

# EXPLORING SHORT LINEAR MOTIFS IN PATHOGENS

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## PART 1: USING JALVIEW WITH Tir PROTEIN ISOLATES FROM PATHOGENIC *E. COLI*

Tir proteins are secreted by pathogenic *E. coli*. They attach to targeted mammalian cells and both the N- and C- termini enter through the membrane, taking over the local cell regulation and, with other inserted proteins, induce the actin pedestal. The central portion of Tir remains extracellular and is bound by the bacterium. Many Tir isolates have been sequenced and are in Uniprot. Load by cut and paste this [already aligned set of Tir proteins](#) into Jalview.

Cyclin box motif - `(.[([KRH].{0,3}))[^EDWNSG][^D][RK][^D]L.{0,1}[FLMP].{0,3}[EDST]`

Long CDK site motif - `...([ST])P..[RK]`

Use the motifs above to find the Cyclin and CDK motif entries and use the regular expressions to create new features in all sequences.

- Do all sequences have both motifs?
- Are they all alignable, or can they move around?

Note that as far as we know in creating this exercise, these motifs have not been studied, but there is some evidence that cell cycle is disrupted by pathogenic *E. coli* (e.g. [PMID: 11598051](#)).

Now put an SH2-binding motif `Y..[IVLM]` regular expression into the alignment and make new features

- Do the sequences have matches to SH2 motifs?
- Do you think the Tir proteins are phosphorylated by Tyrosine Kinases?

Proteins that are natively disordered, and contain linear motifs to control cell regulation, are known to be secreted by pathogens into the cells that they take over.

Now find the PRMT1 Arginine methylase motif **GGRGG** - Do you think Tir is a substrate?

Now find the **NPY** motif which binds the I-BAR domain and is essential for pedestal formation. This motif is well described in bacteria but not yet in a human host cell protein (PMID:21893288).

Tir has a lot of known motifs that interact with host proteins. However there is still a lot of conserved sequence, suggesting that Tir will make more interactions than have yet been described.

## PART 2: USING JALVIEW WITH CagA PROTEIN ISOLATES FROM PATHOGENIC *Helicobacter*

CagA effector proteins are secreted by pathogenic *Helicobacter* directly into the cytosol. These large proteins modulate the actin cytoskeleton and the overall status of the cell. Load by cut and paste the [already aligned set of CagA proteins](#) in Jalview. The EPIYA motif regular expression from ELM is **EP[IL]Y[TAG]** – use it to search the alignment, making a new feature.

- Do the sequences have one EPIYA motif or do they have more?
- Do they all have the same number?
- What is the most EPIYA motifs in one protein?
- Do any of the EPIYA motifs match to typical Y..[IVLM] SH2 motifs?
- Do you think the CagA proteins are phosphorylated by Tyrosine Kinases?

## PART 3:

### A. SEARCHING ELM (<http://elm.eu.org>) FOR BACTERIAL EFFECTOR PROTEINS

ELM contains information for Eukaryotic Linear Motifs although we do capture non-Eukaryotic motifs in cases where motif mimicry might be involved. To explore the bacterial proteins in ELM, we will use the IDP-rich TarP effector from *Chlamydomonas reinhardtii* for which the natural host is guinea pig (*Cavia porcellus*). The Uniprot accession for this protein is Q824H6\_CHLCV; search ELM using this accession.

- How many motifs you retrieve for the protein?
- TarP is extracellular for the bacterium, think if the default search is enough in this case?
- What should be the correct compartment and taxonomic filter?
- Change the compartment and taxonomic filter accordingly and rerun the ELM search.
- How many VBS motifs you have on the protein and what is their biological relevance for pathogen?

### B. EXPLORING ELM (<http://elm.eu.org>) FOR VIRAL PROTEINS - E1A adenoviral Protein

Adenoviruses are non-enveloped DNA virus. Human adenoviruses are responsible for respiratory diseases, croup, and bronchitis outbreaks and gastroenteritis in children. The adenovirus E1A protein is unique to the Mastadenovirus genus. All members of the Mastadenovirus genus infects mammals. E1A plays a role in viral genome replication by driving entry of quiescent cells into the cell cycle. Stimulation of progression from G1 to S phase allows the virus to efficiently use the cellular DNA replicating machinery to achieve viral genome replication.

1. Search in ELM E1A\_ADE05. Remember to define cellular compartments and taxonomic context.

- a) What can you say about the structure of the protein?
- b) How many annotated instances are?
- c) How many annotated instances belong to cellular targets? How many are related?
- d) How many linear motifs for kinases are annotated and how many are predicted?

2. Search in ELM E1A\_ADE02. Remember to define cellular compartments and taxonomic context.

- a) What can you say about the structure of the protein? Is this different from E1A\_ADE05?
- b) How many annotated instances are? Are those different from E1A\_ADE05?
- c) How many annotated instances belong to cellular targets? How many are related?
- d) How many instances are assigned by homology?
- e) How many linear motifs for kinases are annotated and how many are predicted?

3. If you have to test which kinase phosphorylates E1A, which of all the predictions would you test?

4. Search in ELM E1A\_ADECR.

- a) Which is the taxonomic context?
- b) How many instances are annotated? Why do you think is that?
- c) What can you say about the structure of the protein? What can you say in general about E1A proteins?

#### Useful resources:

1. <http://slim.icr.ac.uk/articles/>
2. <http://slim.ucd.ie/slimsearch/>

#### **PUBLICATIONS**

- *Jalview Version 2—a multiple sequence alignment editor and analysis workbench.*  
Waterhouse AM, Procter JB, Martin DM, Clamp M, Barton GJ. Bioinformatics. 2009 May 1;25(9):1189-91. PMID: 19151095

- *Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega.* Sievers F, Wilm A, Dineen D, Gibson TJ, Karplus K, Li W, Lopez R, McWilliam H, Remmert M, Söding J, Thompson JD, Higgins DG. Mol Syst Biol. 2011 Oct 11;7:539. [PMID: 21988835](#)