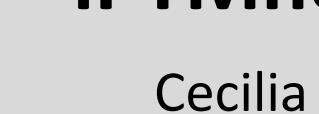
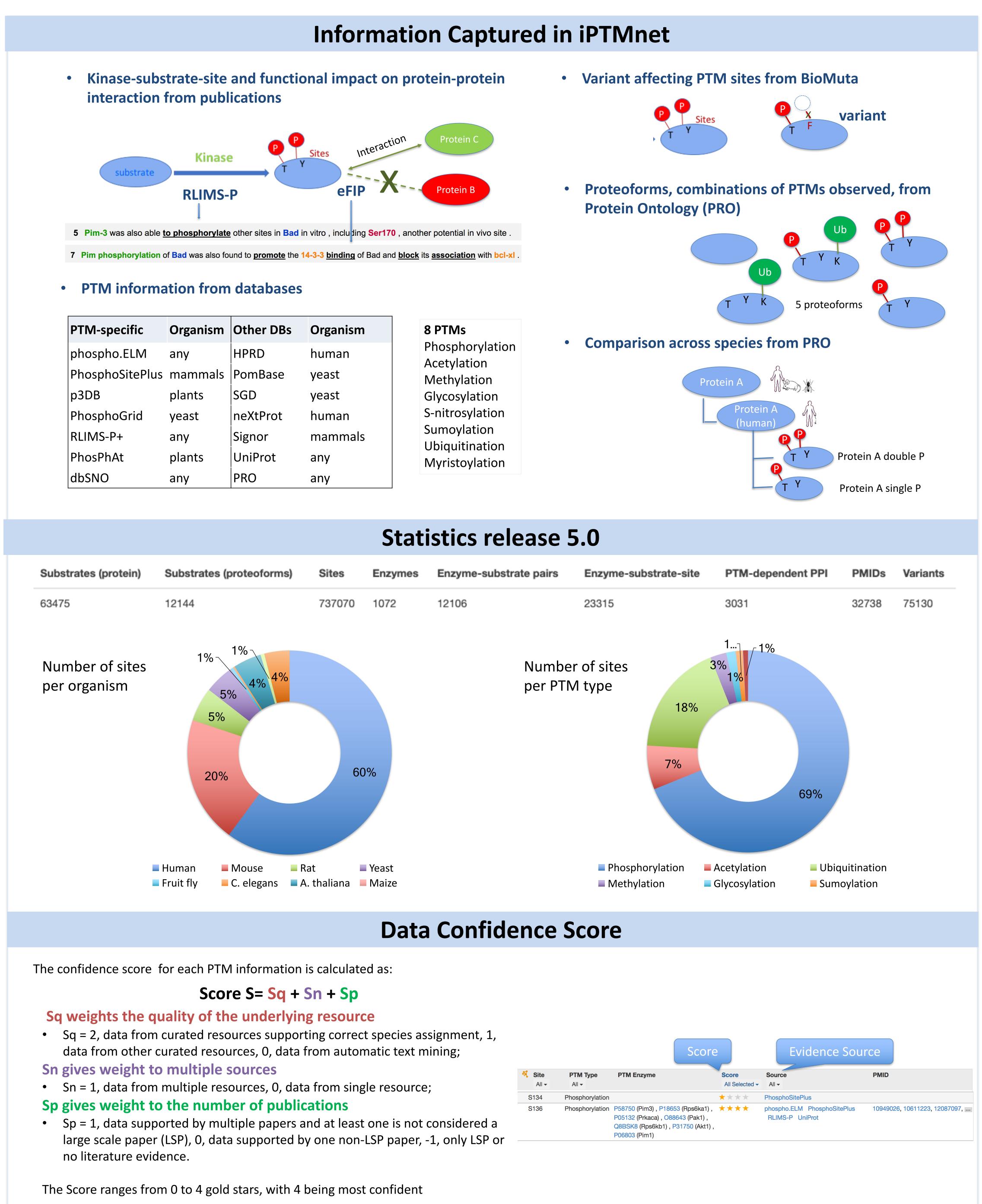
iPTMnet: An Integrated Resource for Protein Post-Translational Modification Network Discovery







Conclusion

iPTMnet connects PTM proteoforms with their modifying enzymes and multiple coordinated PTMs across taxa, thereby unifying fragmented PTM information into a biologically meaningful context for visual and systematic PTM knowledge discovery.

Cecilia Arighi ^{1,2}, Hongzhan Huang^{1,2}, Karen E Ross³, Jia Ren¹, Sachin Gavali¹, Qinghua Wang¹, Julie Cowart¹, K Vijay-Shanker², Cathy H Wu^{1,2,3} 1 CBCB, University of Delaware; 2 CIS, University of Delaware; 3 PIR, Georgetown University Medical Center

iPTMnet for post-translational modification (PTM) knowledge discovery, employs an integrative bioinformatics approach—combining text and data mining, and ontological representation to capture rich PTM information, including PTM enzyme-substrate-site relationships, PTM-specific protein interactions (PPIs), overlapping PTMs, conservation across species and sites affected in variants.

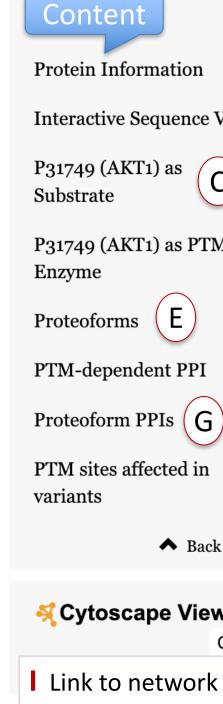
The work presented in this poster is supported by National Institutes of Health U01GM120953

iPTMnet Website (http://proteininfo

1-Search

Use UniProtKB AC/ID, protein or gene name, PRO ID, and PMID. You can restrict search by PTM type (1), enzyme or substrate role (2), and/or organism (3)

