

Current Protocols in Bioinformatics

Exploring Short Linear Motifs using the ELM Database and Tools

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Significance Statement

Short linear motifs (SLiMs) are compact, degenerate and often unstructured peptide sequences that function as interaction modules in a protein. They play essential roles in cell signalling, the cell cycle, intracellular trafficking, and disease, and the number of different motifs is believed to be in the order of millions. Yet, despite their abundance and importance, our understanding of which motifs exist and how they function is still limited, as SLiMs have proven difficult to study both experimentally and computationally. The Eukaryotic Linear Motif (ELM) resource is an online database containing over 3000 manually curated SLiM instances from experimental literature, and a pipeline to detect SLiMs in protein sequences. ELM is a valuable resource to the scientific community studying protein function.

Abstract

The Eukaryotic Linear Motif (ELM) resource (elm.eu.org) is dedicated to the characterization and prediction of short linear motifs (SLiMs). SLiMs are compact, degenerate peptide segments found in many proteins and essential to almost all cellular processes. However, despite their abundance, SLiMs remain largely uncharacterized. The ELM database is a collection of manually annotated SLiM instances curated from experimental literature. In this article we illustrate how to browse and search the database for curated SLiM data, and cover the different types of data integrated in the resource. We also cover how to use this resource in order to predict SLiMs in known as well as novel proteins, and how to interpret the results generated by the ELM prediction pipeline. The ELM database is a very rich resource, and in the following protocols we give helpful examples to demonstrate how this knowledge can be used to improve your own research.

Introduction

The activity and function of a protein is tightly regulated by its cellular environment. To interact with their surroundings, proteins use various types of binding modules that each display distinct binding properties

(Wright and Dyson 1999). One prominent type of binding module consists of short linear motifs (SLiMs) (Diella 2008). These compact binding sites are generally located in intrinsically disordered regions (IDR) of the proteome and commonly bind to the surface of a globular domain in a protein (Davey et al. 2012). SLiMs mediate different types of interactions that regulate protein functionality, and hence are important regulators of the dynamic processes involved in cell signalling (Van Roey et al. 2012) (Van Roey et al. 2014). The number of SLiM instances in the human proteome is currently suggested to be over one million (Tompa et al. 2014). Identifying SLiMs and elucidating their functionality is thus an essential step in understanding cell regulation. The Eukaryotic Linear Motif (ELM) resource contributes to this process by providing the necessary tools to researchers working on motifs. It consists of a database and a prediction tool. The database provides a categorised repository of experimentally validated linear motif classes and instances that were manually curated from the literature. The ELM prediction tool in turn relies on annotated data, both from the ELM database and other resources, to accurately analyse sequences for candidate motifs and assist researchers in selecting the most plausible ones for experimental validation and discard likely false positive hits, saving them valuable time and resources (Dinkel et al. 2012). The following protocols will guide users through the different ELM applications, explaining how to browse the curated data available in ELM, how to analyse a protein sequence for putative motifs, and how to interpret these data and avoid common pitfalls in SLiM discovery.

Protocol 1 Exploring the Content of the ELM Database

The core of the ELM database is a repository of manually annotated motif classes and instances. As of January 2017, ELM contains over 260 motif classes and over 3000 experimentally validated and manually curated motif instances. The motif classes and instances have been uploaded by a large group of annotators from around the globe. The complete catalogue of manually curated data can be searched, browsed and explored on the ELM website.

Each motif class describes a SLiM, a short sequence of amino acids with a dedicated function. Since motifs are often degenerate, each motif class is defined by a regular expression, a symbolic representation expressing a complex pattern of letters (or in this case amino acids). For example, the regular expression “[FY].L.P” indicates a peptide sequence with a phenylalanine ‘F’ or a tyrosine ‘Y’ in the first position, followed by any amino acid ‘.’, then a leucine ‘L’, one more arbitrary amino acid ‘.’ and finally a proline ‘P’.

In all cases, the annotator condenses information from the primary and secondary literature into manageable abstracts, accompanies the motif definition with a list of experimental instances, and adds links to external resources for proteins, biological pathways, and diseases. In this protocol we explore the various data types stored in the database, as well as links to external resources.

Necessary Resources

Software & Hardware

A modern browser such as Firefox, Chrome, or Safari. ELM is best viewed on a laptop or desktop computer, although tablets and smartphones will also work.

Database content overview

The Eukaryotic Linear Motif resource for Functional Sites in Proteins

search ELM Database

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Welcome to the Eukaryotic Linear Motif (ELM) resource

This computational biology resource mainly focuses on annotation and detection of eukaryotic linear motifs (ELMs) by providing both a repository of annotated motif data and an exploratory tool for motif prediction. ELMs, or short linear motifs (SLiMs), are compact protein interaction sites composed of short stretches of adjacent amino acids. They are enriched in intrinsically disordered regions of the proteome and provide a wide range of functionality to proteins (Davey, 2011, Van Roey, 2014). They play crucial roles in cell regulation and are also of clinical importance, as aberrant SLiM function has been associated with several diseases and SLiM mimics are often used by pathogens to manipulate their hosts' cellular machinery (Davey, 2011, Uyar, 2014).

ELM Prediction

The [ELM prediction](#) tool scans user-submitted protein sequences for matches to the regular expressions defined in ELM. Distinction is made between matches that correspond to experimentally validated motif instances already curated in the ELM database and matches that correspond to putative motifs based on the sequence. Since SLiMs are short and degenerate, overprediction is likely and many putative SLiMs will be false positives. However, predictive power is improved by using additional filters based on contextual information, including taxonomy, cellular compartment, evolutionary conservation and structural features.

Protein sequence

Enter Uniprot identifier or accession number: (auto-completion)
e.g. [EPN1_HUMAN](#), [P04637](#), [TAU_HUMAN](#), [\[RANDOM\]](#)

Or paste the sequence (Single letter code sequence only or [FASTA format](#)):

▪ **Cell compartment (one or several):** ▪ **Taxonomic Context**

PDB-Structure [1SDZ](#) showing a peptide from ELM class **LIG_BIR_III_3**

- ELM database update
We have added new instances for: **LIG_APCC_ABBA_1**, **LIG_APCC_ABBAvCdc20_2** as well as **DOC_MAPK_HePTP_8**, **DOC_MAPK_MEF2A_6** and **DOC_MAPK_DCC_7**
- ELM Database Update
We have updated several MOD_CDK motifs and added new instances:
MOD_CDK_1 is now: **LIG_BH_BH3_1**, **MOD_CDK_SPxK_1**, and **MOD_CDK_SPK_2**. **MOD_CDK_SPxxK_3** have been added.
- ELM database update
Several new ELM classes and instances have been added:
LIG_BH_BH3_1, **DEG_COP1_1**
- ELM database update
The class **DOC_PP2A_KARD_1** has been replaced by **DOC_PP2A_B56_1**, and new instances have been added.

Figure 1: The homepage of the ELM resource (elm.eu.org). This page provides a brief introduction to the resource, as well as an overview of the latest changes and additions to ELM. Using the box on the bottom, users can also start from the homepage to search for putative SLiMs in a protein sequence of interest.

1. The ELM database is an online web resource. Open a browser and navigate to elm.eu.org to visit the homepage (Figure 1). This page shows a brief explanation of the ELM resource, and a form to search for SLiMs (which we cover in further detail in [Protocol 3](#) and [Protocol 4](#)). The column to the right is continually updated with the latest news about changes and additions to the database.
2. On the ELM homepage click on the menu link **ELM DB** for an overview of the database statistics (Figure 2). This page displays the types and amounts of annotations contained in the database and a few links to external databases. Each line contains at least one link that will take you to the corresponding contents page. For example: Clicking on **ELM classes** will take you to the page

The ELM relational database stores different types of data about experimentally validated SLiMs that are manually curated from the literature. ELM instances are classified by motif type, functional site and ELM class. A functional site contains one to many ELM classes, which are described by a regular expression and list experimentally validated motif instances matching this sequence pattern. All data curated in ELM DB can be searched on the ELM website according to the following categories:

- 262 annotated ELM classes**
- 3,026** experimentally validated **ELM instances** in **197** taxons
- 113 ELM methods** described in **2,975** articles to experimentally validate ELM instances
- 428 solved PDB structures** for curated ELM instances (from [PDB](#))
- 131 globular ELM binding domains** (from [Pfam](#), [SMART](#), and [InterPro](#))
- 1,425 interactions** mediated by curated ELM instances
- 879 regulatory switches** mediated by curated ELM instances (from [Switches.ELM DB](#))
- 784 pathways** from [KEGG](#) involving linear motifs annotated in **832** Sequences
- 242 viral instances** interfering with host cellular processes
- 11 ELM related diseases** annotated as being caused by aberrant motif function
- 2 examples where pathogens abuse** motifs to deregulate host cells

Search ELM Instances and Classes

Please cite: [ELM 2016-data update and new functionality of the eukaryotic linear motif resource. \(PMID: 26615199\)](#)

ELM data can be downloaded & distributed for non-commercial use according to the [ELM Software License Agreement](#)

feedback@elm.eu.org

ELM database update
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ELM database update
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DEG_COP1_1

ELM database update
The class **DOC_PP2A_KARD_1** has been replaced by **DOC_PP2A_B56_1**, and new instances have been added.

ELM database update
Several new ELM classes and instances have been added:
LIG_CSK_EPIYA_1
LIG_Rb_LxCxE_1
DOC_MAPK_JIP1_4
DOC_MAPK_NFAT4_5

ELM database update
Several new ELM classes and instances have been added:

Figure 2: The ELM database statistics overview page shows the most up-to-date database statistics. As of January 2017, ELM has just over 3000 annotated instances in 262 different motif classes but also associated or derived content such as structures of binding domains, mapped pathways and more.

showing all classes annotated in ELM. We will be exploring these content overview pages in this protocol.

Browsing motif classes and annotated instances

- Click on the sub-menu **ELM classes** under **ELM DB** to visit the page listing all of the ELM classes (Figure 3). For each class, the following information is provided: ELM identifier, short description, regular expression, number of instances annotated for each class, and number of structures available. For details on each class, click on the ELM identifier; to get a list of annotated instances for an individual class, click on the number of instances.

Use the search bar at the top of the page to filter for certain motif classes. For example, typing “MAPK” and hitting submit will perform a full-text search on all motif classes in the ELM database containing the term “MAPK”. The green buttons on the left can also be used to filter

Figure 3: The list of all motif classes annotated in the ELM database. Clicking on the highlighted links brings you to the details page for the individual ELM classes page. The search box on top allows entering keywords for a full-text search of the motif classes, while selecting the green buttons on the left allows filtering the list based on motif type. All data in the table can be exported in tsv format (top right).

this table. For example, toggling the “DOC” button will remove all DOC classes from the table (and clicking it again will bring them back). Lastly, the yellow tsv link can be used to export all motif classes as a “tab separated values” file.

4. Search the table for the term DOC_CYCLIN_1 and click on **DOC_CYCLIN_1** in the left column to navigate to the page with details about the DOC_CYCLIN_1 motif class (Figure 4). This page contains a description of the functional site class (a Cyclin recognition site), and a short description of the ELM and its regular expression, as well as a probability score, the taxonomic distribution of the motif and which domain (if any) is responsible for the interaction.

The probability score is the probability that the regular expression represents a random selection of amino acids (similar to an information content score). A lower score indicates that the motif pattern is more difficult to find by chance in a random sequence.

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«DOC_CKS1_1» »DOC_GSK3_Axin_1»

DOC_CYCLIN_1

Accession: ELME000106

Functional site class: Cyclin recognition site

Functional site description: Functional site that interacts with cyclins, and thereby increases the specificity of phosphorylation by cyclin/CDK complexes.

ELM Description: Substrate recognition site that interacts with cyclin and thereby increases phosphorylation by cyclin/cdk complexes. Predicted proteins should have a CDK phosphorylation site ([MOD_CDK_1](#)). Also used by cyclin/cdk inhibitors.

Pattern: [RK].L.{0,1}[FYLIVMP]

Pattern Probability: 0.0053239

Present in taxon: Eukaryota

Interaction Domain: Cyclin_N (PF00134) Cyclin, N-terminal domain (Stoichiometry: 1 : 1)

PDB Structure: [1JSU](#)



■ See 24 Instances for DOC_CYCLIN_1

■ **Abstract**

The cyclin recognition site (alias Cy or RxL motif) is found in a wide range of cyclin/CDK interacting proteins ([Takeda, 2001](#)). The presence of this motif in CDK substrates substantially increases the level of phosphorylation at [(ST)Px[KR] motifs ([MOD_CDK_1](#)). Example proteins are the retinoblastoma protein, E2F 1-3 and p53. CDK phosphorylation mainly occurs in the nucleus but there also is some evidence for cytoplasmic function. For example, the cytoplasmic SRC and TAU proteins are known cyclin/CDK targets. The motif is recognised by a conserved region in the cyclin protein and binds in a similar manner as the p21Kip cyclin inhibitor ([1JSU](#)).

■ **4 selected references:** [Show](#)

■ **5 GO-Terms:** [Show](#)

Figure 4: The motif details page for DOC_CYCLIN_1. This page contains all the manually annotated details for the DOC_CYCLIN_1 motif, as well as the biological background summarized from the scientific literature, including links to the primary literature and to external resources such as Pubmed (NCBI Resource Coordinators 2017), the Gene Ontology (GO) (Gene Ontology Consortium 2017), PDB (Berman et al. 2000) and more.

5. Scroll further down the DOC_CYCLIN_1 page (Figure 4) to view more details about this motif (Figure 5). The “abstract” contains a description of the biological relevance of the motif (for example its involvement in cellular processes and pathways). Click on the **show** button next to the “selected references” header for a list of publications relevant to this motif. Click on **show** next to “GO terms” for a complete list of all Gene Ontology (GO) terms annotated for this motif.
6. Scroll further down the DOC_CYCLIN_1 page to view the “Instances” header (Figure 5) This table contains the list of all annotated instances for this motif in the database. This includes the protein identifier, the start and end positions of the instance, the specific sequence matching the regular expression representing the motif and the “logic” of the instance. The “# Ev.” indicates the number of experimental evidences associated with the annotation. “Organism” indicates the species in which

Abstract

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4 selected references: [+ Show](#)

5 GO-Terms: [+ Show](#)

24 Instances for DOC_CYCLIN_1
(click table headers for sorting; Notes column: =Number of Switches, =Number of Interactions)

Acc., Gene-, Name	Start	End	Subsequence	Logic	#Ev.	Organism	Notes
P04637 TP53 P53_HUMAN	381	385	GQTSRHKKLMEKTEGPDSD	TP	4	Homo sapiens (Human)	1H26
P46527 CDKN1B CDN1B_HUMAN	30	33	EHPKPSACRNLFGPVDHEEL	TP	5	Homo sapiens (Human)	1H27 1JSU
P38936 CDKN1A CDN1A_HUMAN	19	22	NPCGSKACRRLEGPVDSEQL	TP	4	Homo sapiens (Human)	1 1A
P06789 E1 VE1 HPV18	127	130	NSGQQKAKRRLETTSDSGYG	TP	3	Human papillomavirus type 18	1
Q99741 CDC6 CDC6_HUMAN	94	98	HSHTLKG BRLVFDNQLTIKS	TP	2	Homo sapiens (Human)	2CCH 1A
Q14207 NPAT NPAT_HUMAN	1062	1066	AAKPCHR RVLCFDSTTAPVA	TP	1	Homo sapiens (Human)	
P39880 CUX1 CUX1_HUMAN	1301	1305	NYRSRIR RELFIEEIQAGSQ	TP	1	Homo sapiens (Human)	
P38826 ORC6 ORC6_YEAST	178	182	ESPSITR RKLAFAEDEDEDE	TP	1	Saccharomyces cerevisiae (Baker's yeast)	
Q9WTQ5 Akap12 AKA12_MOUSE	501	504	IKVQGSPL KKLFSSSGLKKL	TP	1	Mus musculus (House mouse)	1A
Q00716 E2F3 E2F3_HUMAN	134	138	GGGPPAK RRLIELGESGHQYL	TP	1	Homo sapiens (Human)	
Q14209 E2F2 E2F2_HUMAN	87	91	AGRIPAK RKLDLEGIGRPVV	TP	1	Homo sapiens (Human)	
Q01094 E2F1 E2F1_HUMAN	90	94	LGRPPVK RRLDILETDHOYLA	TP	3	Homo sapiens (Human)	1H24
P50445 rnx	

Figure 5: The second part of the DOC_CYCLIN_1 motif details page shows the motif abstract, selected references, GO terms, and the list of annotated instances.

the protein is found. Lastly the “Notes” column contains links to any “interactions” or “switches” present in the database, as well as links to PDB, if the structure exists in the PDB.

The instance “logic” is an annotation of whether – at the time the entry was prepared – this is a bona-fide instance, or whether it is a non-functional instance. TP (True Positive) indicates the instance is annotated with experimental evidence that show it is functional. FP (False Positive) instances have experimental evidence suggesting function, but are believed to be non-functional, after careful examination by our annotators. TN (True Negative) instances have been experimentally determined to be non-functional, and U (Unknown) instances do not have enough evidence to determine whether it is functional or not. The overwhelming majority of instances in ELM are TP’s.

- Click on the sub-menu **ELM instances** under **ELM DB** to visit the page where you can search and browse the instances annotated in ELM (Figure 6). Note that only the first hundred instances matching the search criteria are shown. The search form can be used to filter results by a full text

Figure 6: The “instances” page is used to search for instances in the ELM database. The search box on top allows entering keywords for a full-text search of the motif instances, while selecting the green buttons on the left allows filtering based on motif type. In addition, instances can be filtered by instance logic or organism. The search results table can be exported in various formats (orange links at the top right).

search, by instance logic, or by organism.

This table can be filtered by motif class using the green toggle filters on the left hand side. Lastly, the yellow buttons at the top of the page can be used to download the instances in the following formats: GFF, PIR, FASTA or TSV.

8. Type “p53_human” in the search box to search for ELM instances in this protein. Find the row for the ELM class DOC_CYCLIN_1 and click on the instance sub-sequence (highlighted in red) to go to the instance details page of this instance (Figure 7). The top part of the page contains details about the instance and the protein it was identified in, as well as a link to the UniProt entry for the protein (UniProt Consortium 2015).
9. Scroll down to the “Instance Evidence” header to view details on the experimental evidence used

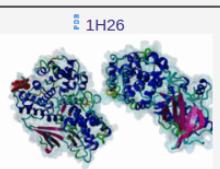
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DOC CYCLIN 1

■ Instance

Accession	Acc. Gene-, Name	Start	End	Subsequence	Logic	PDB	Organism	Length
ELMI000051	P04637 TP53 P53_HUMAN	381	385	GQSTSRH KKLMF KTEGPDSD	TP	 1H26	Homo sapiens (Human)	393

■ Instance evidence

Evidence class	PSMI	Method	BioSource	PubMed	Logic	Reliability	Notes
experimental	MI:0405	competition binding	in vitro	Luciani,2000 [PDF]	support	certain	InteractionDetection
experimental	MI:0074	mutation analysis	in vivo/in vitro	Luciani,2000 [PDF]	support	certain	FeatureDetection
experimental	MI:0065	isothermal titration calorimetry	in vitro	Lowe,2002	support	certain	InteractionDetection
experimental	MI:0114	x-ray crystallography	in vitro	Lowe,2002	support	certain	InteractionDetection FeatureDetection

■ Pathways

The sequence P04637 is implicated in the following 35 Pathways: (color codes: This sequence=red, interacting sequence=orange)

- Amyotrophic lateral sclerosis (ALS)
- Apoptosis
- Basal cell carcinoma
- Bladder cancer
- Cell cycle
- Central carbon metabolism in cancer
- Chronic myeloid leukemia
- Colorectal cancer
- Endometrial cancer
- Epstein Barr virus infection
- Gloma
- HTLV I infection
- Hepatitis B
- Hepatitis C
- Human simplex infection

Figure 7: The instance details page for the DOC_CYCLIN_1 instance annotated for protein P53_HUMAN with start/end position “381–385”. This page also contains links to many external databases including UniProt (UniProt Consortium 2015), PDB (Berman et al. 2002), NCBI taxonomy and Pubmed (NCBI Resource Coordinators 2017), KEGG pathways (Kanehisa et al. 2016), as well as the PSI-MI controlled vocabulary (Kerrien et al. 2007).

to annotate this instance. Each experimental method is annotated using terms from the Proteomics Standards Initiative Molecular Interactions (PSI-MI) ontology (Kerrien et al. 2007), as well as the references in which the experiments were published.

