

iPTMnet Help

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iPTMnet Batch Retrieval

Use this page to retrieve information from the iPTMnet on PTM Enzyme-Site relation, and PTM-dependent PPIs.

1. Provide input

Q7Z7L8 S 112
 Q13017 S 1124
 Q95248 S 1141
 Q9NRY4 S 1150
 Q86UU0 S 118
 Q5VZL5 S 1181
 Q9Y4H2 S 1186
 Q8WW11 S 1231
 Q8N3D4 S 1273
 Q14160 S 1285

[Clear](#) [Input example](#)

or

No file chosen

2. Select output

PTM Enzymes
 PTM Dependent PPIs

Input format:

Paste into the box or upload a text file containing a three column space/comma/tab-delimited list (do not include a header line)

Substrate AC	Site residue	Site position
Q15796	S	465

Query Limit: 500 lines (Large queries may take several minutes to process)

Delimiter: comma, tab, space

Substrate must be provided.

Select desired output:

PTM Enzymes: Displays all iPTMnet PTM enzyme-site relations for the sites on the input list along with evidence source(s).

PTM Dependent PPIs: Displays all PTM-dependent protein-protein interactions for the sites on the input list along with evidence source(s).

for proteins in iPTMnet database

PTM type - Has Role - Restrict by Organism - Sample Report **Batch Retrieval (New!)**

Input Site Found in iPTMnet **217** | Input Site Not Found **26**

[Cytoscape View](#) [Download](#)

PTM with Enzyme

<input type="checkbox"/>	PTM Type	Substrate	Site	PTM Enzyme	Score	Source	PMID
<input checked="" type="checkbox"/>	Phosphorylation	PTM Q15121 (PEA15)	S104	P17252 (PRKCA)	★★★★☆	HPRD Signor	19651622, 15917297, 17287340, ...
<input type="checkbox"/>	Phosphorylation	PTM P00533-1 (EGFR)	S1064	Q9UQM7 (CAMK2A)	★★★★☆	HPRD Signor	18691976, 18669648, 10347170, ...
<input type="checkbox"/>	Phosphorylation	PTM Q9NRY4 (ARHGAP35)	S1150	Q13464 (ROCK1)	★★★★☆	PSP	19103606
<input checked="" type="checkbox"/>	Phosphorylation	PTM P16144 (ITGB4)	S1364	P17252 (PRKCA)	★★★★☆	PSP	15121854
<input checked="" type="checkbox"/>	Phosphorylation	PTM P16144 (ITGB4)	S1364	P17612 (PRKACA)	★★★★☆	PSP Signor	17615294
<input checked="" type="checkbox"/>	Phosphorylation	PTM P16144 (ITGB4)	S1364	Q15418 (RPS6KA1)	★★★★☆	PSP	20870721
<input checked="" type="checkbox"/>	Phosphorylation	PTM Q75116 (ROCK2)	S1374	P53350 (PLK1)	★★★★☆	neXtProt	17446864
<input type="checkbox"/>	Phosphorylation	PTM Q14160 (SCRIB)	S1378	Q13464 (ROCK1)	★★★★☆	PSP	26101221

PTM with no enzyme

PTM Type	Substrate	Site	PTM Enzyme	Score	Source	PMID
Phosphorylation	PTM Q13619 (CUL4A)	S10		★★★★☆	HPRD phospho.ELM PSP UniProt	18691976, 23186163, 18212344, ...
Phosphorylation	PTM Q6TDM6 (DLG5)	S1021		★★★★☆	PSP UniProt	23186163
Phosphorylation	PTM Q6ZRV2 (FAM83H)	S1025		★★★★☆	HPRD PSP UniProt	18669648, 23186163, 20068231
Phosphorylation	PTM Q15164-1 (TRIM24)	S1042		★★★★☆	HPRD PSP UniProt	21406692, 18212344, 20068231
Phosphorylation	PTM Q8ND11-1 (EHBP1)	S1058		★★★★☆	HPRD phospho.ELM PSP UniProt	21406692, 23186163, 19651622, ...

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iPTMnet

iPTMnet can be accessed via the Protein Information Resource (PIR) website

Updated 06/26/2019

(<http://proteininformationresource.org>, **Figure 1**)

The image shows the homepage of the Protein Information Resource (PIR). At the top, there is a navigation bar with the PIR logo, a UniProt Consortium Member badge, and a search bar. Below the navigation bar, the main heading reads "INTEGRATED PROTEIN INFORMATICS RESOURCE FOR GENOMIC, PROTEOMIC AND SYSTEMS BIOLOGY RESEARCH". A central box describes UniProt as "The Universal Protein Resource (UniProt) provides the scientific community with a single, centralized, authoritative resource for protein sequences and functional information." Below this, there are three main sections: "PRO Protein Ontology", "iPTMnet Integrated Protein PTM Resource" (highlighted with a red border), and "iProLINK Literature Information & Knowledge". At the bottom, there are three search options: "OTHER RESOURCE" (with links to Reference Proteomes, ProClass, ProXpress, and RESID), "PEPTIDE SEARCH" (with a database dropdown set to UniProtKB and a search input field), and "TEXT SEARCH" (with a database dropdown set to ProClass and a search input field). A footer section lists "Bioinformatics & Computational Biology Graduate Programs" with links to the MS program at Georgetown University and PhD, MS, PSM and Graduate Certificate programs at the University of Delaware.