Search	for prote	eins in iPT	iPTMnet Mnet databa		irch page					
All	- Search		AKT	1)				Sub	mit	Res
PTM type -	Has Role	Restrict by C	Drganism -	San	nple Repo	rt	Batch Retrie	val (New!)		
M Type		Select All, No	Enzyme or Subst	rate	Select o	rganisms	3	S	elect /	All, None
Acetylation	🗹 N-Glycosyla	ation 🗹 O-Glycos	Enzyme 2		🗌 Human		Mouse		Rat	
C-Glycosylation	S-Glycosyla	ation 🗹 Methylatic	Substrate		Cow		Chicken		Zebr	afish
Myristoylation	Phosphoryla	ation 🗹 Sumoylat	Enzyme and Sub	strat	Fruit fly		C. elegans		Bake	er's yeast
Ubiquitination	S-Nitrosylat	ion			Fission	yeast	A. thaliana		Maiz	e.
		iPTMr	net result page							
1 - 9 of 9 results f	or akt1 in iPTMnet	K Cytoscape View								1
iPTM ID		Protein Name	Gene Name	Orgai	nism	Substrate Role	Enzyme Role	PTM-dependent PPI	Sites	Isoforms
iPTM:P31749	9/ <mark>AKT1_HUMAN</mark> KB PRO	RAC-alpha serine/threonine-protein kinase	Name: <mark>AKT1</mark> Synonyms:PKB,RAC;	Homo (Huma	o sapiens an)	✓ 29 enzymes	✓ 201 substrates	✓ 11 interactants	60	2
iPTM:P31750	0/ AKT1_MOUSE KKB PRO	RAC-alpha serine/threonine-protein kinase	Name: <mark>Akt1</mark> Synonyms:Akt,Rac;	Mus r (Mous	nusculus se)	✓ 10 enzymes	 29 substrates 	✓ 3 interactants	26	0
iPTM:P4719	6/ <mark>AKT1</mark> _RAT	RAC-alpha	Name: Akt1	Rattu	s norvegicus	✓ 3 enzymes	16 substrates	 1 interactant 	10	0



Visualization

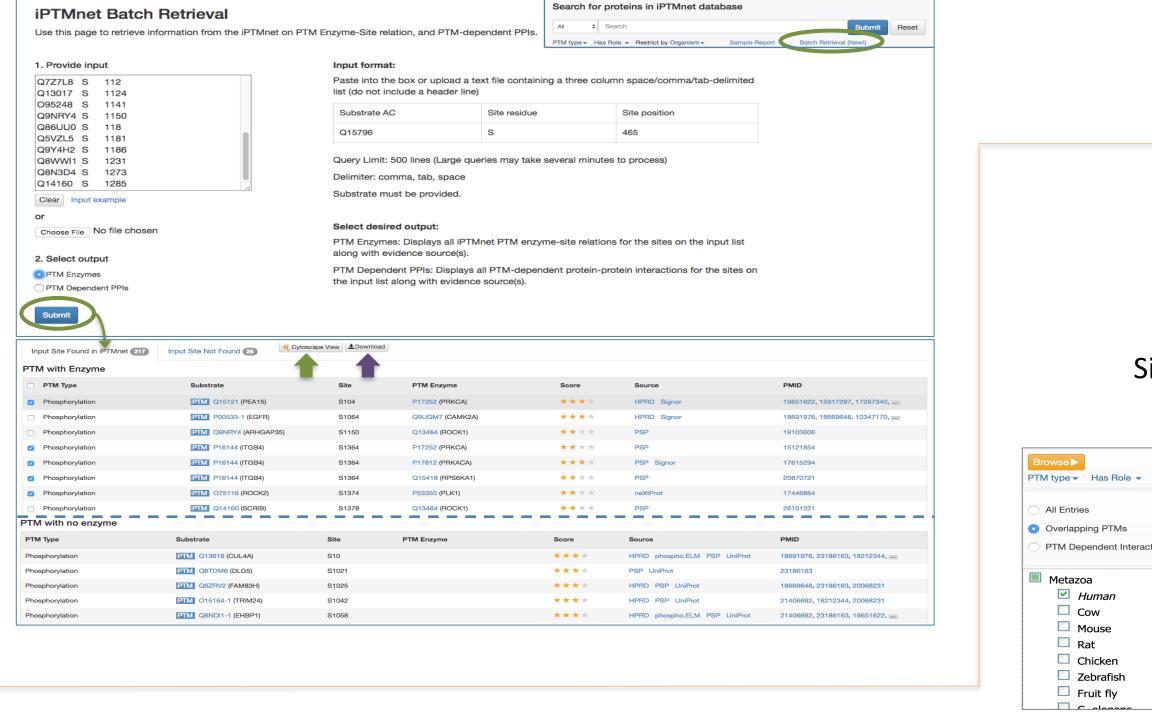
The result page returns candidate entries matching the query ordered by the overall count of all PTM data in descending order

2-Batch Retrieval

serine/threonine-proteir

/ProClass UniProtKB PRO

Allows to obtain PTM enzyme or PTM dependent PPI information for up to 500 PTM sites at a time



MYC PTM site table can be filtered for overlapping PTMs

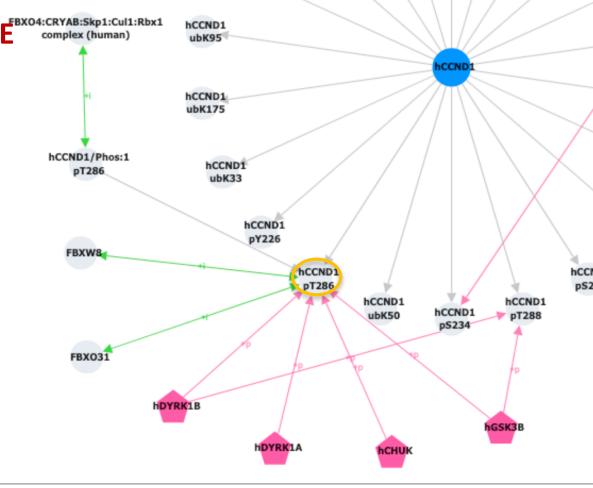
P01106	P01106-1	P	01106-2							Expanded View	
								Search:		Display Overlap PTM	
Site All ▼	PTM Type		PTM Er	nzyme	Score	Source			PMID	Ļ	
	Ubiquitinat	*	Site	PTM Type	PTM Enzyme		Score	Source		PMID	
S6	Phosphory		All 👻	All 👻			4 selected -	All 👻			
Т8	Phosphory		K51	Sumoylation			$\star \star \star \star$	PhosphoSit	ePlus		
			K51	Ubiquitination			****	PhosphoSit	ePlus		
Y12	Phosphory		K52	Sumoylation			****	PhosphoSit	ePlus		
Y16	Phosphory		K52	Ubiquitination			* ***	PhosphoSit	ePlus		
			T58	O-Glycosylation			****	PhosphoSit	ePlus		
			T58	Phosphorylation	P49841 (GSK3B) , P284 P49840 (GSK3A) , P537 P45983 (MAPK8)				hospho.ELM itePlus RLIMS-P Si	,	67756, 21266350, 🖬

4b-Cross species comparison and fun

Deregulated cyclin D1 degradation appears to be responsible for the increased level of cyclin D1 in several cancers. iPTMnet can assist in connecting PTM sites affected i cancer-related variants and their functional consequence. T286 is conserved acros vertebrates (A), and it is phosphorylated (B). This phosphorylation is necessary for subsequent degradation by the proteosome. The PPI section shows phospho dependent interactions with proteosome proteins (C). The variants found in Biomuta for T286 are found in uterine cancer samples (D).