The “biosource” indicates whether method is in vivo, in vitro, in silico or a combination of these. The “logic” column indicates whether this experiment supports or contradicts this instance being functional. Each method is also annotated with a reliability assessment, which can be any of certain, likely, unlikely or unspecified.

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DOC WW Pin1 4

■ Instance

Accession	Acc. Gene-, Name	Start	End	Subsequence	Logic	PDB	Organism	Length
ELMI001957	P04637 TP53 P53_HUMAN	30	35	WKLLPENN VLSPL PSQAMDD	TP	---	Homo sapiens (Human)	393

■ Instance evidence

Evidence class	PSMI	Method	BioSource	PubMed	Logic	Reliability	Notes
experimental	MI:0059	gst pull down	in vivo/in vitro	Wulf,2002 [PDF]	support	certain	InteractionDetection
experimental	MI:0074	mutation analysis	in vivo/in vitro	Wulf,2002 [PDF]	support	certain	FeatureDetection

■ Interactions

Uniprot Id	Domain family	Domain Start	Domain End	Affinity Min/Max (μMol)	Notes
(Q13526) PIN1_HUMAN	PF00397 (WW) WW domain	7	37		[Imtab] [xml]

■ Switches

This ELM instance is part of the following 1 switching mechanism annotated at the switches.ELM resource:

- SWT1000037:

Phosphorylation of S33 in the Pin1-binding motif of Cellular tumor antigen p53 (TP53) induces binding to the Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 (PIN1) protein.

Figure 8: The instance details page for the DOC_WW_PIN1_4 instance found in human p53 (P53_HUMAN) with start/end position “30–35”. For this instance, information is also available about its interaction partner (PIN1_HUMAN) and a phosphorylation-dependant molecular switch that is mediated by this motif instance.

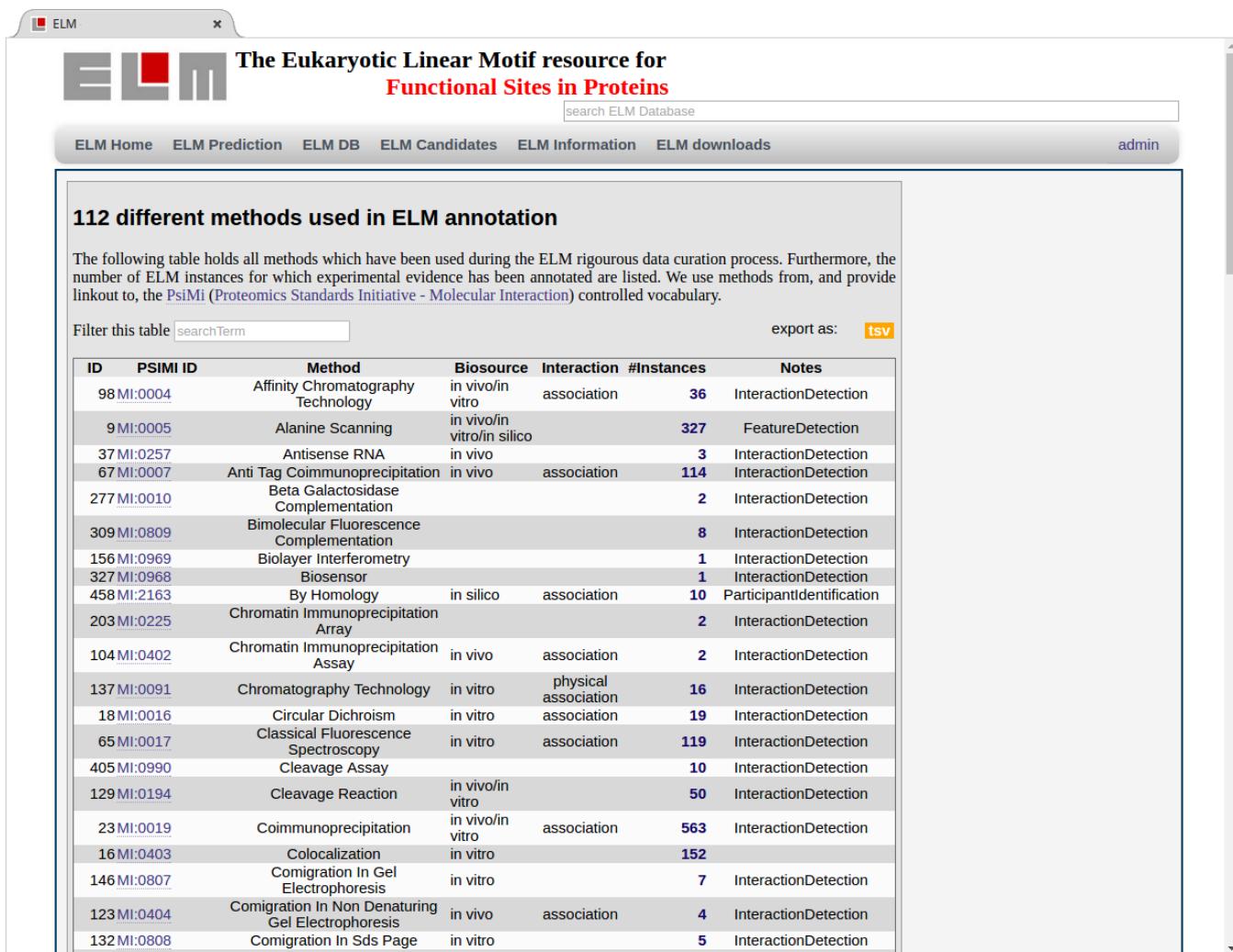
Finding Switches and molecular interactions

- Repeat the previous search by clicking on the sub-menu **ELM instances** under **ELM DB** and type “p53_human” in the search box. This time, find the ELM instance of the motif DOC_WW_PIN1_4 with the start/end position “30–35”. (You can sort the table by clicking on the header lines: click on “Start” to sort by start position). Click on the start/end position or the sub-sequence that will take you to the details page (Figure 8). This page is similar to that described for the p53 instance DOC_CYCLIN_1 (Figure 7). Additionally, for this instance, there is information available about its interaction partner and a molecular switch, which is mediated by this motif instance.
- Scroll down to the “Interactions” header to view information about this instance’s interactions (Figure 8). This instance interacts with PIN1_HUMAN via the “WW” domain (PFAM identifier PF00397;

found on position 7–37 in PIN1_HUMAN. If available, binding affinities are also shown here. Interaction data is made available in *MiTab* and *XML* format (Kerrien et al. 2007), and can be downloaded by clicking on the yellow buttons in the right column.

12. Scroll further down to the “Switches” section for a brief overview of the switches details of this instance obtained from "switches.ELM" (Van Roey et al. 2013) (Figure 8). This particular instance is part of a phosphorylation-dependent molecular switch – only if p53 is phosphorylated on residue serine-33 can it bind to the protein “Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 (PIN1)”. Clicking on the diagram will open an external link to the switches.elm.eu.org website where more detail can be found.

Exploring Links to External Protein Resources



The screenshot shows the ELM (Eukaryotic Linear Motif) website. The main header reads "The Eukaryotic Linear Motif resource for Functional Sites in Proteins". Below the header, there is a search bar labeled "search ELM Database". The navigation menu includes links to "ELM Home", "ELM Prediction", "ELM DB", "ELM Candidates", "ELM Information", "ELM downloads", and "admin".

The main content area displays a table titled "112 different methods used in ELM annotation". The table has columns for "ID", "PSIMI ID", "Method", "Biosource", "Interaction", "#Instances", and "Notes". The table lists various experimental methods such as Affinity Chromatography Technology, Alanine Scanning, Antisense RNA, Anti Tag Coimmunoprecipitation, Beta Galactosidase Complementation, Bimolecular Fluorescence Complementation, Biolayer Interferometry, Biosensor, By Homology, Chromatin Immunoprecipitation Array, Chromatin Immunoprecipitation Assay, Chromatography Technology, Circular Dichroism, Classical Fluorescence Spectroscopy, Cleavage Assay, Cleavage Reaction, Coimmunoprecipitation, Colocalization, Comigration In Gel Electrophoresis, Comigration In Non Denaturing Gel Electrophoresis, and Comigration In Sds Page. The "#Instances" column shows the count of ELM instances annotated with each method, ranging from 1 to 563. The "Notes" column indicates the type of detection, such as InteractionDetection or ParticipantIdentification.

ID	PSIMI ID	Method	Biosource	Interaction	#Instances	Notes
98	MI:0004	Affinity Chromatography Technology	in vivo/in vitro	association	36	InteractionDetection
9	MI:0005	Alanine Scanning	in vivo/in vitro/in silico		327	FeatureDetection
37	MI:0257	Antisense RNA	in vivo		3	InteractionDetection
67	MI:0007	Anti Tag Coimmunoprecipitation	in vivo	association	114	InteractionDetection
277	MI:0010	Beta Galactosidase Complementation			2	InteractionDetection
309	MI:0809	Bimolecular Fluorescence Complementation			8	InteractionDetection
156	MI:0969	Biolayer Interferometry			1	InteractionDetection
327	MI:0968	Biosensor			1	InteractionDetection
458	MI:2163	By Homology	in silico	association	10	ParticipantIdentification
203	MI:0225	Chromatin Immunoprecipitation Array			2	InteractionDetection
104	MI:0402	Chromatin Immunoprecipitation Assay	in vivo	association	2	InteractionDetection
137	MI:0091	Chromatography Technology	in vitro	physical association	16	InteractionDetection
18	MI:0016	Circular Dichroism	in vitro	association	19	InteractionDetection
65	MI:0017	Classical Fluorescence Spectroscopy	in vitro	association	119	InteractionDetection
405	MI:0990	Cleavage Assay			10	InteractionDetection
129	MI:0194	Cleavage Reaction	in vivo/in vitro		50	InteractionDetection
23	MI:0019	Coimmunoprecipitation	in vivo/in vitro	association	563	InteractionDetection
16	MI:0403	Colocalization	in vitro		152	
146	MI:0807	Comigration In Gel Electrophoresis	in vitro		7	InteractionDetection
123	MI:0404	Comigration In Non Denaturing Gel Electrophoresis	in vivo	association	4	InteractionDetection
132	MI:0808	Comigration In Sds Page	in vitro		5	InteractionDetection

Figure 9: The list of all experimental methods used in the ELM database. These methods are annotated as experimental evidence of ELM instances, as can be seen by the number in the “instances” column. For reproducibility, ELM uses the stable external ontology provided by PSI-MI (Kerrien et al. 2007).

13. Click on the sub-menu **ELM methods** under **ELM DB** to see a list of all experimental methods which have been used to identify motifs and instances (Figure 9). This table shows the internal method identifier in the first column, a link to the corresponding entry in the PSI-MI database (Kerrien et al. 2007), and the method name as annotated by the PSI-MI controlled vocabulary, as well as the type of experiment (*in vitro*, *in vivo*, *in silico*, or a combination of these). Clicking on the link in the “instances” column will list all instances annotated using that method.

The filter bar on the top page can be used to filter the list of methods. The TSV link creates a downloadable file in “tab separated values” format.

The screenshot shows the ELM website interface. At the top, there's a navigation bar with links for ELM Home, ELM Prediction, ELM DB, ELM Candidates, ELM Information, ELM downloads, and a user account section. Below the navigation bar, a search bar says "search ELM Database". The main content area has a heading "428 PDBs found:" and a "Filter this table" input field with a "searchTerm" placeholder. To the right of the table, there's a link "Export 428 entries as: tsv". The table itself has four columns: "PDB_ID", "Title", "ELM instance", and "ELM class". Each row contains a PDB ID (e.g., 2FOP, 2FOO, 2G2L, etc.), a brief title/description, the ELM instance identifier (e.g., MDM2_HUMAN, P53_HUMAN, GRIA1_RAT, etc.), and the ELM class (e.g., DOC_USP7_MATH_1, DOC_USP7_MATH_1, LIG_PDZ_Class_1, TRG_AP2beta_CARGO_1, etc.). The table is scrollable, and the bottom right corner shows a small vertical scrollbar.

PDB_ID	Title	ELM instance	ELM class
2FOP	The crystal structure of the n-terminal domain of hausp/usp7 complexed with mdm2 peptide 147-150	MDM2_HUMAN	DOC_USP7_MATH_1
2FOO	The crystal structure of the n-terminal domain of hausp/usp7 complexed with p53 peptide 359-362	P53_HUMAN	DOC_USP7_MATH_1
2G2L	Crystal structure of the second pdz domain of sap97 in complex with a glut-a c-terminal peptide	GRIA1_RAT	LIG_PDZ_Class_1
2G30	Beta appendage of ap2 complexed with arh peptide	ARH_HUMAN	TRG_AP2beta_CARGO_1
2GBQ	Solution nmr structure of the grb2 n-terminal sh3 domain complexed with a ten-residue peptide derived from sos direct refinement against noes, j-couplings, and 1h and 13c chemical shifts, 15 structures	SOS1_MOUSE	LIG_SH3_3
2GPH	Docking motif interactions in the map kinase erk2	PTN7_HUMAN	DOC_MAPK_HePTP_8
2GPO	Estrogen related receptor-gamma ligand binding domain complexed with a synthetic peptide from rip140	NRIP1_HUMAN	LIG_NRBOX
2GTH	Crystal structure of the wildtype mhv coronavirus non-structural protein nsp15	R1AB_CVMA5	LIG_Rb_LxCxE_1
2HE2	Crystal structure of the 3rd pdz domain of human discs large homologue 2, dlg2	AT2B4_HUMAN	LIG_PDZ_Class_1
2HE4	The crystal structure of the second pdz domain of human nherf-2 (slc9a3r2) interacting with a mode 1 pdz binding motif	DHRS2_HUMAN	LIG_PDZ_Class_1
2HGO	Structure of the west nile virus envelope glycoprotein	Q3I0Y8_WNV	MOD_N-GLC_1
2HKQ	Crystal structure of the c-terminal domain of human eb1 in complex with the cap-gly domain of human dynactin-1 (p150-glued)	MARE1_HUMAN	LIG_CAP-Gly_1
2I04	X-ray crystal structure of magi-1 pdz1 bound to the c-terminal peptide of hpv18 e6	VE6 HPV18	LIG_PDZ_Class_1
2I01	X-ray crystal structure of sap97 pdz3 bound to the c-terminal peptide of hpv18 e6	VE6 HPV18	LIG_PDZ_Class_1
2I0L	X-ray crystal structure of sap97 pdz2 bound to the c-terminal peptide of hpv18 e6.	VE6 HPV18	LIG_PDZ_Class_1
2I1N	Crystal structure of the 1st pdz domain of human dig3	AT2B4_HUMAN	LIG_PDZ_Class_1
2I3S	Bub3 complex with bub1 glebs motif	BUB1_YEAST	LIG_GLEBS_BUB3_1
2I3T	Bub3 complex with mad3 (bubr1) glebs motif	MAD3_YEAST	LIG_GLEBS_BUB3_1
2IHS	Crystal structure of the b30.2/spry domain of gustavus in complex with a 20-residue vasa peptide	VASA1_DROME	LIG_SPRY_1
2IVR	Beta appendage in complex with b-arrestin peptide	ARRB1_HUMAN	TRG_AP2beta_CARGO_1

Figure 10: The list of all known PDB structures for which annotated motif instances exist in the ELM database. For each structure, a link to the protein database RCSB (Berman et al. 2002) is provided with a short description as well as the name of the Identifier of the ELM instance / class.

14. Click on the sub-menu **ELM PDB structures** under **ELM DB** to see a list of all macromolecular structures in the ELM database (Figure 10). Structures annotated in ELM ideally (but not always) show both interaction partners (motif and domain). This page also contains links to RCSB/PDB (Berman et al. 2002), the individual instance and the motif class of that instance.

The screenshot shows the ELM (Eukaryotic Linear Motif) website interface. At the top, there is a logo and the title "The Eukaryotic Linear Motif resource for Functional Sites in Proteins". Below the title is a search bar labeled "search ELM Database". A navigation menu includes links for "ELM Home", "ELM Prediction", "ELM DB", "ELM Candidates", "ELM Information", "ELM downloads", and "admin".

The main content area displays a table titled "290 interaction domains annotated in ELM". The table has columns for "ELM identifier", "Interaction Domain Id", "Interaction Domain Name", and "Interaction Domain Description". The table lists various interaction domains, such as Peptidase_M16, Subtilase family, Asparaginase_2, and WD40, along with their corresponding PFAM IDs and brief descriptions.

ELM identifier	Interaction Domain Id	Interaction Domain Name	Interaction Domain Description
CLV_NRD_NRD_1	PF00675	Peptidase_M16	Insulinase (Peptidase family M16)
CLV_PCSK_FUR_1	PF00082	Peptidase_S8	Subtilase family
CLV_PCSK_PC1ET2_1	PF00082	Peptidase_S8	Subtilase family
CLV_PCSK_PCT7_1	PF00082	Peptidase_S8	Subtilase family
CLV_PCSK_SKI1_1	PF00082	Peptidase_S8	Subtilase family
CLV_TASPASE1	PF01112	Asparaginase_2	Asparaginase
old_LIG_14-3-3_1	PF00244	14-3-3	14-3-3 protein
old_LIG_14-3-3_2	PF00244	14-3-3	14-3-3 protein
old_LIG_14-3-3_3	PF00244	14-3-3	14-3-3 protein
LIG_AP_GAE_1	PF02883	Alpha_adaptinC2	Adaptin C-terminal domain
LIG_AP2alpha_1	PF02296	Alpha_adaptin_C	Alpha adaptin AP2, C-terminal domain
LIG_AP2alpha_2	PF02296	Alpha_adaptin_C	Alpha adaptin AP2, C-terminal domain
DEG_APCC_DBOX_1	PF00400	WD40	WD domain, G-beta repeat
DEG_APCC_KENBOX_2	PF00400	WD40	WD domain, G-beta repeat
LIG_BIR_II_1	PF00653	BIR	Inhibitor of Apoptosis domain
LIG_BIR_III_1	PF00653	BIR	Inhibitor of Apoptosis domain
LIG_BIR_III_2	PF00653	BIR	Inhibitor of Apoptosis domain
LIG_BIR_III_3	PF00653	BIR	Inhibitor of Apoptosis domain
LIG_BIR_III_4	PF00653	BIR	Inhibitor of Apoptosis domain
LIG_BRCT_BRCA1_1	PF00533	BRCT	BRCA1 C Terminus (BRCT) domain
LIG_BRCT_BRCA1_2	PF00533	BRCT	BRCA1 C Terminus (BRCT) domain
LIG_BRCT_MDC1_1	PF00533	BRCT	BRCA1 C Terminus (BRCT) domain
LIG_CAP-Gly_1	PF01302	CAP_GLY	CAP-Gly domain
LIG_Clathr_ClatBox_1	PF01394	Clathrin_propel	Clathrin propeller repeat
LIG_Clathr_ClatBox_2	PF01394	Clathrin_propel	Clathrin propeller repeat
DEG_COPI	PF00400	WD40	WD domain, G-beta repeat
LIG_CORNRBOX	PF00104	Hormone_recep	Ligand-binding domain of nuclear hormone receptor
LIG_CtBP_PxDLS_1	PF00389	2-Hacid_dh	D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain
DOC_CYCLIN_1	PF00134	Cyclin_N	Cyclin, N-terminal domain
LIG_Dynamin_DLG_1	PF00000	Domain_light	Domain light chain type 1

Figure 11: This table shows, for each interaction domain, the ELM class, the domain ID, domain name as well as a brief description about the interaction domain. For most ELM classes, an interaction domain is annotated as an interaction partner for the corresponding ELM motif.

