

Tools & Databases of Short Linear Motifs

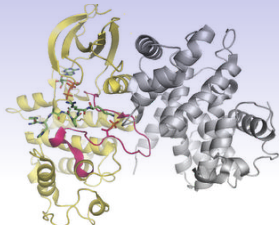
Holger Dinkel

EMBO Practical Course:

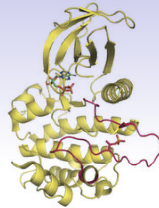
“Computational Analysis of Protein-Protein Interactions:
Sequences, Networks and Diseases”

Budapest, 03. 06. 2016

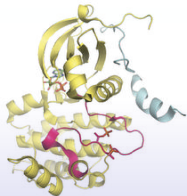
PROTEIN PHOSPHORYLATION SITES



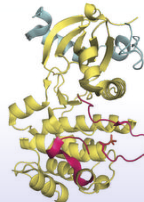
Cdk1/cyclin B



Plk1



Aurora A/TPX2



Aurora B/INCENP

"Spatial exclusivity combined with positive and negative selection of phosphorylation motifs is the basis for context-dependent mitotic signaling"; ALEXANDER ET AL.; (SCI. SIG 2011)

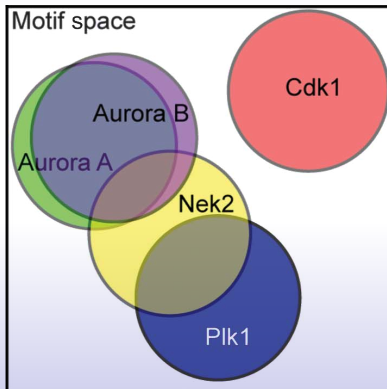
PROTEIN PHOSPHORYLATION SITES

Kinase	-3	-2	-1	0	1	2	3
Cdk1	.	.	.	p[ST]	P	.	[KR]
Plk1	.	[DEN]	.	p[ST]	[ILMVFWY]	.	.
Nek2	[FML]	[!P]	[!P]	p[ST]	[ILMV]	.	.
AuroraA	R	[KR]	.	p[ST]	[!P]	.	.
AuroraB	.	R	[KR]	p[ST]	[!P]	.	.

"Spatial exclusivity combined with positive and negative selection of phosphorylation motifs is the basis for context-dependent mitotic signaling"; ALEXANDER ET AL.; (SCI. SIG 2011)

PROTEIN PHOSPHORYLATION SITES

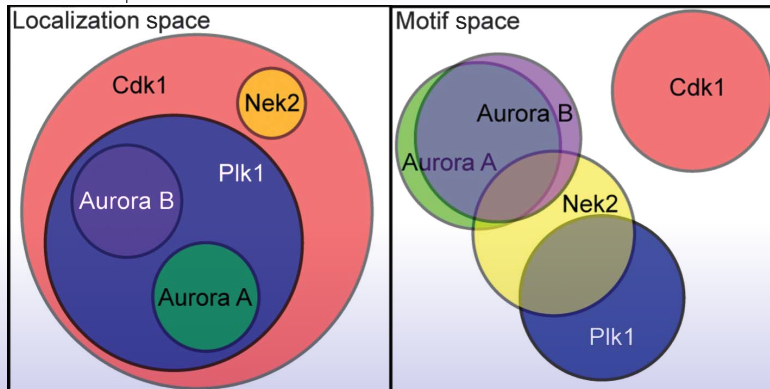
Kinase	-3	-2	-1	0	1	2	3
Cdk1	.	.	.	p[ST]	P	.	[KR]
Plk1	.	[DEN]	.	p[ST]	[ILMVFWY]	.	.
Nek2	[FML]	[!P]	[!P]	p[ST]	[ILMV]	.	.
AuroraA	R	[KR]	.	p[ST]	[!P]	.	.
AuroraB	.	R	[KR]	p[ST]	[!P]	.	.



"Spatial exclusivity combined with positive and negative selection of phosphorylation motifs is the basis for context-dependent mitotic signaling"; ALEXANDER ET AL.; (SCI. SIG 2011)

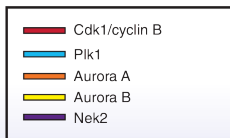
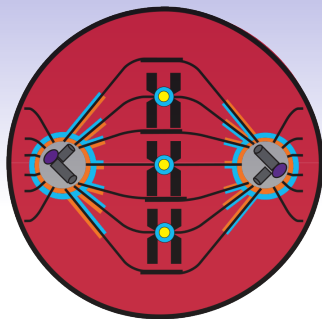
PROTEIN PHOSPHORYLATION SITES

Kinase	-3	-2	-1	0	1	2	3
Cdk1	.	.	.	p[ST]	P	.	[KR]
Plk1	.	[DEN]	.	p[ST]	[ILMVFWY]	.	.
Nek2	[FML]	[!P]	[!P]	p[ST]	[ILMV]	.	.
AuroraA	R	[KR]	.	p[ST]	[!P]	.	.
AuroraB	.	R	[KR]	p[ST]	[!P]	.	.



"Spatial exclusivity combined with positive and negative selection of phosphorylation motifs is the basis for context-dependent mitotic signaling"; ALEXANDER ET AL.; (SCI. SIG 2011)

PROTEIN PHOSPHORYLATION SITES



Kinase localization in Metaphase:

Cdk1 whole cell

Plk1 kinetochores

Aurora A centrosomes & microtubules

Aurora B centromeres & spindle

Nek2 centrosomes

"Spatial exclusivity combined with positive and negative selection of phosphorylation motifs is the basis for context-dependent mitotic signaling"; ALEXANDER ET AL.; (SCI. SIG 2011)

Phospho.ELM

Database of experimentally verified phosphorylation sites in eukaryotic proteins.

Current release contains 8,718 protein entries covering more than 42,500 instances. (Instances are fully linked to literature references.)

Phospho.ELM

a database of S/T/Y phosphorylation sites

[Statistics:](#)

Instances	42.575
Kinases	310
Reference	3.672
Sequences	11.223
Substrates	8.718

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SEARCH

- for phosphorylation sites in proteins using protein name or gene name
(eg. Paxillin, Shc, MAPK)

- by UniPROT accession or Ensembl identifier:
(eg. P12931 or P55211)

- by selected kinase (List):

- by selected phospho-peptide binding domain (List):

- Choose which organisms to include

Caenorhabditis
Drosophila
Vertebrates

- Do not show high throughput data
- Output as Comma-Separated-Values (.csv)

Phospho.ELM

a database of S/T/Y phosphorylation sites

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Substrate: p53 (Cellular tumor antigen p53)

Seq-ID: P04637 [*Homo sapiens*]Interaction Network(s): [STRING](#) [NetworkKIN](#)

External Source(s): PHOSIDA

MINT Interaction(s): [\[show\]](#)GO-Terms: [\[show\]](#)

Conservation:

[Click on table headers for sorting](#)

Res.	Pos.	Sequence	Kinase	PMID	Src	Cons.	ELM	Binding Domain	SMART/Pfam	IUPRED score	PDB	P3D Acc.
S	9	MEEPQSDP S VEPPLSQETP	-	11875057	LTP	0.75		-	P53_TAD	0.94	-	-
S	15	QSDPSVEPPL S QETFSDLWKL	DNA-PK	10446957	LTP	1.00	MOD_PIKK_1	-	P53_TAD	0.66	-	-
S	15	QSDPSVEPPL S QETFSDLWKL	ATM	11875057	LTP	1.00	MOD_PIKK_1	-	P53_TAD	0.66	-	-
T	18	PSVEPPLSQE T PSDLWKLLE	CK1_group	10606744	LTP	1.00	MOD_CK1_1	-	P53_TAD	0.66	-	-
T	18	PSVEPPLSQE T PSDLWKLLE	TTK	19332559	LTP	1.00	MOD_CK1_1	-	P53_TAD	0.66	-	-
T	18	PSVEPPLSQE T PSDLWKLLE	VRK1	10951572	LTP	1.00	MOD_CK1_1	-	P53_TAD	0.66	-	-
T	18	PSVEPPLSQE T PSDLWKLLE	VRK1	15542844	LTP	1.00	MOD_CK1_1	-	P53_TAD	0.66	-	-
S	20	VEPPLSQET S DLWKLLEPENN	-	15254178	LTP	0.95		-	P53_TAD	0.58	-	-
S	20	VEPPLSQET S DLWKLLEPENN	-	15489221	LTP	0.95		-	P53_TAD	0.58	-	-
S	20	VEPPLSQET S DLWKLLEPENN	-	10801407	LTP	0.95		-	P53_TAD	0.58	-	-
S	20	VEPPLSQET S DLWKLLEPENN	-	12111733	LTP	0.95		-	P53_TAD	0.58	-	-