Variants at T286 would avoid proteosomal degradation, as lack of phosphorylation at position 286 would decrease or abolish interaction with proteosomal proteins.

The Cytoscape representation in (E) shows the phosphorylation site T286 along with kinases and PPI partners.



tein Information		3-Entry	,		
Prot AC / UniProt ID tein Name ne Name	P31749 / AKT1_HUMAN RAC-alpha serine/threonine-protein kinase Name: AKT1 Synonyms:PKB,RAC;	A Gen	eral protein Inform	ation	
anism O ID	Homo sapiens (Human) PR:P31749	from l	JniProt and PRO		
O Name inition ort Label egory	RAC-alpha serine/threonine-protein kinase (A RAC-alpha serine/threonine-protein kinase hAKT1 organism-gene			quence with color-coded s	
C Show PRO entrie		ected in variant	▲Select/align proteor	d on PTM types	
Number of sequence: TM:P31749 hAKT1	9 • Alignment length: 480 • Scale: "		180		
R:P31749-2 hAKT1/iso:h2 R:P31749-1 hAKT1/iso:1 KT1 as substrate	- <u>s-k-k-k-t-k</u> - <u>t-</u> t-	TT <u>SSSSK</u> TKKT TT <u>SSSS</u> KTKKT T	Y──K──T-S-C──S-S-K──K─K-K-T-CK+ Y──K──T-S-C── <mark>S</mark> -S-K──K─K-K-T-CK+ Y	-T-T- -T- <mark>D</mark> -	
Site PTM T All - All - S2 Phosp	ype PTM Enzyme	Score Source 4 selected ← All ← ★ ★ ★ ★ PhosphoSitePlus	PMID s RLIMS-P 26440416, 24467442	C Site-centric list. PTM	
K8 Ubiqui K14 Acetyla KT1 as enzyme	tination ation	★ ★ ★ PhosphoSitePlus ★ ★ ★ UniProt	s 21775285	sites with confidence a evidence	
 Substrate All - O14492 (SH2B2) 	Site All - S598	Score Source All ▼ All ▼ ★ ★ ★ ★ neXtProt	PMID t 16141217	D PTM enzymes have	
 O14492-2 (SH2B2) O14745 (SLC9A3F 	•	★★★★ HPRD ★★★★ RLIMS-F		enzyme table with the substrates and sites	
PRO ID (Short Lab All -	All 🗸	PTM Enzyme	Search: Source PMID	E List of proteoforms f	
 PR:000046294 (hAl PR:000046295 (hAl PR:000046296 (hAl 	KT1/Phos:4) pT308 KT1/Phos:1) pT308,pS473		PRO PRO PRO	the entry as described	
PTM-depende	Substrate Site		Seal ssociation type Source PMID		
PhosphorylatiPhosphorylati	ion P31749 (AKT1) S47 ion P31749 (AKT1) S47	Q3U182 (Crtc2) ind '3 P45983 (MAPK8) un	creased_association eFIP 23300 hknown eFIP 22771	³⁸⁷ phosphorylation on PF	
	ion P31749 (AKT1) S47 ion P31749 (AKT1) S47 S	· ,	nknown eFIP 25935 hibited_association eFIP 23303 Set	from toxt mining	
∛ Protein 1 All -	Relation All → (hAKT1/iso:1/Phos:1) Interactio	Protein 2 All - n PR:014746-1 (hTE	Source PMID	G PPIs for proteoform	
PR:000028994 (TM sites affected	hAKT1/iso:1/Phos:1) Interactio	n PR:P41279-1 (hMA	AP3K8/iso:1) PRO 1213820 Search:	from DPO	
Site Variant All • All • K14 N14 K14 I14	Source All - Biomuta Biomuta	PMID Disease [Sample source All → DOID:2994 / germ cell ca DOID:2994 / germ cell ca	ncer [cosmic]	H Variants affecting P	
T65 M65	Biomuta	DOID:9256 / colorectal ca	ancer [icgc, tcga] DOID:1909 / melanoma [cosmic]	sites	
·	T-58 in hum https://research	Synonyms:BHLHE39; Name: RICTOR Synonyms:KIAA1999; An MYC is ph bioinformatics.ude	Homo sapiens (Human) Homo sapiens (Human) • 6 enzy (Human) • 6 enzy el.edu/iptmnet/entry/PC	nes × 1 interactant 150 O-glycosylated 1106	
ample: Ove	Rapamycin-insensitive companion of mTOR T-58 in hum https://research erlapping PT ive Sequence View	Synonyms:BHLHE39; Name: RICTOR Synonyms:KIAA1999; An MYC is ph bioinformatics.ude Ms sites are s Ms sites are s	Homo sapiens (Human) Homo sapiens (Human) osphorylated or el.edu/iptmnet/entry/PC shown in yellow	Role Enzyme Role PPI Sites ymes X 4 interactants 65 Interactant 150 O-glycosylated 1106 In alignment t/align proteoforms across species 63837, 16023596, K S S S K S	
ample: Cove Interacti PRO Ove Interacti PR:P01106-2	N Rapamycin-insensitive companion of mTOR T-58 in hum https://research erlapping PT ive Sequence View i hMYC i hMYC/iso:1 1 hMYC/iso:2 I terpret	Synonyms:BHLHE39; Name: RICTOR Synonyms:KIAA1999; Aan MYC is ph bioinformatics.ude Ms sites are s Ms sites are s 50 y y y kk goT-58 Source: pT-58 (GSK3B) s 15150404 pT-58 (MAPK1) s pT-58 (MAPK1) s pT-58 (MAPK1) s pT-58 (MAPK1) s pT-58 (MAPK1) s	Homo sapiens (Human) Homo sapiens (Human) Homo sapiens (Human) Cosphorylated or ell.edu/iptmnet/entry/PC Shown in yellow Shown in yellow Shown in yellow Shown in yellow	Role Enzyme Role PPI Sites rmes * • 4 interactants 65 mes * • 1 interactant 150 O-glycosylated Interactant Interactant Interactant 1106 Interactant 150 in alignment * • 1 interactant • 1 interactant t/align proteoforms across species • • • • • • • • • • • • • • • • • • •	
Aample: Cove Cove Interacti PR:P01106-1 PR:P01106-1 PR:P01106-2	N Rapamycin-insensitive companion of mTOR T-58 in hum https://research erlapping PT ive Sequence View i hMYC i hMYC/iso:1 i hMYC/iso:2 i hMYC/iso:2 i contemported i contemporte	Synonyms:BHLHE39; Name: RICTOR Synonyms:KIAA1999; Aan MYC is ph bioinformatics.ude Ms sites are s Ms sites are s bu bu bu bu bu bu bu bu bu bu bu bu bu	Homo sapiens (Human) Homo sapiens (Human) Homo sapiens (Human) Homo sapiens (Human) Osphorylated or el.edu/iptmnet/entry/PO shown in yellow Shown in yellow S	Role Enzyme Role PPI Sites ymes × 4 interactants 65 mes × 1 interactant 150 O-glycosylated i106 in alignment t/align proteoforms across species 63837, 16023596, S S S S S S S S S S	