15. Click on the sub-menu **ELM binding domains** under **ELM DB** to see a complete list of all the interaction domains in ELM (Figure 11). This table shows the ELM classes that have been annotated with a corresponding interaction domain divided by the ELM class, a link to the PFAM (Finn et al. 2016), SMART (Letunic et al. 2015) or InterPro (Finn et al. 2017) domain, as well as the name of the interacting domain followed by a brief description.
16. Click on the sub-menu **ELM switches** under **ELM DB** to see a complete list of all the molecular switches annotated in ELM (Figure 12). This table shows the motif class, contains a link to UniProt, as well as the start and stop positions of the motif mediating the switch. The last two columns show links to the switches.elm.eu.org website, and a brief description of the switch (taken from the switches.ELM database, see Van Roey et al. (2013)).

The screenshot shows the ELM (Eukaryotic Linear Motif) database interface. At the top, there's a logo and the title "The Eukaryotic Linear Motif resource for Functional Sites in Proteins". Below the title is a search bar labeled "search ELM Database". The main content area is titled "ELM Switches" and contains a table with the following data:

ELM class	Sequence Id	Start/Stop	Switch Id	Description
LIG_SH2_STAT5	P043561	161-164	SWTI000001	Phosphorylation of Y161 in the SH2-binding motif of <i>Linker for activation of T-cells family member 1 (LAT)</i> induces binding to the <i>1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase gamma-1 (PLCG1)</i> protein.
DOC_AGCK_PIF_1	P31749	469-474	SWTI000002	Phosphorylation of S473 in the PIF motif of <i>RAC-alpha serine/threonine-protein kinase (AKT1)</i> by <i>Serine/threonine-protein kinase mTOR (MTOR)</i> (as part of mTORC2 complex) induces intramolecular interaction with the PIF-binding pocket, resulting in crosactivation of <i>RAC-alpha serine/threonine-protein kinase (AKT1)</i> . Dephosphorylation of the PIF motif by PHLPP1/J2 (PHLPP1 for Akt2/3 and PHLPP2 for Akt1/3) results in reduced Akt activity, probably by disrupting the interaction with the Akt PIF pocket and thus crosactivation.
DOC_AGCK_PIF_1	P05771-2	656-661	SWTI000003	Dephosphorylation of the PIF motif by PHLPP1/J2 results in reduced stability and increased degradation of PKC. This is countered by autophosphorylation of the PIF motif, but mTORC2 might also contribute.
DOC_WW_Pin1_4	Q12800	326-331	SWTI000004	Phosphorylation of T329 in the Pin1-binding motif of <i>Alpha-globin transcription factor CP2 (TFCP2)</i> induces binding to <i>Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 (PIN1)</i> , which isomerizes the peptide bonds in the nearby-phosphorylated SP motifs (S291 and S309) to the trans configuration, thereby facilitating their dephosphorylation, which is required for the transcriptional activity of <i>Alpha-globin transcription factor CP2 (TFCP2)</i> .
LIG_PLK	P30307	129-131	SWTI000005	Phosphorylation of T130 in the PLK-docking motif of <i>M-phase inducer phosphatase 3 (CDC25C)</i> by <i>Cyclin-dependent kinase 1 (CDK1)-Cyclin AB subfamily</i> generates a recruitment site for <i>Serine/threonine-protein kinase PLK1 (PLK1)</i> , which then phosphorylates <i>M-phase inducer phosphatase 3 (CDC25C)</i> . This results in inactivation of the NES of <i>M-phase inducer phosphatase 3 (CDC25C)</i> , thereby promoting its nuclear localization.
LIG_PLK	P30305	49-51	SWTI000006	Phosphorylation of S50 in the PLK-docking motif of <i>M-phase inducer phosphatase 2 (CDC25B)</i> by <i>Cyclin-dependent kinase 1 (CDK1)-Cyclin AB subfamily</i> generates a recruitment site for <i>Serine/threonine-protein kinase PLK1 (PLK1)</i> , which then phosphorylates and activates <i>M-phase inducer phosphatase 2 (CDC25B)</i> .
LIG_FHA_1	P64897	19-25	SWTI000007	Phosphorylation of T21 in the FHA-binding motif of <i>Uncharacterized protein Rv1827/MT1875 (Rv1827)</i> by <i>Probable serine/threonine-protein kinase pknG (pknG)</i> results in auto-inhibition due to an intramolecular interaction with the FHA domain. As a result, phosphorylation-independent interactions of the FHA domain with metabolic enzymes, which regulate the catalytic activity of these enzymes, are blocked (See also switch details).
LIG_14-3-3_3	P30307	213-218	SWTI000008	Phosphorylation of S216 in a 14-3-3-binding motif of <i>M-phase inducer phosphatase 3 (CDC25C)</i> by <i>Serine/threonine-protein kinase Chk1 (CHEK1)</i> induces binding to <i>14-3-3 protein beta/alpha (YWHAB)</i> , which negatively regulates <i>M-phase inducer phosphatase 3 (CDC25C)</i> .

Figure 12: A list of all molecular switches that are based on instances from ELM and which are annotated at the switches.elm.eu.org database. For each switch the ELM class, ELM instance ID, instance motif start position, Switch ID as well as a brief description of the molecular switching mechanism is provided.

Visualizing KEGG pathways from ELM

17. Click on the sub-menu **ELM pathways** under **ELM DB** to see a list of all KEGG pathways contained in ELM (Figure 13). Pathways are taken from and mapped onto the “Kyoto Encyclopedia of Genes and Genomes” (KEGG (Kanehisa et al. 2016)).
18. On the “ELM pathways” page (Figure 14) click on the link **Gallus gallus** to navigate to the page containing all pathways annotated for chicken.
19. On the page with pathways annotated for chicken (Figure 14), click on **Adherens junction** to the KEGG entry for this pathway, with each protein’s color corresponding to ELM classes (see the color legend in the caption of Figure 15).

The screenshot shows the ELM (Eukaryotic Linear Motif) website. At the top, there is a navigation bar with links to "ELM Home", "ELM Prediction", "ELM DB", "ELM Candidates", "ELM Information", "ELM downloads", and "admin". The main content area has a title "Pathways linked from ELM instances". Below the title, a text box says "The following list contains taxons for which sequences at ELM have been mapped to pathways annotated at the "Kyoto Encyclopedia of Genes and Genomes" (KEGG) database." A search bar with placeholder text "Please select a taxon or enter any search term:" and a "submit" button are present. A list of organisms follows:

- [Arabidopsis thaliana](#) (4)
- [Ashbya gossypii ATCC 10895](#) (1)
- [Bos taurus](#) (65)
- [Caenorhabditis elegans](#) (5)
- [Candida albicans SC5314](#) (1)
- [Canis lupus familiaris](#) (3)
- [Danio rerio](#) (6)
- [Drosophila melanogaster](#) (12)
- [Equus caballus](#) (2)
- [Gallus gallus](#) (16)
- [Homo sapiens](#) (231)
- [Mus musculus](#) (167)
- [Oryctolagus cuniculus](#) (29)
- [Plasmodium falciparum](#) 3D7 (1)
- [Rattus norvegicus](#) (139)
- [Saccharomyces cerevisiae](#) (26)
- [Saccharomyces cerevisiae S288c](#) (10)
- [Schizosaccharomyces pombe](#) (11)
- [Schizosaccharomyces pombe](#) 972h- (6)
- [Solanum lycopersicum](#) (1)
- [Strongylocentrotus purpuratus](#) (1)
- [Sus scrofa](#) (30)
- [Vibrio cholerae](#) (2)
- [Xenopus laevis](#) (23)
- [ALL](#) (792)

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feedback@elm.eu.org

Figure 13: A list of organisms for which pathways from KEGG have been mapped to protein sequences of instances in ELM. The number in brackets denotes the number of different pathways per organism. The search box at the top can be used to query pathways for arbitrary keywords (eg. to see a certain pathway in multiple organisms).

Browsing Infections and Diseases

20. Click on the sub-menu **ELM virus instances** under **ELM DB** to see a list of all instances in ELM that have been annotated as being abused by viruses (Figure 16). (The columns are identical to those listed in step 7, see Figure 6).

The green buttons on the left can be used to filter this table by motif type. Click on the yellow links on the top right of the page to download the (complete) table in GFF, PIR, FASTA or TSV format.

21. Click on the sub-menu **ELM diseases** under **ELM DB** to see a list of diseases that are mediated by short linear motifs accompanied by a short description of the disease as well as the role of the motif (Figure 17). Disease information is taken from the “Online Mendelian Inheritance in Man” (OMIM) database (McKusick 2007).

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search ELM Database

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Pathways linked from ELM instances

The following list contains those pathways annotated at the "Kyoto Encyclopedia of Genes and Genomes" (KEGG) database for which at least one sequence is stored in the ELM database (containing at least one ELM instance). Sequences have been mapped from Uniprot to KEGG and colored in the pathway according to a simple colorscheme.

TAXON	Pathway entry	Pathway name	# Instances	# Sequences
	gga04520	Adherens junction	2	2
	gga04144	Endocytosis	2	2
	gga04012	ErbB signaling pathway	4	2
	gga04510	Focal adhesion	9	6
	gga04540	Gap junction	1	1
	gga04912	GnRH signaling pathway	4	2
	gga05168	Herpes simplex infection	3	1
	gga05164	Influenza A	3	1
	gga04010	MAPK signaling pathway	3	1
	gga04810	Regulation of actin cytoskeleton	5	4
	gga05132	Salmonella infection	3	1
	gga04530	Tight junction	1	1
	gga04620	Toll like receptor signaling pathway	3	1
	gga04270	Vascular smooth muscle contraction	2	1
	gga04370	VEGF signaling pathway	2	2
	gga04310	Wnt signaling pathway	4	2

Links redirect to the KEGG database with a color overlay corresponding to ELM classes.

Coloring is as follows:
 CLV (cleavage site)
 DOC (docking site)
 DEG (degradation motif)
 LIG (ligand binding motif)
 MOD (modification site)
 TRG (targeting motif)
 multiple classes per sequence

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Figure 14: A list of all KEGG pathways for the taxon *Gallus gallus* involving proteins annotated in ELM. Note that multiple instances from a single sequence can be annotated for one pathway. The color scheme on the right is used for coloring instances on the KEGG website (see Figure 15).

Finding Help and Frequently Asked Questions

- Click on the **Help** button on the right of the top navigation menu to visit the ELM Help page. This page has answers to the most frequently asked questions, which you can see by clicking on a particular question. For example: Click on “Regular expressions” for a detailed description of the symbols used the regular expressions that define motif classes.

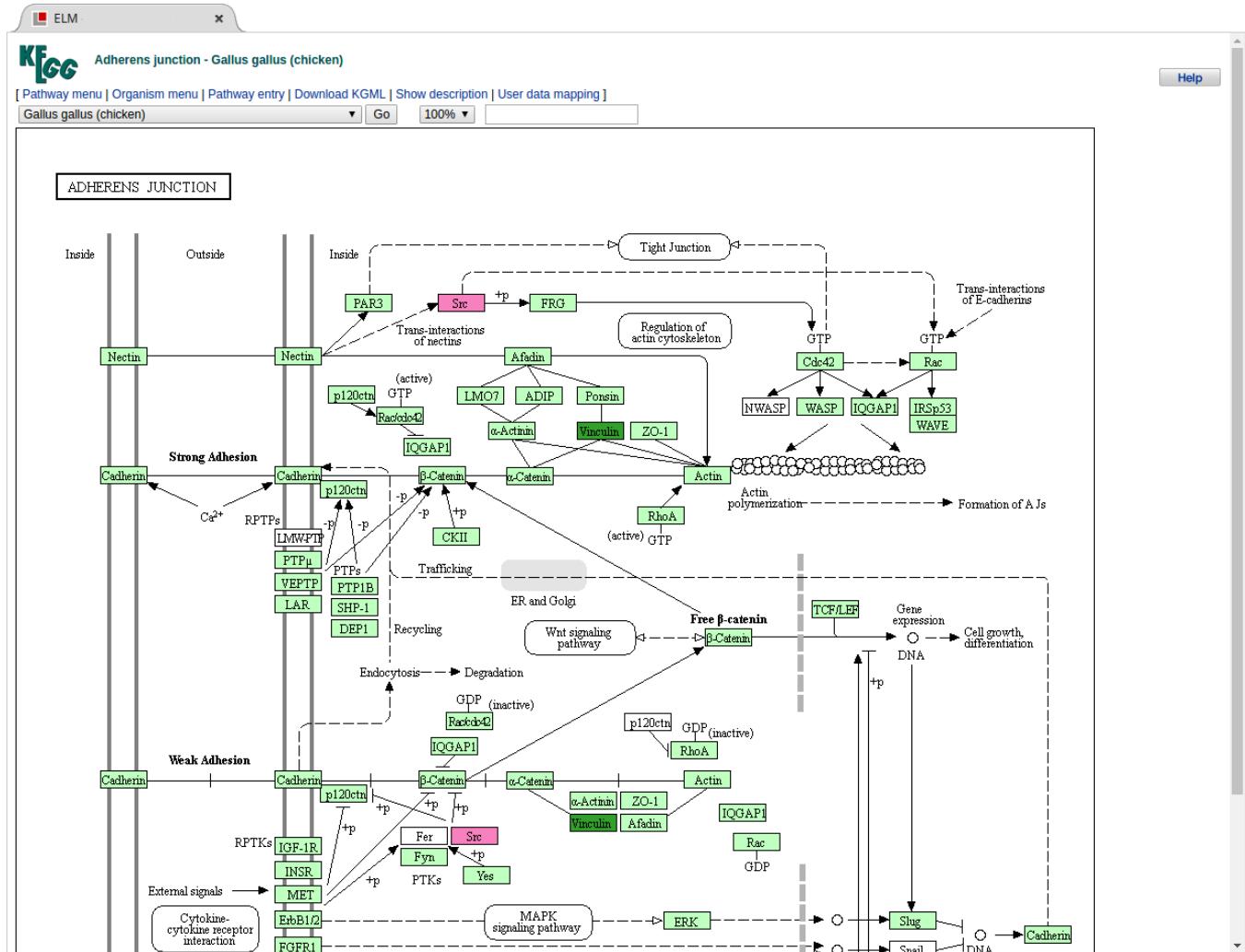


Figure 15: An overlay of ELM annotations of proteins in the “Adherens junction” pathway in *Gallus gallus*. The coloring of proteins is as follows: light blue=CLV (cleavage site), dark blue=DOC (docking site), yellow=DEG (degradation motif), green=LIG (ligand binding motif), pink=MOD (modification site), orange=TRG (targeting motif), red=multiple classes per sequence. Light green boxes are colored by KEGG if a homolog of the protein is present in the selected genome, and represent the KEGG hyperlinks to GENES entries (see KEGG help http://www.kegg.jp/kegg/document/help_pathway.html).

The Eukaryotic Linear Motif resource for
Functional Sites in Proteins

search ELM Database

ELM Home ELM Prediction ELM DB ELM Candidates ELM Information ELM downloads admin

Browse Viral ELM Instances

export 242 instances as: gff | pir | fasta | tsv

(click table headers for sorting; Notes column: =Number of Switches, =Number of Interactions)

CLV	DEG	DOC	LIG	MOD	TRG	ELM identifier	Acc., Gene-, Name	Start	End	Subsequence	Logic	#Ev.	Organism	Notes
						CLV_PCSK_FUR_1	P056861 env ENV_FFV	124	128	GNTSSSSRRRDIYHKLPV	TP	4	Feline foamy virus	1
						CLV_PCSK_FUR_1	P03383 env ENV_HTLV2	305	309	PVPPPATRRRAVPIAVNLV	TP	3	Human T-lymphotro...	1
						CLV_PCSK_FUR_1	P03375 env ENV_HV1B1	508	512	AKRRVVOREKRAVGIGALFL	TP	3	Human immunodefici...	1
						CLV_PCSK_FUR_1	P03420 F FUS_HRSVA	133	137	NVTLSKKRKRFLGFLGVG	TP	3	Human respiratory...	1
						CLV_PCSK_FUR_1	P03188 gB GB_EBVB9	429	433	TPAAVLRRRRDAGNATTPV	TP	1	Human herpesvirus... (Epstein-Barr virus (strain B95-8))	
						CLV_PCSK_FUR_1	P27909 POLG_DEN1B	202	206	SQTGEHRDKRSVALAPHVG	TP	3	Dengue virus 1 Br...	1
						CLV_PCSK_FUR_1	P11223 S SPIKE_IBVB	534	538	KITNGTRRFRRSITENVANC	TP	2	Avian infectious ...	
						CLV_PCSK_FUR_1	P11223 S SPIKE_IBVB	687	691	LLTNPSSRRKRSLIEDLLFT	TP	2	Avian infectious ...	
						CLV_PCSK_FUR_1	Q05320 GP VGP_EBOZM	498	502	GLITGGRRTTREAINVNAQPK	TP	4	Ebola virus - May...	1
						CLV_PCSK_FUR_1	P03107 L2 VL2 HPV16	9	13	RHKRSAKRTKRSATQLYKT	TP	1	Human papillomavi...	1
						CLV_PCSK_FUR_1	P60170 GP VSGP_EBOZM	321	325	EPKTSVVVRVRELLPTQQPT	TP	3	Ebola virus - May...	
						DEG_APCC_KENBOX_2	P03116 E1 VE1_BPV1	27	31	TEAACESDKNEEPPGAGVEL	TP	1	Bovine papillomav...	
						DEG_SCF_FBW7_2	P03070 Large T antigen LT_SV40	699	705	ICRGFTCFKKPTPPPEPET	TP	3	Simian virus 40	1

Figure 16: Table of ELM instances annotated in viral proteins. The high number of instances annotated for a wide range of viruses is an indication of how often viruses abuse existing host cellular machinery by expressing short linear motifs.

The Eukaryotic Linear Motif resource for Functional Sites in Proteins

search ELM Database

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Diseases mediated by short linear motifs

Several diseases are known which are caused by one or more mutations in linear motifs mediating important interactions. Below you find a selection of such diseases; for linear motifs abused by viruses, see the the dedicated [Viruses](#) page. For a large-scale analysis on disease-causing mutations see [\[Proteome-wide analysis of human disease mutations in short linear motifs: neglected players in cancer? Uyar B, et al., 2014\]](#)

DISCLAIMER: Some disease descriptions were adapted from the "Online Mendelian Inheritance in Man - An Online Catalog of Human Genes and Genetic Disorders" [OMIM](#).

Noonan-like Syndrome [OMIM:607721]

A S>G mutation at position 2 creates a novel [MOD_NMyristoyl](#) site (irreversible modification) resulting in aberrant targeting of SHOC2 to the plasma membrane and impaired translocation to the nucleus upon growth factor stimulation [[Cordeau et al., 2007](#)].