Phospho.ELM

a database of S/T/Y phosphorylation sites



MOD_CK2_1 The ELM server ELM details

Phospho site alias: CK2 Phosphorylation site
Phospho site description: KMIF recognized by CK2 for Ser/Thr phosphorylation.
ELM ID: MOD_CK2_1
motif_CK2_1 description: The main determinant of CK2 phosphorylation specificity is a negative charge 3 positions after the modification residue.
Pattern: [D]-[E]-[D]
Present in sequence(s): Vertebrates, Eukaryotes, Zoo flag, Bacteriophages, ctenidia, Dinoflagellates, metazoan(s)
Not represented in (source(s)):

Substrate: Cyclin dependent kinase inhibitor 1B (Cyclin-dependent kinase inhibitor 1B (Cyclin-dependent kinase
Seq-ID: P46527 [Homo sapiens]
Interaction Network(s): STRING NetworkKH
External Source(s):
MINT Interaction(s): [show]
[View Conservation](#)

Res.	Pos.	Sequence	Kinase	PMID	Src	Cons.	ELM	Binding Domain	SMART/Protein	IUPRED score	PDB	PDB Acc.
S	10	...S...P...L...G...G...	-	12492975	LTP	0.20	-	-	-	0.74	-	-
S	10	...S...P...L...G...G...	-	14504288	LTP	0.20	-	-	-	0.74	-	-
S	10	...S...P...L...G...G...	-	15730731	LTP	0.20	-	-	-	0.74	-	-
S	10	...S...P...L...G...G...	-	12642314	LTP	0.20	-	-	-	0.74	-	-
S	10	...S...P...L...G...G...	-	15202936	HTP	0.20	-	-	-	0.74	-	-
S	10	...S...P...L...G...G...	-	16780593	LTP	0.20	-	-	-	0.74	-	-
S	10	...S...P...L...G...G...	PKB_group	12893740	LTP	0.20	-	-	-	0.74	-	-
Y	74	...Y...E...G...E...G...G...	-	18454177	LTP	1.00	-	-	-	0.64	-	-
Y	74	...Y...E...G...E...G...G...	SRC	17254967	LTP	1.00	-	-	-	0.64	-	-
S	83	...S...P...L...G...G...G...	-	15034933	LTP	0.16	MOD_CK2_1	-	-	0.57	1J5U	65.97%
Y	86	...Y...E...G...L...Y...E...F...F...G...G...	-	17254966	LTP	1.00	-	-	-	0.65	1J5U	79.31%
Y	86	...Y...E...G...L...Y...E...F...F...G...G...	-	18193237	LTP	1.00	-	-	-	0.65	1J5U	79.31%
Y	86	...Y...E...G...L...Y...E...F...F...G...G...	SRC	17254967	LTP	1.00	-	-	-	0.65	1J5U	79.31%
Y	89	...Y...E...G...L...Y...E...F...F...G...G...	-	18193237	LTP	0.22	-	-	-	0.63	1J5U	36.68%
Y	89	...Y...E...G...L...Y...E...F...F...G...G...	SRC	17254967	LTP	0.22	-	-	-	0.63	1J5U	36.68%
S	140	...S...P...L...G...G...G...G...G...	-	17525332	HTP	0.85	-	-	-	0.77	-	-
T	157	...T...D...G...C...A...M...K...K...K...K...K...	PKB_group	12244303	LTP	0.94	MOD_PKB_1	-	-	0.84	-	-
T	157	...T...D...G...C...A...M...K...K...K...K...K...	PKB_group	12244302	LTP	0.94	MOD_PKB_1	-	-	0.84	-	-
T	157	...T...D...G...C...A...M...K...K...K...K...K...	PKB_group	12244301	LTP	0.94	MOD_PKB_1	-	-	0.84	-	-
S	178	...S...P...L...G...G...G...G...G...	MAPK1	10621586	LTP	0.15	MOD_PhdCdk_1	-	-	0.94	-	-
T	187	...T...D...G...C...A...M...K...K...K...K...K...	-	15730731	LTP	1.00	MOD_CDK_1	-	-	0.95	-	-
T	187	...T...D...G...C...A...M...K...K...K...K...K...	-	12642314	LTP	1.00	MOD_CDK_1	-	-	0.95	-	-
T	187	...T...D...G...C...A...M...K...K...K...K...K...	-	10621586	LTP	1.00	MOD_CDK_1	-	-	0.95	-	-
T	187	...T...D...G...C...A...M...K...K...K...K...K...	GDK3	12790223	LTP	1.00	MOD_CDK_1	-	-	0.95	-	-
T	198	...T...D...G...C...A...M...K...K...K...K...K...	-	12642314	LTP	0.00	-	YWHQ14-3-3	-	0.94	-	-
T	198	...T...D...G...C...A...M...K...K...K...K...K...	RSK_group	14504289	LTP	0.00	-	YWHQ14-3-3	-	0.94	-	-
T	198	...T...D...G...C...A...M...K...K...K...K...K...	RSK-2	14504289	LTP	0.00	-	YWHQ14-3-3	-	0.94	-	-