Aample: Cove Cove Interacti PR:P01106-1 PR:P01106-1 PR:P01106-2 PR:P01106-2 PR:P01106-2 PR:P01106-2	N Rapamycin-insensitive companion of mTOR T-58 in hum https://research erlapping PT ive Sequence View bMYC/iso:1 hMYC/iso:2	Synonyms:BHLHE39; Name: RICTOR Synonyms:KIAA1999; an MYC is ph bioinformatics.ude Ms sites are s Ms sites are s bu y y y kk pT-58 (GSK3B) s 15150404 pT-58 (MAPK1) s pT-58 (MAPK1) s pT-58 (GSK3B) s 15150404 pT-58 (MAPK1) s pT-58 (MAPK1) s pT-58 (GSK3A) s ation - site affected in variar	Homo sapiens (Human) Homo sapiens (Human) Homo sapiens (Human) Homo sapiens (Human) Osphorylated or el.edu/iptmnet/entry/PO shown in yellow Shown in yellow S	Role Enzyme Role PPI Sites rmes * • 4 interactants 65 mes * • 1 interactant 150 O-glycosylated Interactant Interactant Interactant 1106 Interactant 150 in alignment * • 1 interactant • 1 interactant t/align proteoforms across species • • • • • • • • • • • • • • • • • • •	
ACCND1	N Rapamycin-insensitive companion of mTOR T-58 in hum https://research erlapping PT ive Sequence View ive Sequence View bmYC/iso:2	Synonyms:BHLHE39; Name: RICTOR Synonyms:KIAA1999; Aan MYC is ph bioinformatics.ude Ms sites are s bu bu bu bu bu bu bu bu bu bu bu bu bu	Homo sapiens (Human) Homo sapiens (Human) Homo sapiens (Human) Homo sapiens (Human) Osphorylated or el.edu/iptmnet/entry/PO shown in yellow Shown in yellow S	Role Enzyme Role PPI Sites rmes * • 4 interactants 65 mes * • 1 interactant 150 O-glycosylated Interactant Interactant Interactant 1106 Interactant 150 in alignment * • 1 interactant • 1 interactant t/align proteoforms across species • • • • • • • • • • • • • • • • • • •	
ACCINDI CCNDI	N Rapamycin-insensitive companion of mTOR T-58 in hum https://research erlapping PT ive Sequence View ive Sequence View bmYC/iso:2	Synonyms:BHLHE39; Name: RICTOR Synonyms:KIAA1999; Aan MYC is ph bioinformatics.ude Ms sites are s Ms sites are s	Homo sapiens (Human) Homo sapiens (Human) Homo sapiens (Human) Homo sapiens (Human) Osphorylated or el.edu/iptmnet/entry/PO shown in yellow Shown in yellow S	Role Enzyme Role PPI Sites /mes 	
ACCNDI C	N Rapamycin-insensitive companion of mTOR T-58 in hum https://research erlapping PT ive Sequence View i i hMYC i hMYC/iso:1 i hMYC/iso:2 i hMYC/iso:2 i hMYC/iso:1 i hMYC/iso:2 i hMYC/iso:2 i hMYC/iso:1 i hMYC/iso:2 i hMYC/iso:2 i hMYC/iso:1 i hMYC/iso:2 i hMYC/iso:1 i hMYC/iso:2 i hMYC/iso:2 i hMYC/iso:2 i hMYC/iso:1 i hMYC/iso:2 i hMYC/iso:2 i hMYC/iso:1 i hMYC/iso:2 i hMYC/iso:1 i hMYC/iso:1 i hMYC/iso:2 i hMYC/iso:1 i hMY	Synonyms:BHLHE39; Name: RICTOR Synonyms:KIAA1999; Aan MYC is ph bioinformatics.ude Ms sites are s Ms sites are s	Homo sapiens (Human) Homo sapiens (Human) Homo sapiens (Human) Homo sapiens (Human) Cosphorylated or el.edu/iptmnet/entry/PC shown in yellow Shown in yellow Source: PhosphoSitePlus, Singor PMID: 145 Source: PhosphoSitePlus, PRO, UniProt, 7756, 21266350, Source: PhosphoSitePlus, NeXtProt PMID: 1 hospho.ELM, PhosphoSitePlus, Singor PMID: 145 Source: PhosphoSitePlus, NeXtProt PMID: 1 Source: PhosphoSitePlus, Singor PMID: 145 Source: Scale: "—" ≈ 4 amino acids 4080	Role Enzyme Role PPI Sites rmes 4 interactants 65 mes 1 interactant 0-glycosylated 1106 in alignment t/align proteoforms across species 63837, 16023596, 551811 RUMS-P PMID: 10551811 63837, 16023596, 200, 2160, 200, 240, 280, 200, 240, 280, 200, 240, 280, 200, 240, 280, 200, 240, 280, 280, 290,	
A COVE	Rapamycin-insensitive companion of mTOR T-58 in hum https://research erlapping PT ive Sequence View i hMYC hMYC/iso:1 hMYC/iso:2 i hMYC/iso:2 ence Alignment Align ▶ Modific i Numbe i/Phos:1 PTM Type prive Sephorylation Q136271 (DYRK11 PTM Type All → PTM Er All → Q136271	Synonyms:BHLHE39; Name: RICTOR Synonyms:KIAA1999; Aan MYC is ph .bioinformatics.ude Ms sites are s Ms sites are s Subject of the second secon	Homo sapiens (Human) Homo sapiens (Human) Homo sapiens (Human) Homo sapiens (Human) Cosphorylated or el.edu/iptmnet/entry/PC shown in yellow for the sphositePlus, Paulon HosphoSitePlus PMID: NA Source: PhosphoSitePlus, nextProt PMID: 1 hospho.ELM, PhosphoSitePlus, nextProt PMID: 1 hospho.ELM, PhosphoSitePlus, nextProt PMID: 1 source: PhosphoSitePlus, Singor PMID: 145 Source: PhosphoSitePlus, Singor PMID	Role Enzyme Role PPI Sites rmes * • 4 interactants 65 ines * • 1 interactant 150 O-glycosylated 1106 in alignment t/align proteoforms across species ************************************	