Familial Hypomagnesemia With Hypercalciuria and Nephrocalcinosis (FHHN) [OMIM:248250]

An autosomal recessive wasting disorder of renal Mg²⁺ and Ca²⁺ that leads to progressive kidney failure. Here, motifs mediating interaction to PDZ domains are mutated in [Claudin 16](#), abolishing important interactions to the scaffolding protein [ZO-1](#) resulting in lysosomal mislocalization of the protein [[Müller et al., 2003](#), [Müller et al., 2006](#)].

Golabi-Ito-Hall Syndrome [OMIM:309500]

This syndrome is caused by a missense mutation in the PQBP1 gene exchanging a Tyrosine into Cysteine in the WW interaction domain of [PQBP1_HUMAN](#) [[Lubs et al., 2006](#), [Tapia et al., 2010](#)].

IMAGe Syndrome [OMIM:614732]

IMAGe syndrome is a rare multisystem disorder characterized by intrauterine growth restriction, metaphyseal dysplasia, congenital adrenal hypoplasia, and genital anomalies [[Vilain, E. et al. 1999](#)]. The disease locus was mapped to missense mutations in the carboxy terminus of the "Cyclin-dependent kinase inhibitor 1C" protein [CDKN1C_HUMAN](#) [[Arboleda et al. 2012](#)]. This protein plays a key role in the inhibition of cell-cycle progression and is therefore tightly regulated and repressed in most tissues. It contains a [CRL4-Cdt2 binding PIP degron](#) annotated at position [270](#) which is recognized by the CRL4^{Cdt2} ubiquitin ligase in a PCNA-dependent manner. Mutations in this motif result in excess inhibition of growth and differentiation.

- Diseases mediated by short linear motifs
- Pathogens abusing linear motifs

Figure 17: A list of diseases that are mediated by short linear motifs. Disease description has been adapted from the “Online Mendelian Inheritance in Man“ (OMIM) database ([McKusick 2007](#)) and enriched with information about the role of the motif.

The screenshot shows the ELM Help page. At the top, there is a navigation bar with links to ELM Home, ELM Prediction, ELM DB, ELM Candidates, ELM Information, ELM downloads, and an admin link. Below the navigation bar, the main content area has a title "ELM Help page" and a section titled "Questions and answers". This section contains a list of questions, each preceded by a red square icon:

- What methods are used for detecting functional sites?
- Why are the ELM predictions not scored?
- What does the ELM instance mapper do?
- Why is the context of a functional site important?
- What are the currently implemented context filters?
- Is there a nomenclature for representing functional site motifs?
- How can the ELM DB be accessed programmatically?
- Regular expressions
- Why use Regular Expressions in ELM?

Below this list, there is a note about citation and software license information. To the right of the main content area, there is a sidebar titled "Dictionary" which lists several terms with their definitions:

- Biochemical context**: For [functional sites](#), the biochemical context has several components: the sequence motif, its relation to the local structure and other domains in the protein as well as the protein complex it may reside in.
- Cellular context**: Where and when in the cell a site is functional.
- Context**: The space and time where a [molecular function](#) takes place.
- ELM**: 1. Eukaryotic Linear Motif, 2. The common pattern of a set of linear (sub)sequences that can be related to a [molecular function](#).
- ELM instance**: An experimentally verified instance of an [ELM](#) in a particular polypeptide.
- ELM instance sequence**: A protein sequence carrying one or more experimentally verified [ELM instances](#)
- Filter**: Method for discriminating between likely positive and negative ELM predictions; based on context information.
- Functional site**: A set of short linear (sub)sequences that can be

Figure 18: The ELM “Help” and “Questions & Answers” page also showing a dictionary of most commonly used acronyms. Users are encouraged to contact the authors via email if their questions regarding the ELM database cannot be answered by this page.

Protocol 2 Exploring the Content of the ELM Database Using the General Search

A general search text box is available to query the entire collection of manually curated information in the ELM database. This search field can be found in the header of the ELM database website (see for example Fig. 21). This search performs a full-text query across multiple selected data sources in the ELM database, including ELM classes, instances, candidates, and switches. Using this general search is helpful to get information about a particular protein and its annotation status in the ELM database (eg. full instance vs. candidate).

Necessary Resources

Software & Hardware

A modern browser such as Firefox, Chrome, or Safari. ELM is best viewed on a laptop or desktop computer, although tablets and smartphones will also work.

Using the General Search

1. Use the general search field (on the top of the page) to do a general search for p53 using its UniProt identifier by typing “P04637” in the search field and hitting “Enter”. This will perform a query across multiple tables of the ELM database to find any matches to the search query “P04637”. In this case, the results are grouped into matching instances (Figure 19), candidate classes and switches (Figure 20). As there are no classes with “P04637” in the name or description, no classes are returned for this section of the query.

The “candidate classes” are a collection of putative future ELM classes, which are not yet fully annotated, often submitted by ELM users. Keep in mind that these are first drafts of ELM classes and are still pending curation.

2. Perform a search using the keyword “p53” in the general search field instead of its UniProt identifier “P04637”. The set of results retrieved using this term as the search query (Figure 21) are different, returning 31 instances and 44 switches (instead of 14 and 11). The reason for this is that the phrase “p53” also matches the UniProt identifier of CDH1_YEAST (P53197)! This is probably not what you had in mind when using this search term, so it is important to keep in mind to check for such false positive search results, when searching the database.

The Eukaryotic Linear Motif resource for Functional Sites in Proteins

Search ELM Database

ELM Home ELM Prediction ELM DB ELM Candidates ELM Information ELM downloads admin

Your search for p04637 resulted in 0 ELM classes, 14 ELM Instances, 0 ELM candidate classes, and 11 ELM Switches:

ELM instances

Identifier	Sequence	Start	Stop	Logic	Taxon	Info
DEG_MDM2_SWIB_1	P04637 TP53 P53_HUMAN	19	26	TP	Homo sapiens (Human)	1YCR
DOC_CYCLIN_1	P04637 TP53 P53_HUMAN	381	385	TP	Homo sapiens (Human)	1H26
DOC_USP7_MATH_1	P04637 TP53 P53_HUMAN	359	363	TP	Homo sapiens (Human)	2F1X 2FOO
DOC_USP7_MATH_1	P04637 TP53 P53_HUMAN	364	368	TP	Homo sapiens (Human)	2FOJ
DOC_WW_Pin1_4	P04637 TP53 P53_HUMAN	78	83	TP	Homo sapiens (Human)	1
DOC_WW_Pin1_4	P04637 TP53 P53_HUMAN	312	317	TP	Homo sapiens (Human)	1
DOC_WW_Pin1_4	P04637 TP53 P53_HUMAN	30	35	TP	Homo sapiens (Human)	1
MOD_CDK_SPxxK_3	P04637 TP53 P53_HUMAN	315	319	TP	Homo sapiens (Human)	
MOD_CK1_1	P04637 TP53 P53_HUMAN	15	21	TP	Homo sapiens (Human)	
MOD_GSK3_1	P04637 TP53 P53_HUMAN	30	37	TP	Homo sapiens (Human)	1
MOD_PIKK_1	P04637 TP53 P53_HUMAN	12	18	TP	Homo sapiens (Human)	
MOD_SUMO_for_1	P04637 TP53 P53_HUMAN	385	388	TP	Homo sapiens (Human)	
TRG_NES_CRM1_1	P04637 TP53 P53_HUMAN	339	352	TP	Homo sapiens (Human)	1
TRG-NLS_Bipartite_1	P04637 TP53 P53_HUMAN	305	323	TP	Homo sapiens (Human)	

Figure 19: List of instances retrieved when performing a general search for P53_HUMAN using its UniProt identifier “P04637”.

ELM

ELM Switches

Diagram	Switch	Description
	SWTI000456	Phosphorylation of Cellular tumor antigen p53 (TP53) on T18 (in vitro by Casein kinase I subfamily , requiring prior phosphorylation of S15) inhibits its binding to E3 ubiquitin-protein ligase Mdm2 (MDM2) . In vivo, T18 is phosphorylated in response to DNA damage.
	SWTI000517	Alternative promoter usage and alternative splicing removes the E3 ubiquitin ligase MDM2-binding motif of Cellular tumor antigen p53 (TP53) , abrogating binding to E3 ubiquitin-protein ligase Mdm2 (MDM2) . The splice variant without this motif is resistant to MDM2-mediated degradation, leading to a longer half-life.
	SWTI000519	Alternative splicing removes the deubiquitinating enzyme USP7-binding motif of Cellular tumor antigen p53 (TP53) , abrogating binding to Ubiquitin carboxyl-terminal hydrolase 7 (USP7) .
	SWTI000520	Alternative splicing removes the deubiquitinating enzyme USP7-binding motif of Cellular tumor antigen p53 (TP53) , abrogating binding to Ubiquitin carboxyl-terminal hydrolase 7 (USP7) .
	SWTI000037	Phosphorylation of S33 in the Pin1-binding motif of Cellular tumor antigen p53 (TP53) induces binding to the Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 (PIN1) protein.
	SWTI000038	Phosphorylation of S151 in the Pin1-binding motif of Cellular tumor antigen p53 (TP53) induces binding to the Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 (PIN1) protein.
	SWTI000039	Phosphorylation of T81 in the Pin1-binding motif of Cellular tumor antigen p53 (TP53) induces binding to the Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 (PIN1) protein.

Figure 20: List of molecular switches found when performing a general search for P53_HUMAN using its UniProt identifier “P04637”,

The Eukaryotic Linear Motif resource for Functional Sites in Proteins

search ELM Database

ELM Home ELM Prediction ELM DB ELM Candidates ELM Information ELM downloads admin

Your search for p53 resulted in 0 ELM classes, 31 ELM Instances, 5 ELM candidate classes, and 44 ELM Switches:

ELM instances

Identifier	Sequence	Start	Stop	Logic	Taxon	Info
DEG_APCC_DBOX_1	P53350 PLK1 PLK1_HUMAN	336	344	TP	Homo sapiens (Human)	
DEG_APCC_TPR_1	P53197 CDH1 CDH1 YEAST	564	566	TP	Saccharomyces cerevisiae (Baker's yeast)	
DEG_MDM2_SWIB_1	P04637 TP53 P53_HUMAN	19	26	TP	Homo sapiens (Human)	1YCR
DOC_CYCLIN_1	P04637 TP53 P53_HUMAN	381	385	TP	Homo sapiens (Human)	1H26
DOC_MAPK_gen_1	P53355 DAPK1 DAPK1_HUMAN	1385	1393	FP	Homo sapiens (Human)	
DOC_PP2B_PxIxl_1	P53968 CRZ1 CRZ1 YEAST	330	336	TP	Saccharomyces cerevisiae (Baker's yeast)	
DOC_USP7_MATH_1	P04637 TP53 P53_HUMAN	364	368	TP	Homo sapiens (Human)	2FOJ
DOC_USP7_MATH_1	P04637 TP53 P53_HUMAN	359	363	TP	Homo sapiens (Human)	2F1X 2FOO
DOC_WW_Pin1_4	P04637 TP53 P53_HUMAN	312	317	TP	Homo sapiens (Human)	1A
DOC_WW_Pin1_4	P04637 TP53 P53_HUMAN	30	35	TP	Homo sapiens (Human)	1A
DOC_WW_Pin1_4	P04637 TP53 P53_HUMAN	78	83	TP	Homo sapiens (Human)	1A
Fungi and Amoebozoa.">LIG_APCC_Cbox_2	P53197 CDH1 CDH1 YEAST	55	61	TP	Saccharomyces cerevisiae (Baker's yeast)	
LIG_CaM_IQ_9	P53141 MLC1 MLC1 YEAST	84	102	TP	Saccharomyces cerevisiae (Baker's yeast)	
LIG_CID_NIM_1	P53632 PAP2 PAP2 YEAST	574	583	TP	Saccharomyces cerevisiae (Baker's yeast)	2MOW

Figure 21: List of instances retrieved when performing a general search for P53_HUMAN using the query “p53”. The results are quite different compared to Figure 19.

Protocol 3 Detecting Short Linear Motifs in Protein Sequences

One of the most useful (and used) features in ELM is the ability to detect motifs in proteins and sequences. Given a protein's amino acid sequence, the “ELM Predictions” pipeline searches for occurrences of each motif class using regular expressions, applies a set of filters to minimize false positives and creates a diagram to visualize the resulting set of putative motifs.

In this protocol we will be viewing the manually annotated data of a typical protein, using p53 (UniProt ID: P53_HUMAN/P04637) as an example. We will cover how to find the manually annotated motifs and instances, the references used to annotate each instance, the experimental protocols used, and additional information including relationships to biological pathways (KEGG), diseases (OMIM) and molecular switches (switches.ELM).

Necessary Resources

Software & Hardware

A modern browser such as Firefox, Chrome, or Safari. ELM is best viewed on a laptop or desktop computer, although tablets and smartphones will also work.

Predicting ELM instances: Input form

1. Open a browser and navigate to the ELM homepage: <http://elm.eu.org>. Enter the UniProt ID P53_HUMAN in the search field labelled “Enter a UniProt identifier or accession number”. While typing, the page should autocomplete your input “P53_HUMAN / P04637 (*Homo sapiens*)” and already pre-fill other fields of the input form (Figure 22). Click on this entry to confirm that you want to search for motifs in this protein. Click on **Submit** to send the query to the server.

The autocompletion mechanism queries UniProt for the given protein identifier; if it succeeds, additional information from UniProt will be used to auto-populate the input boxes. In this example, P53_HUMAN is recognized as a human protein, and so “Homo sapiens” is automatically filled in the “Taxonomic Context” field. Also, p53 has been annotated (by UniProt) to be localized to nucleus, cytosol, endoplasmic reticulum and mitochondrion, so these are also automatically applied as search criteria. The motif cutoff of “100” is a sufficiently high (lenient) threshold to ensure no motif class is filtered out based on motif probability.

2. Select the search criteria (optional). To restrict the search to include motifs that are active only in certain cellular compartments, select one or more from the “Cell compartment” list (use the “control” key to select more than one option). It is also possible to select a “Taxonomic Context” to restrict the search to motifs from certain species. Start typing a species name in the “Taxonomic Context” input field to get an auto-completed list of species to select from. Additionally, a “Motif probability cutoff” can be used to only retain ELM classes whose pattern probability is below the given value. These filters are implemented later in Protocol 4. For now, leave all filters at the default values that were auto-populated for p53.

ELM

ELM Prediction

The **ELM prediction** tool scans user-submitted protein sequences for matches to the regular expressions defined in ELM. Distinction is made between matches that correspond to experimentally validated motif instances already curated in the ELM database and matches that correspond to putative motifs based on the sequence. Since SLiMs are short and degenerate, overprediction is likely and many putative SLiMs will be false positives. However, predictive power is improved by using additional filters based on contextual information, including taxonomy, cellular compartment, evolutionary conservation and structural features.

Protein sequence

Enter Uniprot identifier or accession number: (auto-completion)
e.g. [EPN1_HUMAN](#), [P04637](#), [TAU_HUMAN](#), [\[RANDOM\]](#)

Or paste the sequence (Single letter code sequence only or FASTA format):

```
>P53_HUMAN
MEEPQSDPSVEPPLSQETFSDLWKLPPENNVLSPLPSQAMDDILMLSPDDIEQWFTEDPGPDEAPRMPPEAAPVAPAPAAPTFA
APAPAPSWPLSSVPSQRTYGGYGRFLHSGTAKSVTCYSPALNMKQLAKTCTFVQLWMDSTPPPGTRVRAMAIIYKQS
QHMTTEVVRRCFHERCSDSGLAPPQHLLRVEGNLRVEYLDDRTNFHRSVVPYEPPEVGSCTTIIHYNCMNSSCMGGMNRR
PILTIITLEDSSGNNLLGRNSFEVRVACAPGRDRRTEENLKKGEPHHELPGSTKRALPNTSSPQPKKKPLDGEYFTLQI
RGRRERFEMFREIMALELKDAQAGKEPGGSRAHSSHLSKKGQSTSRRHKLMFKTEGPDSD
```

Cell compartment (one or several): not specified
 extracellular
 nucleus
 cytosol
 peroxisome
 glycosome
 glyoxosome
 Golgi apparatus
 endoplasmic reticulum
 lysosome
 endosome
 plasma membrane
 mitochondrion

Taxonomic Context

Type in species name (auto-completion):

Motif Probability Cutoff:

Submit **Reset Form**

ELM DB

The ELM relational database stores different types of data about experimentally validated SLiMs that are manually

peptide from ELM class LIG_SxIP_EBH_1

- ELM database update
We have added new instances for: [LIG_APCC_ABBA_1](#), [LIG_APCC_ABBAvCdc20_2](#) as well as [DOC_MAPK_HePTP_8](#), [DOC_MAPK_MEF2A_6](#) and [DOC_MAPK_DCC_7](#)
- ELM Database Update
We have updated several MOD_CDk motifs and added new instances:
MOD_CDk_1 is now: [MOD_CDk_SPxK_1](#), [MOD_CDk_SPK_2](#), [MOD_CDk_SPxxK_3](#) have been added.
- ELM database update
Several new ELM classes and instances have been added:
[LIG_BH_BH3_1](#), [DEG_COP1_1](#)
- ELM database update
The class DOC_PP2A_KARD_1 has been replaced by [DOC_PP2A_B56_1](#), and new instances have been added.
- ELM database update
Several new ELM classes and instances have been added:
[LIG_CSK_EPIYA_1](#), [LIG_Rb_LxCxE_1](#), [DOC_MAPK_JIP1_4](#), [DOC_MAPK_NFAT4_5](#)
- ELM database update
Several new ELM classes and instances have been added:
[DOC_MAPK_RevD_3](#), [LIG_ANK_PxPxL_1](#), [LIG_CSL_BTD_1](#), [LIG_G3BP_FGDF_1](#), [LIG_KLC1_TPR_1](#), [LIG_PALB2_WD40_1](#), [LIG_UFM1_UFM_1](#)

Figure 22: The ELM input page for predicting motifs in a protein. Here, all fields have been filled in for demonstration purposes (the minimum requirement to perform a search is only to provide the protein's UniProt ID in the first box).

Interpreting the prediction results: Graphical Summary

- Click **submit** to start searching for motifs. You will be brought to an intermediate page indicating that your results are being processed, and should be redirected to the final results page within a minute. You can bookmark this page. The results are stored for a week.

The results are summarized in the first figure on the results page (see Figure 23). The graphical summary shows the results generated by the ELM prediction pipeline, combined with additional filters and information from external resources. The visualization should help you to interpret the results and to assess whether or not a motif is present in a sequence, as well as how likely it is to be functional, based on its structural context and evolutionary conservation. Motif instances that are manually annotated in the database appear as red (TP) or yellow (FP) ovals in the graphic. Blue/gray squares represent predicted motif occurrences.

