFEMHETHDGVQDMACDTFIKIVQKCKYHFVIQQPRESEPFITIRDI
<input checked="" type="checkbox"/>	6X2S	6X2S_C_cPep_6_19_D.pdb	2.5	ELM	D	23.1	100.0	32	RLVAQIGETLQLD--- EALQKLELELNQ--
				Pfam	C	75.8	100.0	83	VIKDLLGLCEQKRGKDNKAIASNIMYIVGQYPRFLRAHWKFLKTVVNLKLFEMHETHDGVQDMACDTFIKIAQKRRHFVQVQVGEVMPFIDEILNNT VIKDLLGLCEQKRGKDNKAVVASDIMYVVGQYPRFLKAHWNFLRTVILKLFEMHETHDGVQDMACDTFIKIVQKCKYHFVIQQPRESEPFITIRDI

Color Codes

- X: Identical residue
- X: contacts <4Å
- X: contacts <6Å
- X: contacts <8Å
- X: contacts >8Å

- Aligned motif sequence
- Peptide template sequence
- Aligned domain sequence
- Domain template sequence

Checkbox to select a template

PDBid and link

SLiMAn-DB template

Structure resolution

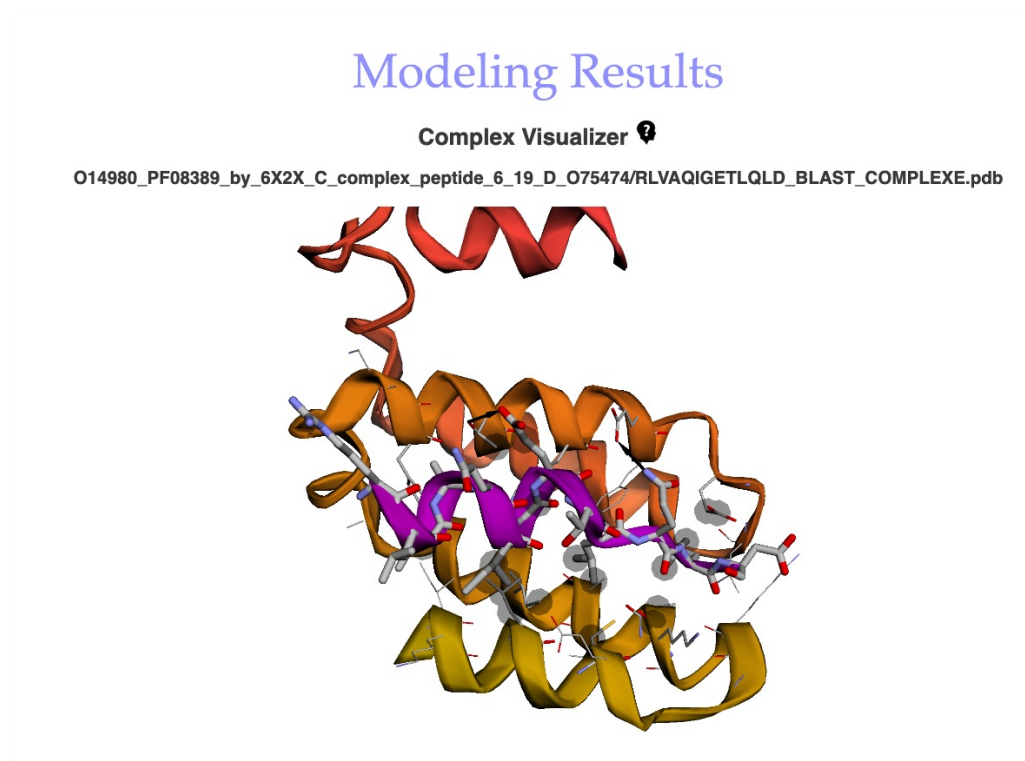
Sequence identity with respect to query

Query & template coverage

Conserved Contact Score (CCS) and %CCS

SLiMAn-IM model visualisation

Generated models are displayed in the SLiMAn-IM result page using both *3Dmol.js** and *BINANA***



BINANA legends

- Hydrogen bonds
- Hydrophobic contact
- VdW clashes

* N. Rego and D. Koes, **3Dmol.js: molecular visualization with WebGL**, *Bioinformatics*, vol. 31, pp. 1322–1324, Apr 2015.