All -	N Rapamycin-insensitive companion of mTOR T-58 in hum https://research erlapping PT ive Sequence View i i hMYC i hMYC/iso:1 i hMYC/iso:2 i hMYC/iso:2 i hMYC/iso:2 i hMYC/iso:1 i hMYC/iso:2 i hMYC/iso:2 i hMYC/iso:2 i hMYC/iso:1 i hMYC/iso:2 i hMYC/iso:2 i hMYC/iso:2 i hMYC/iso:2 i hMYC/iso:3 i hMYC/iso:4 i hMYC/iso:2 i hMYC/iso:1 i hMYC/iso:2 i hMYC/iso:2 i hMYC/iso:3 i hMYC/iso:4 i hMYC/iso:2 i hMYC/iso:3 i hMYC/iso:4 i hMYC/iso:4 i hMYC/iso:3 i hMYC/iso:4 i hMYC/iso:4 i hMYC/iso:4 i hMYC/iso:5 i hMYC/iso:4 i hMYC/iso:5 i hMYC/iso:4 i hMYC/iso:5 i hMYC/iso:6 i hMY	Synonyms:BHLHE39; Name: RICTOR Synonyms:KIAA1999; Aan MYC is ph bioinformatics.ude Ms sites are s Ms sites are s got-58 Source: pT-58 (GSK3B) s 15150404 pT-58 (GSK3B) s 15150404 pT-58 (MAPK1) s pT-58 (MAPK1) s pT-58 (MAPK1) s pT-58 (MAPK1) s pT-58 (GSK3A) s ation - site affected in variar r of sequence: 7 • Alignment length: s hCCND1 2 mCCND1 2 mCCND1 2 hCCND1 2 hCCND1/Phos:1 3 rCCND1 2 hCCND1/Phos:1 3 rCCND1 2 hCCND1/Phos:1 3 rCCND1 3 rCCN	Homo sapiens (Human) Homo sapiens (Human) Homo sapiens (Human) Homo sapiens (Human) Cosphorylated or el.edu/iptmnet/entry/PC shown in yellow for the sphositePlus, Paulon HosphoSitePlus PMID: NA Source: PhosphoSitePlus, nextProt PMID: 1 hospho.ELM, PhosphoSitePlus, nextProt PMID: 1 hospho.ELM, PhosphoSitePlus, nextProt PMID: 1 source: PhosphoSitePlus, Singor PMID: 145 Source: PhosphoSitePlus, Singor PMID	Role Enzyme Role PPI Sites rmes X 4 interactants 65 nes X 1 interactant 150 O-glycosylated 1106 in alignment t/align proteoforms across species 63837, 16023596, 53837, 16023596, S1811 RUMS-P PMID: 10551811 83837, 16023596, PMID 160 200 240 240 240 240 240 240 240 240 240 240 240 240 PMID 8 PMID 10766840, 15735756, 261576	
All - CCND1 CC	Rapamycin-insensitive companion of mTOR T-58 in hum https://research erlapping PT ive Sequence View i hMYC hMYC/iso:1 hMYC/iso:2 i hMYC/iso:2 ence Alignment Align ▶ Modific i Numbe i/Phos:1 PTM Type prive Sephorylation Q136271 (DYRK11 PTM Type All → PTM Er All → Q136271	Synonyms:BHLHE39; Name: RICTOR Synonyms:KIAA1999; Aan MYC is ph bioinformatics.ude Ms sites are s Ms sites are s	Homo sapiens (Human) Homo sapiens (Human) Homo sapiens (Human) Homo sapiens (Human) Osphorylated or el.edu/iptmnet/entry/PC shown in yellow Shown in yellow Source: PhosphoSitePlus, Singor PMID: 145 Source: Source Not SitePlus, Singor PMID: 145 Source: PhosphoSitePlus, Singor PMID: 145 Source: Source Source All Selected All All HPRD neXtProt PRO PhosphoSi RLIMS-P Signor	Role Enzyme Role PPI Sites rmes X 4 interactants 65 nes X 1 interactant 150 O-glycosylated 1106 in alignment (4000) (400) (
All - CCND1 CC	N Rapamycin-insensitive companion of mTOR T-58 in hum https://research erlapping PT ive Sequence View i hMYC i hMYC i hMYC i hMYC i hMYC/iso:1 i hMYC/iso:2 i hMYC/iso:2 i hMYC/iso:2 i hMYC/iso:2 i hMYC/iso:3 i hMYC/iso:4 i hMYC/iso:2 i hMYC/iso:4 i hMYC/iso:5 i hMYC/iso:1 i hMYC/iso:2 i hMYC/iso:2 i hMYC/iso:2 i hMYC/iso:2 i hMYC/iso:3 i hMYC/iso:4 i hMYC/iso:2 i hMYC/iso:4 i hMYC/iso:5 i hMYC/iso:2 i hMYC/iso:3 i hMYC/iso:4 i hMYC/iso:5 i hMYC/iso:1 i hMYC/iso:2 i hMYC/iso:3 i hosphorylation i i hosphorylation i i i i i i i i i i i i i i i i i i i	Synonyms:BHLHE39; Name: RICTOR Synonyms:KIAA1999; Aan MYC is ph bioinformatics.ude Ms sites are s Ms sites are s	Homo sapiens (Human) Homo sapiens (Human) Homo sapiens (Human) Homo sapiens (Human) Cosphorylated or el.edu/iptmnet/entry/PC shown in yellow Shown in yellow Source: PhosphoSitePlus, Singor PMID: 145 Source: PhosphoSitePlus, neXtProt PMID: 1 Source: PhosphoSitePlus, neXtProt PMID: 145 Source: PhosphoSitePlus, singor PMID: 15 Source: Source All Selected ~ All ~ Source: Source All Selected ~ All ~	PPI Sites rmes X 4 interactants 65 mes X 1 interactant 150 O-glycosylated 1106 in alignment t/align proteoforms across species O-glycosylated Sites A Sites A Sites Interactant 150 O-glycosylated Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant <td colspan<="" td=""></td>	
All - COVE Cample: COVE	N Rapamycin-insensitive companion of mTOR T-58 in hum https://research erlapping PT ive Sequence View ive Sequence View immyCisci imm	Synonyms:BHLHE39; Name: RICTOR Synonyms:KIAA1999; Aan MYC is ph bioinformatics.ude Ms sites are s Ms sites are s fisto404 pT-58 (GSK3B) s pT-58 (MAPK1) s pT-58 (MAPK1) s pT-58 (MAPK1) s pT-58 (MAPK1) s pT-58 (GSK3A) s Addition of sequence: 7 • Alignment length: s hCCND1 chick-CCND1 chic	Homo sapiens 18 enz (Human) Homo sapiens 6 enzy (Human) Homo sapiens 6 enzy (Human) Cosphorylated or el.edu/iptmnet/entry/PC Shown in yellow Source: PhosphoSitePlus, Singor PMID: 145 Source: PhosphoSitePlus, neXtProt PMID: 1 hospho.ELM, PhosphoSitePlus, NC, UniProt, 120. 10551811 Source: PhosphoSitePlus, neXtProt PMID: 145 Source: PhosphoSitePlus, Singor PMID: 145 PhosphoSitePlus, Singor PMID: 145 Source: PhosphoSitePlus, Sin	PPI Sites rmes X 4 interactants 65 mes X 1 interactant 150 O-glycosylated 1106 1106 1106 in alignment X Sites X Sites Y/align proteoforms across species Sites Sites X Sites Sites X Sites Sites Sites Sites X Sites Sites Sites Sites X Sites Sites Sites Sites Sites Sites Sites Sites Sites	