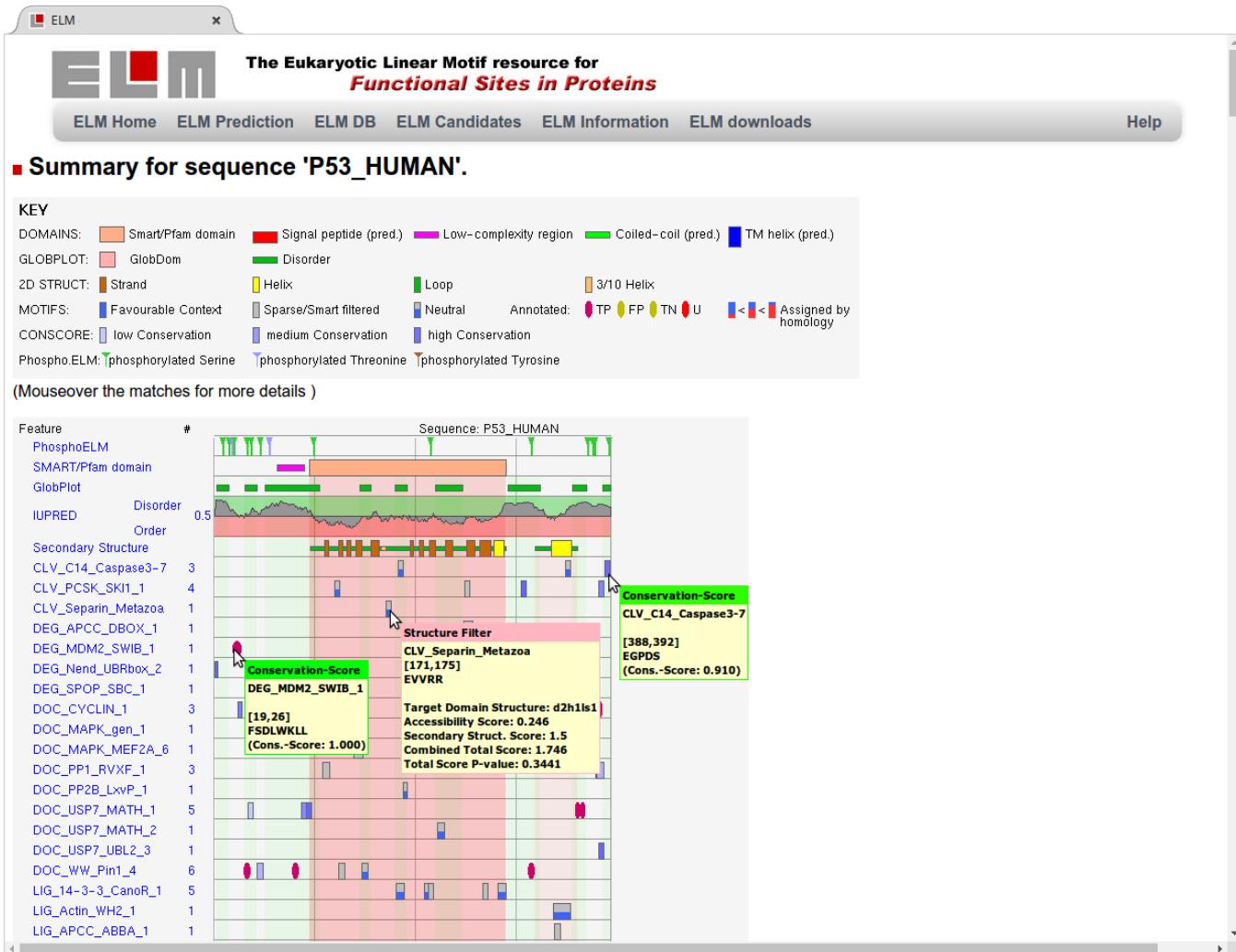


Figure 23: The graphical results summary of the ELM prediction pipeline for P53_HUMAN. Note that not all motif detections are shown (the image is truncated at the bottom). The top five rows show a set of structural features. Annotated and predicted motifs are shown as differently colored ovals/boxes. The information screens for three motifs are shown: CLV_C14_CASPASE3-7, DEG_MDM2_SWIB_1 and CLV_SEPARIN_METAZOA (this figure shows all three pop-up info screens at the same time; normally they are only shown when the cursor is placed over a motif).

4. The first row contains phosphorylation sites, as retrieved from PhosphoELM (Dinkel et al. 2011), and shows whether the phosphorylated amino acid is a serine, threonine or tyrosine. PhosphoELM is a database of manually annotated phosphorylation sites, obtained from scientific publications describing low and high-throughput experiments. You can follow the link to PhosphoELM by clicking on the phosphorylation site in the image to get more information on individual phosphorylation sites.

Phosphorylation sites are only available when the search is performed with a protein accession (eg. not with a FASTA sequence alone) in step 1 and when relevant information is annotated in the PhosphoELM database. Phosphorylation sites are relevant to interpret ELM motif predictions, for instance when the predicted motif is required to be phosphorylated (as in several docking and

ligand binding motifs) or in the case of a predicted phosphorylation motif.

5. The second row shows SMART and PFAM domains detected by the SMART database ([Schultz et al. 1998](#); [Letunic et al. 2015](#); [Schultz et al. 1998](#)) (Figure 23). Hover the mouse over these domains to see their names and exact start and end positions.

In order to be functional, motifs need to be accessible, and therefore they are usually not found within globular domains or structured regions ([Davey et al. 2012](#)). Any motif detected by the ELM prediction pipeline inside a SMART domain is less likely to be functional, and therefore is shown with a gray box background (see commentary section "Structure Filter" at page 45).

6. The third row shows globular and disordered regions in the sequence, as predicted by GlobPlot ([Linding et al. 2003](#)). The fourth and fifth rows contain results from IUPred ([Dosztányi et al. 2005](#)), another predictor of disordered protein regions. Protein segments with an IUPred score above 0.5 are considered to be disordered (see commentary section "Disorder Filter" at page 45).

Motifs are typically only functional when found in intrinsically disordered regions. Any motif occurrence detected by the ELM prediction pipeline that falls within a disordered region is more likely to be functional.

7. The sixth row (Figure 23) contains information on the protein's structure (see commentary section "Structure Filter" at page 45). The secondary structure is predicted by mapping the motif occurrence onto high quality reference domain structures ([Via et al. 2009](#)). Check the graphical representation, and whether the output of the secondary structure filter and the disorder predictors agree with each other with respect to which parts of the sequence are considered structured or disordered.
8. The remainder of the figure (below "secondary structure" output) displays predicted and annotated motif instances, overlaid with the structural context from rows 2 and 3 (SMART domains and GlobPlot). A blue square indicates a single motif occurrence, and the intensity of the color indicates the conservation of this sequence across a group of homologous proteins. Boxes in gray are motif occurrences that have been filtered out by the structure filter. Boxes that are blue & gray are neutral, i.e. within a globular domain but part of a loop according to the secondary structure predictions. If a motif instance in this sequence has already been annotated in the ELM database, it is shown as an oval. Lastly, any detected motif that is already annotated as a functional instance in a homologous sequence, is shown as a red & blue rectangle (see commentary section "Instance Mapper" at page 46).

In the case that not enough homologous sequences were detected to build an alignment, no conservation score can be calculated. Therefore all of the motif occurrences will be shown in a uniform shade of blue.

9. Place the cursor over the blue box for motif occurrence CLV_C14_CASPASE3-7 at the end of the sequence (position 388–392). This will trigger the green and yellow information screen shown on the top right in Fig. 23. This motif is in a disordered region, and has not been filtered out by the structural filter. Also, its conservation score of 0.910 is very high, indicating that this motif is highly conserved.

The conservation score is based on how conserved the sequence is across a set of homologous proteins (see commentary section "Conservation Filter" at page 46).

10. Place the cursor over the blue & gray rectangle for motif CLV_SEPARIN_METAZOA at position 171–175, a motif which was flagged as “neutral” by the ELM prediction pipeline. This will trigger the information screen (with the pink header) shown in Figure 23 to appear. This motif resides inside the p53 PFAM domain, and thus has been subjected to “structural filtering”. However, the secondary structure prediction suggests that this motif occurs within the looped region of this domain, so may be accessible.

The information screen pop-up shows scores for all of the individual criteria used by the secondary structure filter: The name of the domain, the accessibility score, secondary structure score, a combined total score, and the associated total score P-value (Via et al. 2009).

11. Place the cursor over the red oval for DEG_MDM2_SWIB_1 at position 19–26. This motif is an annotated instance in the ELM database, and is therefore a bona-fide experimentally validated instance.

The screenshot shows the ELM software interface. At the top, it says "Filtering summary". Below that, it lists user-supplied cellular locations: nucleus, cytosol, endoplasmic reticulum, mitochondrion, Cytoplasm. It also lists the user-supplied taxon: Homo sapiens. A note states "(An ELM is listed as filtered when all its matching instances have been filtered out.)".

		Elms	Instances
FILTERED BY:	Species	4	26
	Cellular location (counts only those ELMs not already excluded by species.)	5	11
	Structural score (below medium threshold score)	8	29
	Smart (in a domain and no structural filter info available)	0	0
TOTAL FILTERED:		17	66
RETAINED BY:	Smart (outside domain and no structural filter info available)	12	48
	Structural score (at or above medium threshold score)	32	58
TOTAL RETAINED:		44	106
TOTAL	all found (before filtering)	61	172

Query sequence:
>P53_HUMAN
MEEPQSDPSVEPPLSQETFSDLWKLPPENNVLSPPLPSQAMDDMLSPDDIEQWFTEDPGP
DEAPRMPPEAAPPVAPAPAAPTAAAPAPASWPWLSSVPSSQTYQGSYGRFLGLHSGTAK
SVCCTYSPALNKMFCQLAKTCPVOLWVDSTPPGTRVRAMAIIYKQSQHMTEVRRCPHHE
RCSDSDGLAPPQHLIRVEGNLREYLDNRTRHSVVVPPYEPPEVGSDCTIHYNYMCNS
SCMGGMNRNPILTIIITLESSGNLGRNISFEVRVCACPGRDRTEEENLRKKGEPHHELP
PGSTKRALPNNTSSSPOPKKKPLDGEYFTLQIRGRERFEMFRELNEALELKDAQAGKEPG
GSRAHSSHLKSKGQSTSRRHKKLMFKTEGPDS

Globular domains/ TM domains and signal peptide detected by the SMART server

Domain	Start	End
Pfam:P53	95	289

The ELMs in the following table are known instances annotated from the literature.

Click on the link at positions to see experimental evidence.

Elm Name	Instances (Matched Sequence)	Positions	Logic	Elm Description	Cell Compartment	Pattern
MOD_PIKK_1	PPLSQET	12-18	true positive	(ST)Q motif which is phosphorylated by PIKK family members.	nucleus	...([ST])Q...
DOC_USP7_MATH_1	PGGSR AHSSH	359-363 364-368	true positive true positive	The USP7 MATH domain binding motif variant based on the MDM2 and p53 interactions.	nucleus	[PA][^P][^FYWIL]S[^P]
			Some proteins re-exported from the nucleus contain a	((DEQ).(0,1)[LIM].{2,3}[LIVMF][^P]{2,3}[LMVF])

Figure 24: This section of the results lists the user-provided search parameters and summarizes the details of the filtering results and provides a list of globular domains that have been detected in the query sequence.

12. Scroll down to below the results graphic to find additional information on the ELM prediction pipeline’s results (Figure 24). The first section contains links to download or view the multiple sequence alignments of homologous proteins used to calculate the conservation score. Click on the link “Click here to enable the multiple sequence alignment viewer” to open the alignment in Jalview (note: this requires the Java browser plugin, which might not be available on some browsers, and is now officially deprecated.). Alternatively you can also download the “alignment”, “conservation features” and “phosphosite features” files separately to view on a desktop (non-browser) installation of Jalview (Waterhouse et al. 2009).

The search for possible homologues is performed against the UniRef90 database, a dataset of protein sequences with less than 90 percent identity between any two of them (Suzek et al. 2007). It may occur that the BLAST results are not finished when the results page is shown: We suggest to refresh the page if you see the message “Either not enough data available to calculate a sequence alignment or the calculations haven’t finished yet”. In some cases it is also possible that no homologues will be detected. If you have refreshed the page after waiting for more than 3 minutes, this is most likely the case.

13. Scroll down to the section titled “Filtering Summary” to view some statistics about how many motifs and instances were filtered out (Fig. 24). The first two lines contain information on which filters were applied in step 1 of this protocol. In this case 4 motifs representing 26 instances were filtered out as they did not occur in *Homo sapiens*. An additional 5 motifs (representing 11 instances) were filtered out because they are not annotated to the cell compartments automatically filled in on the search page (step 1). The next three lines (“SMART” & “Structural score”) show how many motifs and instances were not removed by the SMART and Secondary structure filters. A total of 42 motifs (representing 106 instances) passed the structural filter.

Note that the graphical summary above does not contain sequences filtered out by the “cell compartment” and “taxonomic context” filters. However those filtered out by the SMART and Structural scores are shown in the graphic above (as gray rectangles).

14. Scroll down to the section with the header “Globular domains/ TM domains and signal peptide detected by the SMART server” (Figure 24). This section contains information on which domains were detected by the SMART server, and their positions. Clicking on their names will bring you to the entry for that domain on the SMART or PFAM homepage. In this case the only domain detected is the “p53” PFAM domain.
15. On the results page, scroll down to the heading: “The ELMs in the following table are known instances annotated from the literature” (25). This table has details of the motifs and instances which have been manually annotated in the ELM database. The columns show each motif name, the sequence(s) that matched the motif as well as their starting and ending positions and the logic of the annotation followed by a short description of each motif, to which cell compartments its has been associated, and finally the regular expression of the motif.
16. Scroll further down to the section title “Results of ELM motif search after globular domain filtering, structural filtering and context filtering” to obtain an overview of all of the motifs and motif instances detected (26) Each of the rows is a “predicted” motif: A sequence matching a motif’s regular expression has been detected that has also passed the “structural filter”. Each row displays the motif identified, the matching peptide sequence and its position. Additional information is shown about

■ The ELMs in the following table are known **instances** annotated from the literature.

Click on the link at positions to see experimental evidence.

Elm Name	Instances (Matched Sequence)	Positions	Logic	Elm Description	Cell Compartment	Pattern
MOD_PIKK_1	PPLSQET	12-18	true positive	(ST)Q motif which is phosphorylated by PIKK family members.	nucleus	...((ST)Q..
DOC_USP7_MATH_1	PGGSR AHSSH	359-363 364-368	true positive true positive	The USP7 MATH domain binding motif variant based on the MDM2 and p53 interactions.	nucleus	[PA][^P][^FYWIL]S[^P]
TRG_NES_CRM1_1	EMFRELNEALELKD	339-352	true positive	Some proteins re-exported from the nucleus contain a Leucine-rich nuclear export signal (NES) binding to the CRM1 exportin protein.	nucleus, cytosol	((DEQ){,0,1}[LIM]{,2,3}[LIVMF][^P]{,2,3}[LMVF][LMIV]{,0,3}[DE]{,0,1}[LIM]{,2,3}[LIVMF][^P]{,2,3}[LMVF][LMIV]{,0,3}[DEO])
DEG_MDM2_SWIB_1	FSDLWKLL	19-26	true positive	An amphipathic α -helix found in p53 family members that binds in the hydrophobic cleft of MDM2's SWIB domain.	nucleus, cytosol	F[^P]{,3}W[^P]{,2,3}[VIL]
DOC_CYCLIN_1	KKLMF	381-385	true positive	Substrate recognition site that interacts with cyclin and thereby increases phosphorylation by cyclin/cdk complexes. Predicted proteins should have a CDK phosphorylation site. Also used by cyclin/cdk inhibitors.	cytosol, nucleus	[RK].L.{,0,1}[FYLIVMP]
MOD_SUMO_for_1	FKTE	385-388	true positive	Motif recognised for modification by SUMO-1	nucleus, PML body	[VILMAFP]{,1}[K].E
MOD_GSK3_1	NVLSPLPS	30-37	true positive	GSK3 phosphorylation recognition site	cytosol, nucleus	...((ST))...[ST]
DOC_WW_Pin1_4	NVLSPL AAPTPA TSSSPQ	30-35 78-83 312-317	true positive true positive true positive	The Class IV WW domain interaction motif is recognised primarily by the Pin1 phosphorylation-dependent prolyl isomerase.	cytosol, nucleus	...((ST))P.
MOD_CK1_1	SQETFSD	15-21	true positive	CK1 phosphorylation site	cytosol, nucleus	S..((ST))...
TRG_NLS_Bipartite_1	KRALPNNTSSSPQPKKKPL	305-323	true positive	Bipartite variant of the classical basically charged NLS.	nucleus, Nuclear pore, NLS-dependent protein nuclear import complex	[KR][K]R.{,7,15}[^DE]{,((K)R)(K)([^DE][K]R){,((K)[^DE])}{,^DE}}

Figure 25: The ELM prediction pipeline section displaying a table of all known experimentally confirmed motifs that have been annotated in the ELM database for the query sequence (p53/P04637).

the motif, its cell compartment and its regular expression. If the motif was detected in a homologue, the column “PHI-Blast Instance mapping” contains a link to the multiple sequence alignment of the homologous proteins. If a motif instance has been filtered out by the “structural filter”, the “Structural filter info” column contains a link to a page with details on why. The last column contains information on the Probability filter: the probability reflects the chance to observe this motif in any random amino acid sequence (see section [Protocol 1](#))

17. Scroll further down to the heading “List of excluded ELMs falling inside SMART/PFAM domains and/or scoring poorly with the structural filter (if applicable).” (Figure 27) This table is similar to the one described above, but shows motif matches which were rejected by the structural filter.

■ Results of ELM motif search after globular domain filtering, structural filtering and context filtering.

Matches falling inside globular protein domains are excluded from this list unless having an acceptable structural score (if the structural filter (BETA version) is applicable). If the structural filter (BETA version) is applicable it is possible to view these structures with Jmol

Elm Name	Instances (Matched Sequence)	Positions	View in Jmol	Elm Description	Cell Compartment	Pattern	PHI-Blast Instance Mapping	Structural Filter Info	
CLV_C14_Caspase3-7	SDSDG ELKDA EGPDS	183-187 [A] 349-353 [A] 388-392 [A]	183-187 349-353 -	Caspase-3 and Caspase-7 cleavage site.	cytosol, nucleus	[DSTE][^P] [^DEWHFYC]D[GSAN]	-	Output	3.094e-03
CLV_Separase_Metazoa	EVVRR	171-175 [A]	171-175	Separase cleavage site, best known in sister chromatid separation.	centrosome, nucleus, cytosol	E[IMPVL][MLVP]R.	-	Output	3.410e-04
DEG_MDM2_SWIB_1	FSDLWKLL	19-26	-	An amphipathic α -helix found in p53 family members that binds in the hydrophobic cleft of MDM2's SWIB domain.	nucleus, cytosol	F[^P](3)W[^P](2,3)[VIL]	Output Summary	-	2.125e-05
DEG_SPOP_SBC_1	PLSSS	92-96 [A]	92-96	The S/T rich motif known as the SPOP-binding consensus (SBC) of the MATH-BTB protein, SPOP, is present in substrates that undergo SPOP/Cul3-dependant ubiquitination.	nuclear speck, nucleus, Cul3-RING ubiquitin ligase complex	[AVP].[ST][ST][ST]	-	Output	9.380e-04
DOC_CYCLIN_1	KLLP RALP KKLMF	24-27 [A] 306-309 [A] 381-385	- - -	Substrate recognition site that interacts with cyclin and thereby increases phosphorylation by cyclin/cdk complexes. Predicted proteins should have a CDK phosphorylation site. Also used by cyclin/cdk inhibitors.	cytosol, nucleus	[RK].L.(0,1)[FYLIVMP]	Output Summary	-	5.324e-03
DOC_PP1_RVXF_1	RHKKLMFK HKKLMFK	379-386 [A] 380-386 [A]	- -	Protein phosphatase 1 catalytic subunit (PP1c) interacting motif binds targeting proteins that dock to the substrate for dephosphorylation. The motif defined is [RK](0,1)[VI][P][FW].	nucleus, protein phosphatase type 1 complex, cytosol	..[RK].(0,1)[VIL][^P][FW].	-	-	8.301e-04
DOC_PP2B_LxvP_1	LAPP	188-191 [A]	188-191	Docking motif in calcineurin substrates that binds at the interface of the catalytic CNA and regulatory CNB subunits.	cytosol, calcineurin complex, nucleus	L.[LIVAPM]P	-	Output	2.296e-03
DOC_USP7_MATH_1	PLPSQ PAPSW PLSSS	34-38 [A] 87-91 [A] 02-06 [A]	- - 02-06	The USP7 MATH domain binding motif variant based on the MDM2 and p53 interactions.	nucleus	[PA][^P][^FYWILJS][^P]	Output Summary	Output	1.239e-02

Figure 26: This table contains the list of putative motifs detected in the query sequence (p53/P04637). These are “predictions” in the sense that each of these motifs has been detected in the sequence after applying (structure/context) filtering, however no experimental evidence has been annotated (yet) to confirm biological function.