J. Young, N. Garikipati, and J. D. Durrant, **BINANA 2: Characterizing Receptor/Ligand Interactions in Python and JavaScript, *J Chem Inf Model*, vol. 62, pp. 753–760, Feb 2022

SLiMAn-IM Result table

Generated models are accessible from the in the SLiMAn-IM result table.

List of **discarded** models

Note: Discarded models will be erased

Click to **download all** complexes

List of **validated** models.

Note: Validated models are forwarded to the SLiMAn-IP table

SLiMI- Models Accession Table

-> Download Analysis.zip <-

Discarded

Validated

• O14980_PF08389_by_6X2X_C_complex_peptide_6_19_D_O75474/SCWRL/BLAST

• O14980_PF08389_by_6X2X_C_complex_peptide_6_19_D_O75474/SCWRL/MAFFT

Save Selection

Click to **discard / validate** models

Currently displayed model

	PDB	SLiMIM	Reso.	%Ident	Software	Alignment	PFam Domain Model	Motifs	Peptide Model	Complexes	Validation
	6X2X PDB	6X2X_C_complex_peptide_6_19_D	2.5	73.3	SCWRL	BLAST	MODEL TEMPLATE FASTA	RLVAQIGETLQLD--- EALQKKLEEELELDE--	MODEL TEMPLATE FASTA	COMPLEX	<input checked="" type="radio"/> <input type="radio"/> <input type="radio"/>
						MAFFT	MODEL TEMPLATE FASTA	RLVAQIGETLQLD--- EALQKKLEEELELDE--	MODEL TEMPLATE FASTA	COMPLEX	<input type="radio"/> <input type="radio"/> <input checked="" type="radio"/>

