

# *Current Protocols in Bioinformatics*

## Eukaryotic Linear Motifs on the ELM database

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### Keywords

Linear motifs, Bioinformatics, Protein-Protein Interaction, Molecular switches, Cell regulation

### Significance statement

#### Abstract

The Eukaryotic Linear Motif (ELM) resource ([elm.eu.org](http://elm.eu.org)) is a manually curated database of short linear motifs (SLiMs). This protocol explains how to best use this resource and explains how to access the database content (both manual and scripted access), how to interpret the output, and how to predict novel putative motifs in any given protein sequence.

### 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 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 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 annotated from the literature. The ELM prediction tool in turn relies on annotated data, both from the ELM database and other resources, to accurately analyse unknown 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). 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 Explore the content of the ELM DB

The core of the ELM database is a repository of manually annotated motifs and instances. As of December 2016, ELM contains over 260 motif classes and over 3000 experimentally validated and manually curated instances. The motif classes and motif 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 is a short genenerate sequence of amino acids with a given function. Since the sequences are genenerate, each motif class is represented using a “regular expression”: a symbolic representation expressing a complex pattern of letters (or amino acids). For example, the regular expression “[FY].L.P” is to be read as: The first amino acid is a phenylalaline (F) or a Tyrosine (Y) followed by any one amino acid (.), a Leucine (L), one more arbitrary amino acid (.) and finally a Proline (P).

Each motif class is annotated by an expert molecular biologist based on literature cited experiments. In all cases the annotator accompanies the motif definition with the list of instances, as well as links to external resources including Biological Pathways, Diseases, Gene Ontology and other Protein resources. In this protocol we explore the several datatypes 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.

#### Protocol 1.1 Database content overview

1. The ELM database is an online web resource. Open a browser and navigate to [elm.eu.org](http://elm.eu.org) to visit the homepage (Fig. 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 the news column, and 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 (Fig. 2). This page displays the types and amounts of annotations contained in the database and a few links to third-part databases. Each line contains at least one link which will take you to the corresponding contents page (for example, clicking on **ELM instances** will take you to the page displaying all of the annotated instances in the 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: [MOD\\_CDK\\_SPxK\\_1](#), and [MOD\\_CDK\\_SPK\\_2](#)  
[MOD\\_CDK\\_SPxxK\\_3](#) has 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 database ([elm.eu.org](http://elm.eu.org)).

## Protocol 1.2 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 (Fig. 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 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.*

- Search the table for the term **DOC\_CYCLIN\_1** and click on **DOC\_CYCLIN\_1** in the left column to

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

Recent Database Updates:

- 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.

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.

navigate to the page with details about the **DOC\_CYCLIN\_1** motif class (Fig. 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.*

5. Scroll further down the **DOC\_CYCLIN\_1** page (Fig. 4) to view more details about the manually annotated data and instances in the database (Fig. 5) The “abstract” contains a more detailed description of the motif annotation. 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.

| ELM Identifier           | Description  | RegEx  | Instances | Instances in PDB |
|--------------------------|--|--|-----------|------------------|
| CLV_C14_Caspase3-7       | Caspase-3 and Caspase-7 cleavage site.   | [DSTE][^P][^DEWHYCF]D[GSAN]                            | 39        | 0                |
| CLV_MEL_PAP_1            | Prophenoloxidase-activating proteinase (PAP) cleavage site ([ILV]-X-X-R-[FV]-[GS]-X).  | [ILV]..R[FV][GS].                                      | 12        | 0                |
| CLV_NRD_NRD_1            | N-Arg dibasic convertase (NRD/Nardilysin) cleavage site (X-[R-K] or R-[R-X]).  | (.RK) (RR[KR])   | 2         | 0                |
| CLV_PCSK_FUR_1           | Furin (PACE) cleavage site (R-X-[RK]-R-[X]).   | R.[RK]R.   | 13        | 0                |
| CLV_PCSK_KEX2_1          | Yeast kexin 2 cleavage site (K-R-[X] or R-R-[X]).  | [KR]R.   | 1         | 0                |
| CLV_PCSK_PC1ET2_1        | NEC1/NEC2 cleavage site (K-R-[X]).   | KR.  | 6         | 0                |
| CLV_PCSK_PC7_1           | Proprotein convertase 7 (PC7, PCSK7) cleavage site (R-X-X-[RK]-R-[X]).   | R...[KR]R.   | 1         | 0                |
| CLV_PCSK_SKI1_1          | Subtilisin/kexin isozyme-1 (SKI1) cleavage site ([RK]-X-[hydrophobic]-[LTKF]-[X]).   | [RK].[AILMFV][LTKF].                                   | 2         | 0                |
| CLV_Separin_Fungi        | Separase cleavage site, best known in sister chromatid separation. Also involved in stabilizing the anaphase spindle and centriole disengagement.  | S[IVLMH]E[IVPFMLYAQR]GR.                               | 4         | 0                |
| CLV_Separin_Metazoa      | Separase cleavage site, best known in sister chromatid separation.   | E[IIMPLV][MLVP]R.                                      | 5         | 0                |
| CLV_TASPASE1             | Taspase1 is a threonine aspartase which was first identified as the protease responsible for processing the trithorax (MLL) type of histone methyltransferases.                                    | Q[MLV]DG..[DE]   | 2         | 0                |
| DEG_APCC_DBOX_1          | 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  | .R...L...[LIVM].                                       | 11        | 0                |
| DEG_APCC_KENBOX_2        | Motif conserving the exact sequence KEN that binds to the APC/C subunit Cdh1 causing the protein to be targeted for 26S proteasome mediated degradation.   | .KEN.  | 16        | 1                |
| DEG_APCC_TPR_1           | This short C-terminal motif is present in co-activators, the Doc1/APC10 subunit and some substrates of the APC/C and mediates direct binding to TPR-containing APC/C core subunits.                | .[ILM]RS   | 22        | 0                |
| DEG_COP1_1               | A destruction motif interacts with the COP1 WD 40 domain for target ubiquitination and degradation.  | [STDE]{1,3}..{0,2}[TSDE].{2,3}VP[STDE]G{0,1}[FLIMVYPA] | 12        | 1                |
| DEG_CRL4_CDT2_1          | This degron overlaps a PCNA interaction protein (PIP) box and is recognised by the CRL4 <sup>Cdt2</sup> ubiquitin ligase in a PCNA- and chromatin-dependent manner.                                | [NQ]{0,1}..[ILMV][ST][DEN][FY][FY].[2,3][KR]{2,3}[^DE] | 6         | 0                |
| DEG_CRL4_CDT2_2          | This degron, occurring in non-Vertebrates, overlaps a PCNA interaction protein (PIP) box and is recognised by the CRL4 <sup>Cdt2</sup> ubiquitin ligase in a PCNA- and chromatin-dependent manner. | [NQ]{0,1}..[ILMV]T[DEN][HMFY][FMY].[2,3][KR]{2,3}[^DE] | 1         | 0                |
| DEG_Kelch_actininfilin_1 | A hydrophobic degron motif present in some kainate receptors necessary to interact with kelch domain of actininfilin protein for efficient ubiquitination and degradation.                         | [AP]P[MV][IM]V   | 1         | 0                |
| DEG_Kelch_Keap1_1        | Motif that binds to the Kelch domain of KEAP1 with high affinity. This high affinity motif is required for the efficient recruitment of target proteins to the Cul3-based E3 ligase.               | [DNS]..[DES][TNS]GE                                    | 13        | 4                |
| DEG_Kelch_Keap1_2        | Motif that binds to the Kelch domain of KEAP1 with low affinity. This low affinity motif is important for ubiquitination and degradation of target proteins.                                       | QD.DLGV  | 1         | 1                |
| DEG_Kelch_KLHL3_1        | An Acidic degron motif present in wnk kinases necessary to interact with kelch domain of KLHL2 and KLHL3 proteins for efficient ubiquitination degradation.  | E.EE.E[AV]DQH  | 4         | 0                |
| DEG_MDM2_SWIB_1          | An amphipathic $\alpha$ -helix found in p53 family members that binds in the hydrophobic slot of MDM2 SWIB domain.   | F[^P]{3}W[^P]{2,3}[VIL]                                | 5         | 2                |

Figure 3: The list of all motif classes annotated in the ELM database.

6. Scroll further down the DOC\_CYCLIN\_1 page to view the “Instances” header (Fig. 5) This table contains the list of all annotated DOC\_CYCLIN\_1 instances in the database of this motif. 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 in which species in which 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 this structure exists in PDB.

The instance “logic” is an annotation of whether 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 showing 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

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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 of the manual annotation details for the DOC\_CYCLIN\_1 motif, the biological background summarized from the scientific literature including links to the primary literature and to external resources (Pubmed [Coordinators \(2017\)](#), the Gene Ontology [Consortium \(2017\)](#), PDB ([Berman et al. \(2002\)](#)) and more).

not. The overwhelming majority of instances in ELM are TPs.

- Click on the sub-menu **ELM instances** in **ELM DB** to visit the page where you can search and browse the instances annotated in ELM. (Fig. 6). Note that only the first 100 instances matching the search criteria are shown. The search form can be used to filter results by a full text search, by instance logic, or organisms.