■ List of excluded ELMs falling inside SMART/PFAM domains and/or scoring poorly with the structural filter (if applicable).

Matches in this list are only likely to be of interest if they are in accessible surface-exposed loops. Motif matches buried in stably folded cores of globular domains are not plausible candidates.

If the structural filter (BETA version) is applicable it is possible to view these structures with Jmol. For more info consult the PDB structure entry used for structure filtering or the SMART or PFAM entries for useful links to solved 3D structures.

Elm Name	Positions	View in Jmol	Elm Description	Cell Compartment	Pattern	PHI-Blast Instance Mapping	Structural Filter Info	Probability
DEG_APCC_DBOX_1	248-256 [A]	248-256	An RxxL-based motif that binds to the Cdh1 and Cdc20 components of APC/C thereby targeting the protein for destruction in a cell cycle dependent manner	nucleus, cytosol	.R..L..,[LIVM].	-	Output	
DOC_MAPK_gen_1	248-254 [A]	248-254	MAPK interacting molecules (e.g. MAPKKs, substrates, phosphatases) carry docking motif that help to regulate specific interaction in the MAPK cascade. The classic motif approximates (R/K)xxxx#x# where # is a hydrophobic residue.	nucleus, cytosol	[KR]{0,2}[KR].[0,2][KR]{2,4}[ILVM].[ILVF]	-	Output	
DOC_MAPK_MEF2A_6	139-147 [A]	139-147	A kinase docking motif that mediates interaction towards the ERK1/2 and p38 subfamilies of MAP kinases.	cytosol, Transcription factor complex, nucleus	[RK]{2,4}[LIVMP].[LIV].[LIVMF]	-	Output	
DOC_PP1_RVXF_1	108-114 [A]	108-114	Protein phosphatase 1 catalytic subunit (PP1c) interacting motif binds targeting proteins that dock to the substrate for dephosphorylation. The motif defined is [RK]{0,1}[V/I][^P][FW].	nucleus, protein phosphatase type 1 complex, cytosol	.,[RK]{0,1}[VIL][^P][FW].	-	Output	
DOC_WW_Pin1_4	124-129 [A]	124-129	The Class IV WW domain interaction motif is recognised primarily by the Pin1 phosphorylation-dependent prolyl isomerase.	cytosol, nucleus	...([ST])P.	Output Summary	Output	
LIG_14-3-3_CanoR_1	213-217 [A] 267-271 [A]	213-217 267-271	Canonical Arg-containing phospho-motif mediating a strong interaction with 14-3-3 proteins.	cytosol, internal side of plasma membrane, nucleus	R{0,2}[DDEGI]{0,2}([DFWYLMV].)([P]RKGNJP)([^P]RKGNJ){2,4}[VILMFYWYP])	-	Output	
LIG_APCC_ABBA_1	338-343 [A]	338-343	Amphipathic motif that is involved in APC/C inhibition by binding of CDH1/CDC20. In metazoan cyclin A, the motif also acts as a degron, enabling the cyclin's degradation in prometaphase.	spindle pole, nucleus, cytosol	[ILVMF].[ILMV[P][FHY]:[DE]	-	Output	
LIG_FHA_1	198-214 [A]	198-	Phosphothreonine motif binding a subset of	nucleus	./[T]./[I].V.	-	Output	

Figure 27: This table contains the list of putative motifs that were detected in the query sequence (p53/P04637) but were excluded by the structural or context filter.

Protocol 4 Detecting Short Linear Motifs in Novel Protein Sequences

The ELM motif detection pipeline provides a powerful tool to obtain information about the putative motifs that are present in a protein sequence and about its structural context. However, determining which motifs are actually true positive detections requires interpreting all of these results, as well as incorporating as much biological knowledge as possible. In this protocol we will be following a typical example of how one might use the ELM pipeline to search for motifs in novel sequences.

Some pathogens have evolved short linear motifs in effector proteins to modify intracellular signalling in their host cells for their own convenience (Via et al. 2015). The Gram-negative bacteria *Chromobacterium violaceum* is an opportunistic pathogen of humans whose mechanism of pathogenicity remains poorly understood. Its genome encodes a type III secretion system (T3SS) that is used by different pathogens to translocate bacterial proteins into the infected cells. Interestingly, the genes encoding this T3SS as well as other genes located in the same genomic location are very similar to the ones in *Salmonella spp.*, with the exception of few genes such as the modular protein SptP (de Brito et al. 2004). SptP in *Salmonella spp.* is a secreted protein tyrosine phosphatase (Kaniga et al. 1996) whose closest homolog in *C. violaceum* is the protein CV_0974. To better understand the possible biological function of the protein cv_0974, we will use it as an example application of the ELM server motif detection pipeline.

Necessary Resources

Software & Hardware

A modern browser such as Firefox, Chrome, or Safari. ELM is best viewed on a laptop or desktop computer, although tablets and smartphones will also work.

Files

You need to download the following file from UniProt containing the FASTA sequence of cv_0974/Q7NZE8: <http://www.uniprot.org/uniprot/Q7NZE8.fasta>

Submitting a query to ELM

1. Click on the “ELM Predictions” button in the menu to access the search query page (Fig. 28). Here you should provide the amino acid sequence of CV_0974 from UniProt (<http://www.uniprot.org/uniprot/Q7NZE8.fasta>), and enter it as FASTA format into the “sequence input text box”.
2. In the “Taxonomic Context” field, enter the text “Homo sapiens”. This will limit the search to motif classes which have been annotated for human proteins.

Certain human diseases occur when motifs are hijacked by opportunistic pathogens (see Step 20 in Protocol 1 and Figure 16). By limiting the search to human motifs, we will identify motifs which are known to exist in humans and thus may be the target of motif hijacking.

3. The bacterial protein CV_0974 is probably an effector protein, similar to its homologue SptP. As SptP localizes to the cytosol, we assume the same for CV_0974, so you should select “cytosol” in the “Cell compartment” field.

The ELM prediction tool scans user-submitted protein sequences for matches to the regular expressions defined in ELM. Distinction is made between matches that correspond to experimentally validated motif instances already curated in the ELM database and matches that correspond to putative motifs based on the sequence. Since SLiMs are short and degenerate, overprediction is likely and many putative SLiMs will be false positives. However, predictive power is improved by using additional filters based on contextual information, including taxonomy, cellular compartment, evolutionary conservation and structural features.

Protein sequence

Enter Uniprot identifier or accession number: (auto-completion)
e.g. EPN1_HUMAN, P04637, TAU_HUMAN, [RANDOM]

Or paste the sequence (Single letter code sequence only or FASTA format):
 >CV_0974
 MSTIQTGIGLGGGRQLDLSRLDSLSGVNADKARIGIRKDGTLLVYTGRSYLLHPDQTRRADQFLKHDLIPGQKPREFRLAQI
 FDRPMALTQRNTQANETIARIPTQDVTGRGKPKLWADQAARPSGEPSGERASLQRRGAELHLKLAQPRAEARPEKH
 DAIKTELALRGSSDQPSGLLQLKAQVGSSAEGARFLNDVGQARFRDPTAAATQVRAPDGAPLPAKRVQVGGVNVATASQY
 PKAQALESYFGMLAANRTPVLVVLASADMAKQGRIGKADLPDYFSQSGRYVEVESKSKGSTTLEGGLEVRAYHVNVRGAD
 HKSVSIPLHVNPWNADFEAQGATALKALAQHVDAVADKTTAFYRDNNSSALNDPDKLLPV1HCRAGVGRGTGQLIAABELLKPG
 ASSLESIVADMGRGSRNHLMVQTSGQLSTLVLAQQQGRAILQPETAAEPIYANQQAQAEPIYANDAPPPPRRRP

Cell compartment (one or several):

- not specified
- extracellular
- nucleus
- cytosol**
- peroxisome
- glycosome
- glycosome
- Golgi apparatus
- endoplasmic reticulum
- lysosome
- endosome
- plasma membrane
- mitochondrion

Taxonomic Context

Type in species name (auto-completion):
Homo sapiens

Motif Probability Cutoff:

100

Submit **Reset Form**

ELM DB

The ELM relational database stores different types of data about experimentally validated SLiMs that are manually

▪ ELM database update
We have added new instances for LIG_APCC_ABBA_1, LIG_APCC_ABBAvCdc20_2 as well as
DOC_MAPK_HePTP_8, DOC_MAPK_MEF2A_6 and DOC_MAPK_DCC_7

▪ ELM Database Update
We have updated several MOD_CDK motifs and added new instances:
MOD_CDK_1 is now: MOD_CDK_SPxK_1, and MOD_CDK_SPK_2
MOD_CDK_SPxxK_3 have been added.

▪ ELM database update
Several new ELM classes and instances have been added:
LIG_BH_BH3_1
DEG_COP1_1

▪ ELM database update
The class DOC_PP2A_KARD_1 has been replaced by DOC_PP2A_B56_1, and new instances have been added.

▪ ELM database update
Several new ELM classes and instances have been added:
LIG_CSK_EPIYA_1
LIG_Rb_LxCxE_1
DOC_MAPK_JIP1_4
DOC_MAPK_NFAT4_5

▪ ELM database update
Several new ELM classes and instances have been added:
DOC_MAPK_RevD_3
LIG_ANK_PxLPxL_1
LIG_CS1_BT1_1
LIG_G3BP_FGDF_1
LIG_KLC1_TPR_1
LIG_PALB2_WD40_1
LIG_UFM1_UFIM_1

These ELM classes have been

Figure 28: The ELM input page for predicting motifs in a protein. The sequence for *C. violaceum* protein “Probable Tyrosine phosphate” CV_0974 is used as an example for this protocol.

- For now, you should set the “Motif probability cutoff” to the same value you used in [Protocol 3](#) and enter “100” into this box.

Interpreting the results

- Hit **Submit** to send the query to the ELM prediction pipeline. The results are summarized in the first figure on the results page (see Fig. 29) See steps 3 – 10 of [Protocol 3](#) for a description of the graphical summary output. In this case, there are a lot of putative motif hits and it will be difficult to investigate all of these. At this point, it is a good idea to limit your search to the most promising candidates first, by trying to remove false positive hits.
- Go back to the “ELM Predictions” page (it’s probably still open in another browser tab) and enter the same values as used before in steps 1-4. Now however, in order to reduce false positive hits, you should set the “Motif probability cutoff value” to a more stringent threshold: Enter “0.001” for this

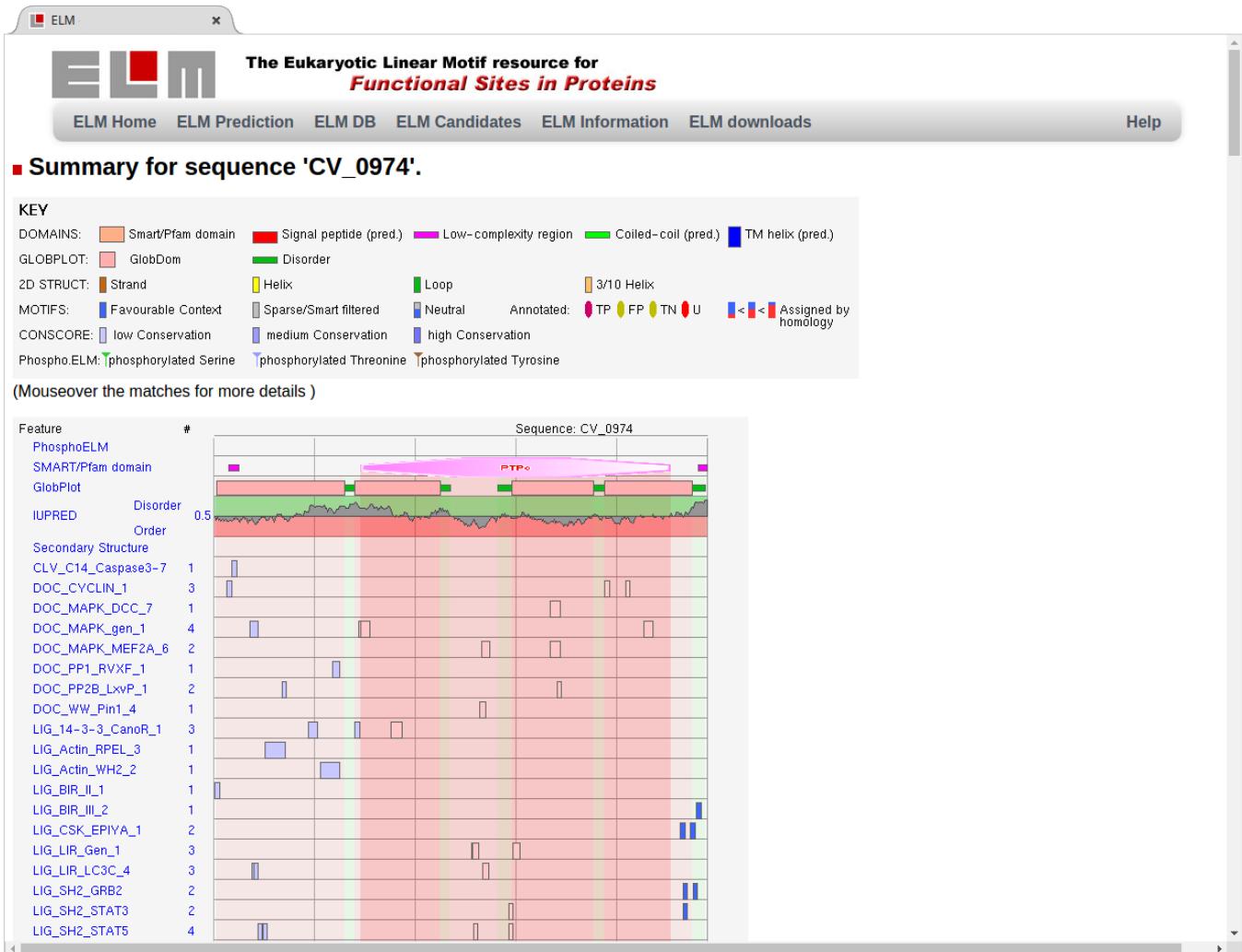


Figure 29: The graphical results summary of the ELM prediction pipeline for protein CV_0974. Note that not all motif detections are shown as the image is truncated at the bottom.

- value. This will exclude all motifs with a probability score higher than this, limiting the results to motifs which are less likely to be found by random chance.
7. Hit **Submit** to send the query to the ELM prediction pipeline. The results are summarized in the first figure on the results page (see Fig. 30). The amount of motif classes detected has been reduced from 54 to 17, and the number of instances from from 156 to 22. Of the remaining 17 motifs, 1 does not occur in *Homo sapiens*, 2 do not localize to the cytosol, and 3 are inside of the PTPc domain (see the “Filtering summary” below the graphical result summary).
 8. By focussing on motif instances with a high probability you have successfully limited the list of ELM motif classes down to 11. (Now would be a good point in time to read up on the details of the remaining motif classes to get a better idea, about which motifs might be functional in your protein. Click on the motif identifiers on the left side of the graphical summary to go to the details page for the motif classes). For this protocol, however, click on the motif identifier LIG_CSK_EPIYA_1 on

the left side of the graphical summary to go to the details page for this motif class.

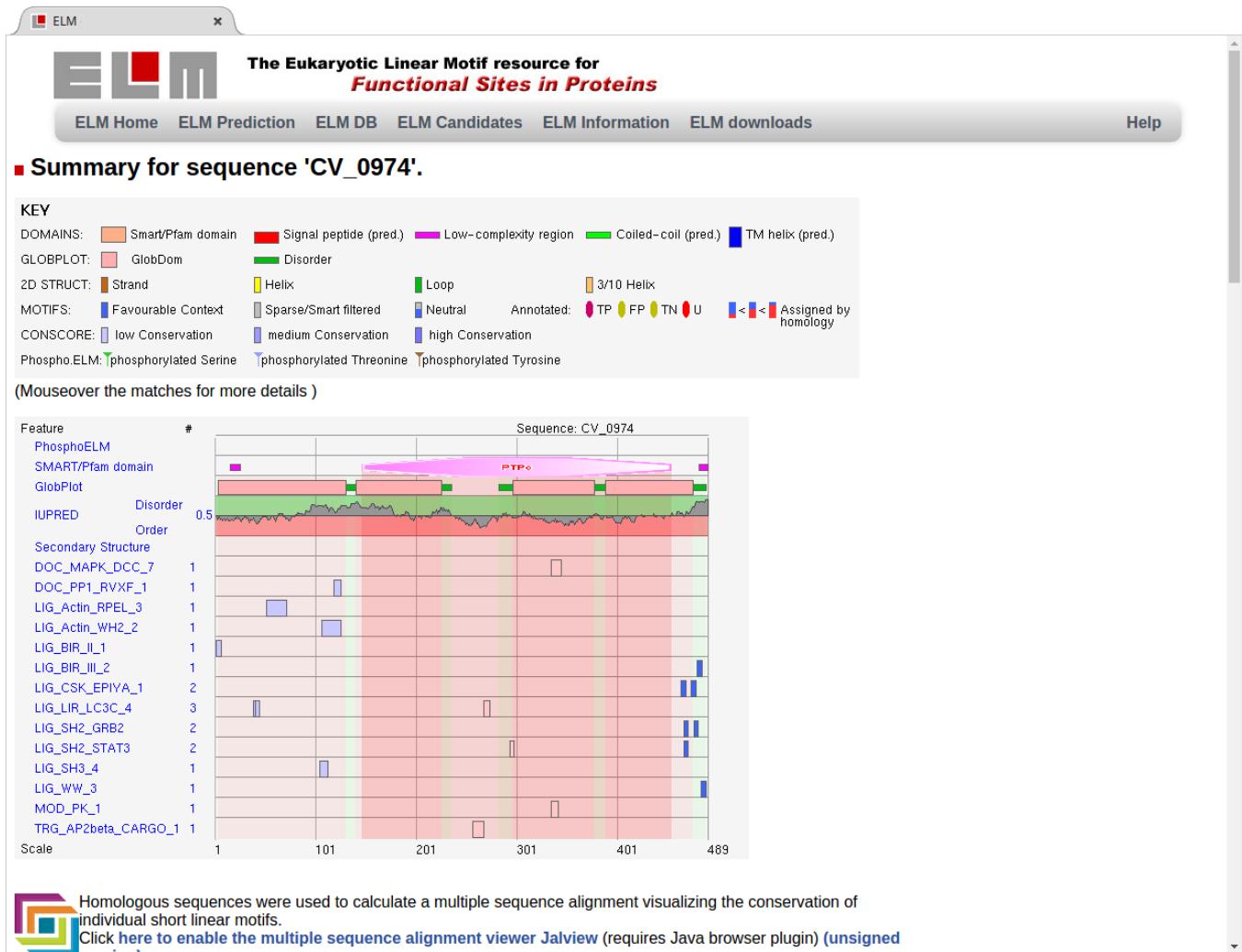


Figure 30: The graphical results summary of the ELM prediction pipeline for CV_0974 using a more stringent probability cutoff of 0.001. The number of motifs predicted is far less than when using the default threshold of 100 (Figure 30)

9. On the LIG_CSK_EPIYA_1 details page the “Functional site description” states that ‘bacterial proteins usually have repeats of EPIYA motifs.’ The ELM prediction results did indeed also detect two EPIYA motifs in a 20 amino acid range (30), lending further support to the likelihood that there are indeed two functional EPIYA motifs in CV_0974, which in turn suggests that these motifs may be involved in *C. violaceum*’s pathogenicity.