PDB entry: 1j5u

P27KIP1/SH2/SH3/SH600/SH7/SH8/SH9/SH10/SH11/SH12/SH13/SH14/SH15/SH16/SH17/SH18/SH19/SH20/SH21/SH22/SH23/SH24/SH25/SH26/SH27/SH28/SH29/SH30/SH31/SH32/SH33/SH34/SH35/SH36/SH37/SH38/SH39/SH40/SH41/SH42/SH43/SH44/SH45/SH46/SH47/SH48/SH49/SH50/SH51/SH52/SH53/SH54/SH55/SH56/SH57/SH58/SH59/SH60/SH61/SH62/SH63/SH64/SH65/SH66/SH67/SH68/SH69/SH70/SH71/SH72/SH73/SH74/SH75/SH76/SH77/SH78/SH79/SH80/SH81/SH82/SH83/SH84/SH85/SH86/SH87/SH88/SH89/SH90/SH91/SH92/SH93/SH94/SH95/SH96/SH97/SH98/SH99/SH100/SH101/SH102/SH103/SH104/SH105/SH106/SH107/SH108/SH109/SH110/SH111/SH112/SH113/SH114/SH115/SH116/SH117/SH118/SH119/SH120/SH121/SH122/SH123/SH124/SH125/SH126/SH127/SH128/SH129/SH130/SH131/SH132/SH133/SH134/SH135/SH136/SH137/SH138/SH139/SH140/SH141/SH142/SH143/SH144/SH145/SH146/SH147/SH148/SH149/SH150/SH151/SH152/SH153/SH154/SH155/SH156/SH157/SH158/SH159/SH160/SH161/SH162/SH163/SH164/SH165/SH166/SH167/SH168/SH169/SH170/SH171/SH172/SH173/SH174/SH175/SH176/SH177/SH178/SH179/SH180/SH181/SH182/SH183/SH184/SH185/SH186/SH187/SH188/SH189/SH190/SH191/SH192/SH193/SH194/SH195/SH196/SH197/SH198/SH199/SH200/SH201/SH202/SH203/SH204/SH205/SH206/SH207/SH208/SH209/SH210/SH211/SH212/SH213/SH214/SH215/SH216/SH217/SH218/SH219/SH220/SH221/SH222/SH223/SH224/SH225/SH226/SH227/SH228/SH229/SH230/SH231/SH232/SH233/SH234/SH235/SH236/SH237/SH238/SH239/SH240/SH241/SH242/SH243/SH244/SH245/SH246/SH247/SH248/SH249/SH250/SH251/SH252/SH253/SH254/SH255/SH256/SH257/SH258/SH259/SH260/SH261/SH262/SH263/SH264/SH265/SH266/SH267/SH268/SH269/SH270/SH271/SH272/SH273/SH274/SH275/SH276/SH277/SH278/SH279/SH280/SH281/SH282/SH283/SH284/SH285/SH286/SH287/SH288/SH289/SH290/SH291/SH292/SH293/SH294/SH295/SH296/SH297/SH298/SH299/SH300/SH301/SH302/SH303/SH304/SH305/SH306/SH307/SH308/SH309/SH310/SH311/SH312/SH313/SH314/SH315/SH316/SH317/SH318/SH319/SH320/SH321/SH322/SH323/SH324/SH325/SH326/SH327/SH328/SH329/SH330/SH331/SH332/SH333/SH334/SH335/SH336/SH337/SH338/SH339/SH340/SH341/SH342/SH343/SH344/SH345/SH346/SH347/SH348/SH349/SH350/SH351/SH352/SH353/SH354/SH355/SH356/SH357/SH358/SH359/SH360/SH361/SH362/SH363/SH364/SH365/SH366/SH367/SH368/SH369/SH370/SH371/SH372/SH373/SH374/SH375/SH376/SH377/SH378/SH379/SH380/SH381/SH382/SH383/SH384/SH385/SH386/SH387/SH388/SH389/SH390/SH391/SH392/SH393/SH394/SH395/SH396/SH397/SH398/SH399/SH400/SH401/SH402/SH403/SH404/SH405/SH406/SH407/SH408/SH409/SH410/SH411/SH412/SH413/SH414/SH415/SH416/SH417/SH418/SH419/SH420/SH421/SH422/SH423/SH424/SH425/SH426/SH427/SH428/SH429/SH430/SH431/SH432/SH433/SH434/SH435/SH436/SH437/SH438/SH439/SH440/SH441/SH442/SH443/SH444/SH445/SH446/SH447/SH448/SH449/SH450/SH451/SH452/SH453/SH454/SH455/SH456/SH457/SH458/SH459/SH460/SH461/SH462/SH463/SH464/SH465/SH466/SH467/SH468/SH469/SH470/SH471/SH472/SH473/SH474/SH475/SH476/SH477/SH478/SH479/SH480/SH481/SH482/SH483/SH484/SH485/SH486/SH487/SH488/SH489/SH490/SH491/SH492/SH493/SH494/SH495/SH496/SH497/SH498/SH499/SH500/SH501/SH502/SH503/SH504/SH505/SH506/SH507/SH508/SH509/SH510/SH511/SH512/SH513/SH514/SH515/SH516/SH517/SH518/SH519/SH520/SH521/SH522/SH523/SH524/SH525/SH526/SH527/SH528/SH529/SH530/SH531/SH532/SH533/SH534/SH535/SH536/SH537/SH538/SH539/SH540/SH541/SH542/SH543/SH544/SH545/SH546/SH547/SH548/SH549/SH550/SH551/SH552/SH553/SH554/SH555/SH556/SH557/SH558/SH559/SH560/SH561/SH562/SH563/SH564/SH565/SH566/SH567/SH568/SH569/SH570/SH571/SH572/SH573/SH574/SH575/SH576/SH577/SH578/SH579/SH580/SH581/SH582/SH583/SH584/SH585/SH586/SH587/SH588/SH589/SH590/SH591/SH592/SH593/SH594/SH595/SH596/SH597/SH598/SH599/SH600/SH601/SH602/SH603/SH604/SH605/SH606/SH607/SH608/SH609/SH610/SH611/SH612/SH613/SH614/SH615/SH616/SH617/SH618/SH619/SH620/SH621/SH622/SH623/SH624/SH625/SH626/SH627/SH628/SH629/SH630/SH631/SH632/SH633/SH634/SH635/SH636/SH637/SH638/SH639/SH640/SH641/SH642/SH643/SH644/SH645/SH646/SH647/SH648/SH649/SH650/SH651/SH652/SH653/SH654/SH655/SH656/SH657/SH658/SH659/SH660/SH661/SH662/SH663/SH664/SH665/SH666/SH667/SH668/SH669/SH670/SH671/SH672/SH673/SH674/SH675/SH676/SH677/SH678/SH679/SH680/SH681/SH682/SH683/SH684/SH685/SH686/SH687/SH688/SH689/SH690/SH691/SH692/SH693/SH694/SH695/SH696/SH697/SH698/SH699/SH700/SH701/SH702/SH703/SH704/SH705/SH706/SH707/SH708/SH709/SH710/SH711/SH712/SH713/SH714/SH715/SH716/SH717/SH718/SH719/SH720/SH721/SH722/SH723/SH724/SH725/SH726/SH727/SH728/SH729/SH730/SH731/SH732/SH733/SH734/SH735/SH736/SH737/SH738/SH739/SH740/SH741/SH742/SH743/SH744/SH745/SH746/SH747/SH748/SH749/SH750/SH751/SH752/SH753/SH754/SH755/SH756/SH757/SH758/SH759/SH760/SH761/SH762/SH763/SH764/SH765/SH766/SH767/SH768/SH769/SH770/SH771/SH772/SH773/SH774/SH775/SH776/SH777/SH778/SH779/SH780/SH781/SH782/SH783/SH784/SH785/SH786/SH787/SH788/SH789/SH790/SH791/SH792/SH793/SH794/SH795/SH796/SH797/SH798/SH799/SH800/SH801/SH802/SH803/SH804/SH805/SH806/SH807/SH808/SH809/SH810/SH811/SH812/SH813/SH814/SH815/SH816/SH817/SH818/SH819/SH820/SH821/SH822/SH823/SH824/SH825/SH826/SH827/SH828/SH829/SH830/SH831/SH832/SH833/SH834/SH835/SH836/SH837/SH838/SH839/SH840/SH841/SH842/SH843/SH844/SH845/SH846/SH847/SH848/SH849/SH850/SH851/SH85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Links to:

- STRING
- NetworKin
- Phosida
- Phospho3D

Display:

- MINT interactions
- GO-Terms

Substrate:**Caspase 9** (Cysteine protease)**Seq-ID:****P55211** [*Homo sapiens*]**Interaction Network(s):**
 **STRING**
 **NetworKin**
External Source(s):**PHOSIDA**

[hide]

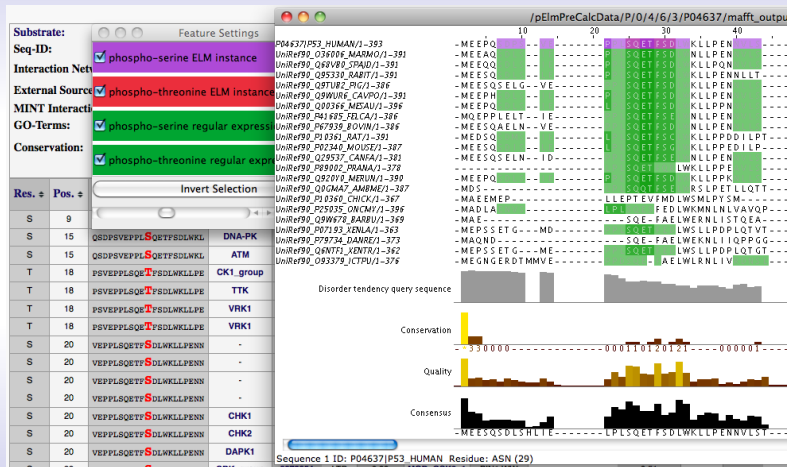
MINT-15372 APAF_HUMAN
 MINT-18815 CASP3_HUMAN
 MINT-25026 XIAP_HUMAN

[hide]

MINT Interaction(s):**Molecular Function****GO-Terms:**

cysteine-type endopeptidase activity,
 protein binding,
 enzyme activator activity

Precalculated conservation scores for the phosphorylation sites are presented using **Jalview**

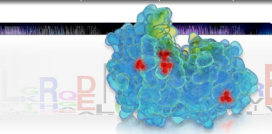




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Protein Name: p53

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Aug 2014 **Download PTM-VarMut dataset:** Overlap of disease missense mutations & genetic variants, with their corresponding PTMs and flanking sequences.

Jul 2012 **Download Datasets of Regulatory or Disease-Associated Sites.**

Dec 2011 **Download "PhosphoSitePlus: a comprehensive resource..."** in January 2012 issue of *Nucleic Acids Research*.

Jul 2011 **Multiple Sequence Alignment (MSA)** added to the Protein Page.

Jul 2011 **Download PyMOL & Chimera Scripts** from the Structure Viewer window.

Phosphorylation Site Statistics

Non-redundant sites:	239,738
Non-redundant proteins:	19,680
Sites curated from literature:	136,109
All sites using site-specific (SS) methods:	12,528
All sites using discovery-mode MS (MS) methods:	127,064
Sites using both SS and MS methods:	6,010
MS sites observed at CST:	151,472
Number of curated papers:	16,428

Other Modification Site Statistics

Acetylation:	27,657	Caspase cleavage:	481
Di-methylation:	2,555	Methylation:	163
Mono-methylation:	4,992	O-GalNAc:	2,118
O-GlcNAc:	1,390	Succinylation:	4,657
Sumoylation:	816	Tri-methylation:	321
Ubiquitination:	51,255		



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Protein Page:
p53 (human)

Overview

p53 a transcription factor and major tumor suppressor that plays a major role in regulating cellular responses to DNA damage and other genomic aberrations. Activation of p53 can lead to either cell cycle arrest and DNA repair or apoptosis. More than 50 percent of human tumors contain a mutation or deletion of the TP53 gene. p53 is modified post-translationally at multiple sites. DNA damage induces phosphorylation of p53 at S15, S20 and S37, reducing its interaction with the oncoprotein MDM2. MDM2 inhibits p53 accumulation by targeting it for ubiquitination and proteasomal degradation. Phosphorylation by many kinases including Chk2 and Chk1 at S20, enhancing its tetramerization, stability and activity. The phosphorylation by CAK at S392 is increased in human tumors and has been reported to influence the growth suppressor function, DNA binding and transcriptional activation of p53. Phosphorylation of p53 at S44 regulates the ability of p53 to induce apoptosis. The acetylation of p53 appears to play a positive role in the accumulation of p53 during the stress response. Following DNA damage, p53 becomes acetylated at K382, enhancing its binding to DNA. Deacetylation of p53 can occur through interaction with SIRT1, a deacetylase that may be involved in cellular aging and the DNA damage response. p53 regulates the transcription of a set of genes encoding endosomal proteins that regulate endosomal functions. These include STEAP3 and CHMP4C, which enhance exosome production, and CAV1 and CHMP4C, which produce a more rapid endosomal clearance of the EGFR from the plasma membrane. DNA damage regulates a p53-mediated secretory pathway, increasing the secretion of some proteins such as Hsp90, SERPINE1, SERPINB5, NKEF-A, and CyPA, and inhibiting the secretion of others including CTSL and IGFBP-2. Two alternatively spliced human isoforms have been reported. Isoform 2 is expressed in quiescent lymphocytes. Seems to be non-functional. May be produced at very low levels due to a premature stop codon in the mRNA, leading to nonsense-mediated mRNA decay. Note: This description may include information from UniProtKB.