All - COVE Cample: Cove Co	N Rapamycin-insensitive companion of mTOR T-58 in hum https://research erlapping PT ive Sequence View ive Sequence View imMYC imMYC/iso:1 imMYC/iso:2 imMYC/iso:2 imMYC/iso:1 immyc/iso:1 <td>Synonyms:BHLHE39; Name: RICTOR Synonyms:KIAA1999; Aan MYC is ph bioinformatics.ude Ms sites are s Ms sites are s fisto404 pT-58 (GSK3B) s pT-58 (MAPK1) s pT-58 (MAPK1) s pT-58 (MAPK1) s pT-58 (MAPK1) s pT-58 (GSK3A) s Addition of sequence: 7 • Alignment length: s hCCND1 chick-CCND1 chic</td> <td>Homo sapiens 18 enz (Human) Homo sapiens 6 enzy (Human) Homo sapiens 6 enzy (Human) Cosphorylated or el.edu/iptmnet/entry/PC Shown in yellow Source: PhosphoSitePlus, Particle Source: PhosphoSitePlus, Singor PMID: 145 Source: PhosphoSitePlus, neXtProt PMID: 1 hospho.ELM, PhosphoSitePlus, NC, UniProt, 120. 10551811 Source: PhosphoSitePlus, neXtProt PMID: 145 Source: PhosphoSitePlus, neXtProt PMID: 145 Source: PhosphoSitePlus, neXtProt PMID: 145 Source: PhosphoSitePlus, neXtProt PMID: 145 Source: PhosphoSitePlus, Singor PMID: 145 PhosphoSitePlus, Singor PMID: 145 Source: PhosphoSitePlus, Singor PMID: 145 PhosphoSitePlus, Singor PMID: 145 Source: PhosphoSitePlus, Singor PMID: 145 Source: PhosphoSitePlus, Singor PMID: 145 PhosphoSitePlus, Singor PMID: 145 PhosphoSitePlus, Singor PMID: 145 PhosphoSitePlus, Singor PMID: 145 Source: PhosphoSitePlus, Singor PMID: 145 PhosphoSitePlus, Singor PMID: 145 PhosphoSi</td> <td>PPI Sites rmes X 4 Interactants 65 mes X 1 Interactant 150 O-glycosylated 1106 in alignment X 2 Interactant 150 t/align proteoforms across species 2 Interactant 150 Sites X 2 Interactant 150 t/align proteoforms across species 2 Interactant Interactant Interactant Sites Interactant Interactant Interactant Interactant Sites Interactant Interactant Interactant Interactant Interactant t/align proteoforms across species Interactant Interactant Interactant Interactant Sister Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant</td>	Synonyms:BHLHE39; Name: RICTOR Synonyms:KIAA1999; Aan MYC is ph bioinformatics.ude Ms sites are s Ms sites are s fisto404 pT-58 (GSK3B) s pT-58 (MAPK1) s pT-58 (MAPK1) s pT-58 (MAPK1) s pT-58 (MAPK1) s pT-58 (GSK3A) s Addition of sequence: 7 • Alignment length: s hCCND1 chick-CCND1 chic	Homo sapiens 18 enz (Human) Homo sapiens 6 enzy (Human) Homo sapiens 6 enzy (Human) Cosphorylated or el.edu/iptmnet/entry/PC Shown in yellow Source: PhosphoSitePlus, Particle Source: PhosphoSitePlus, Singor PMID: 145 Source: PhosphoSitePlus, neXtProt PMID: 1 hospho.ELM, PhosphoSitePlus, NC, UniProt, 120. 10551811 Source: PhosphoSitePlus, neXtProt PMID: 145 Source: PhosphoSitePlus, neXtProt PMID: 145 Source: PhosphoSitePlus, neXtProt PMID: 145 Source: PhosphoSitePlus, neXtProt PMID: 145 Source: PhosphoSitePlus, Singor PMID: 145 PhosphoSitePlus, Singor PMID: 145 Source: PhosphoSitePlus, Singor PMID: 145 PhosphoSitePlus, Singor PMID: 145 Source: PhosphoSitePlus, Singor PMID: 145 Source: PhosphoSitePlus, Singor PMID: 145 PhosphoSitePlus, Singor PMID: 145 PhosphoSitePlus, Singor PMID: 145 PhosphoSitePlus, Singor PMID: 145 Source: PhosphoSitePlus, Singor PMID: 145 PhosphoSitePlus, Singor PMID: 145 PhosphoSi	PPI Sites rmes X 4 Interactants 65 mes X 1 Interactant 150 O-glycosylated 1106 in alignment X 2 Interactant 150 t/align proteoforms across species 2 Interactant 150 Sites X 2 Interactant 150 t/align proteoforms across species 2 Interactant Interactant Interactant Sites Interactant Interactant Interactant Interactant Sites Interactant Interactant Interactant Interactant Interactant t/align proteoforms across species Interactant Interactant Interactant Interactant Sister Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant Interactant	
