

Schilling, auf dem Keller, and Overall (2011):

Subsite Mapping of Factor Xa Using Proteome-Derived Peptide Libraries.

Short instructions for WebPICS

WebPICS is hosted at <http://clipserve.clip.ubc.ca/pics/>

The screenshot shows the WebPICS web application interface. At the top, there is a navigation bar with the title "CLIP-PICS" and the logo for "THE OVERALL LAB". Below the navigation bar, there are four tabs: "ABOUT", "MANUAL", "ANALYSIS", and "RESULTS". The main content area contains a form for submitting peptide sequences and analysis parameters. Five numbered callouts are overlaid on the form:

1. Paste prime-side sequences
2. Name test protease
3. Select digestion protease
4. Select proteome source
5. Start data analysis

The form includes a text area for pasting peptide sequences, a text input for the protease name (set to "Factor_Xa"), radio buttons for selecting the digestion protease (Chymotrypsin is selected), radio buttons for selecting the proteome source (Human cell culture is selected), radio buttons for subsite cooperativity analysis (No is selected), and a text input for the minimum difference in percentage points (set to 10). A "Press" button is used to start the analysis. A warning message at the bottom states: "PROCESSING WILL TAKE SEVERAL MINUTES. PLEASE SUBMIT ONLY ONCE! There is no progress bar - the result page will load as soon as results are available".

CLIP-PICS



ABOUT

MANUAL

ANALYSIS

RESULTS

Your file **Interact.pep.xls** was uploaded. Thank you!
Test protease: Factor_Xa
Digestion protease: C
Origin of proteome: Human
Directory for analysis: 25235206
90 total entries, 89 unique entries
1

[Click here for your PICS results](#)

6. Wait for this website and follow link for results.

[Results \(including html files\) in one compressed file for local use.](#)

(tar file can be opened with most de-compressing applications. Renaming of folder is possible and does not interfere with html files.)

The links do not work? The result file is missing?
Please check the following:

- Did you upload a properly formatted list of peptides?
- Did you select an enzyme and a proteome source?
- Name of test protease without blank spaces?

CLIP-PICS



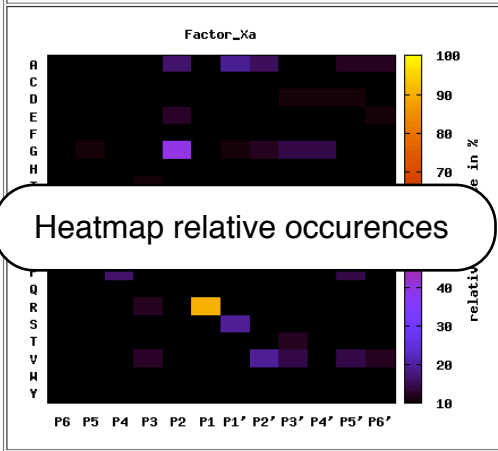
ABOUT **MANUAL** **A**

Further options:
 dependency analysis
 sequence logos
 redraw heatmaps

dependency analysis cleavage sites for logos redraw heatmaps

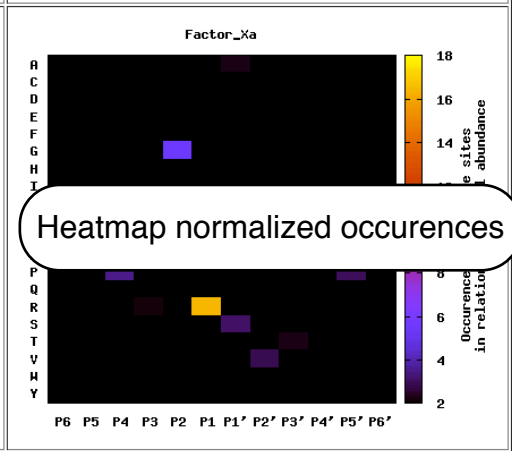
PICS analysis of protease: Factor_Xa
 87 cleavage sites analyzed (total was 90)
 PICS library made with (T)rypsin, (G)luC or (C)hymotrypsin: C

Positional occurrences
Values > 10 % are shown
 (table for [total](#) and [relative \(in %\)](#) values)



Heatmap relative occurrences

Occurrences relative to natural abundance
Values > 2 fold natural abundance are shown
 ([table](#))



Heatmap normalized occurrences

[Results \(including this html file\) in one compressed file for local use.](#)

Total occurrences ([open csv](#))

	P6	P5	P4	P3	P2	P1	P1prime	P2prime	P3prime	P4prime	P5prime	P6prime
A	1	1	2	2	14	0	16	13	7	8	10	10
G	8	9	2	4	34	0	9	10	12	12	6	4

Tables displaying total, relative, and normalized occurrences