Figure 1 iPTMnet link in PIR website

Or by typing the URL: <http://proteininformationresource.org/iPTMnet>

iPTMnet functionalities are compatible with the latest versions of Chrome and Firefox browsers.

In the homepage (**Figure 2**), you can query the database (1) which contains the protein post-translational modification (PTM) data from multiple expert curated databases (see database sources section) and results from text mining (RLIMS-P and eFIP tools). You can also perform a literature search (2) using the RLIMS-P text mining tool to find relevant papers with protein phosphorylation information for the topic of interest. In addition, the homepage presents the menu (3) with links to browsing, database statistics, general project information, programmatic access (API), help document, License and Citation information.

iPTMnet


iPTMnet is a bioinformatics resource for integrated understanding of protein post-translational modifications (PTMs) in systems biology context.

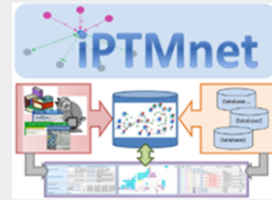
It connects multiple disparate bioinformatics tools and systems text mining, data mining, analysis and visualization tools, and databases and ontologies into an integrated cross-cutting research resource to address the knowledge gaps in exploring and discovering PTM networks.

- [Browse](#)
- [Statistics](#)
- [Project Info](#) ▾
- [API](#)
- [Help](#)
- [License](#)
- [Citation](#)



3-iPTMnet Menu

 (NSF grants ABI-1062520)
NIH/NIGMS grants U01GM120953



Search for proteins in iPTMnet database

1-Database Search

All ▾ Search

PTM type ▾ Has Role ▾ Restrict by Organism ▾ [Sample Report](#) [Batch Retrieval \(New!\)](#)

Search phosphorylation information in the literature

2-Literature Mining Search



Enter Keywords (accepts Boolean operators (AND, OR, NOT))

Input keyword

Exclude review papers, Restrict by Organism ▾

Figure 2 iPTMnet homepage

Database Search

Figure 3 shows that the database search allows searching the iPTMnet database based on the following search fields (1) UniProtKB identifiers (e.g. O22476/BRI1_ARATH), protein/gene name (e.g. Protein BRASSINOSTEROID INSENSITIVE 1/BRI1), or PMID (e.g., 21855796). The search can be restricted by PTM type (2), by role (3), whether the protein act as enzyme or is a substrate, and/or by organism (4).

1-Search Fields Search in iPTMnet database

All Search Submit Reset

Restrict by Organism Sample Report Batch Retrieval (New!)

UniProt AC/ID
Protein/Gene Name
PMID

Search phosphorylation information in the literature

RLIMS-P
A Rule-based Literature Mining System for Protein Phosphorylation

Enter keywords (accepts Boolean operators (AND, OR, NOT))

2-Select which PTM Select All, None

Acetylation N-Glycosylation O-Glycosylation
 C-Glycosylation S-Glycosylation Methylation
 Myristoylation Phosphorylation Sumoylation
 Ubiquitination S-Nitrosylation

3-Select which role

Enzyme or Substrate
 Enzyme
 Substrate
 Enzyme and Substrate

4-Select organism Select All, None

Select organisms

Human Mouse Rat
 Cow Chicken Zebrafish
 Fruit fly C. elegans Baker's yeast
 Fission yeast A. thaliana Maize
 M. truncatula Rice (japonica) Rice (indica)

Or input other organisms
 Separate by comma

Figure 3 iPTMnet Database Search functionality

Literature Search

Figure 4 shows the literature search box which uses RLIMS-P tool [1] to identify papers with information on protein phosphorylation, along with information on kinase, substrate and site. The search is PubMed style search, you can use Boolean, also indicate Mesh terms, etc. (e.g. jasmonic AND wound) (1). Review articles can be excluded (2) in case only articles with experiments are important for the user; and the search can be restricted by organism(s) of interest (3).

Search phosphorylation information in the literature

RLIMS-P
A Rule-based Literature Mining System for Protein Phosphorylation

Enter Keywords (accepts Boolean operators (AND, OR, NOT))

1 Input keyword Submit Reset

2 Exclude review papers, Restrict by Organism

3 Select organisms

Human Cow Mouse
 Rat Chicken Zebrafish
 Fruit fly C. elegans Baker's yeast
 Fission yeast A. thaliana Maize
 M. truncatula Rice (japonica) Rice (indica)

Figure 4 Literature Search functionality with RLIMS-P

Updated 06/26/2019

iPTMnet Menu

Browsing: to view database based on specific organism or group of organisms (see Browse section)

Statistics: to view the release information and the distribution of iPTMnet data based on PTM type (**Table 1**), by organism, or by data source.