*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.*

- 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 subsequence (highlighted in red) to go to

ELM

**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](#)

**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<br>P53_HUMAN     | 381   | 385  | GQSTSRH <b>KKLME</b> KTEGPDS   | TP    | 4    | Homo sapiens (Human)                     | ⚡ 1H26                  |
| P46527 CDKN1B<br>CDN1B_HUMAN | 30    | 33   | EHPKPSAC <b>RNLFG</b> PVDHEEL  | TP    | 5    | Homo sapiens (Human)                     | 1H27 ⚡ 1JSU<br>1⚡<br>1⚠ |
| P38936 CDKN1A<br>CDN1A_HUMAN | 19    | 22   | NPCGSKAC <b>RRLE</b> GPVDSEQL  | TP    | 4    | Homo sapiens (Human)                     | 1⚠<br>1⚠                |
| P06789 E1<br>VE1 HPV18       | 127   | 130  | NSGQKKAK <b>RRLE</b> TISDSGYG  | TP    | 3    | Human papillomavirus type 18             | 1🌐                      |
| Q99741 CDC6<br>CDC6_HUMAN    | 94    | 98   | HSHTLKG <b>BRLVFD</b> DNQLTIKS | TP    | 2    | Homo sapiens (Human)                     | ⚡ 2CCH<br>1⚠            |
| Q14207 NPAT<br>NPAT_HUMAN    | 1062  | 1066 | AAKPCHR <b>RVLCF</b> DSTTAPVA  | TP    | 1    | Homo sapiens (Human)                     |                         |
| P39880 CUX1<br>CUX1_HUMAN    | 1301  | 1305 | NYRSRIR <b>RELFI</b> EEIQAGSQ  | TP    | 1    | Homo sapiens (Human)                     |                         |
| P38826 ORC6<br>ORC6_YEAST    | 178   | 182  | ESPSITR <b>RKLA</b> FEEDEDEDE  | TP    | 1    | Saccharomyces cerevisiae (Baker's yeast) |                         |
| Q9WTQ5 Akap12<br>AKA12_MOUSE | 501   | 504  | IKVQGSPL <b>KKLF</b> SSSGLKKL  | TP    | 1    | Mus musculus (House mouse)               | 1⚠                      |
| Q00716 E2F3<br>E2F3_HUMAN    | 134   | 138  | GGGPPAK <b>RRL</b> EGESGHQYL   | TP    | 1    | Homo sapiens (Human)                     |                         |
| Q14209 E2F2<br>E2F2_HUMAN    | 87    | 91   | AGRIPAK <b>RKLDL</b> EGIGRPVV  | TP    | 1    | Homo sapiens (Human)                     |                         |
| Q01094 E2F1<br>E2F1_HUMAN    | 90    | 94   | LGRPPVK <b>RRLDI</b> ETDHOYLA  | TP    | 3    | Homo sapiens (Human)                     | ⚡ 1H24                  |
| P50445 rux                   | ...   | ...  | ...                            | ...   | ...  | ...                                      | ...                     |

Figure 5: The second part of the **DOC\_CYCLIN\_1** motif details page shows the motif abstract GO terms, and the list of annotated instances.

the instance details page of this instance (Fig. 7) The top part of the page contains details about the instance and the protein it was identified in, and link to the Uniprot entry for the protein [Consortium \(2015\)](#).

9. Scroll down to the “Instance Evidence” header to view details on the experimental evidence used to annotate this instance. The each experimental method is annotated using the Proteomics Standards Initiative Method Identifier (PSI-MI) [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”, which can be any of “certain”, “likely”, “unlikely” or “unspecified”.*

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### Search ELM Instances

Full-Text Search (use "\*" to get all instances)

Filter by instance Logic  
Filter by organism

submit Reset

export 100 instances as: gff pir fasta tsv

| CLV              | DEG                          | DOC   | LIG  | MOD                   | TRG   | latest 100 Instances   |  |            |
|------------------|------------------------------|-------|------|-----------------------|-------|--|--|------------|
|                  |                              |       |      |                       |       | (click table headers for sorting; Notes column: ⚡ =Number of Switches, 🌐=Number of Interactions) |  |            |
| ELM identifier   | Acc., Gene-, Name            | Start | End  | Subsequence           | Logic | #Ev.   | Organism                                       | Notes      |
| DOC_MAPK_HePTP_8 | P08018 PBS2<br>PBS2_YEAST    | 217   | 234  | SLSARRGLKLPPGGMSLKMP  | U     | 1  | Saccharomyces cerev...<br>1                    | 1🌐         |
| DOC_MAPK_HePTP_8 | P35236 PTPN7<br>PTN7_HUMAN   | 38    | 50   | HVRQLERRGSNSVALLDVRS  | TP    | 6  | Homo sapiens (Human)<br>1                      | 2GPH       |
| DOC_MAPK_HePTP_8 | P15822 HIVEP1<br>ZEP1_HUMAN  | 1422  | 1437 | PILERRGPLVROISLNIAPI  | TP    | 1  | Homo sapiens (Human)<br>2                      | 2🌐         |
| DOC_MAPK_HePTP_8 | Q15256 PTPRR<br>PTPRR_HUMAN  | 333   | 345  | PIGLQERRGSNSVSLTDMSSS | TP    | 3  | Homo sapiens (Human)<br>1                      | 1🌐         |
| DOC_MAPK_HePTP_8 | P54829 PTPN5<br>PTN5_HUMAN   | 239   | 251  | SMGLQERRGSNSVSLTDMSCT | TP    | 5  | Homo sapiens (Human)<br>3                      | 3🌐         |
| DOC_MAPK_HePTP_8 | Q62132 Ptprr<br>PTPRR_MOUSE  | 332   | 344  | PIGLQERRGSNSVSLTDMSSS | TP    | 3  | Mus musculus (House mouse)<br>2                | 2🌐         |
| DOC_MAPK_HePTP_8 | P06784 STE7<br>STE7_YEAST    | 7     | 19   | RKTQLBRNLKGLNLNLHPDV  | TP    | 9  | Saccharomyces cerev...<br>(Baker's yeast)<br>3 | 2B9H<br>3🌐 |
| DOC_MAPK_HePTP_8 | P38590 MSG5<br>MSG5_YEAST    | 26    | 38   | PRSLQRNRTKHLSDLIAALH  | TP    | 3  | Saccharomyces cerev...<br>(Baker's yeast)<br>1 | 2B9I<br>1🌐 |
| DOC_MAPK_HePTP_8 | Q6PJF5 RHBDF2<br>RHDf2_HUMAN | 19    | 31   | SSRLQSRKPPNLSITIPPE   | TP    | 1  | Homo sapiens (Human)<br>1                      | 1🌐         |
| DOC_MAPK_HePTP_8 | Q96CC6 RHBDF1<br>RHDF1_HUMAN | 12    | 24   | TSSLQRKPPNWLKDIPSAV   | TP    | 3  | Homo sapiens (Human)<br>1                      | 1🌐         |

Figure 6: The “instances” page can be used to search for instances in the ELM database.

## 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 DOC\_WW\_PIN1\_4 motif 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 subsequence which will take you to the details page (Fig. 8). This page is similar to that described for the P53 instance DOC\_CYCLIN\_1 (Fig. 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 (Fig. 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.

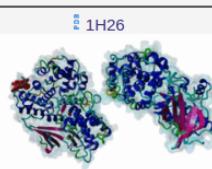
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**DOC CYCLIN\_1**

■ Instance

| Accession  | Acc. Gene-, Name         | Start | End | Subsequence                    | Logic | PDB   | Organism             | Length |
|------------|--------------------------|-------|-----|--------------------------------|-------|---|----------------------|--------|
| ELMI000051 | P04637 TP53<br>P53_HUMAN | 381   | 385 | GQSTSRRH <b>KKLMF</b> 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 Consortium (2015), PDB Berman et al. (2002), NCBI taxonomy, Pubmed Coordinators (2017), and KEGG Pathways Kanehisa et al. (2016), as well as the PSI-MI controlled vocabulary Kerrien et al. (2007).

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)) (Fig. 8). This particular instance is involved in the switch phosphorylating P53. Clicking on the diagram will open an external link to the switches.ELM website.

## Exploring Links External Protein Resources

13. Click on the sub-menu **ELM methods** in **ELM DB** to see a list of all experimental methods which have been used to identify motifs and instances (Fig 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

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**DOC WW Pin1 4**

■ Instance

| Accession  | Acc. Gene-, Name         | Start | End | Subsequence                            | Logic | PDB | Organism             | Length |
|------------|--------------------------|-------|-----|--|-------|-----|----------------------|--------|
| ELMI001957 | P04637 TP53<br>P53_HUMAN | 30    | 35  | WKLLPEN <b>N</b> VLSP <b>L</b> 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)<br>WW domain | 7            | 37         |                         | [tsv]<br>[xml] |

■ Switches

This ELM instance is part of the following 1 switching mechanism annotated at the [switches.ELM](#) resource:

- 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.

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”.

of experiment (in vitro/in vivo). 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.*

- Click on the sub-menu **ELM pdb structures** in **ELM DB** to see a list of all macromolecular structures in the ELM database (Fig. 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 filter bar on the top page can be used to filter the list of structures shown. The yellow tsv link creates a downloadable file in “tab separated values” format.*

- Click on the sub-menu **ELM binding domains** under **ELM DB** to see a complete list of all the interaction domains in ELM (Fig. 11). This table shows the ELM classes which have been annotated

The screenshot shows the ELM (Eukaryotic Linear Motif) database 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 "admin". Below the navigation is a search bar labeled "search ELM Database". The main content area has a title "112 different methods used in ELM annotation". A sub-section below it states: "The following table holds all methods which have been used during the ELM rigorous data curation process. Furthermore, the number of ELM instances for which experimental evidence has been annotated are listed. We use methods from, and provide linkout to, the PsiMi (Proteomics Standards Initiative - Molecular Interaction) controlled vocabulary." A table follows, with columns: ID, PSIMI ID, Method, Biosource, Interaction, #Instances, and Notes. The table contains 22 rows of data.

| 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, along with their PSI-MI identifiers.

with a corresponding interaction domain. This table shows 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.