All - CONDI CO	N Rapamycin-insensitive companion of mTOR T-58 in hum https://research erlapping PT ive Sequence View i <td< td=""><td>Synonyms:BHLHE39; Name: RICTOR Synonyms:KIAA1999; Aan MYC is ph bioinformatics.ude Ms sites are s Ms sites are s source: p 5150404 pT-58 (GSK3B) s 5150404 pT-58 (GSK3B) s (GSK3A) s ation - site affected in variar of sequence: 7 • Alignment length: a hCCND1 shcCND1 chick-CCND1 chick-CCND1 chick-CCND1 shcCND1</td><td>Homo sapiens (Human) Homo sapiens (Human) Homo sapiens (Human) Homo sapiens (Human) Homo sapiens (Human) Cosphorylated or el.edu/iptmnet/entry/PC shown in yellow Source: PhosphoSitePlus, nextProt PMID: 145 Source: PhosphoSitePlus, Singor PMID: 145 Sour</td><td>Role Enzyme Role PPI Sites Imes X 4 interactants 65 Ines X 1 interactant 150 O-glycosylated 1106 in alignment Interactant (100.0500) O-glycosylated Interactant <td colsp<="" td=""></td></td></td<>	Synonyms:BHLHE39; Name: RICTOR Synonyms:KIAA1999; Aan MYC is ph bioinformatics.ude Ms sites are s Ms sites are s source: p 5150404 pT-58 (GSK3B) s 5150404 pT-58 (GSK3B) s (GSK3A) s ation - site affected in variar of sequence: 7 • Alignment length: a hCCND1 shcCND1 chick-CCND1 chick-CCND1 chick-CCND1 shcCND1	Homo sapiens (Human) Homo sapiens (Human) Homo sapiens (Human) Homo sapiens (Human) Homo sapiens (Human) Cosphorylated or el.edu/iptmnet/entry/PC shown in yellow Source: PhosphoSitePlus, nextProt PMID: 145 Source: PhosphoSitePlus, Singor PMID: 145 Sour	Role Enzyme Role PPI Sites Imes X 4 interactants 65 Ines X 1 interactant 150 O-glycosylated 1106 in alignment Interactant (100.0500) O-glycosylated Interactant Interactant <td colsp<="" td=""></td>	
All - Cove	N Rapamycin-insensitive companion of mTOR T-58 in hum https://research erlapping PT ive Sequence View i <td< td=""><td>Synonyms:BHLHE39; Name: RICTOR Synonyms:KIAA1999; Aan MYC is ph bioinformatics.ude Ms sites are s Ms sites are s output sites are s output sites (SK38) s ou</td><td>Homo sapiens (Human) Homo sapiens (Human) Homo sapiens (Human) Cosphorylated or el.edu/iptmnet/entry/PC shown in yellow Shown in yellow PhosphoSitePlus PMID: NA Source: PhosphoSitePlus,sextProt PMID: 145 Source: PhosphoSitePlus,Singor PMID: 145 Source: PhosphoSitePlus,</td><td>Role Enzyme Role PPI Sites mes × < 4 interactants</td> 65 nes × < 1 interactant</td<>	Synonyms:BHLHE39; Name: RICTOR Synonyms:KIAA1999; Aan MYC is ph bioinformatics.ude Ms sites are s Ms sites are s output sites are s output sites (SK38) s ou	Homo sapiens (Human) Homo sapiens (Human) Homo sapiens (Human) Cosphorylated or el.edu/iptmnet/entry/PC shown in yellow Shown in yellow PhosphoSitePlus PMID: NA Source: PhosphoSitePlus,sextProt PMID: 145 Source: PhosphoSitePlus,Singor PMID: 145 Source: PhosphoSitePlus,	Role Enzyme Role PPI Sites mes × < 4 interactants	
All - PRO ID All - PRO ID PRO ID PRO ID PRO ID PRO ID PRO	Rapamycin-insensitive companion of mTOR T-58 in hum https://research https://research erlapping PT ive Sequence View immyCisol immyCisol<	Synonyms:BHLHE39; Name: RICTOR Synonyms:KIAA1999; Aan MYC is ph bioinformatics.ude Ms sites are s Ms sites are s output pt-58 (GSK3B) 5 1515040 pt-58 (GSK3A) 5 ARAPK1) 5 pt-58 (GSK3A) 5 AARACLE pt-58 (GSK3A) 5 AARACLE pt-58 (GSK3B) 5 (CHUK) Sites AII ~ 1) pT286 Cyclin D1 degradation res FBX031 and phosphoryl Site AII ~ 1) pT286 Cyclin D1 degradation res FBX031 and phosphoryl Site AII ~ 1) pT286 Cyclin D1 degradation res FBX031 and phosphoryl Site AII ~ 1) T286 D1) T286	Homo sapiens 18 enz (Human) Homo sapiens 6 enzy Homo sapiens 6 enzy el.edu/iptmnet/entry/PC shown in yellow Source: PhosphoSitePlus, Singor PMID: 145 Source: PhosphoSitePlus, neXtProt PMID: 1 Source: PhosphoSitePlus, neXtProt PMID: 145 Source: PhosphoSitePlus, neXtProt PMID: 145 Source: PhosphoSitePlus, neXtProt PMID: 145 Source: PhosphoSitePlus, singor PMID: 145 Source: All = 4 amino acids 40	PROI Enzyme Role PPI Sites mes X 4 interactants 65 nes X 1 interactants 150 O-glycosylated 1106 in alignment t/align proteoforms across species 63837, 16023596, 7 7 7 7 7 7 8 7 8 9 <td< td=""></td<>	
All - PRO COVE COVE COVE COVE COVE COVE COVE PR:P01106-1 PR:P01106-2 PR:P0110 PR:P0100 PR:P0110 PR:P0110 PR:P010 PR:P0100 PR:P010 PR:P0100 PR:P010 PR:P010 PR:P0100 PR:P0	N Rapamycin-insensitive companion of mTOR T-58 in hum https://research erlapping PT ive Sequence View i hMYC hMYC/iso:1 i hMYC hMYC/iso:2 i hMYC hMYC hMYC hMYC hMYC hMYC hMYC hMYC	Synonyms:BHLHE39; Name: RICTOR Synonyms:KIAA1999; Aan MYC is ph bioinformatics.ude Ms sites are s over the source: pT-58 (GSK3B); pT-58 (GSK3A); ation - gite affected in variar r of sequence: 7 • Alignment length: scond i gite affected in variar r of sequence: 7 • Alignment length: bicKND1 scCND1 chick-CCND1 chick-CCND1 chick-CCND1 stes hCCND1 chick-CCND1 chick-CCND1 scCND1	Homo sapiens 18 enz (Human) Homo sapiens 6 enzy Homo sapiens 6 enzy (Human) Cosphorylated or el.edu/iptmnet/entry/PC shown in yellow PhosphoSitePlus PMID: NA Source: PhosphoSitePlus,Singor PMID: 145 Source: All + Amino acids 40. 80. 120. 120 Source: PhosphoSitePlus,Singor PMID: 145 Source: PhosphoSitePlus,Singor PMID: 145 Source: PhosphoSitePlus,Singor PMID: 145 Source: PhosphoSitePlus,Singor PMID: 145 Source: Source All Selected ~ All ~ All	PROI Enzyme Role PPI Sites mes X 4 interactants 65 nes X 1 interactants 150 O-glycosylated 1106 in alignment t/align proteoforms across species 63837, 16023596, 7 7 7 7 7 7 8 7 8 9 <td< td=""></td<>	