Table 1 Example of iPTMnet Database Statistics for PTMs for release 5.0

iPTMnet v5.0 Updated on June 6, 2019

Substrates (protein)	Substrates (proteoforms)	Sites	Enzymes	Enzyme-substrate pairs	Enzyme-substrate-site	PTM-dependent PPI	PMIDs	Variants
63475	12144	737070	1072	12106	23315	3031	32738	75130

Event type

	Substrates (protein)	Substrates (proteoforms)	Sites	Enzymes	Enzyme-substrate pairs	Enzyme-substrate-site	PTM-dependent PPI	PMIDs	Variants
Phosphorylation	57182	10779	507757	1048	11963	23044	871	28772	50543
Acetylation	17261	1016	51807	19	135	258	0	1207	3997
Ubiquitination	21501	918	133041	1	2	4	0	272	14614
Methylation	7450	240	18788	4	4	7	0	380	5920
N-Glycosylation	2486	30	5987	0	0	0	0	1565	399
O-Glycosylation	1420	17	4971	0	0	0	0	302	671
C-Glycosylation	20	1	197	0	0	0	0	17	20
S-Glycosylation	5	0	5	0	0	0	0	6	0
Sumoylation	2711	118	8403	0	2	2	0	18	1253
Myristoylation	283	20	308	0	0	0	0	197	15
S-Nitrosylation	2924	0	5806	0	0	0	0	150	397

Project Info: to view general information on the project, the publications, and how to contribute.

API: to use RESTful API for iPTMnet. R package and Python package are also provided in this link.

Help: to access the help document (this document).

License: to check license and disclaimer information.

Citation: to access citation information for iPTMnet and its underlying sources.

iPTMnet Search Results

The result table presents the results based on level of match to query. For text search like the example shown in **Figure 5**, the queried text is highlighted and the results are shown for exact match first and then partial match. The table columns are

1-iPTM ID for each entry matching the query, along with links to iProClass, UniProtKB and Protein Ontology entry reports (2)

3-Protein name (from UniProtKB)

4-Gene Names and synonyms (from UniProtKB)

5-Organism

6-Role: These columns present information on whether the entry has information as substrate or/and enzyme (green checked). The number next to the check indicate the number of enzymes modifying substrate, or number of substrates, for substrate and enzyme roles, respectively.

7-PTM (post translational modification)-dependent PPI (protein-protein interaction)

8-Sites show the number of distinct sites collected from the multiple sources

9-Number of additional protein isoforms for which there is PTM information

10-Provides links network view for selected entries in Cytoscape

1	2	3	4	5	6	7	8	9	10
IPTM ID	Protein Name	Protein Name	Gene Name	Organism	Substrate Role	Enzyme Role	PTM-dependent PPI	Sites	Isoforms
IPTM:Q22476/ BRI1_ARATH	Protein BRASSINOSTEROID INSENSITIVE 1 precursor	Protein BRASSINOSTEROID INSENSITIVE 1 precursor	Name: BRI1 OrderedLocusNames:At4g39400;ORFNames:F23K16.30;	Arabidopsis thaliana (Mouse-ear cress)	✓ 6 enzymes	✓ 1 substrate	✗	28	1
IPTM:Q9FMZ0/ BK1_ARATH	BRI1 kinase inhibitor 1	BRI1 kinase inhibitor 1	Name: BK1 OrderedLocusNames:At5g42750;ORFNames:MB21.13;	Arabidopsis thaliana (Mouse-ear cress)	✓ 1 enzyme	✗	✗	9	0
IPTM:Q6K624/ Q6K624_ORYSJ	BRI1 -KD interacting protein 135	BRI1 -KD interacting protein 135	Name: BRI1 OrderedLocusNames:Os02g0612800;ORFNames:OJ1004_A05.34,OsJ_07506,OSNPB_020612800;	Oryza sativa subsp. japonica (Rice)	✓	✗	✗	9	0
IPTM:Q92WC8/ BRL1_ARATH	Serine/threonine-protein kinase BRI1 -like 1 precursor	Serine/threonine-protein kinase BRI1 -like 1 precursor	Name: BRL1 OrderedLocusNames:At1g55610;ORFNames:F20N2.4;	Arabidopsis thaliana (Mouse-ear cress)	✓	✗	✗	4	0
IPTM:Q9LJF3/ BRL3_ARATH	Receptor-like protein kinase BRI1 -like 3 precursor	Receptor-like protein kinase BRI1 -like 3 precursor	Name: BRL3 OrderedLocusNames:At3g13380;ORFNames:MRP15.1;	Arabidopsis thaliana (Mouse-ear cress)	✓	✗	✗	2	0

Figure 5 Literature Search Result Table

iPTMnet Browse

Use browsing to have a glance at iPTMnet data for specific species or group of species. To view the entries see example in **Figure 6**: click on the organism(s) of interest (1) and then select Click to browse (2). The result table (3) contains the same column information as that described for **Figure 5**. However, the data displayed can be filtered by entity role or PTM type (4).