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

- Click on the sub-menu **ELM switches** in **ELM DB** to see a complete list of all the switches in ELM (Fig. 12). This table shows the motif class, contains a link to Uniprot, and the start and stop positions of the motif mediating the switch. The last two columns have links to switches.ELM, and a brief description of the switch also taken from switches.ELM [Van Roey et al. \(2013\)](#).

*The filter bar on the top page can be used to quickly filter the list of interactions shown.*

The screenshot shows the ELM (Eukaryotic Linear Motif) 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 "admin". A search bar labeled "search ELM Database" is also present. The main content area displays a table titled "428 PDBs found:".

**Table Headers:**

- PDB\_ID
- Title
- ELM instance
- ELM class

**Table Data:**

|                      |   |             |                     |
|----------------------|---|-------------|---------------------|
| <a href="#">2FOP</a> | The crystal structure of the n-terminal domain of hausp/usp7 complexed with mdm2 peptide 147-150  | MDM2_HUMAN  | DOC_USP7_MATH_1     |
| <a href="#">2FOO</a> | The crystal structure of the n-terminal domain of hausp/usp7 complexed with p53 peptide 359-362   | P53_HUMAN   | DOC_USP7_MATH_1     |
| <a href="#">2G2L</a> | Crystal structure of the second pdz domain of sap97 in complex with a glut-a c-terminal peptide   | GRIA1_RAT   | LIG_PDZ_Class_1     |
| <a href="#">2G30</a> | Beta appendage of ap2 complexed with arh peptide  | ARH_HUMAN   | TRG_AP2beta_CARGO_1 |
| <a href="#">2GBQ</a> | 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           |
| <a href="#">2GPH</a> | Docking motif interactions in the map kinase erk2   | PTN7_HUMAN  | DOC_MAPK_HePTP_8    |
| <a href="#">2GPO</a> | Estrogen related receptor-gamma ligand binding domain complexed with a synthetic peptide from rip140  | NRIP1_HUMAN | LIG_NRBOX           |
| <a href="#">2GTH</a> | Crystal structure of the wildtype mhv coronavirus non-structural protein nsp15  | R1AB_CVMA5  | LIG_Rb_LxCxE_1      |
| <a href="#">2HE2</a> | Crystal structure of the 3rd pdz domain of human discs large homologue 2, dlg2  | AT2B4_HUMAN | LIG_PDZ_Class_1     |
| <a href="#">2HE4</a> | 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     |
| <a href="#">2HGO</a> | Structure of the west nile virus envelope glycoprotein  | Q3I0Y8_WNV  | MOD_N-GLC_1         |
| <a href="#">2HKQ</a> | 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       |
| <a href="#">2I04</a> | X-ray crystal structure of magi-1 pdz1 bound to the c-terminal peptide of hpv18 e6  | VE6 HPV18   | LIG_PDZ_Class_1     |
| <a href="#">2I01</a> | X-ray crystal structure of sap97 pdz3 bound to the c-terminal peptide of hpv18 e6   | VE6 HPV18   | LIG_PDZ_Class_1     |
| <a href="#">2IOL</a> | X-ray crystal structure of sap97 pdz2 bound to the c-terminal peptide of hpv18 e6.  | VE6 HPV18   | LIG_PDZ_Class_1     |
| <a href="#">2I1N</a> | Crystal structure of the 1st pdz domain of human dig3   | AT2B4_HUMAN | LIG_PDZ_Class_1     |
| <a href="#">2I3S</a> | Bub3 complex with bub1 glebs motif  | BUB1_YEAST  | LIG_GLEBS_BUB3_1    |
| <a href="#">2I3T</a> | Bub3 complex with mad3 (bur1) glebs motif   | MAD3_YEAST  | LIG_GLEBS_BUB3_1    |
| <a href="#">2IHS</a> | Crystal structure of the b30.2/spry domain of gustavus in complex with a 20-residue vasa peptide  | VASA1_DROME | LIG_SPRY_1          |
| <a href="#">2IVR</a> | Beta apoindole in complex with b-arrestin neotide   | ARRB1_HUMAN | TRG_AP2beta_CARGO_1 |

Figure 10: The list of all known structures in PDB which are also in ELM.

## Visualizing KEGG pathways from ELM

17. Click on the sub-menu **ELM pathways** in **elm DB** to see a list of all KEGG pathways contained in ELM (Fig. 13). Pathways are from the “Kyoto Encyclopedia of Genes and Genomes” (KEGG Kanehisa et al. (2016)) database mapped to ELM instances.
18. On the “ELM pathways” page (Fig. 14) click on the link **gallus gallus** to navigate to the page containing all pathways annotated for chicken.
19. One the page with chicken pathways (Fig. 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 right side of figure 15).

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290 interaction domains annotated in ELM

Filter this table

export as: [tsv](#)

| 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_COP1             | 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               | Dynamin_light           | Dynamin light chain-type 1                                      |

Figure 11: A list of all interactions annotated in the database.

## 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 (Fig. 18). The columns are identical to those listed in Step 7 (Fig. 6).

*The green buttons on the left can be used to filter this table by motif class. 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 all motif classes that have been annotated with a disease (Fig. 17). Disease information is taken from the Online Mendelian Inheritance in Man (OMIM) database McKusick (2007).

The screenshot shows the ELM (Eukaryotic Linear Motif) website interface. At the top, there's a navigation bar with links to 'ELM Home', 'ELM Prediction', 'ELM DB', 'ELM Candidates', 'ELM Information', 'ELM downloads', and a user account section for 'admin'. Below the navigation is a search bar labeled 'search ELM Database'. The main content area is titled 'The Eukaryotic Linear Motif resource for Functional Sites in Proteins'. A sub-section titled 'ELM Switches' is shown, with a table listing various switches. The table columns are: 'ELM class', 'Sequence Id', 'Start/Stop', 'Switch Id', and 'Description'. Each row provides a detailed description of the switch's function and context within a protein.

| 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 <a href="#">switch details</a> ).  |
| 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</i> .   |

Figure 12: A list of all switches annotated switches.ELM also contained in ELM.

## 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 to build regular expressions to define motif classes.

## Protocol 2 General Search Box

A general search text box is available to query the entire collection of manually curated information in ELM DB. This search field can be found at the top of almost all pages on the ELM website (for example in Fig. 21). This search is a full-text search across multiple selected data sources in the database, including protein and ELM class.

The screenshot shows the Eukaryotic Linear Motif (ELM) website. At the top, there is a logo consisting of the letters 'ELM' in a stylized font. Below the logo, the text 'The Eukaryotic Linear Motif resource for Functional Sites in Proteins' is displayed. A search bar labeled 'search ELM Database' is present. The navigation menu includes links for 'ELM Home', 'ELM Prediction', 'ELM DB', 'ELM Candidates', 'ELM Information', 'ELM downloads', and 'admin'. The main content area has a heading 'Pathways linked from ELM instances'. Below this, a sub-headline states: '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 input field and a 'submit' button are shown. A large list of taxon names follows, each with a count in parentheses:

- [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)

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

Figure 13: A list of all Pathways from KEGG with proteins in 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.

### Using the General Search

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.

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 search across in-

The screenshot shows the ELM (Eukaryotic Linear Motif) website interface. 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 this, a table lists various KEGG pathways and their details. To the right of the table, there is a sidebar with information about pathway coloring and links to KEGG.

| 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           |

Please cite: ELM 2016-data update and new functionality of the eukaryotic linear motif resource. (PMID: 26615199) [feedback@elm.eu.org](mailto:feedback@elm.eu.org)

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

Figure 14: A list of all KEGG pathways in *Gallus gallus* involving proteins annotated in ELM.

stances, motif classes and switches to find any matches to the search query “P04637”. The results are grouped into matching instances (Fig. 19) candidate classes and switches (Fig. 20). As there are no classes with “P04637” in the name, no classes are returned with this query.

*The “candidate classes” are a separate part of ELM, where users can propose novel classes to be annotated. Although these are returned by the general search, we would advise users not to use this data, as it is 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 search query (Fig. 21) in this case 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 important to keep in mind when using the general search field.