Protein Type: DNA binding protein; Nuclear receptor co-regulator; Motility/polarity/chemotaxis; Transcription factor; Activator protein; Tumor suppressor

Cellular Component: PML body; transcription factor TFIIID complex; protein complex; nuclear matrix; mitochondrion; endoplasmic reticulum; replication fork; cytosol; nucleoplasm; nuclear body; mitochondrial matrix; cytoplasm; nuclear chromatin; nucleolus; chromatin; nucleus

Molecular Function: identical protein binding; protease binding; zinc ion binding; protein phosphatase 2A binding; p53 binding; protein N-terminus binding; receptor tyrosine kinase binding; transcription factor binding; protein phosphatase binding; protein kinase binding; histone acetyltransferase binding; protein binding; cytosol binding; histone deacetylase regulator activity; enzyme binding; DNA binding; protein heterodimerization activity; chaperone binding; ubiquitin protein ligase binding; damaged DNA binding; chromatin binding; transcription factor activity; ATP binding

Biological Process: central nervous system development; viral reproduction; positive regulation of apoptosis; multicellular organismal development; positive regulation of transcription, DNA-dependent; T cell differentiation in the thymus; gastrulation; determination of adult life span; DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest; response to antibiotic; regulation of apoptosis; cellular response to glucose starvation; protein localization; negative regulation of neuroblast proliferation; base-excision repair; transforming growth factor beta receptor signaling pathway; protein complex assembly; cell cycle arrest; ER overload response; response to X-ray; somitogenesis; release of cytochrome c from mitochondria; chromatin assembly; cell aging; RNA transcription; positive regulation of peptide-tyrosine phosphorylation; negative regulation of DNA replication; negative regulation of fibroblast proliferation; embryonic organ development; positive regulation of transcription from RNA polymerase II promoter; regulation of mitochondrial membrane permeability; negative regulation of transcription, DNA-dependent; regulation of tissue remodeling; negative regulation of apoptosis; G1 DNA damage checkpoint; DNA damage response, signal transduction by p53 class mediator; apoptosis; negative regulation of transcription from RNA polymerase II promoter; response to salt stress; negative regulation of cell proliferation; positive regulation of protein oligomerization; positive regulation of histone deacetylation; DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator; regulation of transcription, DNA-dependent; T cell proliferation during immune response; double-strand break repair; positive regulation of neuron apoptosis; response to gamma radiation; cell differentiation; DNA damage response, signal transduction by p53 class mediator resulting in induction of apoptosis; protein tetramerization; notch signaling pathway; in utero embryonic development; multicellular organism growth; B cell lineage commitment; cell proliferation; neuron apoptosis; T cell lineage commitment; negative regulation of helicase activity; nucleotide-excision repair; protein import into nucleus, translocation; DNA strand renaturation; Ras protein signal transduction; negative regulation of cell growth; negative regulation of transforming growth factor beta receptor signaling pathway; blood coagulation; response to DNA damage stimulus

Reference #: P04637 (UniProtKB)

Select Structure to View Below

p53



1A1U - A/C=324-358 (human)

Open Viewer

Modification Sites in Parent Protein, Orthologs, and Isoforms

Show Multiple Sequence Alignment

SS	MS	human	mouse	rat	rabbit	monkey
6	0	P4 ___HEEPQSDPaVE	54-p ___HEE+QSDIsLE	54-p ___HEE+QSDIsLE	54 ___HEESQSDLSLE	P4 ___HEEPQSDPSIE
31	4	56-p ___HEEPQSDPaVEFP	56-p ___HEE+QSDIsLEFP	56-p ___HEE+QSDIsLEFP	56 ___HEESQSDLSLEFP	56 ___HEEPQSDPSIEFP
34	3	59-p EEKQSDPaVEFPLeQ	59-p EEK+QSDIsLEFLaQ	59-p EEK+QSDIsLEFLaQ	59 EEKSDSDLSIEFLaQ	59 EEKQSDPSIEFLaQ
358	2	515-p PaVEFPLeQETPaDL	515-p IsLEFLPaQETPaGL	515-p HaIEFLPaQETPaGL	515 LSLEFLPaQETPaDL	515-p PSEIEFPLeQETPaDL
28	0	T18-p EPFLaQETPaDLWKL	T18-p ELFLaQETPaDLWKL	T18-p ELFLaQETPaDLWKL	T18 EPFLaQETPaDLWKL	T18 EPFLaQETPaDLWKL
110	1	S20-p PLaQETPaDLWKLFP	S20-p PLaQETPaDLWKLFP	S20-p PLaQETPaDLWKLFP	S20 PLaQETPaDLWKLFP	PLaQETPaDLWKLFP
30	3	S33-p LPEHMLVPLPaQAK	F33 LPFDLPLPaPHCHDD	F33 LPFDLPLPaPHCHDD	L33 LPEHMLTLSLHPFV	S33-p LPEHMLVPLPaQAK
65	3	S37-p NVLsPLPaQMDDLK	S34-p PFDLPLPaPHCHDD	S35-p LFTTATGPaPHSHEDL	H37 MLTLSLHPFVDDLL	S37 NVLsPLPaQMDDLK
85	2	S46-p RDDDLLaPDDLEIQL	L43 HCHDDLLLPQDVEEF	L48 HSHDEFLPaQVMAEL	S45 PFVDDLLSHEVAMV	S46 RDDDLLaPDDLaQW
15	0	T53-p DDIEQWLEDGPaDE	- gap	- gap	H54 EDVAMMLHEPGEGL	T53 DDLaQWLEDGPaDE
2	0	D61 FEDGPaDEAPRHE	S55-p EEFEGPaEALRVSG	E60 RELLEGPaEALQVSA	E58 HWLHEGPaEALRVPA	D61 LETDGPDeAPRHE
8	2	T81-p APAPAPAPAPAPA	G75 DPVTETPaPVAPAPA	A76 EPGETAPAPAPASA	A78 APAPAPAPAPAPA	T81 APAPAPAPAPAPA
0	2	S99-p PLSSVFPaQATYQG	S93 PLSSVFPaQRTYQGN	S97 PLSSVFPaQRTYQGN	S96 PLSSVFPaQRTYQGN	S99 PLSSVFPaQRTYQGN
1	2	K101-nb SSSVFPaQATYQGeG	K95 SSVFPaQRTYQGN	K99 SSVFPaQRTYQGN	K94 SSVFPaQRTYQGN	K101 SSVFPaQRTYQGeG
1	0	S106-p sQATYQGeGPaLGP	H180 SQRTYQGeGPaLGP	H184 SQRTYQGeGPaLGP	H183 SQRTYQGeGPaLGP	S106 SQRTYQGeGPaLGP
0	1	R118-nl YQGeGPaLQFLHSG	H184 YQGeGPaLQFLHSG	H188 YQGeGPaLQFLHSG	R187 YQGeGPaLQFLHSG	R118 YQGeGPaLQFLHSG
0	1	H115-nl GPaLQFLHSGPaTSV	Q189 GPaLQFLHSGPaTSV	Q113 GPaLQFLHSGPaTSV	H112 GPaLQFLHSGPaTSV	H115 GPaLQFLHSGPaTSV
23	1	K128-ac FLASGTaKSVTCYs	K114-ac FLASGTaKSVCTYS	K118-ac FLASGTaKSVCTYS	K117 FLASGTaKSVCTYS	K128 FLASGTaKSVCTYS
1	19	K128-nb FLASGTaKSVTCYs	K114 FLASGTaKSVCTYS	K118 FLASGTaKSVCTYS	K117 FLASGTaKSVCTYS	K128 FLASGTaKSVCTYS
1	0	Y126-p AKSVTCYsPaLRRH	Y126 AKSVCTYSPaLRRH	Y124 AKSVCTYSPaLRRH	Y123 AKSVTCYsPaLRRH	Y126 AKSVCTYSPaLRRH
1	1	K132-nb TYSPLMRPaCOLAK	K126 TYSPLMRPaCOLAK	K130 TYSPLMRPaCOLAK	K129 TYSPLMRPaCOLAK	K132 TYSPLMRPaCOLAK
1	0	K139-nb RPaCOLRPaCPVQLW	K133 RPaCOLRPaCPVQLW	K137 RPaCOLRPaCPVQLW	K136 RPaCOLRPaCPVQLW	K139 RPaCOLRPaCPVQLW
3	1	S149-p PVQLWPaSTPaPAGaR	A143 PVQLWPaSTPaPAGaR	S147 PVQLWPaSTPaPAGaR	S146 PVQLWPaSTPaPAGaR	S149 PVQLWPaSTPaPAGaR
1	1	S149-gV PVQLWPaSTPaPAGaR	A143 PVQLWPaSTPaPAGaR	S147 PVQLWPaSTPaPAGaR	S146 PVQLWPaSTPaPAGaR	S149 PVQLWPaSTPaPAGaR
4	8	T158-p VQLWPaSTPaPAGaRV	T144 VQLWPaSTPaPAGaRV	T148 VQLWPaSTPaPAGaRV	T147 VQLWPaSTPaPAGaRV	T158 VQLWPaSTPaPAGaRV
4	1	T155-p DaSTPaPAGaRVPaRAI	S149-p DaSTPaPAGaRVPaRAI	T153 DaSTPaPAGaRVPaRAI	T152 DaSTPaPAGaRVPaRAI	T155 DaSTPaPAGaRVPaRAI
4	1	K164-ac VRMAIYKsQHQITE	K158 VRMAIYKsQHQITE	K162 VRMAIYKsQHQITE	K161 VRMAIYKsQHQITE	K164 VRMAIYKsQHQITE
1	1	K164-nb VRMAIYKsQHQITE	K158 VRMAIYKsQHQITE	K162 VRMAIYKsQHQITE	K161 VRMAIYKsQHQITE	K164 VRMAIYKsQHQITE
2	0	S183-p CPDHERCaSDGGLaP	S177 CPDHERCaSDGGLaP	S181 CPDHERCaSDGGLaP	S180 CPDHERCaSDGGLaP	S183 CPDHERCaSDGGLaP
0	1	R209-nl RVEYLDaRPaTRHsV	R203 RVEYLDaRPaTRHsV	R207 RVEYLDaRPaTRHsV	R206 RVEYLDaRPaTRHsV	R209 RVEYLDaRPaTRHsV
1	0	T211-p EYLDaRPaTRHsVVV	T205 EYLDaRPaTRHsVVV	T209 EYLDaRPaTRHsVVV	T208 EYLDaRPaTRHsVVV	T211 EYLDaRPaTRHsVVV
0	1	R213-nl LDDaRPaTRHsVVVFP	R207 LDDaRPaTRHsVVVFP	R211 LDDaRPaTRHsVVVFP	R210 LDDaRPaTRHsVVVFP	R213 LDDaRPaTRHsVVVFP
4	0	S215-p DRPaTRHsVVVFPaEP	S209 DRPaTRHsVVVFPaEP	S213 DRPaTRHsVVVFPaEP	S212 DRPaTRHsVVVFPaEP	S215 DRPaTRHsVVVFPaEP
1	0	Y228-p RPaTRHsVVVFPaEPaGS	Y214 RPaTRHsVVVFPaEPaGS	Y218 RPaTRHsVVVFPaEPaGS	Y217 RPaTRHsVVVFPaEPaGS	Y228 RPaTRHsVVVFPaEPaGS
0	1	C229 PFEVGSaCITTHDHY	Y223-p PFEVGSaCITTHDHY	Y227 PFEVGSaCITTHDHY	C226 PFEVGSaCITTHDHY	C229 PFEVGSaCITTHDHY