2-Click Browse

3-Result page

4-Filter by entity role or PTM type

1-Select organism

1	2	3	4	5	6	7	8	9	10
IPTM ID	Protein Name	Protein Name	Gene Name	Organism	Substrate Role	Enzyme Role	PTM-dependent PPI	Sites	Isoforms
			Name: BRI1 OrderedLocusNames:At4g39400;ORFNames:F23K16.30;	Arabidopsis thaliana (Mouse-ear cress)	✓ 6 enzymes	✓ 1 substrate	✗	28	1
IPTM:Q39026/ MPK6_ARATH	Mitogen-activated protein kinase 6	Mitogen-activated protein kinase 6	Name: MPK6 OrderedLocusNames:At2g43790;ORFNames:F18O19.10;	Arabidopsis thaliana (Mouse-ear cress)	✓	✓ 9 substrates	✗	5	0
IPTM:Q48814/ BIK1_ARATH	Serine/threonine-protein kinase BIK1	Serine/threonine-protein kinase BIK1	Name: BIK1 OrderedLocusNames:At2g39660;ORFNames:F12L6.32,F17A14.3;	Arabidopsis thaliana (Mouse-ear cress)	✓ 2 enzymes	✓ 1 substrate	✗	22	1
IPTM:F4JZW1/ PBL13_ARATH	Serine/threonine-protein kinase PBL13	Serine/threonine-protein kinase PBL13	Name: PBL13 OrderedLocusNames:At5g35580;ORFNames:K2K18.3;	Arabidopsis thaliana (Mouse-ear cress)	✓ 1 enzyme	✓ 1 substrate	✗	21	0
IPTM:Q9A9F7/ PDPK1_ARATH	3-phosphoinositide-dependent protein kinase 1	3-phosphoinositide-dependent protein kinase 1	Name: PDPK1 Synonyms:PDK1;OrderedLocusNames:At5g04510;ORFNames:T32M21.110;	Arabidopsis thaliana (Mouse-ear cress)	✓ 1 enzyme	✓ 1 substrate	✗	11	1

Figure 6 Browse iPTMnet data by organism

iPTMnet Report

The report contains sections that are displayed upon existing content. A complete report would have the sections shown in **Figure 7**, <https://research.bioinformatics.udel.edu/iptmnet/entry/P31749/>

Content

Protein Information **A**

Interactive Sequence View **B**

P31749 (AKT1) as Substrate **C**

P31749 (AKT1) as PTM Enzyme **D**

Proteoforms **E**

PTM-dependent PPI **F**

Proteoform PPIs **G**

PTM sites affected in variants **H**

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Cytoscape View **I**
Clear

Link to network Visualization

Protein Information

UniProt AC / UniProt ID: P31749 | AKT1_HUMAN
 Protein Name: RAC-alpha serine/threonine-protein kinase
 Gene Name: Name: AKT1
 Synonyms: PKB, RAC
 Organism: Homo sapiens (Human)

PRO ID: PR:P31749
 PRO Name: RAC-alpha serine/threonine-protein kinase (human)
 Definition: A RAC-alpha serine/threonine-protein kinase that is encoded in the genome of human.
 Short Label: AKT1
 Category: organism-gene

Interactive Sequence View

Show PRO entries: Modification: site affected in variant:

Number of sequence: 9 • Alignment length: 490 • Scale: "x" = 6 amino acids

AKT1 as substrate

Site	PTM Type	PTM Enzyme	Score	Source	PMID
S2	Phosphorylation	***	***	PhosphoSitePlus	26440416, 24467442
K8	Ubiquitination	***	***	PhosphoSitePlus	
K14	Acetylation	***	***	UniProt	21778285

AKT1 as enzyme

Substrate	Site	Score	Source	PMID
O14492 (SH2B2)	S598	***	neXtProt	16141217
O14492-2 (SH2B2)	S641	***	HPRD	16141217
O14745 (SLC9A3R1)	T156	***	RLIMS-P+	25492869

Proteoforms

PRO ID (Short Label)	Sites	PTM Enzyme	Source	PMID
PR:000048294 (hAKT1/Phos:3)	pS473		PRO	
PR:000048295 (hAKT1/Phos:4)	pT308		PRO	
PR:000048296 (hAKT1/Phos:1)	pT308,pS473		PRO	