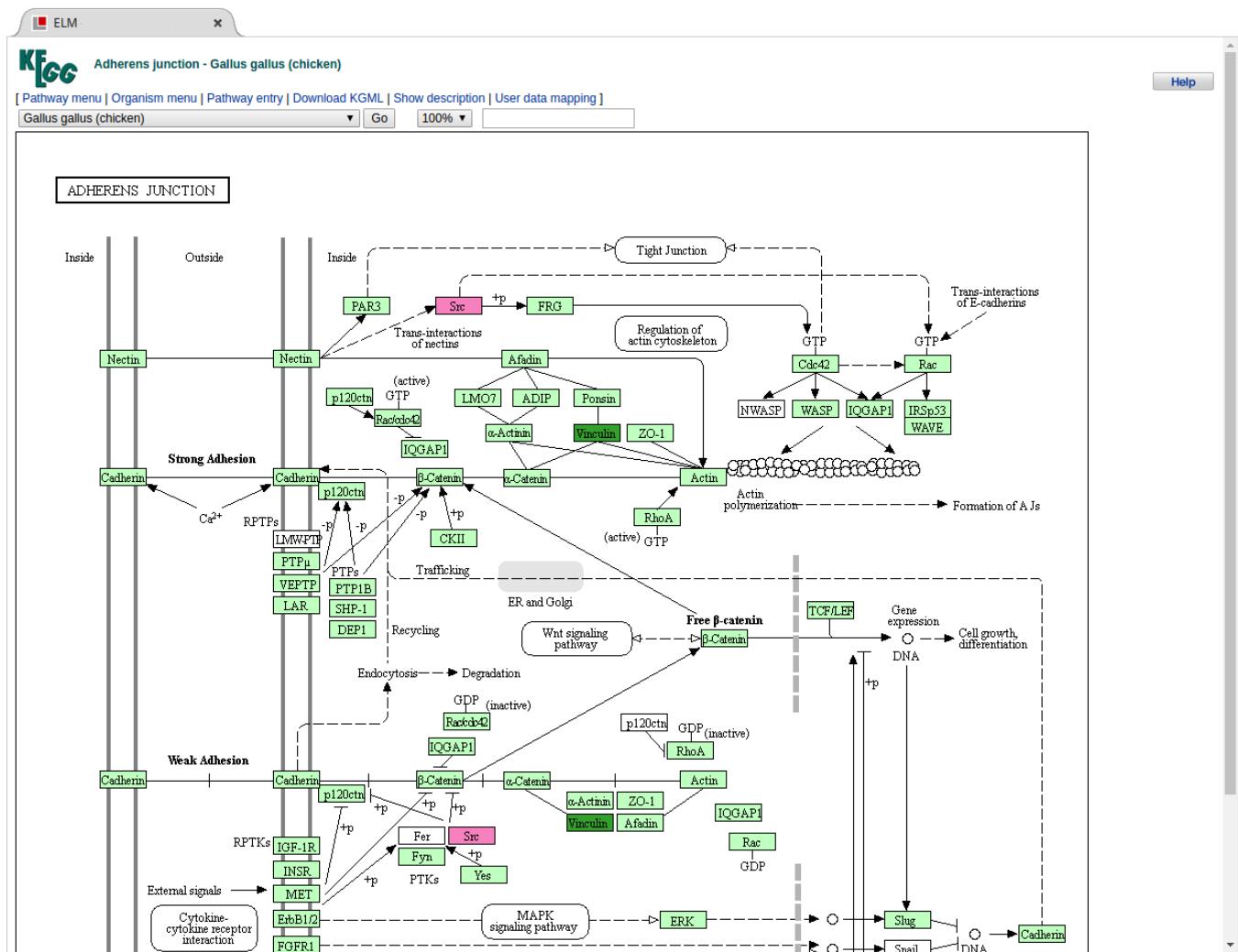


Figure 15: A list of all annotated pathways for taxon *Gallus gallus*

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: gif pir fasta tsv

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

| ELM identifier    | Acc., Gene-, Name              | Start | End | Subsequence                        | Logic | #Ev. | Organism   | Notes |
|-------------------|--------------------------------|-------|-----|------------------------------------|-------|------|--|-------|
| CLV_PCSK_FUR_1    | Q056861 env ENV_FFV            | 124   | 128 | GNTSSSSR <del>RRRD</del> IQYHKLPV  | TP    | 4    | Feline foamy virus                                       | 1⚡🌐   |
| CLV_PCSK_FUR_1    | P03383 env ENV_HTV2            | 305   | 309 | PVPPPAT <del>RRRA</del> VPIAVWLW   | TP    | 3    | Human T-lymphotro...                                     | 1🌐    |
| CLV_PCSK_FUR_1    | P03375 env ENV_HV1B1           | 508   | 512 | AKRRVVQ <del>REKRA</del> VGIGALFL  | TP    | 3    | Human immunodefic...                                     | 1🌐    |
| CLV_PCSK_FUR_1    | P03420 F FUS_HRSVA             | 133   | 137 | NVTLSSKK <del>RKRRF</del> LGFLLGVG | TP    | 3    | Human respiratory...                                     | 1🌐    |
| CLV_PCSK_FUR_1    | P03188 gB GB_EBVB9             | 429   | 433 | TPAAVL <del>RRRD</del> AGNATPPV    | TP    | 1    | Human herpesvirus... (Epstein-Barr virus (strain B95-8)) |       |
| CLV_PCSK_FUR_1    | P27909 POLG_DEN1B              | 202   | 206 | SQTGEHR <del>RDKRS</del> VALAPHVG  | TP    | 3    | Dengue virus 1 Br...                                     | 1🌐    |
| CLV_PCSK_FUR_1    | P11223 S SPIKE_IBVB            | 534   | 538 | KITNGTR <del>RFRRS</del> ITENVANC  | TP    | 2    | Avian infectious ...                                     |       |
| CLV_PCSK_FUR_1    | P11223 S SPIKE_IBVB            | 687   | 691 | LLTNPSS <del>RRKRS</del> LIEDLLFT  | TP    | 2    | Avian infectious ...                                     |       |
| CLV_PCSK_FUR_1    | Q05320 GP VGP_EBOZM            | 498   | 502 | GLITGGR <del>RTTRE</del> AIVNAQPK  | TP    | 4    | Ebola virus - May...                                     | 1⚡🌐   |
| CLV_PCSK_FUR_1    | P03107 L2 VL2 HPV16            | 9     | 13  | RHKRS <del>AKRTKRA</del> SATQLYKT  | TP    | 1    | Human papillomavi...                                     | 1🌐    |
| CLV_PCSK_FUR_1    | P60170 GP VSGP_EBOZM           | 321   | 325 | EPKTSVV <del>RVRRE</del> LLPTQGPT  | TP    | 3    | Ebola virus - May...                                     |       |
| DEG_APCC_KENBOX_2 | P03116 E1 VE1_BPV1             | 27    | 31  | TEAECES <del>DKENE</del> EPGAGVEL  | TP    | 1    | Bovine papillomav...                                     |       |
| DEG_SCF_FBW7_2    | P03070 Large T antigen LT_SV40 | 699   | 705 | ICRGFTCFKK <del>PTPPPPE</del> PET  | TP    | 3    | Simian virus 40  | 1⚡    |

Figure 16: A table of the ELM instances abused by viruses.

The screenshot shows the ELM (Eukaryotic Linear Motif) website interface. 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". A search bar labeled "search ELM Database" is also present. The main content area has a title "The Eukaryotic Linear Motif resource for Functional Sites in Proteins". Below this, a section titled "Diseases mediated by short linear motifs" lists several diseases. To the right of this section is a sidebar with two items: "Diseases mediated by short linear motifs" and "Pathogens abusing linear motifs".

**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 [[Cordedu et al., 2007](#)].

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

An autosomal recessive wasting disorder of renal Mg<sup>2+</sup> and Ca<sup>2+</sup> 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<sup>Cdt2</sup> ubiquitin ligase in a PCNA-dependent manner. Mutations in this motif result in excess inhibition of growth and differentiation.

Figure 17: A list of all diseases in ELM.

The screenshot shows the ELM (Eukaryotic Linear Motif) website's help and questions & answers 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 section. The main content area has a title "The Eukaryotic Linear Motif resource for Functional Sites in Proteins". Below the title is a search bar labeled "search ELM Database". The left sidebar contains a heading "ELM Help page" and a section titled "Questions and answers" with a list of questions:

- 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?

At the bottom of the left sidebar, there are links for "Please cite" (PMID: 26615199), "Software License Agreement", and an email address "feedback@elm.eu.org".

The right sidebar is titled "Dictionary" and contains definitions for several terms:

- 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.

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

Figure 19: The instances retrieved when performing a general search for P53\_HUMAN using its Uniprot identifier “P04637”.

ELM

### ELM Switches

| Diagram | Switch     | Description   |
|---------|------------|---|
|         | SWTI000456 | Phosphorylation of <a href="#">Cellular tumor antigen p53 (TP53)</a> on T18 (in vitro by <a href="#">Casein kinase I subfamily</a> , requiring prior phosphorylation of S15) inhibits its binding to <a href="#">E3 ubiquitin-protein ligase Mdm2 (MDM2)</a> . 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 <a href="#">Cellular tumor antigen p53 (TP53)</a> , abrogating binding to <a href="#">E3 ubiquitin-protein ligase Mdm2 (MDM2)</a> . 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 <a href="#">Cellular tumor antigen p53 (TP53)</a> , abrogating binding to <a href="#">Ubiquitin carboxyl-terminal hydrolase 7 (USP7)</a> .   |
|         | SWTI000520 | Alternative splicing removes the deubiquitinating enzyme USP7-binding motif of <a href="#">Cellular tumor antigen p53 (TP53)</a> , abrogating binding to <a href="#">Ubiquitin carboxyl-terminal hydrolase 7 (USP7)</a> .   |
|         | SWTI000037 | Phosphorylation of S33 in the Pin1-binding motif of <a href="#">Cellular tumor antigen p53 (TP53)</a> induces binding to the <a href="#">Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 (PIN1)</a> protein.   |
|         | SWTI000038 | Phosphorylation of S151 in the Pin1-binding motif of <a href="#">Cellular tumor antigen p53 (TP53)</a> induces binding to the <a href="#">Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 (PIN1)</a> protein.  |
|         | SWTI000039 | Phosphorylation of T81 in the Pin1-binding motif of <a href="#">Cellular tumor antigen p53 (TP53)</a> induces binding to the <a href="#">Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 (PIN1)</a> protein.   |

Figure 20: The 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: The results retrieved when performing a general search for P53\_HUMAN using the query “p53”.