When this motif is tyrosine-phosphorylated it is recognized by C-terminal kinase. Different effector proteins from human pathogens like Bartonella henselae, Helicobacter pylori and Haemophilus ducreyi have been reported to use this motif to interfere with the host signalling network to induce proliferation or to avoid phagocytosis (Selbach et al. 2009; Tsutsumi 2002; Dodd et al. 2014). Also, you may notice that there are no conservation scores for either of these motifs. A closer

examination of the alignments of homologous proteins shows that none of the other proteins have this part of the sequence, and are gapped, and it is not possible to calculate a conservation score.

10. It is now up to the experimenter to decide whether to undertake validation experiments that would confirm the LIG_CSK_EPIYA_1 predictions and function in controlling the host cell. Bioinformatics predictions are never certain, and this is especially true for SLiM prediction. At this point it would be important to consult other bioinformatics tools and to search literature published after the motif was annotated. (See the [Protocol 6](#))

Protocol 5 (Alternative Protocol) Searching the ELM database using the REST API

Many researchers are interested in large-scale analyses rather than information about individual protein sequences. To this end, individual queries to the ELM webserver with a single protein ID at a time, are not practical.

For this reason, as much information as practicable is made available via a REST interface ([Fielding and Taylor 2002](#)). This allows the user to interact with the ELM database and ELM webserver via scriptable URL requests. Each request can easily be tested in the browser before it is being automated in a script.

In this section we will explore the various ways in which data can be downloaded both in using the browser as well as via the commandline.

Necessary Resources

Software

A modern browser such as Firefox, Chrome, or Safari. ELM is best viewed on a laptop or desktop computer, although tablets and smartphones will also work. There exist several REST client plugins for different browsers, however these are not needed for this protocol. Ideally use a commandline tool such as `curl` (<http://curl.haxx.se/>) in a terminal window. This program is available in any of the major operating systems: OSX, Windows and Linux. Of course, `curl` is only one of many different ways to access web content programmatically, and we suggest to use whichever program you feel is better suited for your tasks.

Downloading all ELM classes

1. Direct your browser to the URL 'elm.eu.org/downloads' or select **ELM Downloads** from the main menu (Figure 31). This page contains links and descriptions on how to download ELM data in text format. The datasets are split into several smaller collections (for example "Classes", "Instances", etc). Each table contains links (in orange) to download the data in appropriate formats.

Each table also shows the 'last modified date' indicating when the data was last updated. This information is useful if you want to know when to update your local data with the most up to date ELM data as it allows you to determine whether you need to update or not.

The screenshot shows the ELM Downloads page. At the top, there's a navigation bar with links for ELM Home, ELM Prediction, ELM DB, ELM Candidates, ELM Information, ELM downloads, and Help. To the right of the navigation is a search bar labeled "Search ELM Database". Below the navigation is a sidebar with a dark blue background containing a list of links: Classes, Instances, Interactions, Interaction Domains, Methods, PDBs, GOTerms, Renamed ELM classes, and Media / Files.

Classes

Last modified on: Dec. 7, 2016, 5:28 p.m.

Here you can download a list of ELM classes, either all at once or limit the list by providing a query term "q".

Name	Example	URL
all	html	/elms/elm_index.html
all	tsv	/elms/elms_index.tsv
by query term	tsv	/elms/elms_index.tsv?q=PCSK
by ELM id	html	/ELME000012.html

Instances

Last modified on: Dec. 8, 2016, 2:56 p.m.

Annotated ELM instances can be queried in a variety of ways. You are encouraged to use the [search form](#) to get a feeling for the parameters. Common examples include limiting the query by either instance logic or taxon.

Name	Example	URL
all	html	/elms/instances.html?q=*
by Uniprot acc	fasta	instances.fasta?q=P12931
by Uniprot name	gff	instances.gff?q=SRC_HUMAN
by Uniprot acc	tsv	instances.tsv?q=P12931
by query term	pir	instances.pir?q=PCSK
by query term	tsv	instances.tsv?q=src
by query term	mitab	instances.mitab?q=src
by query term	xml	instances.psimi?q=src
by query term using additional parameter "instance logic"	tsv	instances.tsv?q=src&instance_logic=true+positive
by Instance id	html	/ELMI000123.html
All docking motifs annotated in taxon "mouse"	tsv	instances.tsv?q=DOC_&taxon=mus+musculus

Figure 31: The ELM downloads page, which holds information about the different types of data (such as “Classes”, “Instances”, etc; see menu to the right) that can be obtained from the server. The orange boxes are clickable links, the URL following them are used to highlight the URL scheme used by the server (**bold** font denotes specifics used in the examples such as query terms, or formats).

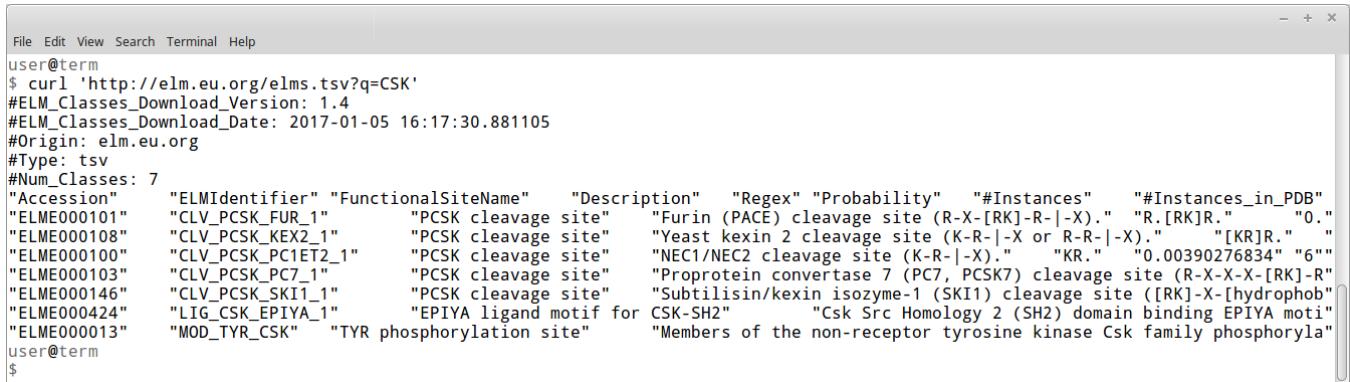
2. Click on the first orange **html** link in the table “Classes” to navigate to the following URL: 'elm.eu.org/elms/elm_index.html'. This page shows all of the annotated ELM classes in the database. This page is the same one as shown in Figure 3.
3. Navigate to the following URL: 'elm.eu.org/elms.html?q=CSK' specifying **q=CSK** to limit the list of ELMs to those matching the search query “CSK”. This page is again similar to the one shown in Figure 3, but with less classes.

This search result is identical to the result you would obtain by doing a “manual” search on the ELM Classes page (eg. typing ‘CSK’ in the search box and clicking submit) as described in step 3 of Protocol 1 (see Figure 3).

4. Open the following URL: 'elm.eu.org/elms.tsv?q=CSK' to download a list of classes that match

the search query “CSK” (as in the previous step) in the “tab separated values” format. Note that this time we used the file extension ‘.tsv’ instead of ‘.html’ as before. By exchanging the ‘.html’ part of the URL with ‘.tsv’, we ask the webserver to give us the data in “tab-separated values” format.

Depending on which browser you are using, the file may open directly in your browser, or you may be prompted to download the file or save it to a separate location. In the latter two cases you can open the downloaded file using a (plain) text file viewer, or possibly a spreadsheet viewer (such as Microsoft Excel or LibreOffice Calc).



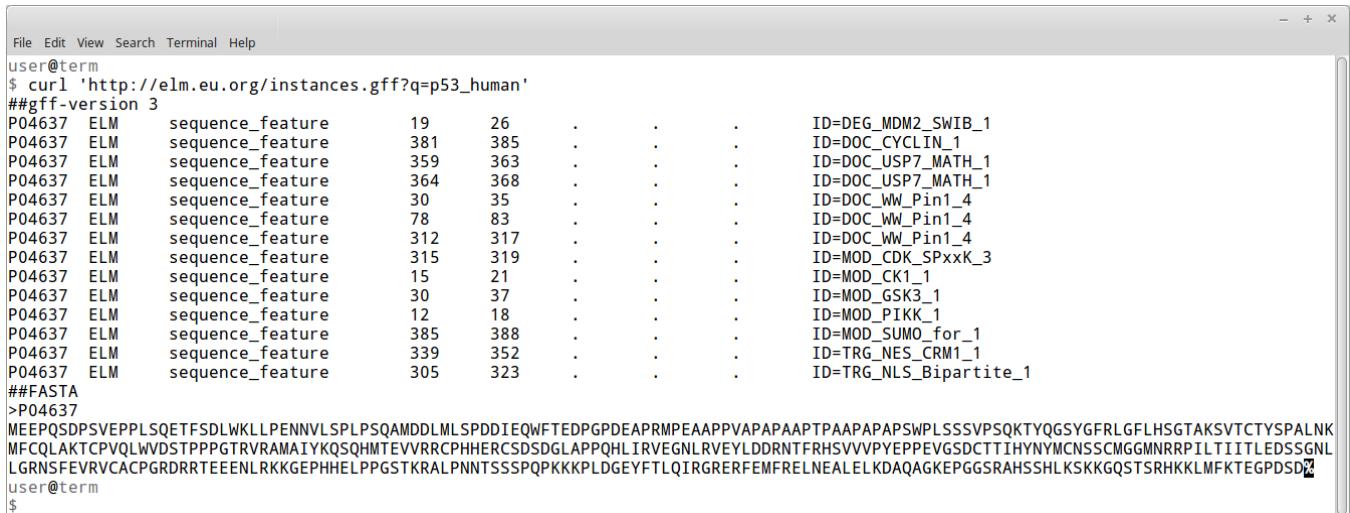
```

File Edit View Search Terminal Help
user@term
$ curl 'http://elm.eu.org/elms.tsv?q=CSK'
#ELM_Classes_Download_Version: 1.4
#ELM_Classes_Download_Date: 2017-01-05 16:17:30.881105
#Origin: elm.eu.org
#Type: tsv
#Num_Classes: 7
"Accession" "ELMIdentifier" "FunctionalSiteName" "Description" "Regex" "Probability" "#Instances" "#Instances_in_PDB"
"ELME000101" "CLV_PCSK_FUR_1" "PCSK cleavage site" "Furin (PACE) cleavage site (R-X-[RK]-R|-X)." "R,[RK]R." "0."
"ELME000108" "CLV_PCSK_KEX2_1" "PCSK cleavage site" "Yeast kexin 2 cleavage site (K-R|-X or R-R|-X)." "[KR]R." "0."
"ELME000100" "CLV_PCSK_PC1ET2_1" "PCSK cleavage site" "NEC1/NEC2 cleavage site (K-R|-X)." "KR." "0.00390276834" "6"
"ELME000103" "CLV_PCSK_PC7_1" "PCSK cleavage site" "Protein convertase 7 (PC7, PCSK7) cleavage site (R-X-X-[RK]-R)"
"ELME000146" "CLV_PCSK_SKI1_1" "PCSK cleavage site" "Subtilisin/kexin isozyme-1 (SKI1) cleavage site ([RK])-X-[hydrophob]"
"ELME000424" "LIG_CSKEPIYA_1" "EPIYA ligand motif for CSK-SH2" "Csk Src Homology 2 (SH2) domain binding EPIYA motif"
"ELME00013" "MOD_TYR_CSK" "TYR phosphorylation site" "Members of the non-receptor tyrosine kinase Csk family phosphoryla"
user@term
$
```

Figure 32: A screenshot of a terminal window using `curl` to download all ELM classes matching the term ‘CSK’.

- Type the following command into a command line terminal to download the same data from the previous step directly into the terminal: `curl 'http://elm.eu.org/elms/elms_index.tsv?q=CSK'`. The output should look similar to Figure 32. The column names are the same as shown in Figure 3.

Use the curl option “–o” to save the results directly to a file. For example: `curl -o classes.tsv 'http://elm.eu.org/elms/elms_index.tsv?q=CSK'` will save the data to a file called classes.tsv.



```

File Edit View Search Terminal Help
user@term
$ curl 'http://elm.eu.org/instances.gff?q=p53_human'
##gff-version 3
P04637 ELM sequence_feature 19 26 . . . ID=DEG_MDM2_SWIB_1
P04637 ELM sequence_feature 381 385 . . . ID=DOC_CYCLIN_1
P04637 ELM sequence_feature 359 363 . . . ID=DOC_USP7_MATH_1
P04637 ELM sequence_feature 364 368 . . . ID=DOC_USP7_MATH_1
P04637 ELM sequence_feature 30 35 . . . ID=DOC_WW_Pin1_4
P04637 ELM sequence_feature 78 83 . . . ID=DOC_WW_Pin1_4
P04637 ELM sequence_feature 312 317 . . . ID=DOC_WW_Pin1_4
P04637 ELM sequence_feature 315 319 . . . ID=MOD_CDK_SPxxK_3
P04637 ELM sequence_feature 15 21 . . . ID=MOD_CK1_1
P04637 ELM sequence_feature 30 37 . . . ID=MOD_GSK3_1
P04637 ELM sequence_feature 12 18 . . . ID=MOD_PIKK_1
P04637 ELM sequence_feature 385 388 . . . ID=MOD_SUMO_for_1
P04637 ELM sequence_feature 339 352 : : . ID=TRG_NES_CRM1_1
P04637 ELM sequence_feature 305 323 : : . ID=TRG_NLS_Bipartite_1
##FASTA
>P04637
MEEQPSDPSVEPPLSQETFSDLWKLLPENNVLSPPLSQAMDDMLSPDDIEQWFTEDPGPDEAPRMPEAAPPVAPAPAAPTAAAPPAPAPSWLSSSVPSQKTYQGSYGFRLGFLHSGTAKSVTCTYSPALNK
MFQLAKTCPVQLWDSTPPPGTRVRAMAIFYKQSQHMTEVRRCPHHERCSDSDGLAPPQHLIRVEGNLRVEYLDRNTFRHSVVVPYEPPEVGSDCTTIHYNYMCNSCMGGMNRRPILTTIILEDSSGNL
LGRNSFEVRVCACPGRDRRTEENLRKKGEPHELPPGSTKRALPNNTSSSPQPKKKPLDGEYFTLQIRGRERFEMFRELNEALELKDAQAGKEPGGSRAHSSHLSKKGQSTSRRKKLMFKTEGPDSM
user@term
$
```

Figure 33: Screenshot of a terminal window using `curl` to download all ELM instances annotated for sequence P53_HUMAN.

- To download a list of all motif instances detected in the protein sequence of human p53, type the following command into a terminal: `curl 'http://elm.eu.org/instances.gff?q=p53_human'`. The output should look similar to that shown in Figure 34. The output is in the “General Feature Format” (see www.ensembl.org/info/website/upload/gff.html#moreinfo), with the FASTA formatted sequence appended to the end of the output.

Many other file formats are available for downloading instances annotations; see the downloads page for available options including the FASTA, GFF, PIR, or PSI-MI format (either XML or MiTab).

- To download a list of all instances matching the search query “CLV” annotated for the taxon “yellow fever mosquito (*Aedes aegypti*)”, enter the following command into a terminal: `curl 'http://elm.eu.org/instances.tsv?q=CLV&taxon=aedes+aegypti'` (In general, any species name can be used, however remember to replace all “spaces” with “+”). This should return a single instance, the only one matching CLV in *A. aegypti*.
- More data (interactions, domains, methods, etc.) can be downloaded from ELM in analogous fashion as shown in the preceding steps. Take a look at the ELM Downloads page (elm.eu.org/downloads, figure 31) for an overview of which datasets can be downloaded, and what different filters and formats are available for each dataset.

Protocol 6 (Alternate Protocol) Detecting Short Linear Motifs in Sequences using the REST API

Querying ELM for motifs in a given sequence (as described in [Protocol 3](#) and [Protocol 4](#)), gives you a nice overview of putative and annotated motifs in your query protein with a graphical representation using colors to highlight different regions of the protein sequence (eg. disordered vs. globular). It is however difficult to analyse a large set of protein sequences in this manner. Therefore, the ELM server provides an interface which you can use to submit your sequence in a programmatic way. Of course, this way, you won’t receive the graphical output representation, but are limited to textual data representation.

Currently, there exists a single URL (elm.eu.org/start_search/) to accept such queries. You can choose to either submit a UniProt name or accession (eg. `'elm.eu.org/start_search/P53_HUMAN.tsv'`) or submit your raw sequence (e.g. `'elm.eu.org/start_search/MAPRGFSCLLLTSEIDLPVKRRA'`). If the URL ends in ‘.tsv’ then the server assumes you are using a UniProt id or accession; if it doesn’t, then it assumes you are using raw sequence. See below for details.

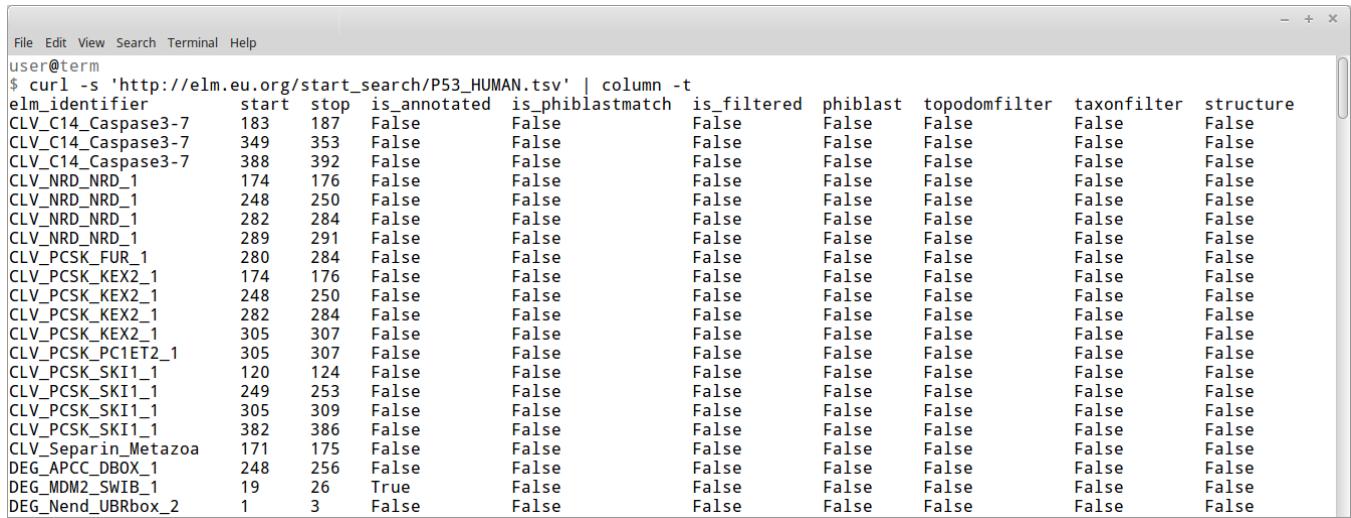
Necessary Resources

Software

A modern browser such as Firefox, Chrome, or Safari. ELM is best viewed on a laptop or desktop computer, although tablets and smartphones will also work. There exist several REST client plugins for different browsers, however these are not needed for this protocol. Ideally use a commandline tool such as

`curl` (<http://curl.haxx.se/>) in a terminal window. This program is available in any of the major operating systems: OSX, Windows and Linux. Of course, `curl` is only one of many different ways to access web content programatically, and we suggest to use whichever program you feel is better suited for your tasks. (Note that in some of the following screenshots, we append the following command to the commandline “`| column -t`” to make the output more readable. All this does is to properly align all columns at tabstops.)