PTM-dependent PPI

PTM type	Substrate	Site	Interactant	Association type	Source	PMID
Phosphorylation	P31749 (AKT1)	S473	Q3U182 (Crtc2)	increased_association	eFIP	23300339
Phosphorylation	P31749 (AKT1)	S473	P45983 (MAPK8)	unknown	eFIP	22771387
Phosphorylation	P31749 (AKT1)	S473	P07900 (HSP90AA1)	unknown	eFIP	25935150
Phosphorylation	P31749 (AKT1)	S473	Q68ED7 (Crtc1)	inhibited_association	eFIP	23303455

Proteoform PPIs

Protein 1	Relation	Protein 2	Source	PMID
PR:000028994 (hAKT1/iso:1/Phos:1)	Interaction	PR:Q14746-1 (hTERT/iso:1)	PRO	12586360
PR:000028994 (hAKT1/iso:1/Phos:1)	Interaction	PR:P41279-1 (hMAP3K8/iso:1)	PRO	12138205

PTM sites affected in variants

Site	Variant	Source	PMID	Disease [Sample source]
K14	N14	Biomuta		DOID:2994 / germ cell cancer [cosmic]
K14	I14	Biomuta		DOID:2994 / germ cell cancer [cosmic]
T65	M65	Biomuta		DOID:9256 / colorectal cancer [lgs, toga] DOID:1909 / melanoma [cosmic]

A General protein Information from UniProt and PRO

B Sequence with color-coded sites based on PTM types
■ Phosphorylation
■ Acetylation

C Site-centric list. PTM sites with confidence and evidence

D PTM enzymes have an enzyme table with their substrates and sites

E List of proteoforms for the entry as described in PRO.

F Impact of phosphorylation on PPIs from text mining

G PPIs for proteoforms from PRO

H Variants affecting PTM sites

Figure 7 Summary of entry content for AKT1 human

Here is a more detailed description of the sections:

A-Protein Information. The basic information about the protein (name, gene names and organism) coming from UniProtKB. In addition, information about the corresponding term from the Protein Ontology: PRO term name, ID, synonyms, definition and level in the ontology are displayed, with links to hierarchy. This section is common to all reports.

B-The sequence interactive view The sequence interactive view displays the collection of modified residues highlighted in the canonical sequence and isoforms (if present). Use the magnifier glass to view the actual sequence. In addition, sequences with known specific combinations of modifications (proteoforms) are shown based on the Protein Ontology data. Residues in grey show conservation of sequence in different forms.

Example: AKT1 human



Figure 8 Sequence view. (a) Canonical sequence and isoform with color-coded modifications and variants (with black border). (b) Multiple sequence alignment including proteoforms across organisms

Use Modification to select the type of modification to be highlighted. Modifications are color-coded. Yellow indicates sites where there is annotation for more than one PTM type (e.g., S-129 Phosphorylation and O-glycosylation in AKT1 human)

The screenshot shows the Modification selection interface on the left and a table of PTM sites for AKT1 on the right.

The Modification selection interface includes a dropdown menu for "Modification" and a checkbox for "site affected in variant". The "Select: All, None" option is selected. The list of modifications includes:

- Phosphorylation (checked)
- Acetylation (checked)
- N-Glycosylation (unchecked)
- O-Glycosylation (checked)
- C-Glycosylation (unchecked)
- S-Glycosylation (unchecked)
- Methylation (checked)
- Ubiquitination (checked)
- Myristoylation (unchecked)
- S-Nitrosylation (checked)
- Other (checked)
- Multiple (checked)

The table of PTM sites for AKT1 is as follows:

Site	PTM Type	Source	PubMed ID (PMID)
goS-129	Phosphorylation	PhosphoSitePlus, UniProt	22629392
pS-129 (CSNK2A1)	Phosphorylation	PhosphoSitePlus, Singor, neXtProt	21735093, 21159648, 15818404
pS-129	Phosphorylation	phospho.ELM, PhosphoSitePlus, UniProt, RLIMS-P	21735093, 23186163, 17081983, ...

The URL <https://research.bioinformatics.udel.edu/iptmnet/entry/P31749/#msa> is displayed below the table.

C-Site information for the entry protein with role as substrate

This table lists all PTM sites for the query protein in iPTMnet database. The results are sorted based on the position of the modified site. For each site, the PTM type, the modifying enzyme, the confidence score, source and PubMed ID (PMID) are displayed.

P31749 (AKT1) as Substrate

P31749 [P31749-1](#) [Expanded View](#)

Search: [Display Overlap PTM](#)

Site	PTM Type	PTM Enzyme	Score	Source	PMID
S2	Phosphorylation		★★★★	PhosphoSitePlus RLIMS-P	26440416, 24467442
T34	Phosphorylation	O15530 (PDPK1), Q05513 (PRKCZ)	★★★★	neXtProt PhosphoSitePlus RLIMS-P+ RLIMS-P	14560023, 25912234
T72	Phosphorylation	P31749 (AKT1)	★★★☆☆	neXtProt PhosphoSitePlus RLIMS-P	16549426
S124	Phosphorylation		★★★★	phospho.ELM PhosphoSitePlus RLIMS-P UniProt	12149249, 18669648, 24670416, ...
S129	Phosphorylation	P68400 (CSNK2A1)	★★★★	neXtProt phospho.ELM PhosphoSitePlus RLIMS-P Signor UniProt	21735093, 23186163, 17081983, ...