## Protocol 3 Predicting ELMs in proteins

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 remove false positives and creates a diagram to visualize 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, and how to find the motif 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”. The page should autocomplete/suggest the protein “P53\_HUMAN / P04637 (Homo sapiens)” (Fig. 22). Click on this entry to confirm that we want to search for motifs in this protein. Click on **Submit** to submit the query to the server.

*The autocompletion mechanism queries Uniprot for protein identifier; if it succeeds, then additional information from Uniprot will be used to pre-populate the filter 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 allow all other detected motifs to be shown.*

2. Select the search criteria (optional). It is possible to limit the results by “cell compartment”, “taxonomic context” or by changing the “motif probability cutoff”. To restrict the search to include motifs that are active in certain cellular compartments, select one or more from the 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. For the current protocol, leave all of these at their default values: “not specified”, “100” and no “taxonomic context”

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](#), [\[RANDOM\]](#)  
[P53\\_HUMAN](#)

Or paste the sequence (Single letter code sequence only or FASTA format):  
>P53\_HUMAN  
MEEPQSDPSVEPPLSQETFSDLWKLPPENNVLSPLPSQAMDDILMSLPDDIEQWFTEDPGPDEAPRMPEAAPVAPAPAAPTAA  
APAPAPSWPLSSVPSQRTYGGYGRFLGFLHSGTAKSCTVCTYSPALNMFCQLAKTCCPVLQWLWDSTPPPGTRVRAMAIIYKQS  
QHMTTEVVRRCFPHERCSDSDGLAPPQHLLRVEGNLRVEYLDRNTFRHSVVPVPEPPEVGSCTTIHNYMCNSCMGGMNRR  
PILTIITLEDSSGNLLGRNSFEVRCACPGDRRTEENLKKGEPHHELPGSTRKRALPNNTSSPQPKKKPLDGEYFTLQI  
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):  
[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\\_PxPxL\\_1](#), [LIG\\_CSL\\_BTD\\_1](#), [LIG\\_G3BP\\_FGDF\\_1](#), [LIG\\_KLC1\\_TPR\\_1](#), [LIG\\_PALB2\\_WD40\\_1](#), [LIG\\_UFM1\\_UFIM\\_1](#)

These ELM classes have been updated:

Figure 22: The ELM input page for predicting motifs in a protein.

TODO: Repeat search using stringent filters (homo sapiens, nucleus, 0.01) Do we want to do this? - Marc

### 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 interpreting 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 which are manually annotated in the database appear as red (TP) or yellow (FP) ovals in the graphic. Blue/gray squares represent predicted motif occurrences.*

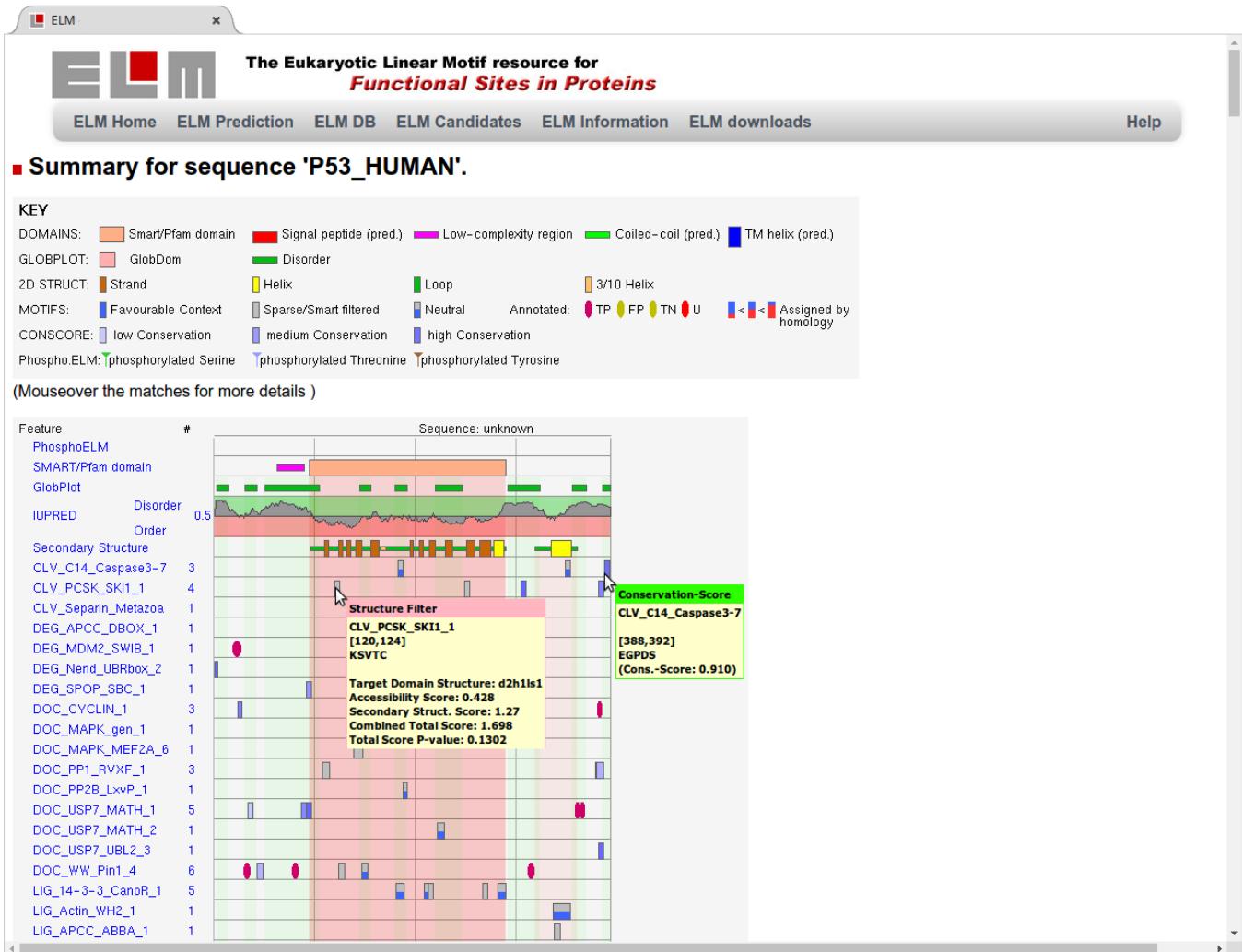


Figure 23: The graphical results summary of the ELM Prediction pipeline for P53\_HUMAN . Note that not all motif detections are shown (the image is truncated at the bottom). The top five rows show a set of structural features. Annotated and predicted motifs are shown as differently colored ovals/boxes. The info screens for two motifs are shown: CLV\_C14\_CASPASE3-7 and CLV\_PCSK\_SKI1\_1 .

4. The first row contains phosphorylation sites as retrieved from phospho.ELM Dinkel et al. (2011), and whether the phosphorylated amino acid is a serine, threonine or tyrosine. Phospho.ELM is a database of manually annotated phosphorylation sites obtained from scientific publications from low and high-throughput experiments. You can follow the link to phospho.ELM 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 there is relevant information annotated in the phospho.ELM database. Phosphorylation sites are relevant to interpret ELM motif predictions when the predicted motif requires to be phosphorylated (as in several docking and ligand binding motifs) and for predicting phosphorylation motifs.*

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) (Fig. 23). Hover the mouse over these domains to see their names and exact start and end positions.

*In order to be functional motifs to be accessible, and therefore they are usually not found within globular domains and structured regions (Davey et al. (2012)). Any motifs detected by the ELM prediction pipeline inside of a smart domain are less likely to be functional, and are shown as a gray box background (see also the “structural filter” described in Protocol 6).*

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.

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

7. The 5th row (Fig. 23) contains information on secondary structure. The secondary structure is predicted using a pipeline mapping motif occurrence onto high quality reference domain structures Via et al. (2009). Check the graphical representation, and if the output of the secondary structure filter and the disorder predictors agree with respect to which parts of the sequence are considered structured and which disordered.
8. The remainder of the figure (below “secondary structure” output) displays predicted and annotated motif instances, overlayed with the structural context from rows 2 and 3 (SMART domains and GlobPlot). A blue square indicates a single motif occurrence, and intensity of the color indicates the conservation of this sequence across a group of homologous proteins. Boxes in gray are motif occurrences which have been filtered out by the structure filter. Boxes that are blue & gray are neutral (residing in structural context, but the secondary structure detected a loop region). If the sequence is already present in the ELM database, any motif instances that have already been annotated are shown as ovals. Lastly, any motifs detected which are annotated to be functional in homologous sequences, are shown as red & blue rectangles.

*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.*

TODO: EXPLAIN / SHOW ANNOTATED INSTANCES Marc: Use mouse over in this figure.