CURIOSITY

"For every answer, there are but two more questions."

motifake.com

The Eukaryotic Linear Motif resource for *Functional Sites in Proteins*

The ELM resource

is a collection of more than 240 thoroughly annotated motif classes with over 2700 annotated instances.

It is also a prediction tool to detect these motifs in protein sequences employing different filters to distinguish between **functional** and **non-functional** motif instances.

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Functional sites	ELM classes		ELM instances		PDB structures	GO terms		PubMed links
Total	159	246	2702	348		549	2439	
By category	LIG	137	Human	1594				
	MOD	31	Mouse	253	Biological Process	283	From class	1174
	DEG	25	Rat	130				
	DOC	22	Yeast	94	Cellular Compartment	119	From instance	1746
	TRG	20	Fly	90				
	CLV	11	Other	541	Molecular Function	147		

ELM Class

Condensed information about a motif. Regular Expressions used to annotate the motif (eg. "[KR]xLx{0,1}[FYLIIVMP] for Cyclin motif)

DOC_CYCLIN_1

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 with this model:	#DOC_CYCLIN_1
Description:	Substrate recognition site that interacts with cyclin and thereby increases phosphorylation by cyclin/cdk complexes. Predicted proteins should have a CDK phosphorylation site (#M000_CDK_1). Also used by cyclin/cdk inhibitors.
Pattern:	[KR].L.L(0,1)[FYLIIVMP]
Pattern Probability:	0.0053239
Present in taxon:	Eukaryota
Interaction Domain:	#Cyclin_N (PF00134) Cyclin, N-terminal domain (Stoichiometry: 1 : 1)

PDB Structure: [1HE24](#)

ELM Class

Condensed information about a motif. Regular Expressions used to annotate the motif (eg. "[KR]xLx{0,1}[FYLIIVMP] for Cyclin motif)

■ 24 instances for DOC_CYCLIN_1

(click table headers for sorting. Notes column: Δ =Number of Switches, $\#$ =Number of Interactions)

Protein Name	Gene Name	Start	End	Subsequence	Logic	#Ev.	Organism	Notes
RL_HUMAN	RE1	873	877	GGPPFYKQLGLFVIGDSEK	TP	3	Homo sapiens (Human)	1H25 14
QBLWJB_CHICK	CDH1-A	394	398	KLDSREYVQLLAKHPDSEK	FP	1	Gallus gallus (Chicken)	
PMY1_HUMAN	PKMYT1	486	489	GGPPFYVQLLAFVDFLD	TP	1	Homo sapiens (Human)	
E2F3_HUMAN	E2F3	90	94	LGGPPFYVQLLFTDQFLA	TP	3	Homo sapiens (Human)	1H24
CDN1C_HUMAN	CDKN1C	31	34	VLPPTSAVQLLCPVDSSEK	TP	1	Homo sapiens (Human)	
RLUX_DROME	rux	248	251	PEARRCYVQLLFTDQFEEK	TP	1	Drosophila melanogaster (Fruit fly)	
E2F2_HUMAN	E2F2	87	91	ADRLFAVQLLFDIDPFYV	TP	1	Homo sapiens (Human)	
E2F3_HUMAN	E2F3	134	138	GGPPFAVQLLFDQDQETK	TP	1	Homo sapiens (Human)	
AKA12_MOUSE	Akap12	501	504	TEPDEYVQLLFDVDEEK	TP	1	Mus musculus (House mouse)	14
CDC5_HUMAN	CDC5	94	98	RRRLAVQLLFDGLTEK	TP	2	Homo sapiens (Human)	2CCH 14
CDN1A_HUMAN	CDKN1A	19	22	WPSDEAVQLLFDVDSSEK	TP	4	Homo sapiens (Human)	16 14
CDN1A_HUMAN	CDKN1A	155	159	SNQDFFVRRRLFDVRRFP	TN	1	Homo sapiens (Human)	
ORC5_YEAST	ORC5	178	182	SPNPTAVQLLFDQDSEK	TP	1	Saccharomyces cerevisiae (Baker's yeast)	
TP53_HUMAN	TP53	381	385	IQDTERVQLLFTDQDFEK	TP	5	Homo sapiens (Human)	1H26
RBL1_HUMAN	RBL1	638	641	QPTADEAVQLLFDQDFEEN	TP	3	Homo sapiens (Human)	1H28
RBL2_HUMAN	RBL2	680	684	PPASPTVQLLFTDQDFSEK	TP	1	Homo sapiens (Human)	
HRA_HUMAN	HRA	629	633	KASLFAVQLLFDVYDEEK	TP	1	Homo sapiens (Human)	

DOC_CYCLIN_1

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 with this model:** #DOC_CYCLIN_1**Description:** Substrate recognition site that interacts with cyclin and thereby increases phosphorylation by cyclin/cdk complexes. Predicted proteins should have a CDK phosphorylation site (#KDD_CDK_1). Also used by cyclin/cdk inhibitors.**Pattern:** [KR].{0,1}[FYLIIVMP]**Pattern Probability:** 0.0053239**Present in taxon:** Eukaryota**Interaction Domain:** #Cyclin_N (PF00134) Cyclin, N-terminal domain (Stoichiometry: 1:1)

PDB Structure: 1H24




ELM Instance

An experimentally verified instance of an ELM class in a particular sequence.