The confidence score is calculated as follows:

$$\text{Score } S = S_q + S_n + S_p$$

S_q weights the quality of the underlying resource

- S_q = 2, data from curated resources supporting correct species assignment, 1, data from other curated resources, 0, data from automatic text mining;

S_n gives weight to multiple sources

- S_n = 1, data from multiple resources, 0, data from single resource;

S_p gives weight to the number of publications

- S_p = 1, data supported by multiple papers and at least one is not considered a large scale paper (LSP), 0, data supported by one non-LSP paper, -1, only LSP or no literature evidence.

The Score ranges from 0 to 4 gold stars, with 4 being most confident

D-Substrate information for the entry protein with role as enzyme

This table lists the substrates that are modified by the query protein (if the protein is a PTM enzyme). For each substrate (of AKT1 in the example), the site modified (by AKT1 in the example), the score (calculated as indicated in previous point), the source, and PubMed ID (PMID), if known, are displayed.

P31749 (AKT1) as PTM Enzyme

Protein as Phosphorylation Enzyme Search:

Substrate	Site	Score	Source	PMID
<input type="checkbox"/> O14492 (SH2B2)	S598	★★★☆☆	neXtProt	16141217
<input type="checkbox"/> O14492-2 (SH2B2)	S641	★★★☆☆	HPRD	16141217
<input type="checkbox"/> O14745 (SLC9A3R1)	T156	★★★☆☆	RLIMS-P+	25492869
<input type="checkbox"/> O14746 (TERT)	S227	★★★☆☆	HPRD neXtProt PhosphoSitePlus Signor	10224060
<input type="checkbox"/> O14746 (TERT)	S824	★★★☆☆	neXtProt PhosphoSitePlus Signor	10224060

E-Proteome

This table lists the different PTM combinations described in the literature and curated in PRO. E.g., for human AKT1 there are 3 phosphorylated forms, 2 singly phosphorylated and 1 proteoform that is doubly phosphorylated.

Proteome

Search:

PRO ID (Short Label) All ▾	Sites All ▾	PTM Enzyme	Source All ▾	PMID
<input type="checkbox"/> PR:000046294 (hAKT1/Phos:3)	pS473		PRO	
<input type="checkbox"/> PR:000046295 (hAKT1/Phos:4)	pT308		PRO	
<input type="checkbox"/> PR:000046296 (hAKT1/Phos:1)	pT308,pS473		PRO	

F- PTM-dependent PPI

Protein-protein interactions that are affected by the PTM. Currently iPTMnet only shows phosphorylation. The information about phosphor-dependent PPI comes from the text mining tool eFIP (note that false positives may occur)

PTM-dependent PPI

PTM type All ▾	Substrate P31749 (AKT1) ▾	Site All ▾	Interactant 9 selected ▾	Association type All ▾	Source All ▾	PMID
<input type="checkbox"/> Phosphorylation	P31749 (AKT1)	S473	P20936 (RASA1)	unknown	eFIP	14707121
<input type="checkbox"/> Phosphorylation	P31749 (AKT1)	S473	Q3U182 (Crtc2)	increased_association	eFIP	23300339
<input type="checkbox"/> Phosphorylation	P31749 (AKT1)	S473	P45983 (MAPK8)	unknown	eFIP	22771387
<input type="checkbox"/> Phosphorylation	P31749 (AKT1)	T308	Q15118 (PDK1)	inhibited_association	eFIP	22629392
<input type="checkbox"/> Phosphorylation	P31749 (AKT1)	S473	P07900 (HSP90AA1)	unknown	eFIP	25935150
<input type="checkbox"/> Phosphorylation	P31749 (AKT1)	S473	Q68ED7 (Crtc1)	inhibited_association	eFIP	23303455
<input type="checkbox"/> Phosphorylation	P31749 (AKT1)	S473	Q3U182 (Crtc2)	inhibited_association	eFIP	23272152
<input type="checkbox"/> Phosphorylation	P31749 (AKT1)	T308	O15530 (PDPK1)	unknown	eFIP	19402821
<input type="checkbox"/> Phosphorylation	P31749 (AKT1)	S473	Q15118 (PDK1)	increased_association	eFIP	27481935
<input type="checkbox"/> Phosphorylation	P31749 (AKT1)	T308	Q15118 (PDK1)	inhibited_association	eFIP	22629392
<input type="checkbox"/> Phosphorylation	P31749 (AKT1)	S473	Q53ET0 (CRTC2)	inhibited_association	eFIP	22384145

G-Proteome PPI

Protein-protein interactions of the proteome in previous sections are annotated in this section.