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 confidence score is based on how conserved the sequence is across a set of homologous proteins from other sequences. A full description of the method can be found in Chica et al. (2008). The higher the conservation score (max. 1), the more conserved the motif’s sequence is, and the more likely it is a functional motif for this prediction.*

10. Place the cursor over the blue & gray rectangle for motif CLV\_PCSK\_SKI1\_1 at position 120-124, a motif which was flagged as “neutral” by the ELM prediction pipeline. This will trigger the information screen (with the pink header) shown in Fig. 23 to appear. This motif resides inside of the P53 Pfam domain, and thus has been subjected to “structural filtering”. However, the secondary structure prediction suggests 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, combined total score, and the associated total score P-value Via et al. (2009).*

The screenshot shows the ELM web interface with the following sections:

- Filtering summary:**
  - User supplied cellular location(s): nucleus, cytosol, endoplasmic reticulum, mitochondrion, Cytoplasm
  - User supplied taxon: Homo sapiens
  - (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 MEEPQSDPSVEPPPLSQETFSDLWKLPPENNVLSPLSQAMDDLMLSPDDEIEQWFTEDPGP DEAPRMPPEAAPPVAPAPAAPTAAAPAPAPSPWLSSVSPSQKTYQGSYGRFLGLHSGTAK SVTCCTSPALNPKMFQLAKTCPVQLWVDSTPPGTRVRAMAIFYKQSQHMTEVVRRCPHHE RCDSDSGDGLAPPQHLIRVEGNLRLVEYLDDRNTRFRHSVVVPYEPPEVGSDCTTIHYNYMCNS SCMGGMNRPRPILTIIITLEDSSGNLLGRNIFEVRYVCACPGRDRTEEENLRKKGEPHHELP PGSTKRALPNNTSSSPKPKKPLDGEYFTLQIRGRERFEMFRELNEALELKDAQAGKEPG GSRAHSSHLSKKGQSTSRRHKKLMFKTEGPDS
- 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<br>364-368 | true positive<br>true positive | The USP7 MATH domain binding motif variant based on the MDM2 and p53 interactions.                                    | nucleus          | [PA][^P][FYWIL]S[^P]    |
| DEG_MDM2_SWIB_1 | FSDLWKLL                     | 19-26              | true positive                  | An amphipathic $\alpha$ -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] |

Figure 24: This section of the results contains additional details on the homologue alignments used to calculate the conservation score, filtering results and globular domains.

11. Scroll down to below the results graphic to find additional information on the ELM prediction pipeline’s results (Fig. 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). 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.*

12. 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 whether and which filters were applied in step 1 of this protocol. In this case 4 motifs (elms) 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).*

13. Scroll down to the section with the header “Globular domains/ TM domains and signal peptide detected by the SMART server” (Fig. 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 domains detected is the “P53” Pfam domain.
14. 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.
15. 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 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

■ 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<br>(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<br>AHSSH                  | 359-363<br>364-368        | true positive<br>true positive                                   | The USP7 MATH domain binding motif variant based on the MDM2 and p53 interactions.  | nucleus   | [PA][^P][FYWIL]S[^P]   |
| DEG_MDM2_SWIB_1     | FSDLWKLL                        | 19-26                     | true positive  | An amphipatic $\alpha$ -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](K).E   |
| MOD_GSK3_1          | NVLSPPLS                        | 30-37                     | true positive  | GSK3 phosphorylation recognition site   | cytosol, nucleus  | ...([ST])...[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][KR].(7,15)[^DE]<br>((K[RK])(RK))(([^DE]<br>[KR]) ([KR][^DE])) ^DE]  |
| MOD_CK1_1           | SQETFSD                         | 15-21                     | true positive  | CK1 phosphorylation site  | cytosol, nucleus  | S..([ST])...   |
| DOC_WW_Pin1_4       | NVLSPPL<br>AAPTPA<br>TSSSPQ     | 30-35<br>78-83<br>312-317 | true positive<br>true positive<br>true positive<br>true positive | The Class IV WW domain interaction motif is recognised primarily by the Pin1 phosphorylation-dependent prolyl isomerase.  | cytosol, nucleus  | ...([ST]).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]) ((DE),<br>(0,1)[LIM].(2,3)[LIVMF].[^P](2,3)[LMVF].[LMIV].[0,3][DEQ]) |

Figure 25: The ELM prediction pipeline section displaying the P53 motifs that are “known”, and have been annotated in the ELM database.

information on the Probability filter: the probability reflects the chance to observe this motif in any random amino acid sequence (see section [Protocol 1](#))

16. 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).” (Fig. 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<br>ELKDA<br>EGPDS      | 183-187 [A]<br>349-353 [A]<br>388-392 [A] | 183-187<br>349-353<br>- | Caspase-3 and Caspase-7 cleavage site.  | cytosol,<br>nucleus  | [DSTE][^P]<br>[^DEWHFYC]D[GSAN] | -                          | Output                 | 3.094e-03 |
| CLV_Separin_Metazoa | EVRRR                        | 171-175 [A]                               | 171-175                 | Separin cleavage site, best known in sister chromatid separation.   | centrosome,<br>nucleus,<br>cytosol                                 | E[IMPVL][MLVP]R.                | -                          | Output                 | 3.410e-04 |
| DEG_MDM2_SWIB_1     | FSDLWKLL                     | 19-26                                     | -                       | An amphipatic $\alpha$ -helix found in p53 family members that binds in the hydrophobic cleft of MDM2's SWIB domain.  | nucleus,<br>cytosol  | F[^P](3)W[^P](2,3)[VIL]         | Output Summary             | -                      | 2.125e-05 |
| DEG_SP0P_SBC_1      | PLSSS                        | 92-96 [A]                                 | 92-96                   | The S/T rich motif known as the SP0P-binding consensus (SBC) of the MATH-BTB protein, SP0P, is present in substrates that undergo SP0P/Cu3-dependant ubiquitination.  | nuclear speck,<br>nucleus,<br>Cu3-RING<br>ubiquitin ligase complex | [AVP].[ST][ST][ST]              | -                          | Output                 | 9.380e-04 |
| DOC_CYCLIN_1        | KLLP<br>RALP<br>KKLMF        | 24-27 [A]<br>306-309 [A]<br>381-385       | -<br>-<br>-             | 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,<br>nucleus  | [RK].L.(0,1)[FYLIVMP]           | Output Summary             | -                      | 5.324e-03 |
| DOC_PP1_RVXF_1      | RHKKLMFK<br>HKKLMFK          | 379-386 [A]<br>380-386 [A]                | -<br>-                  | 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,<br>protein phosphatase type 1 complex,<br>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,<br>calcineurin complex,<br>nucleus                        | L.[LIVAPM]P                     | -                          | Output                 | 2.296e-03 |
| DOC_USP7_MATH_1     | PLPSQ<br>PAPSW<br>PLSSS      | 34-38 [A]<br>87-91 [A]<br>02-06 [A]       | -<br>-<br>02-06         | The USP7 MATH domain binding motif variant based on the MDM2 and p53 interactions.  | nucleus  | [PA][^P][^FYWIL]S[^P]           | Output Summary             | Output                 | 1.239e-02 |

Figure 26: This table contains the list of motifs detected in the sequence (only the top part of the table is shown). These are predictions in the sense that the sequence is present, however its is known whether they are *bona-fide* motifs which are biologically functional.

■ 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].  | -                              | <a href="#">Output</a> |             |
| 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]                                  | -                              | <a href="#">Output</a> |             |
| 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]   | -                              | <a href="#">Output</a> |             |
| 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].  | -                              | <a href="#">Output</a> |             |
| 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.  | <a href="#">Output Summary</a> | <a href="#">Output</a> |             |
| LIG_14-3-3_CanoR_1 | 213-217 [A]<br>267-271 [A] | 213-217<br>267-271 | Canonical Arg-containing phospho-motif mediating a strong interaction with 14-3-3 proteins.  | cytosol, internal side of plasma membrane, nucleus   | R[^DE]{0,2}[DDEPGI](ST)([FWYLMV].)[(^PRIKGNJP)](^APRIKGN){2,4}[VILMFYWYP]) | -                              | <a href="#">Output</a> |             |
| 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].[ILMVP][FHY][DE]   | -                              | <a href="#">Output</a> |             |
| LIG_FHA_1          | 198-214 [A]                | 198-               | Phosphothreonine motif binding a subset of   | nucleus  | .(T).II.VI.  | -                              | <a href="#">Output</a> |             |

Figure 27: This table contains the list of motifs detected in the sequence (only the top part of the table is shown) which were excluded by the structural filter.

## Protocol 4 Predicting ELMs in novel sequences

TODO: DESCRIBE MOST PROBABLE MOTIF INSTANCES (COMPARED TO FILTERED)

We will use protein CV\_0974 (uniprot ID: Q7NZE8) as an example, a “probable tyrosine phosphatase” from *Chromobacterium violaceum*. This protein is predicted to be a tyrosine phosphatases because it has a “tyrosine phosphatase” (PTPc) domain.

### 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.

#### 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 can provide either a protein accession (from uniprot) or an amino acid sequence (simply the sequence, or a FASTA formatted entry) in which you want to detect SLiMs. Retrieve the FASTA formatted sequence from Uniprot (<http://www.uniprot.org/uniprot/Q7NZE8.fasta>), and enter it into the “sequence input text box”.