Complex validation

- To be discarded
- Unannotated model
- Validated model

PDBid, link and download

SLiMAn-DB template, and download

Structure resolution

Modeling tool

Identity to domain

Alignment tool

Domain modeling process
- Domain model
- Domain template
- Query sequence

Aligned query and template motif sequence

Motif modeling process
- Motif model
- Motif template
- Query sequence

Click to **visualize** complex

Click to **download** complex

SLiMAn – PPI extension results

AND/OR Logical operator switch defining how to combine both databases

Switch On/Off partners from BioGRID

Lower boundary of BioGRID low throughput experiment

Lower boundary of BioGRID high throughput experiment

Lower boundary of BioGRID low + high throughput experiment

Switch On/Off partners from IntAct

Lower boundary of IntAct interaction count

Lower boundary of HuRI interaction count

Lower boundary of IntAct + HuRI interaction count

Quick Launch

GIPC1_HUMAN, MYO6_HUMAN, SH3B4_HUMAN, LRP2_HUMAN, ARHGAP2_HUMAN, PKHA2_HUMAN, TPBG_HUMAN, LSHR_HUMAN, ITA6_HUMAN, TYRP1_HUMAN, RGS19_HUMAN, ADRB1_HUMAN, LRP1_HUMAN, ITA5_HUMAN, KIF1B_HUMAN, GTR1_HUMAN, ACTN1_HUMAN, C1QR1_HUMAN, CAR10_HUMAN, LPAR1_HUMAN, NRP1_HUMAN, SDC4_HUMAN, DDIT3_HUMAN, BMI1_HUMAN, VE6_HP18, GEM14_HUMAN, NUP93_HUMAN, MCM7_HUMAN, SYMC_HUMAN, MMS19_HUMAN, TAGL_HUMAN, PDXD1_HUMAN, MYO1C_HUMAN, DRD3_HUMAN, LRP8_HUMAN, NTRK1_HUMAN, NTRK2_HUMAN, GSK3B_HUMAN, ZN408_HUMAN, GIPC2_HUMAN, SEM4C_HUMAN, DP13B_HUMAN, DP13A_HUMAN, DOCK9_HUMAN, LPAR2_HUMAN, ESR1_HUMAN, NCAP_SARS2, RHOB_HUMAN, PRKN_HUMAN, TGBR3_HUMAN, CDV3_HUMAN, HECW2_HUMAN, GGA1_HUMAN, GNAS3_HUMAN, OGT1_HUMAN, FCL_HUMAN, EWS_HUMAN, CADH1_HUMAN, TRI25_HUMAN, BRCA1_HUMAN, LZTS2_HUMAN, GULP1_HUMAN, S1L3_HUMAN, FHI1A_HUMAN, STRN3_HUMAN, FMNL3_HUMAN, TM1L2_HUMAN, TOLIP_HUMAN, TRIP6_HUMAN, STRN4_HUMAN, PHOCN_HUMAN, STRN_HUMAN, FRMD6_HUMAN, TOM1_HUMAN, FBP1L_HUMAN, AT2B4_HUMAN, ESR2_HUMAN, RNF41_HUMAN, BID_HUMAN, RFIP5_HUMAN, CYLD_HUMAN, PKHA4_HUMAN, KIF14_HUMAN, PKHG5_MOUSE, PKHG6_HUMAN, HNRH1_HUMAN, BioID_4383950, NUPR1_HUMAN, BRD4_HUMAN, RIGI_HUMAN, PROF1_HUMAN, RAB5A_HUMAN, TRI37_HUMAN, GIPC3_HUMAN, MGME1_HUMAN, KLH13_HUMAN, KLHL9_HUMAN, NBR1_HUMAN, SNX27_HUMAN, MYCN_HUMAN, MYC_HUMAN, EFNMT_HUMAN, YTHD2_HUMAN, OVOL2_HUMAN, BAP1_HUMAN, GATA4_HUMAN, HSP7C_HUMAN, BCR_HUMAN, KPCA_HUMAN, null, NOC2L_HUMAN, SSRD_HUMAN, COPB2_HUMAN, SYC_FRATT, A0A3G5L7D7, A0A380PGB4, A0A2U2H0M0, ALR_YERPE, PTBP3_HUMAN, NS1_I34A1, NS1_I59A0, Q2PJP0, Q6DP93, PKHA7_HUMAN, Q3KR16-1, Q66T02-1, Q9NZN5-1, P0C6X7-PRO_0000037319, CADH1_CANLF

Quick launch button:

Click to send current list to SLiMAn.
Alternatively, copy-paste the list in the SLiMAn input section

List of proteins interacting with query. Partners are sorted according to the total number of interactions found in BioGRID, IntAct and HuRI.

Note: The first protein in the list is the query.

SLiMAN – Webserver results

<https://sliman2.cbs.cnrs.fr>

[Webserver results](#)

[Documentation](#)

[Contacts](#)

[Cite us](#)

SLiMAN Open-Access results

Study Name	Entries	Date	Version	Mode
QL_PPI_PGAM5_HUMAN_B1_L0_H0_IU1_I0_U0	237	2023-12-18 09h25	2.6.08022023	Read - Write
QL_PPI_CRK_HUMAN_B1_L1_H0_IU1_I0_U0	37	2023-11-27 14h20	2.6.08022023	Read - Write
QL_PPI_CSK_HUMAN_B1_L0_H0_IU1_I0_U0	69	2023-11-27 13h47	2.6.08022023	Read - Write
QL_PPI_AIEM1_HUMAN_B2_L0_H1_IU2_I0_U0	53	2023-11-27	2.6.08022023	Read - Write

This page contains a list of open-access SLiMAN projects sorted by dates. It allows users to retrieve their runs or visualize runs performed by other scientists.

Note: Project initialized from the 'PPI Extension' meta-interactomes (starting by QL_PPI) are always open-access as we consider that the corresponding data is not sensible and already accessible elsewhere.

How to cite SLiMAN

Reys V., Pons J.-L., and Labesse G. **SLiMAN2: meaningful navigation through peptide-protein interaction networks.** *Nucleic Acids Research webserver issue* (2024) (in preparation)

Reys V. and Labesse G. **SLiMAN: an integrative web server for exploring short linear motif-mediated interactions in interactomes.** *Journal of Proteomic Research* (2022)
doi: 10.1021/acs.jproteome.1c00964

Questions ? Remarks ?

If you have any remarks or questions related to the use of SLiMAn, please reach us at:

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