ELM Class

Condensed information about a motif. Regular Expressions used to annotate the motif (eg. "[KR]xLx{0,1}[FYLIIVMP] for Cyclin motif)

Instance

Sequence	Start	End	Subsequence	Logic	PDB	Organism	Length
(Q99741) CDCR_HUMAN	94	98	RRRTLAGRRGQDRQLTTRQ	TP		Homo sapiens (Human)	560

Instance evidence

Evidence class	PSM	Method	BioSource	PubMed	Logic	Reliability	Notes
experimental	M0114	x-ray crystallography	in vitro	Chang,2006	support	certain	InteractionDetection FeatureDetection
experimental	M0096	pull down	in vivo/in vitro	Petersen,1999	support	certain	InteractionDetection

This ELM instance is part of the following switching mechanism(s) annotated at the [iSwitches](#) ELM resource:

SWT000335:



DOC_CYCLIN_1

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 with this model: [DOC_CYCLIN_1](#)

Description: Substrate recognition site that interacts with cyclin and thereby increases phosphorylation by cyclin/cdk complexes. Predicted proteins should have a CDK phosphorylation site ([M000_CDK_1](#)). Also used by cyclin/cdk inhibitors.

Pattern: [KR]_L_{0,1}[FYLIIVMP]

Pattern Probability: 0.0053239

Present in taxon: [Eukaryota](#)

Interaction Domain: [Cyclin_N \(PF00134\)](#) Cyclin, N-terminal domain (Stoichiometry: 1:1)

PDB Structure: [1H24](#)



ELM Instance


An experimentally verified instance of an ELM class in a particular sequence.

- Experimental Evidences
- Methods
- References
- Interactions

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Pattern: [KR], L., [D], L [FTLIVMP]
Pattern Probability: 0.0053239
Present in taxon: Eukaryota
Interaction Domain: #Cyclin_N (PF00134) Cyclin, N-terminal domain (Stoichiometry: 1 : 1)
 PDB Structure: [1H24](#)



ELM Instance

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ELM Class

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Pattern Probability: 0.0053239

Present in taxon: Eukaryota

Interaction Domain: [Cyclin_N \(PF00134\)](#) Cyclin, N-terminal domain (Stoichiometry: 1:1)

PDB Structure: [1H24](#)



ELM Instance


An experimentally verified instance of an ELM class in a particular sequence.

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This ELM instance is part of the following switching mechanism(s) annotated at the [iSwitches](#) ELM resource:

SWT000339:



DOC_CYCLIN_1

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 with this model: #DOC_CYCLIN_1

Description: Substrate recognition site that interacts with cyclin and thereby increases phosphorylation by cyclin/cdk complexes. Predicted proteins should have a CDK phosphorylation site (#M000_CDK_1). Also used by cyclin/cdk inhibitors.

Pattern:

[KR]_L_{0,1}[FYLIIVMP]

Pattern Probability:

0.0053239

Present in taxon:

Eukaryota

Interaction Domain:

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

PDB Structure: [1H24](#)



ELM Instance


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Pattern:

[KR], L, (0, 1) [FYLIIVMP]

Pattern Probability:

0.0053239

Present in taxon:

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Interaction Domain:

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

PDB Structure: 1H24



ELM Instance

An experimentally verified instance of an ELM class in a particular sequence.

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The Eukaryotic Linear Motif resource for Functional Sites in Proteins

ELM Home ELM Prediction ELM DB ELM Candidates ELM

ELM classes

ELM instances

ELM pdb structures

ELM binding domains

ELM switches

ELM pathways

ELM related diseases

ELM viral instances

ELM pathogenic abuse

ELM experiments

ELM GO Terms

SEARCH the ELM

The ELM relational database is curated from the literature. This site contains one to many ELM validated motif instances matched to a protein sequence on this website according to the following criteria:

- 239 annotated **ELM classes**
- 2,675 experimentally validated **ELM instances**
- 100 **ELM methods** described
- 358 solved **PDB structures**
- 118 globular **ELM binding domains**
- 1,031 **interactions** mediated by [ELM instances](#)
- 836 regulatory **switches** mediated by curated ELM instances (from [Switches](#), ELM DB)
- 784 **pathways** from [KEGG](#) involving linear motifs annotated in **832** Sequences
- 219 **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

kelch1

ELM CLASS: DEG_Kelch_actinfilin_1

ELM CLASS: DEG_Kelch_Keap1_1

ELM CLASS: DEG_Kelch_Keap1_2

ELM CLASS: DEG_Kelch_KLHL3_1

INSTANCE: P42260 GRIK2_RAT [881:885] DEG_Kelch_actinfilin_1

INSTANCE: Q14494 NF2L1_HUMAN [231:236] DEG_Kelch_Keap1_1

INSTANCE: Q16236 NF2L2_HUMAN [77:82] DEG_Kelch_Keap1_1

INSTANCE: P20482 CNC_DROME [458:463] DEG_Kelch_Keap1_1

INSTANCE: Q13501 SQSTM_HUMAN [347:352] DEG_Kelch_Keap1_1

INSTANCE: Q96HS1-1 PGAM5_HUMAN [77:82] DEG_Kelch_Keap1_1

INSTANCE: O14920 IKKB_HUMAN [34:39] DEG_Kelch_Keap1_1

INSTANCE: Q5JTC6 AMER1_HUMAN [286:291] DEG_Kelch_Keap1_1

INSTANCE: Q86YC2 PALB2_HUMAN [89:94] DEG_Kelch_Keap1_1

INSTANCE: Q13402 MYO7A_HUMAN [1636:1641] DEG_Kelch_Keap1_1

INSTANCE: Q12830 BPTF_HUMAN [729:734] DEG_Kelch_Keap1_1

- DEG_SPOP_SBC_1
- DOC_GSK3_Axin_1
- LIG_CID_NIM_1
- LIG_GBD_WASP_1
- LIG_Mtr4_Alr2_1
- LIG_Mtr4_Trif4_1
- LIG_Mtr4_Trif4_2
- LIG_Pex14_3
- LIG_Pex14_4
- LIG_RPA_C_Funoi
- LIG_RPA_C_Insects
- LIG_RPA_C_Plants
- LIG_RPA_C_Vert
- MOD_SUMO_rev_2



TRG_AP2beta_CARGO_1

Accession: [ELME000247](#)

Functional site class: AP-2 beta2 appendage CCV component motifs

Functional site description: Several motifs are responsible for the binding of accessory endocytic proteins to the beta2-subunit appendage of the adaptor protein complex AP-2 as part of their recruitment to the site of clathrin coated vesicle (CCV) formation. Proteins binding the platform subdomain have been found to be cargo family specific (for example can load all GPCRs, or all LDL receptor family members) clathrin adaptors. Accessory proteins which help in CCV formation bind the sandwich subdomain site or the alpha ear domain.

ELM Description: Motif binding as a helix in a depression on the top surface of the AP-2 beta appendage platform subdomain. The pattern [ED]x(1,2)Fxx[FL]xxxR is conserved in beta Arrestins, ARH and Epsin-1, -2 of vertebrates. It is also found in homologues of other metazoans, but the pattern is sometimes not matched exactly, meaning that the ELM regular expression will not provide a match. In other lineages, if there is an equivalent motif, the pattern is likely to have diverged.