TODO: MENTION NOT TO USE “CHROMOBACTERIUM VIOLACEUM” IN THE ORGANISM BOX AND WHY

2. The Results are summarized in the first figure on the results page (see Fig. 29) The Graphical summary shows all of the final and intermediate results generated by the ELM Prediction pipeline, and can be used infer 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.
3. Check the first row to see whether there are phosphorylation sites acid is a serine, threonine or tyrosine. In this case, no phosphorylation data could be found in the Phospho.ELM database (Dinkel et al. (2011)).
4. Check the second row showing SMART and Pfam domains. Hover the mouse over these domains to see their names and exact start and end positions.
5. The third row shows globular and disordered regions in the sequence as predicted by GlobPlot (Linding et al. (2003)). The 4th & 5th rows contain results from IUPred (Dosztányi et al. (2005)), another unstructured region prediction tool. Protein segments with an IUPred score above 0.5 are 95% likely to be disordered.
6. Place the cursor over the blue box for motif occurrence “DOC\_USP7\_MATH\_1” at position 129-133. This motif is in a disordered region, and has not been filtered out by the structural filter. However, its conservation score is extremely low: 0.000, indicating it is not conserved in homologous proteins.

**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):  
>CV\_0974  
MSTIQTGIGQLGGRQLDLSRLDSLSGVNADKARIGIRKDGTLLVYTGRSYLLHPDQTRRADQFLKKHDLLIPGQKPREFRLAQI  
FDRPMALTQRNTQANETIARIPTQDVDTVRGGKPKLRLWDQAARPSGEPSGERASLKQRRAEHLKLQAPRAEARPEKH  
DAIKTELASRLGSSDQPSGLLQLKAQVGSSAEGARFLNDVGQARFRDIPITAATQVRAPDGAPL PANRVQVGGVNVAIASQY  
PKAAQLESYFGMLAANRTPVLVVLASADAMAKQGRGKADLPDYFSQSGRYVEVESKSKGSTTLEGGLEVRAYHLNRGAD  
HKSVSIPLVHPNWADFGAQGATALKALAQHVDAVADKTTAFYRDNNSSALNDPDKLLPVIIHRAGVGRGTGQIJAABELLKPG  
ASSLESIVADMGRGSRNHLMVQTSGQLSTLVDLAQQQGRAILQPETAAEPIYANQQAQAEPIYANDAPPPPRRRP

**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):

**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

**peptide from ELM class LIG\_PT\_B\_Apo\_2**

- 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\_PxLPxL\_1**, **LIG\_CSL\_BTD\_1**, **LIG\_G3BP\_FGDF\_1**, **LIG\_KLC1\_TPR\_1**, **LIG\_PALB2\_WD40\_1**, **LIG\_UFM1\_UFIM\_1**

Figure 28: **Figure BACT-BP-1:** The input query page for finding motifs in ELM. The sequence for *C. vilaceum* protein CV\_0974 was used as an example for this protocol.

Place the cursor over motif “DOC\_MAPK\_DCC\_7” at positions “334-343”. Despite the high conservation score (1.000), this motif is inside the PTPc domain (and a Globular regions), and therefore has been filtered out.

TODO: CHECK CONSERVATION FILTER

### Interpreting the prediction results: Additional Information

TODO: DESCRIBE HOW TO INTERPRETE THE PREDICTIONS USING THIS BACTERIAL EXAMPLE (OF WHICH NOT MUCH IS KNOWN). FOCUS ON HOW ONE SHOULD INTERPRETE THESE PREDICTIONS (LOOK AT DISORDER/GLOBULARITY, CONSERVATION)



Figure 29: **Figure BACT-BP-2:** The graphical results summary of the ELM Prediction pipeline for Probable Tyrosine phosphate (CV\_0974). Note that not all motif detections are shown (the image is truncated at the bottom). The top five rows show a handful of structural features. The motif occurrence are shown as blue boxes, the intensity of which indicates the conservation score. See steps XXX to YYY for more information.

## Protocol 5 Predicting ELMS in sequences using the 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 possibly 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.

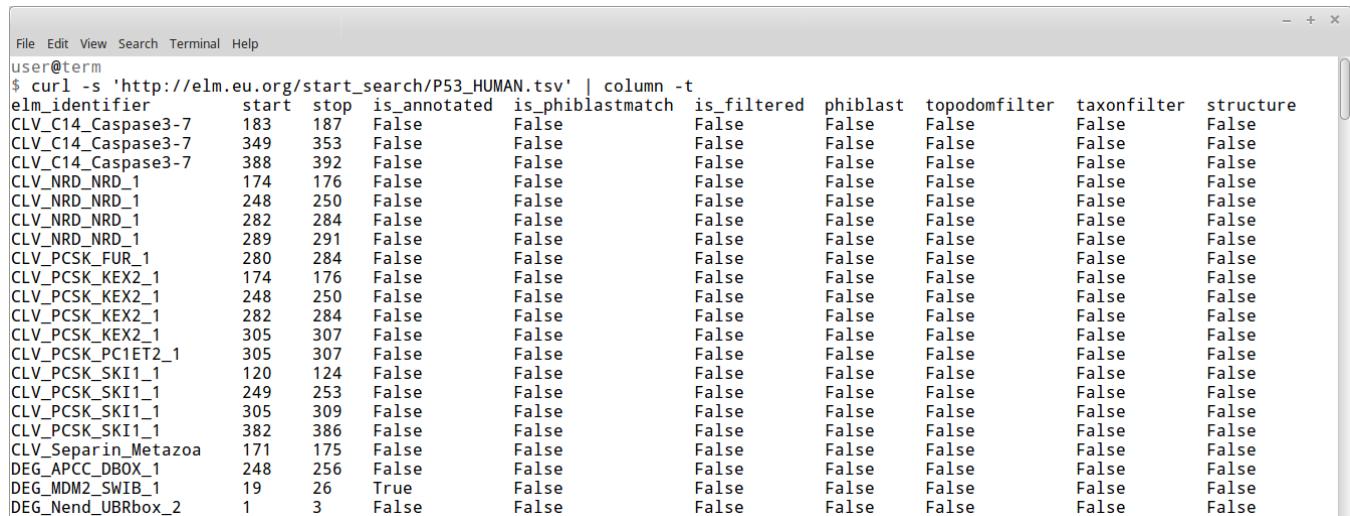
Currently, there exists a single URL ([elm.eu.org/start\\_search/](http://elm.eu.org/start_search/)) to accept such queries. You can choose to either submit a uniprot name or accession (eg. '[elm.eu.org/start\\_search/P53\\_HUMAN.tsv](http://elm.eu.org/start_search/P53_HUMAN.tsv)') or submit your raw sequence (e.g. '[elm.eu.org/start\\_search/MAPRGFSCLLLTSEIDLGVKRRA](http://elm.eu.org/start_search/MAPRGFSCLLLTSEIDLGVKRRA)'). 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

Ideally use curl [curl.haxx.se/](http://curl.haxx.se/) on the commandline. This program can be launched from the terminal 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 programmaticaly, and we suggest anyone to use which ever program they feel is better suited for their tasks.

### Submitting a query to ELM via the REST API



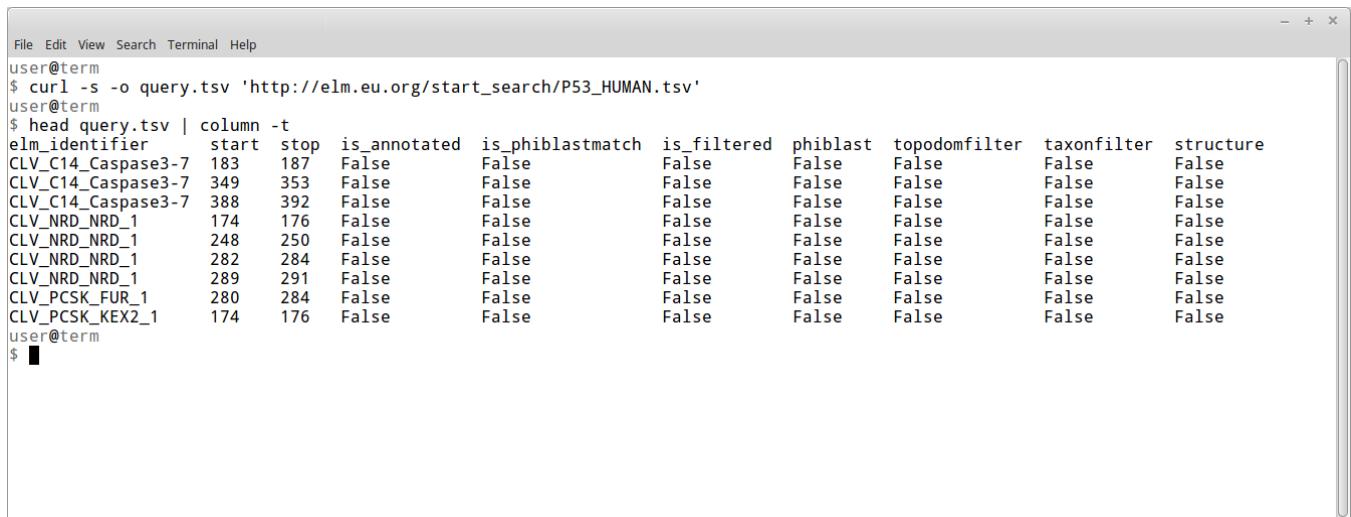
```
File Edit View Search Terminal Help
user@term
$ curl -s 'http://elm.eu.org/start_search/P53_HUMAN.tsv' | column -t
elm_identifier      start  stop  is_annotated  is_phiblastmatch  is_filtered  phiblast  topodomfilter  taxonfilter  structure
CLV_C14_Caspase3-7  183   187   False    False          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 30: The commandline output when curl is used to download all motifs predicted in Human P53. Note that we used a more advanced command that curl alone to make the columns align nicely (see text for an explanation).

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](http://elm.eu.org/start_search/P53_HUMAN.tsv)’’. Each row represents a motif detection, and the first column “elm\_identifier” indicates which class was identified. The columns “start” and “stop” show that first and last amino acid positions that matched form part of the motif. Column “is annotated” is True if this motif has been annotated in the database as an (experimentally validated) motif instance. The column “is phiblastmatch” is True if ?????. The column “is filtered” shows whether or not this motif was rejected by the ELM Prediction structure filter. Column “phibast” indicates whether ?????. The “topodomfilter” and “taxonfilter” shown whether ?????. The last column “structure” ?????

*In figure 30 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).*

TODO: Holger: what are the columns that are not described in the above section for?