Proteome PPIs


Protein 1 All ▾	Relation All ▾	Protein 2 All ▾	Source All ▾	PMID
<input type="checkbox"/> PR:000028994 (hAKT1/iso:1/Phos:1)	Interaction	PR:O14746-1 (hTERT/iso:1)	PRO	12586360
<input type="checkbox"/> PR:000028994 (hAKT1/iso:1/Phos:1)	Interaction	PR:P41279-1 (hMAP3K8/iso:1)	PRO	12138205

H-PTM sites affected in variants

This section shows the variants that affect PTM sites. The data is collected from Biomuta. The site (in canonical sequence), the variant one, the source, the PMID, the disease and sample source are listed. PMIDs are provided when the data from Biomuta is collected by its text mining tool. DOID are terms from the disease ontology.

PTM sites affected in variants					Search: <input type="text"/>
Site	Variant	Source	PMID	Disease [Sample source]	
All ▾	All ▾	All ▾		All ▾	
K14	N14	Biomuta		DOID:2994 / germ cell cancer [cosmic]	
K14	I14	Biomuta		DOID:2994 / germ cell cancer [cosmic]	
T65	M65	Biomuta		DOID:9256 / colorectal cancer [icgc, tcga] DOID:1909 / melanoma [cosmic]	
T65	K65	Biomuta		DOID:3571 / liver cancer [icgc]	
T211	I211	Biomuta		DOID:3070 / malignant glioma [cosmic, icgc, tcga]	
T305	N305	Biomuta		DOID:3571 / liver cancer [icgc]	
S378	F378	Biomuta		DOID:2994 / germ cell cancer [cosmic]	
Y417	C417	Biomuta		DOID:10534 / stomach cancer [cosmic, icgc, tcga]	
T443	M443	Biomuta		DOID:3371 / chondrosarcoma [cosmic]	
S457	R457	Biomuta		DOID:3571 / liver cancer [icgc]	
S475	L475	Biomuta		DOID:10534 / stomach cancer [tcga]	
S477	R477	Biomuta		DOID:3571 / liver cancer [icgc]	

I-Cytoscape view

The  **Cytoscape View** icon shows the substrate centric view with modifications, e.g., phosphorylation (edges with +p), and interaction relations (edges with +i or -i). The protein-protein interaction (PPI) relation source is the annotation in Protein Ontology and eFIP. The edges are in solid green for interactions (+i) or in broken green line for interactions that are decreased or inhibited by the modification (-i). The source for the information can be viewed by clicking on the PPI edge. Clicking on the nodes shows the source of the information plus external links when available (**Figure 9**).

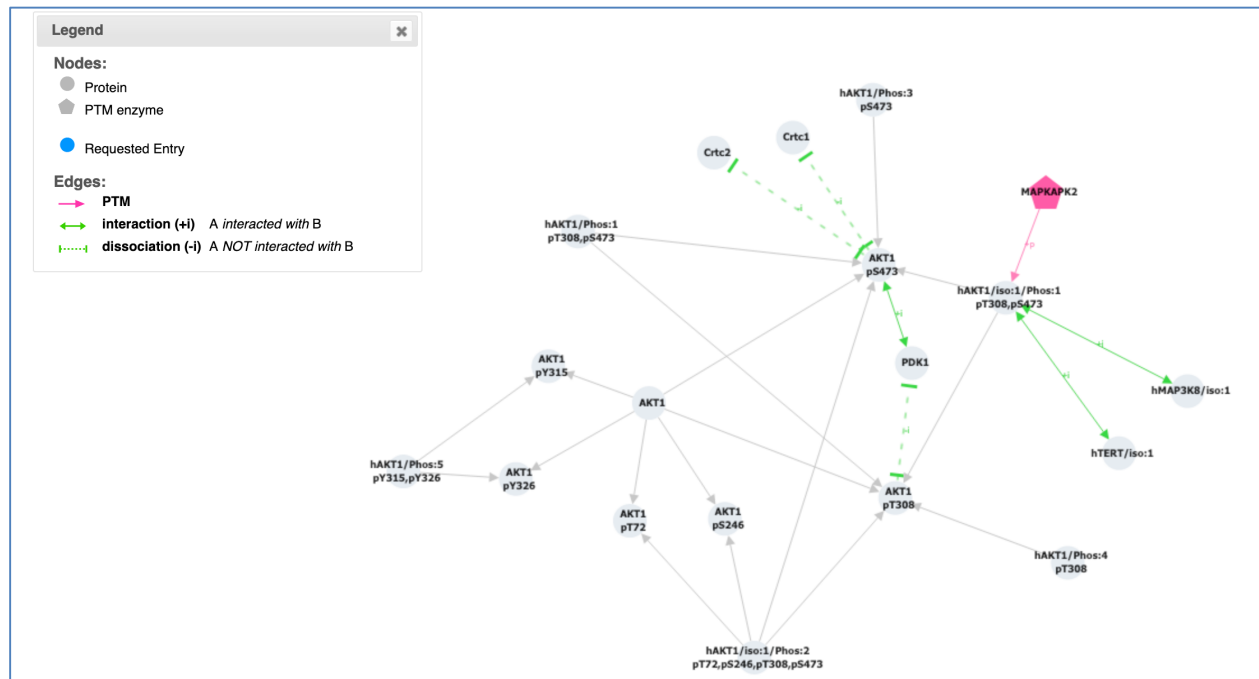


Figure 9-Cytoscape view for selected nodes in AKT1 network displaying AKT1 phosphorylation sites, proteoforms and PPIs.