Submitting a query to ELM via the REST API

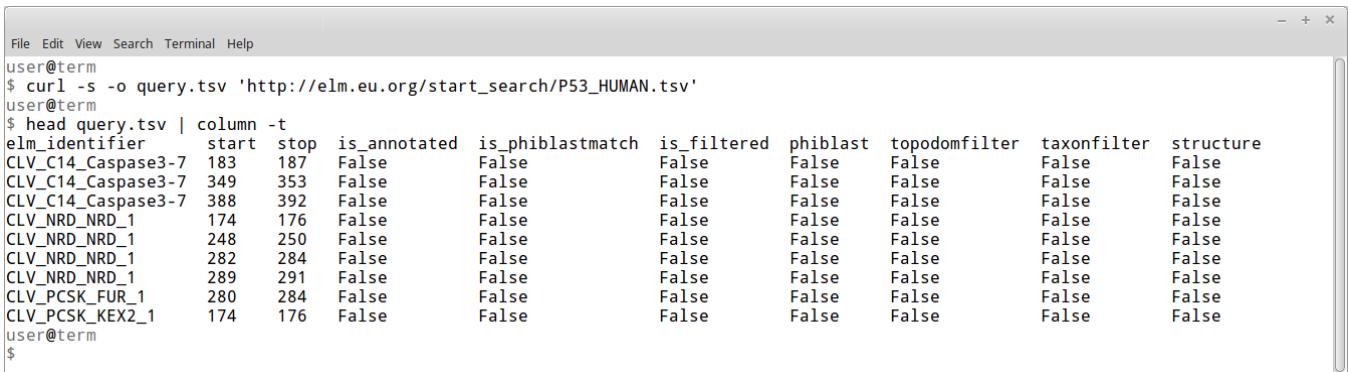


```
File Edit View Search Terminal Help
user@term $ curl -s 'http://elm.eu.org/start_search/P53_HUMAN.tsv' | column -t
elm_identifier start stop is_annotated is_phiblastmatch is_filtered phiblast topodomfilter taxonfilter structure
CLV_C14_Caspase3-7 183 187 False False False False False False False
CLV_C14_Caspase3-7 349 353 False False False False False False False
CLV_C14_Caspase3-7 388 392 False False False False False False False
CLV_NRD_NRD_1 174 176 False False False False False False False
CLV_NRD_NRD_1 248 250 False False False False False False False
CLV_NRD_NRD_1 282 284 False False False False False False False
CLV_NRD_NRD_1 289 291 False False False False False False False
CLV_PCSK_FUR_1 280 284 False False False False False False False
CLV_PCSK_KEX2_1 174 176 False False False False False False False
CLV_PCSK_KEX2_1 248 250 False False False False False False False
CLV_PCSK_KEX2_1 282 284 False False False False False False False
CLV_PCSK_KEX2_1 305 307 False False False False False False False
CLV_PCSK_PC1ET2_1 305 307 False False False False False False False
CLV_PCSK_SKI1_1 120 124 False False False False False False False
CLV_PCSK_SKI1_1 249 253 False False False False False False False
CLV_PCSK_SKI1_1 305 309 False False False False False False False
CLV_PCSK_SKI1_1 382 386 False False False False False False False
CLV_Separin_Metazoa 171 175 False False False False False False False
DEG_APCC_DBOX_1 248 256 False False False False False False False
DEG_MDM2_SWIB_1 19 26 True False False False False False False
DEG_Nend_UBRbox_2 1 3 False False False False False False False
```

Figure 34: Screenshot of a terminal window using `curl` to download all motifs predicted in human p53.

1. Use `curl` to query ELM for all motifs predicted to occur in human p53 by typing the following into a terminal: ‘`curl ‘http://elm.eu.org/start_search/P53_HUMAN.tsv’`. See Figure 34 for example output. Each resulting row represents a motif detection, and the first column “elm_identifier” indicates which ELM class was identified, multiple matches to the same class are represented in multiple lines. The columns “start” and “stop” show the first and last amino acid positions that matched the motif. The column “is_annotated” is True if this motif has been annotated in the ELM database as an (experimentally validated) motif instance. The column “is_phiblastmatch” is True if a match was found by the ELM Instance mapper indicating that an experimentally validated instance in a homologous sequence was found (see commentary section “Instance Mapper” at page 46). The column “is_filtered” shows whether or not this motif was rejected by any of the ELM prediction filters (structure, topodom, taxon), whereby “topodomfilter” uses information from UniProt to determine the protein’s “topology” with respect to trans-membrane domains or extracellular regions. The columns “taxonfilter” and “structure” indicate that an instance has been filtered by the taxonomy or secondary structure filter, respectively (see commentary sections “Taxon Filter” and “Structure Filter”).

In FigureF34 we use a slightly more advanced command to get the output to look nice in the terminal. We specified the `-s` option to silence all `curl` output other than the downloaded file, and piped the output directly to the `column` command (this command exists on most Linux and OSX machines).



```

File Edit View Search Terminal Help
user@term
$ curl -s -o query.tsv 'http://elm.eu.org/start_search/P53_HUMAN.tsv'
user@term
$ head query.tsv | column -t
elm_identifier    start  stop  is_annotated  is_phiblastmatch  is_filtered  phiblast  topodomfilter  taxonfilter  structure
CLV_C14_Caspase3-7 183   187   False        False           False        False      False          False        False
CLV_C14_Caspase3-7 349   353   False        False           False        False      False          False        False
CLV_C14_Caspase3-7 388   392   False        False           False        False      False          False        False
CLV_NRD_NRD_1      174   176   False        False           False        False      False          False        False
CLV_NRD_NRD_1      248   250   False        False           False        False      False          False        False
CLV_NRD_NRD_1      282   284   False        False           False        False      False          False        False
CLV_NRD_NRD_1      289   291   False        False           False        False      False          False        False
CLV_PCSK_FUR_1     280   284   False        False           False        False      False          False        False
CLV_PCSK_KEX2_1     174   176   False        False           False        False      False          False        False
user@term
$
```

Figure 35: Screenshot of a terminal window using `curl` with the option “`-o`” to download directly to the file `query.tsv`, and using a combination of the `head` and `column` commands to display the first 10 rows to the terminal.

2. Use `curl` to query ELM via protein sequence by using the URL 'elm.eu.org/start_search/MAPRGFSCLLLLTSEIDLPKRRA' (Figure 35). In this case the query is an arbitrary short peptide sequence, but this can (of course) contain any sequence you are interested in analysing. The output format is exactly the same as in the previous step.

This way of querying ELM is unfortunately not stable for long protein sequences. Different browsers and computers have different maximum lengths for URLs, and the excess text is often simply ignored. We recommend not using this method for sequences longer than 2000 amino acids.

Guidelines for Understanding Results

The annotations in the ELM database have all been created manually, and in most cases you can safely assume that the annotations present in the database are of high confidence. These annotators have a lot of experience in reading the scientific literature, and know how to distinguish high confidence from suggestive experiments [Gibson et al. \(2015\)](#). However, bioinformatics databases are never perfect, and some annotations in ELM may be 10 years old, so there could be updated literature. You are also encouraged to dig deeper into each annotation. In all cases, each entry contains descriptions of the experiments performed and links to the original research.

Understanding the results generated by the ELM prediction pipeline can sometimes require some extra work. In [Protocol 3](#) and [Protocol 4](#) we gave a few examples of how to read and interpret the results from the ELM prediction pipeline. These are bioinformatics predictions, and therefore will rely on a heuristic which might make mistakes. In general the prediction pipeline attempts to make as many predictions as possible, at the risk of making some False Positive predictions as well.

In cases all of the intermediate results generated by the ELM prediction pipeline are made available to aid you in deciding which predictions are worth further investigation. Looking at the multiple sequence alignments used to generate the conservation score can (for example) help determine why a seemingly likely motif may have a (falsely) low confidence score. However, contrary you may have reason to believe

that a predicted motif that was rejected by ELM's structure filter may actually exposed in a different structural conformation. We highly recommend you do not use ELM in isolation. Always make sure to check the literature and to use other bioinformatics tools to check alignments, structures and conservation (See the [Protocol 6](#) for a handful of suggestions)

Commentary:

Background Information

In order to interpret the data contained in ELM and the results produced by the ELM prediction tool, it is important to have a basic understanding of SLiMs and how they are affected by their structural and biological context. This background information summarizes the different functionalities of SLiMs, describes the degenerate nature of motif sequences, and emphasizes the need for contextual data for confident SLiM prediction.

ELM categorises SLiMs depending on their functionality

SLiMs mediate different types of interactions, and based on this functionality, the ELM classes annotated in the ELM database are grouped into six main ELM types (Figure 36, [Dinkel et al. \(2014\)](#)). They can function as ligand binding sites or as sites for post-translational modification (PTM). Some ligand SLiMs are recognised by components of the cellular transport machinery and function as localisation signals that target proteins to specific sub-cellular compartments (TRG type). Other ligand SLiMs are abundantly present in interfaces that mediate the assembly of large macromolecular complexes and in highly modular scaffold proteins that act as multivalent platforms for protein complex assembly (LIG type). Docking motifs are ligand SLiMs that recruit modification enzymes to their substrates by binding to a site on the enzyme that is distinct from the active site (DOC type). A subset of these, known as degrons, recruit ubiquitin ligases, which subsequently polyubiquitylate their substrates and hence target them for proteasomal degradation (DEG type). SLiMs that act as sites for PTM can be targeted by specific enzymes for the addition or removal of a small chemical group (e.g. phosphorylation), a sugar molecule (e.g. glycosylation), a protein (e.g. ubiquitylation), or another moiety (e.g. lipidation) (MOD type). Other PTM SLiMs mediate proteolytic cleavage by acting as target site for proteolytic enzymes (CLV type), or are recognised for structural modification by isomerases that catalyse cis-trans isomerisation of the peptide backbone (DOC type), see [Van Roey et al. \(2014\)](#) and [Lee et al. \(2015\)](#).

ELM regular expressions reflect the degenerate nature of SLiMs

As their name suggests, SLiMs are compact, being composed of a limited number of adjacent amino acids. Most of a motif's binding specificity however is conferred by only a subset of these amino acids. Those few residues that directly interact with the binding partner are evolutionarily conserved, although in many cases a subset of amino acids that share certain properties (such as similar charge, size or hydrophobicity) are allowed in these hotspot positions. In the motif positions that contribute little to the interaction, there are even less constraints, i.e. a broader range of amino acids is allowed in these positions ([Davey et al. 2012](#)). This sequence flexibility is captured in the regular expressions that are defined for each motif class. A first consequence of this degeneracy is that SLiMs co-operatively engage in interactions of relatively low

affinity. Hence these binding events are transient and reversible, and can be readily modulated, for instance by PTM. These characteristics make SLiM-based interactions ideal mediators of the dynamic processes involved in cell signalling (Van Roey et al. 2012). Another consequence is that it might take only a few or even a single point mutation to generate or disrupt a functional motif in a protein. The associated ability to evolve convergently might underlie the proliferation of SLiMs and the rewiring of interactomes (Davey et al. 2015; Kim et al. 2012). Conversely, several SLiM-associated diseases have been characterised to date, for instance Liddle syndrome (Furuhashi et al. 2005).

ELM integrates data to increase the confidence of SLiM prediction

Due to their degenerate nature, motif sequences contain only very little information, and many short sequences in a proteome will match motif patterns. However, most of these matches will not represent functional motifs, and hence, scanning a proteome for putative motifs using only the motif sequence patterns will yield a large number of false positive instances, far exceeding the number of true motifs. This is painful both for bioinformaticians and experimentalists. Therefore, reliable motif detection cannot go without experimental validation of candidate motifs, using different types of experiments and techniques (Gibson et al. 2015). This however does not mean that bioinformatics analysis cannot guide researchers towards a subset of candidate motifs that have a higher probability to be functional and help rule out those candidate motifs that are likely to be false positives. Taking into account additional information, besides a match to a sequence pattern defining a SLiM, can greatly narrow the selection of putative motifs for experimental validation. Additional data for in silico analysis include conservation of the motif sequence, the location of the motif within the protein's structure and its accessibility for its binding partner, validated interaction with the binding partner, and in-cell co-localisation with the binding partner. The availability and usefulness of these additional data for SLiM discovery depend on their extensive and correct biocuration. A vast and increasing amount of biological data is available in a wide variety of sources, including the literature and large-scale datasets. In order to facilitate integration of data, they need to be collected, annotated and formatted in central data and knowledge repositories. The ELM database provides such a repository for experimentally validated linear motif classes and instances. The ELM prediction tool in turn relies on annotated data, both from the ELM database and other resources, to accurately analyse sequences for candidate motifs and assist researchers in selecting the most plausible ones for experimental validation and discard likely false positive hits, saving them valuable time and assets (Dinkel et al. 2012).

ELM Filters

Disorder Filter ELM uses two different predictors of globularity/disorder: Firstly, GlobPlot developed by Linding et al. (2003), uses amino acid propensities derived from a set of proteins to detect regions of globularity/disorder in any given protein sequence. Secondly, IUPred by Dosztányi et al. (2005), which, unlike GlobPlot, has not been trained on any dataset, but rather uses a position-specific scoring scheme assessing the tendency of any given amino acid to reside in either an ordered or disordered region. IUPred assigns a score between 0.0 to 1.0 to each amino acid of a protein sequence, whereby protein segments with an IUPred score above 0.5 are considered to be disordered. ELM displays IUPred scores as a colored line on either green (disordered) or red (globular) background, see rows four and five of Figure 23.

Structure Filter The structural filter, especially developed for ELM by Via et al. (2009), assesses accessibility and secondary structural context derived from experimentally solved protein structures. It maps

putatively functional motif occurrences onto a representative domain structure and scores these motifs for solvent-accessibility and secondary structure context. ELM displays this information as overlay boxes in the graphical output, whereby the user needs to hover over individual instance entries within structural context (see the CLV_PCSK_SKI1_1 example in fig. 23).

Conservation Filter This filter method for scoring the conservation of linear motif instances was developed by Chica et al. (2008) and subsequently implemented into the ELM pipeline. It requires only primary sequence-derived information (e.g. a multiple alignment and the sequence tree) and implicitly takes into account the degenerate nature of short linear motif patterns. By auto-generating multiple sequence alignments from a non-redundant database, generating distance-trees and taking into account motif degeneracy, it assesses for each ELM motif class found in any given sequence its conservation. The conservation score ranges from 0.0 (the predicted instance is present only in the query sequence) to 1.0 (full conservation of the motif regular expression in all the informative sequences). In the graphical representation, motif conservation is indicated by coloring instances in different shades of blue, whereby darker shades of blue represent higher conservation. In the case that not enough homologous sequences were detected to build an alignment, no conservation score can be calculated. Therefore all of the motif occurrences will be shown in a uniform shade of blue.

Since conserved motifs in structural regions are most likely conserved for structural integrity rather than motif function, one always has to assess the context when inspecting conservation score. Generally, best motif candidates are those with high conservation scores in regions of unstructured, unconserved regions.

Taxon Filter Each ELM class is annotated with one or more taxonomic ranges, for which experimental evidence has been found for the particular class (see "Present in Taxon: Eukaryota" in figure 4). This information is then used to filter taxons outside the annotated range whenever a user submits a query sequence to the ELM database (see the **taxonomic context** field in the ELM search input form in fig. 22).

Instance Mapper The ELM instance mapper takes all annotated instances from the ELM database, generates a BLAST database from it and uses PHI-BLAST (Zhang et al. 1998) to detect sequence stretches in the query sequence which are similar to sequences in this database. This allows the instance mapper to effectively map known instances (for which experimental evidence exists) onto homologous sequences of unknown function.

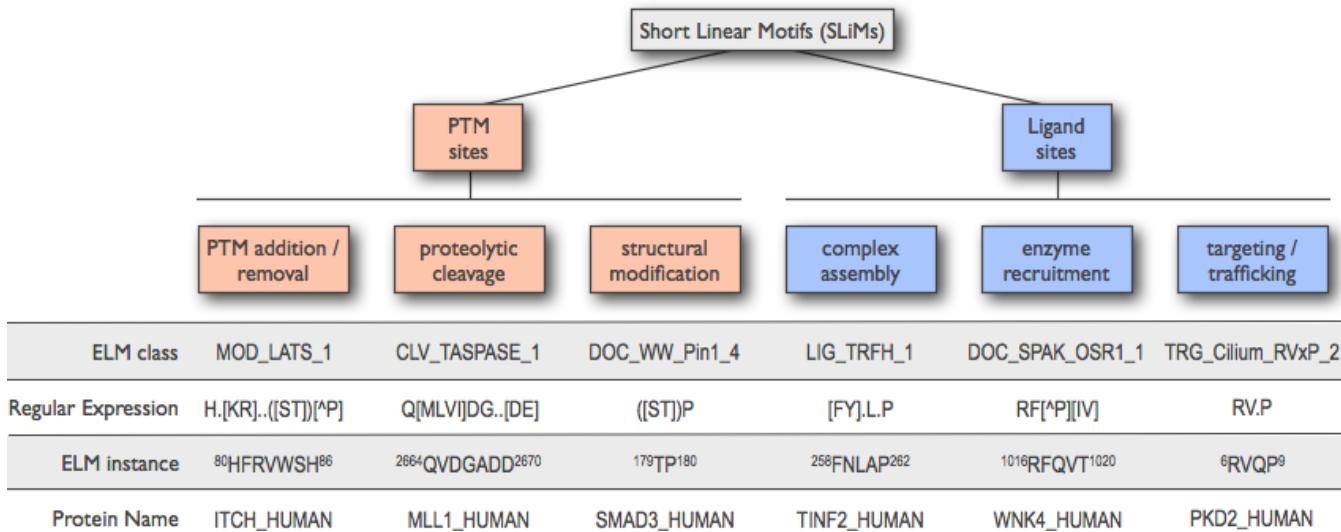


Figure 36: Classification of ELM motif classes. For each ELM class, the functional category to which it belongs is indicated by a three-letter prefix (such as “MOD” for “MOD_LATS_1”). Each ELM class is defined by a regular expression. Peptide sequences in proteins that match the regular expression of a specific ELM class and that were experimentally validated to be functional motifs are captured as ELM instances of that class. Figure adapted from Lee et al. (2015).

Key References with Annotation

- “ELM 2016-data update and new functionality of the eukaryotic linear motif resource.” (Dinkel et al. 2016). This is the latest publication on the ELM database highlighting the newest features.
- “Experimental detection of short regulatory motifs in eukaryotic proteins: tips for good practice as well as for bad” (Gibson et al. 2015). This guide is meant for experimentalists working on detecting/validating short linear motif instances.
- “Attributes of short linear motifs.” (Davey et al. 2012). This review summarizes the biochemical properties of short linear motifs.
- “Short linear motifs: ubiquitous and functionally diverse protein interaction modules directing cell regulation.” (Van Roey et al. 2014). Comprehensive review about short linear motifs with extensive biological examples.

Internet Resources with Annotations

- www.clustal.org/omega Clustal Omega (Sievers et al. 2011) is a tool for the alignment of multiple nucleic acid and protein sequences.
- www.jalview.org Jalview (Waterhouse et al. 2009) is a Java desktop application (and browser applet) that employs web services for sequence alignment and visualization.

- proviz.ucd.ie ProViz (Jehl et al. 2016) is an interactive protein exploration tool, which searches several databases for information about a given query protein. Data relevant to the protein like an alignment of homologues, linear motifs, post translational modifications, domains, secondary structure, sequence variations and others are graphically represented relative to their position in the protein.

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