Pattern: [DE] . {1,2} F [^ P] [^ P] [FL] [^ P] [^ P] [^ P] R

Pattern Probability: 0.0000182

Present in taxon: Metazoa

Interaction Domain: [B2-adapt-app_C \(PF09066\)](#) Beta2-adaptin appendage, C-terminal sub-domain (Stoichiometry: 1 : 1)

PDB Structure: [2G30](#)





The Eukaryotic Linear Motif resource for
Functional Sites in Proteins

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Search ELM Instances

Full-Text Search (to show all instances, enter 'all' or '')

Filter by instance Logic: true positive | Filter by organism: Homo sapiens

submit Reset

export 58 instances as: [fasta](#) [tsv](#)

■ 58 instances for search term 'ap2':

(click table headers for sorting)

CLV
LIG
MOD
TRG

ELM identifier	Sequence	Start	End	Subsequence	Instance Logic	#Evidence	PDB	Organism
TRG_LysEnd_APsAcLL_1	OPRD_HUMAN	241	246	GLMLRL RSV RLLSGSKEKD	true positive	8	---	Homo sapiens (Human)
TRG_AP2beta_CARGO_1	ARRB1_HUMAN	385	395	TNDD IVFDF ARQLKGRK	true positive	5	2IV8	Homo sapiens (Human)
TRG_LysEnd_APsAcLL_1	HG2A_HUMAN	19	24	DQKVM DQRDL SNNEQLP	true positive	5	---	Homo sapiens (Human)
LIG_AP2alpha_2	EPS15_HUMAN	672	674	DPFATSS DPF SAANSSIT	true positive	4	---	Homo sapiens (Human)
LIG_AP2alpha_2	EPS15_HUMAN	692	694	SVETLKH NDPF APGGTVVAA	true positive	4	---	Homo sapiens (Human)
LIG_AP2alpha_2	EPS15_HUMAN	709	711	VAASD SATDPF ASVFGNESF	true positive	4	---	Homo sapiens (Human)
LIG_AP2alpha_2	EPS15_HUMAN	737	739	TLKVN NDPF RSATSSSVS	true positive	4	---	Homo sapiens (Human)
TRG_AP2beta_CARGO_1	EPN1_HUMAN	377	386	FDTE PDEFSD RLRLTALPT	true positive	4	---	Homo sapiens (Human)
TRG_LysEnd_APsAcLL_1	ATP7A_HUMAN	1483	1488	SVTSE PDKHSL LVGDFRED	true positive	4	---	Homo sapiens (Human)
LIG_SxIP_EBH_1	CLAP2_HUMAN	492	502	ASA QRKRSKIP RSVSGCSREAS	true positive	3	---	Homo sapiens (Human)
LIG_SxIP_EBH_1	CLAP2_HUMAN	515	525	LSVA RSSRI PRPSVSGQCSR	true positive	3	---	Homo sapiens (Human)
TRG_LysEnd_APsAcLL_1	BCAM_HUMAN	604	609	HSGSEQ EQTE LLMGGASGG	true positive	3	---	Homo sapiens (Human)
TRG_LysEnd_APsAcLL_1	NPC1_HUMAN	1271	1276	KSCATEERYK GERER LLNF	true positive	3	---	Homo sapiens (Human)
LIG_APCC_KENbox_2	CKAP2_HUMAN	80	84	KLKTK MADKEN KRPAESKN	true positive	2	---	Homo sapiens (Human)
LIG_MAPK_1	MP2K1_HUMAN	3	11	HPKKKPTPI QLNPAPDGSVA	true positive	2	---	Homo sapiens (Human)
LIG_MAPK_1	MP2K4_HUMAN	40	48	SSMQ KRKALK LNFA ^{NP} PK	true positive	2	---	Homo sapiens (Human)
TRG_AP2beta_CARGO_1	ARH_HUMAN	256	266	DDGL DEAF SRLAQSR ^{TN} POV	true positive	2	2G30	Homo sapiens (Human)
TRG_LysEnd_APsAcLL_1	CD44_HUMAN	708	713	GEASK SEMV HLN ^{KES} SET	true positive	2	---	Homo sapiens (Human)
LIG_AP2alpha_1	AMPH_HUMAN	324	328	QENI SF FED ^{FN} VPETSVTT	true positive	1	1KY7	Homo sapiens (Human)
LIG_AP2alpha_2	EP15R_HUMAN	599	601	RGSFG ANDPF KNKALLFSN	true positive	1	---	Homo sapiens (Human)
LIG_AP2alpha_2	EP15R_HUMAN	618	620	NNTQEL HPDP QTE ^{DP} PKSD	true positive	1	---	Homo sapiens (Human)



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 dedicated **Viruses** page. For a large-scale analysis on disease-causing mutations see [\[Proteome-wide analysis of human disease mutations in short linear motifs: neglected players in cancer? Uyar B, et al., 2014\]](#)

Noonan Syndrome

The developmental disorder "Noonan Syndrome" can be caused by mutations in [Raf-1](#) which abrogate the interaction with 14-3-3 proteins mediated by corresponding motifs and thereby deregulate the Raf-1 kinase activity [[Pandit et al., 2007](#)]. The [Raf-1](#) sequence features two **LIG_14-3-3_1** binding sites, which are annotated at **256-261** and **618-623**.

Noonan-like Syndrome

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](#)].

Usher's Syndrome

"Usher's Syndrome" is the most frequent cause of hereditary deaf-blindness in humans [[Eudy and Sumeji, 1999](#)], affecting one child in 25 000. This disease can be caused by mutations in either PDZ domains in [Harmonin](#) or the corresponding PDZ interaction motifs in the [SANS](#) protein (annotated at **456-461**) [[Weil et al., 2003](#), [Kalay et al., 2005](#)].

Another example implicating PDZ domains is "*familial hypomagnesemia with hypercalciuria and nephrocalcinosis*" (FHWHN), an autosomal recessive wasting disorder of renal Mg²⁺ and Ca²⁺ that leads to progressive kidney failure. Here, motifs mediating interaction to PDZ domains are mutated in [Claudin 16](#), abolishing important interactions to the scaffolding protein [ZO-1](#) resulting in lysosomal mislocalization of the protein [[Müller et al., 2003](#), [Müller et al., 2006](#)].



Functional site prediction

Protein sequence

Enter Uniprot identifier or accession number: (auto-completion)

e.g. [EPN1_HUMAN](#), [P04637](#), [TAU_HUMAN](#), [\[RANDOM\]](#)

EPN1
 CARP_CRYPA [P11838] Cryphonectria parasitica
 EPD1_CARAU [P13506] Carassius auratus
[EPN1_ARATH](#) [Q8VY07] Arabidopsis thaliana
[EPN1_HUMAN](#) [Q9Y6I3] Homo sapiens
[EPN1_MOUSE](#) [Q80VP1] Mus musculus
[EPN1_RAT](#) [O88339] Rattus norvegicus
 F2QLC2_PICP7 [F2QLC2] Kornagataella pastoris
 K0KY34_WICCF [K0KY34] Wickerhamomyces ciferrii
 A0A024R4S1_HUMAN [A0A024R4S1] Homo sapiens
 K7EMP4_HUMAN [K7EMP4] Homo sapiens
 W8B7F4_CERCA [W8B7F4] Ceratitidis capitata
 A8X4H2_CAEBR [A8X4H2] Caenorhabditis briggsae
 Q9BI71_CAEEL [Q9BI71] Caenorhabditis elegans
 Q9B1B6_CAEEL [Q9B1B6] Caenorhabditis elegans

cytosol
 peroxisome
 glycosome
 glyoxisome

FASTA format:

```

SEIMSHIWKRLNDHGKKNRWIRVYKAMTL
LRDEDRLREERAHALKTEKLAQTATA
QLALSLSREEDKKEIRIGDDLRQM
DPWGGPPVFPAADPWGGPAPTASGDP
AFSPDWGGSPAKFSTNGTTAAGGFDTE
ISPPAANTFTPTTFFKRTPEFLGFNAA
RLSPVFPVPGAPPTYISPLGGGPGLEFP
  
```

Taxonomic Context

Type in species name (auto-completion):

Homo sapiens

Motif Probability Cutoff:

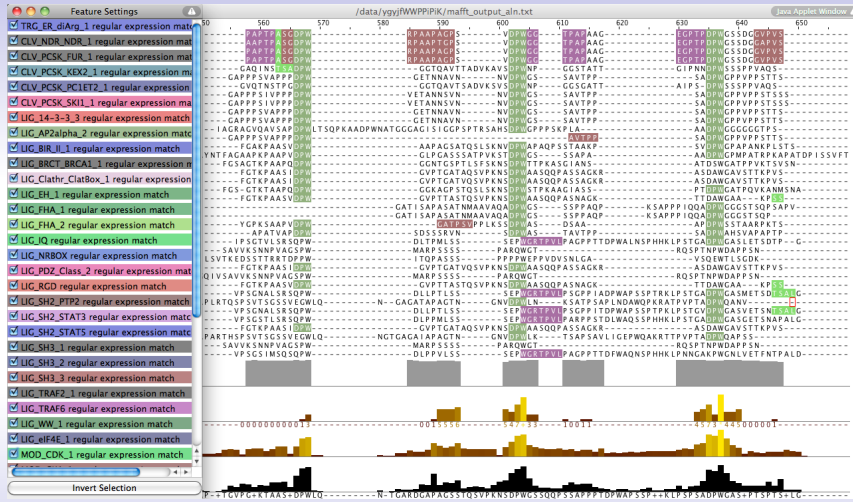
ELM database update

The following elm classes have been added to the database:

- [DEG Kelch actinfilin 1](#)
- [DEG Kelch Keap1 1](#)
- [DEG Kelch Keap1 2](#)
- [DEG Kelch KLHL3 1](#)
- [DEG Nend Nbox 1](#)
- [DEG Nend UBRbox 1](#)
- [DEG Nend UBRbox 2](#)
- [DEG Nend UBRbox 3](#)
- [DEG Nend UBRbox 4](#)
- [DEG SPOD SBC 1](#)
- [DOC GSK3 Axin 1](#)
- [LIG CID NIM 1](#)
- [LIG GBD WASP 1](#)
- [LIG Mtr4 Air2 1](#)
- [LIG Mtr4 Trf4 1](#)
- [LIG Mtr4 Trf4 2](#)
- [LIG Pex14 3](#)
- [LIG Pex14 4](#)
- [LIG RPA C Fungj](#)
- [LIG RPA C Insects](#)
- [LIG RPA C Plants](#)
- [LIG RPA C Vert](#)
- [MOD SUMO rev 2](#)

Many new instances of

VIEW CONSERVATION IN JALVIEW



Questions?