Batch retrieval

Useful when you want to learn about modifying enzymes and phosphor-dependent interactions linked to particular sites.

(a) access to batch retrieval from home page, (b) iPTMnet batch retrieval form with examples. You can enter up to 500 PTM sites at a time. (c) Example of results for PTM enzymes found for the set submitted in (b), and (d) list of results from (b) where no PTM enzyme were found.

iPTMnet Batch Retrieval

Use this page to retrieve information from the iPTMnet on PTM Enzyme-Site relation, and PTM-dependent PPIs.

a for proteins in iPTMnet database

Search

Submit Reset

PTM type Has Role Restrict by Organism Sample Report **Batch Retrieval (New)**

1. Provide input

Q7Z7L8 S 112
 Q13017 S 1124
 Q95248 S 1141
 Q9NRY4 S 1150
 Q86JU0 S 118
 Q5VZL5 S 1181
 Q9Y4H2 S 1186
 Q8WWI1 S 1231
 Q8N3D4 S 1273
 Q14160 S 1285

Clear [Input example](#)

or

Choose File No file chosen

2. Select output

PTM Enzymes

PTM Dependent PPIs

Input format:

Paste into the box or upload a text file containing a three column space/comma/tab-delimited list (do not include a header line)

Substrate AC	Site residue	Site position
Q15796	S	465

Query Limit: 500 lines (Large queries may take several minutes to process)

Delimiter: comma, tab, space

Substrate must be provided.

Select desired output:

PTM Enzymes: Displays all iPTMnet PTM enzyme-site relations for the sites on the input list along with evidence source(s).

PTM Dependent PPIs: Displays all PTM-dependent protein-protein interactions for the sites on the input list along with evidence source(s).

Input Site Found in iPTMnet 217 Input Site Not Found 26 [Cytoscape View](#) [Download](#)

PTM with Enzyme

<input type="checkbox"/> PTM Type	Substrate	Site	PTM Enzyme	Score	Source	PMID
<input checked="" type="checkbox"/>	PTM Q15121 (PEA15)	S104	P17252 (PRKCA)	★★★★☆	HPRD Signor	19651622, 15917297, 17287340, ...
<input type="checkbox"/>	PTM P00533-1 (EGFR)	S1064	Q9UQM7 (CAMK2A)	★★★★☆	HPRD Signor	18691976, 18689648, 10347170, ...
<input type="checkbox"/>	PTM Q9NRY4 (ARHGAP35)	S1150	Q13464 (ROCK1)	★★★★☆	PSP	19103606
<input checked="" type="checkbox"/>	PTM P16144 (ITGB4)	S1364	P17252 (PRKCA)	★★★★☆	PSP	15121854
<input checked="" type="checkbox"/>	PTM P16144 (ITGB4)	S1364	P17612 (PRKACA)	★★★★☆	PSP Signor	17615294
<input checked="" type="checkbox"/>	PTM P16144 (ITGB4)	S1364	Q15418 (RPS6KA1)	★★★★☆	PSP	20870721
<input checked="" type="checkbox"/>	PTM Q75116 (ROCK2)	S1374	P53350 (PLK1)	★★★★☆	neXIProt	17446864
<input type="checkbox"/>	PTM Q14160 (SCRIB)	S1378	Q13464 (ROCK1)	★★★★☆	PSP	26101221

PTM with no enzyme

PTM Type	Substrate	Site	PTM Enzyme	Score	Source	PMID
Phosphorylation	PTM Q13619 (CUL4A)	S10		★★★★☆	HPRD phospho.ELM PSP UniProt	18691976, 23186163, 18212344, ...
Phosphorylation	PTM Q8TDM6 (DLG5)	S1021		★★★★☆	PSP UniProt	23186163
Phosphorylation	PTM Q6ZRV2 (FAM83H)	S1025		★★★★☆	HPRD PSP UniProt	18689648, 23186163, 20068231
Phosphorylation	PTM O15164-1 (TRIM24)	S1042		★★★★☆	HPRD PSP UniProt	21406692, 18212344, 20068231
Phosphorylation	PTM Q8ND1-1 (EHBP1)	S1058		★★★★☆	HPRD phospho.ELM PSP UniProt	21406692, 23186163, 19651622, ...