```

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 31: It is possible to send amino acid sequences to the ELM Prediction pipeline. In this case we have used the curl option -o to download directly to the file query.tsv, and use 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/MAPRGFSCLLLTSEIDLPKRRA](http://elm.eu.org/start_search/MAPRGFSCLLLTSEIDLPKRRA)' (Fig. 31). 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.*

## Protocol 6 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 possible 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 downloaded both in using the browser as well as via the commandline.

### Necessary Resources

#### Software

Ideally use curl <curl.haxx.se/> on the commandline. This program can be launched from the terminal 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 programmaticaly, and we suggest anyone to use which ever program they feel is better suited for their tasks.

#### Downloading all ELM classes

1. Direct your browser to the URL '[elm.eu.org/downloads](http://elm.eu.org/downloads)' or select 'ELM Downloads' from the main menu (Fig. 32). 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 various formats.

*Each table also shows the 'last modified date' indicating when the data was last updated. This is useful if you want to know when to update your local data with the most up to date ELM data.*

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](http://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. Navidate to the folling URL: '[elm.eu.org/elms.html?q=CSK](http://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 described in step 3 of Protocol 1 (Fig. 3).*

4. Open the following URL: '[elm.eu.org/elms.tsv?q=CSK](http://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. By exchanging the '.html' part of the url with '.tsv', we ask the webserver to give us the data in "tab-separated values" format.

The screenshot shows the ELM Downloads page. At the top, there's a navigation bar with links to ELM Home, ELM Prediction, ELM DB, ELM Candidates, ELM Information, ELM downloads, and Help. A search bar is also present. To the right, a sidebar lists categories: 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.

| Name          | Example              | URL                         |
|---------------|----------------------|-----------------------------|
| all           | <a href="#">html</a> | /elms/elm_index.html        |
| all           | <a href="#">tsv</a>  | /elms/elms_index.tsv        |
| by query term | <a href="#">tsv</a>  | /elms/elms_index.tsv?q=PCSK |
| by ELM id     | <a href="#">html</a> | /ELME000012.html            |

**Instances**

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

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

Figure 32: 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).

*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).*

- 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 33. The column names are the same ones as shown in the table 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/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." ""
"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)
"Subtilisin/kexin isozyme-1 (SKI1) cleavage site ([RK]-X-[hydrophobic])
"ELME000146" "CLV_PCSK_SKI1_1" "PCSK cleavage site" "Members of the non-receptor tyrosine kinase Csk family phosphoryla"
"ELME000424" "LIG_CSK_EPIYA_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 33: A screenshot of a terminal window using curl to download all ELM classes matching the term ‘CSK’.

```

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
MEEPQSDPSVEPPLSQETFSDLWKLLPENNVLSPPLPSQAMDDMLLSPDDIEQWFTEDPGPDEAPRMPAAPPVAPAPAAPTAAAPAPAPSPLSSSVPSQKTYQGSYGRFLGFLHSGTAKSVTCTYSPLNPK
MFQLAKTCPVQLWVDSTPPGTRVRAMAIVKQSQHMTEVVRRCPHHERCSDSDGLAPPQHLIRVEGNLRVEYLDRNTFRHSVVVPYEPPEVGSDCTTIHYNYMCNSCMGGMNRRPILTIITLEDSSGNL
LGRNSFEVRVCACPGRDRRTEENLRKKGEPHELPPGSTKRALPNNTSSSPQPKKPLDGEYFTLQIRGRERFEMFRELNEALELKDAQAGKEPGGSRAHSSHLSKKGQSTSRRKKLMFKTEGPDSDF
user@term
$ 

```

Figure 34: 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 Human P53, type the followin command into a terminal: curl ‘[http://elm.eu.org/instances.gff?q=p53\\_human](http://elm.eu.org/instances.gff?q=p53_human)’. The output should look similar to that shown in figure 30. The output is in the “General Feature Format” (see [www.ensembl.org/info/website/upload/gff.html#moreinfo](http://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, including the FASTA, GFF, PIR, OR PSI-MI format (either xml or MiTab)*

- To download a list of all instances matchin th search query “CLV” in the yellow fever mosquito (*Aedes agypti*), enter the following command into a terminal: curl ‘<http://elm.eu.org/instances.tsv?query=CLV>’
- In general any species name can be used, always replacing the “space” with a “+”. This should return

- a single instance, the only one matching CLV in *A. aegypti*.
8. 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](http://elm.eu.org/downloads), figure 32) for an overview of which datasets can be downloaded, and what the different possible filters and formats are for each dataset.

## Guidelines for Understanding Results

*instructions: A brief discussion of the theory and applications of your*

*notes: Maybe mention how findings are relevant to the lab? For example: Manually annotated content should be reliable, although one should look at the ‘confidence’ in the instance annotation. Predictions are probably trustworthy, but you need to take into account the ‘confidence score’, and other features like whether its in a domain, etc...*

## Commentary:

*instructions: A brief discussion of the theory and applications of your*

## 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 SLiM’s and how they are affected by their structural and biological context. This background information summarises the different functionalities of SLiMs, describes the degenerate nature of motif sequences, and emphasises 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 35) (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) Van Roey et al. (2014); 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 evolutionary 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, when 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. 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 proteinâŽs 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 depends 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 unknown 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**

### **Structure Filter**

### **Disorder Filter**

### **Conservation Filter**

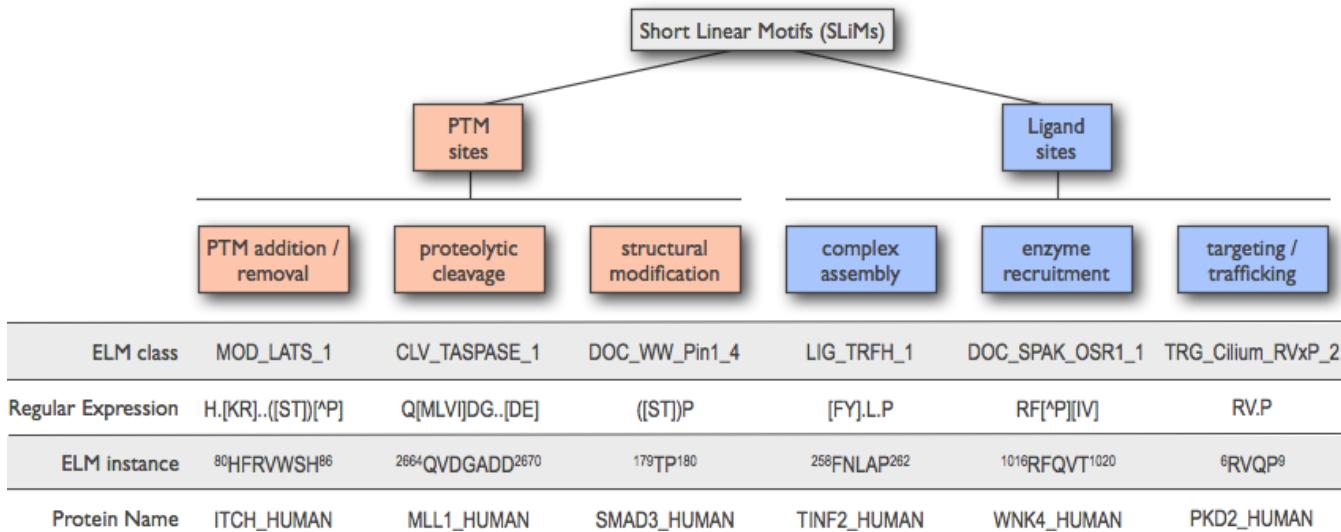


Figure 35: **Figure functional\_classification\_of\_SLiMs** For each ELM class, the functional category to which it belongs is indicated by a three-letter prefix. Each ELM class is defined by a regular expression. Peptide sequences in proteins that match the regular expression of a specific ELM class and that were experimentally validated to be functional motifs are captured as ELM instances of that class. Degrons are a specific subtype of enzyme-recruiting docking motifs (see text for a detailed description).

## Instance Mapper

## Critical Parameters and Troubleshooting

*Factors that influence the protocol and to which special attention should be paid. Common problems with the protocols, their causes, and potential solutions. The information may be presented in tabular form or it may be combined with Critical Parameters.*

## Internet Resources with Annotations

<http://www.clustal.org/omega> Clustal Omega ([Sievers et al. \(2011\)](#)) is a tool for the alignment of multiple nucleic acid and protein sequences.

<http://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.

<http://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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