CURIOSITY

Do you really want to know?

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Short Linear Motifs

- are compact, degenerate protein interaction interfaces (in IDRs)
- are ubiquitous in eukaryotic proteomes and mediate many regulatory functions:
 - directing ligand binding
 - providing docking sites for modifying enzymes
 - controlling protein stability
 - acting as signals to target proteins to specific subcellular locations

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Motif-mediated interactions

- occur with low affinity,
- are transient & reversible
- can be easily modulated.

Short Linear Motifs

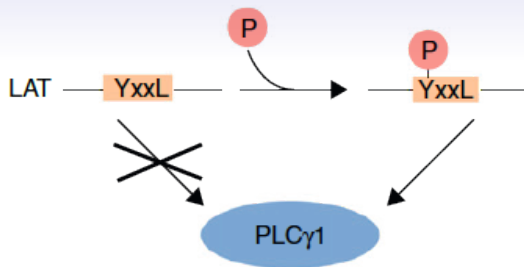
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Motif-mediated interactions

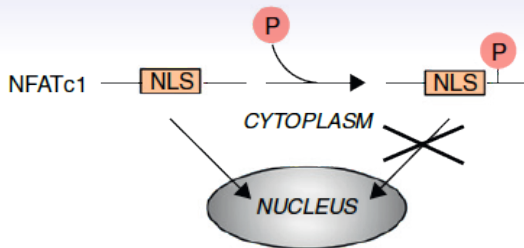
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- are transient & reversible
- can be easily modulated.

Motifs mediate switches

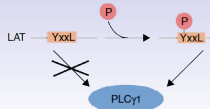
This makes SLiMs ideal regulatory modules and enable them to conditionally **switch** between “on” and “off” states or between multiple, functionally distinct on states.

PTM-induced binding

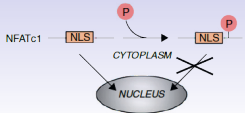
PTM-induced incompatibility



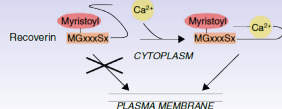
(a) Binary switch
PTM-induced binding



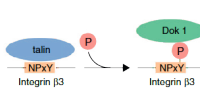
PTM-induced incompatibility



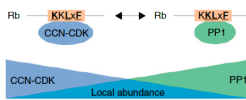
Allostery



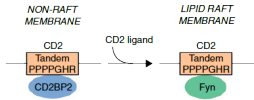
(b) Specificity switch
Intrinsic affinity switch



Competition switch

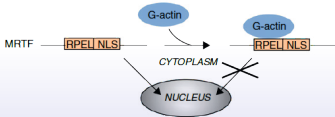


Localisation switch



(c) Motif hiding

PTM-independent



PTM-dependent

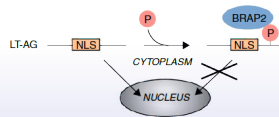
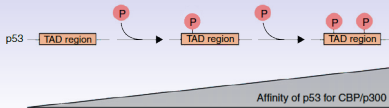


Figure legend

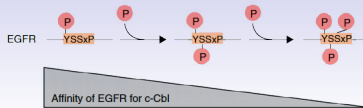
- Protein
- Protein
- Small molecule
- Post-translational modification
- Motif (Regular expression)
- Motif (Name / Abbreviation)

(a) Cumulative switch

Positive rheostat

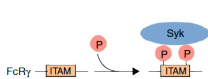


Negative rheostat

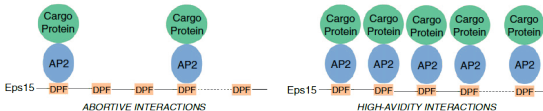


(b) Avidity-sensing switch

PTM-dependent



PTM-independent



(c) Sequential switch

Priming PTM



Sequential specificity switch

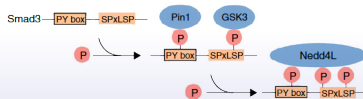


Figure legend

- Protein
- Protein
- Small molecule
- Post-translational modification
- Motif (Regular expression)
- Motif (Name / Abbreviation)

The switches.ELM **database** curates experimentally validated motif-based molecular switches.

In addition, based on these validated instances, the switches.ELM **prediction** tool was developed to identify possible switching mechanisms that might regulate a motif-containing protein of interest.

switches.ELM

Home Browse Analyse Search Submit Definitions Help About

Introduction

The switches.ELM resource, hosted by the ELM consortium at the European Molecular Biology Laboratory (EMBL), consists of a database that curates experimentally validated motif-based molecular switches and a prediction tool to identify possible switching mechanisms that might regulate a user-submitted motif of interest. This tool helps to extend knowledge and direct research on how motifs mediate cooperative decision-making in a context-dependent manner and direct reliable and robust cell regulation.

Submit a paper for curation

Enter a PubMed ID

Links

[View predicted switches in the ELM database.](#)
[View switches currently awaiting curation.](#)

Switch of the month

A Smad action turnover switch operated by WW domain readers of a phosphoserine code.
 Aragon *et al.*, Genes Dev, 2011

Links: [PubMed](#) [Genes Dev](#) [switches.ELM](#)

Browse database by

Search database

Enter search term

Examples: Phosphorylation | Mouse | LIG_CYCLIN_1

Analyse proteins for novel switches

Enter protein

Examples: P04637 | TP53 | Tumor suppressor p53

[SyBass](#) [EMBL](#) [EU](#) [FR](#)

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Switch #: SWT1000055	Switch type: Binary	Switch subtype: Physicochemical compatibility
--------------------------------------	---------------------	---

Switch Description:

Phosphorylation of S203 in the Pin1-binding motif of Steroidogenic factor 1 (Nr5a1) induces binding to the Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 (Pin1) protein.



Participants:

- Steroidogenic factor 1 (Nr5a1)
- Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 (Pin1)

Interactions

Interaction #1 Nr5a1 - Pin1

Interfaces

- LIG_WW_Pin1_4 motif (YASPP)₂₀₆ in Steroidogenic factor 1 (Nr5a1)
- WW domain (7-37) in Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 (Pin1)

Interaction Regulation

PTM-dependent Induction (Phosphorylation of S203 on Steroidogenic factor 1 (Nr5a1) of the Steroidogenic factor 1 (Nr5a1) LIG_WW_Pin1_4 motif - Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 (Pin1) WW domain interaction)

References

- Pin1 facilitates the phosphorylation-dependent ubiquitination of SF-1 to regulate gonadotropin beta-subunit gene transcription. Luo et al. *Mol. Cell Biol.* (2010)

See also

Other switches involving participants

Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 (Pin1) - 26 more (view)

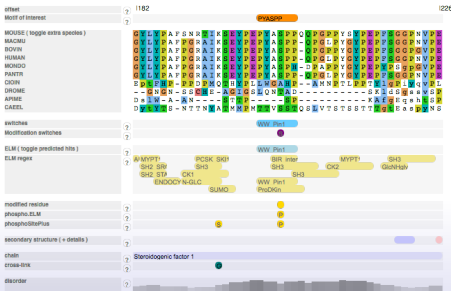
Other switches involving interfaces

LIG-WW_Pin1-4+69 more (view)

WW domain - 102 more (view)

Steroidogenic factor 1 (Nr5a1)

Alignment Motifs Modification Switches Structure Mutation Isoforms SNPs Features Disorder



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ProViz <http://proviz.ucd.ie/> is a tool to visualize biological data allowing the investigation of functional and evolutionary protein features. The tool is designed to be an intuitive and accessible resource to allow users with limited bioinformatic skills to rapidly access and visualise data pertinent to their research.

PROTEIN VISUALIZATION (PROVIZ)



"ProViz-a web-based visualization tool to investigate the functional and evolutionary features of protein sequences."; JEHL P, MANGUY J, SHIELDS DC, HIGGINS DG, DAVEY NE.; (NUCLEIC ACIDS RES. 2016 APR 16)

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Questions?



CURIOSITY KILLED THE CAT

Good boy curiosity.....
Good boy!!

motifake.com