All - CONDI CO	N Rapamycin-insensitive companion of mTOR T-58 in hum https://research erlapping PT ive Sequence View i hMYC i hMYC/iso:2 i hMYC/iso:2 <td>Synonyms:BHLHE39; Name: RICTOR Synonyms:KIAA1999; Aan MYC is ph bioinformatics.ude Ms sites are s Ms sites are s output for the source: T-58 (GSK3B) (p1-58 (MAPK1) (p1-58 (GSK3B) (p1-58 (MAPK1) (p1-58 (GSK3B) (CALL (ation - site affected in variant is InCCND1 site affected in variant is Increased Interna is Increased Intern</td> <td>Homo sapiens 18 enz (Human) Homo sapiens 6 enzy Homo sapiens 6 enzy el.edu/iptmnet/entry/PC shown in yellow Source: PhosphoSitePlus, Singor PMID: 145 Source: PhosphoSitePlus, neXtProt PMID: 1 Source: PhosphoSitePlus, neXtProt PMID: 145 Source: PhosphoSitePlus, neXtProt PMID: 145 Source: PhosphoSitePlus, neXtProt PMID: 145 Source: PhosphoSitePlus, singor PMID: 145 Source: All = 4 amino acids 40</td> <td>PPI Sites mes × 4 interactants 65 mes × 1 interactants 65 O-glycosylated 1106 in alignment t/align proteoforms across species 10051811 63837, 16023596, 10051811 63837, 16023596, 10051811 63837, 16023596, 10051811 63837, 16023596, 10051811 63837, 16023596, 10051811 63837, 16023596, 10050840, 15735756, 261576 10766840, 15735756, 261576 PMID B consplication type Source PMID Source PMID Source PMID Source PMID Source PMID All - PRO 17407 convin eFIP 1941 convin eFIP</td>	Synonyms:BHLHE39; Name: RICTOR Synonyms:KIAA1999; Aan MYC is ph bioinformatics.ude Ms sites are s Ms sites are s output for the source: T-58 (GSK3B) (p1-58 (MAPK1) (p1-58 (GSK3B) (p1-58 (MAPK1) (p1-58 (GSK3B) (CALL (ation - site affected in variant is InCCND1 site affected in variant is Increased Interna is Increased Intern	Homo sapiens 18 enz (Human) Homo sapiens 6 enzy Homo sapiens 6 enzy el.edu/iptmnet/entry/PC shown in yellow Source: PhosphoSitePlus, Singor PMID: 145 Source: PhosphoSitePlus, neXtProt PMID: 1 Source: PhosphoSitePlus, neXtProt PMID: 145 Source: PhosphoSitePlus, neXtProt PMID: 145 Source: PhosphoSitePlus, neXtProt PMID: 145 Source: PhosphoSitePlus, singor PMID: 145 Source: All = 4 amino acids 40	PPI Sites mes × 4 interactants 65 mes × 1 interactants 65 O-glycosylated 1106 in alignment t/align proteoforms across species 10051811 63837, 16023596, 10051811 63837, 16023596, 10051811 63837, 16023596, 10051811 63837, 16023596, 10051811 63837, 16023596, 10051811 63837, 16023596, 10050840, 15735756, 261576 10766840, 15735756, 261576 PMID B consplication type Source PMID Source PMID Source PMID Source PMID Source PMID All - PRO 17407 convin eFIP 1941 convin eFIP	
ACCONST COVE COVE COVE COVE COVE COVE COVE COVE PROTION PROTION PROTION COVE COVE PROTION PROTION COVE COVE PROTION COVE COVE COVE PROTION COVE COVE PROTION COVE COVE COVE PROTION COVE COVE COVE PROTION COVE COVE COVE PROTION COVE COVE COVE PROTION COVE COVE COVE PROTION COVE COVE COVE PROTION COVE COVE PROTION COVE COVE PROTION COVE PROTION COVE PROTION COVE COVE PROTION COVE PROTION COVE PROTION COVE PROTION COVE PROTION COVE COVE PROTION COVE COVE COVE COVE PROTION COVE COVE COVE PROTION COVE COVE COVE PROTION COVE COVE COVE COVE PROTION COVE	N Rapamycin-insensitive companion of mTOR T-58 in hum https://research erlapping PT ive Sequence View i hMYC i hMYC/iso:2 i hMYC/iso:2 <td>Synonyms:BHLHE39; Name: RICTOR Synonyms:KIAA1999; Aan MYC is ph bioinformatics.ude Ms sites are s Ms sites are s potoget sites are s potoget sites are s potoget potoget sites are s potoget potoget sites are s potoget potoget sites are s potoget potoget sites are s potoget potoget sites are s source: potoget potoget sites are s source: potoget potoget sites are s sites are s source: potoget sites are s source: potoget sites are s are source: potoget sites are s sites are s potoget potoget sites are s are source: potoget sites are s sites are s are source: potoget sites are s are source: sites are s are source: sites are s are source: sites are s are source: are source: sites are s are source: sites are source: sites</td> <td>Homo sapiens 18 enz (Human) Homo sapiens 6 enzy (Human) Cosphorylated or el.edu/iptmnet/entry/PC shown in yellow Source: PhosphoSitePlus,nextProt PMID: 145 Source: PhosphoSitePlus,nextPhosphoSitePlus,nextPhosphoSitePlus,nextPhosphoSit</td> <td>PRIO Enzyme Role PPI Sites mes × 4 interactants 65 mes × 1 interactants 65 O-glycosylated 1106 in alignment t/align proteoforms across species 10051811 63837, 16023596, 10051811 63837, 16023596, 10051811 63837, 16023596, 10051811 63837, 16023596, 10051811 63837, 16023596, 10051811 63837, 16023596, 10051811 10051811 10051811 10051811 10051811 10051811 10051811 10051811 10051811 10050840, 15735756, 261576 PMID B PHID B PHID B PHID B PHID B PHID P PHID P PHID P PHID P P P P P P P P P P<!--</td--></td>	Synonyms:BHLHE39; Name: RICTOR Synonyms:KIAA1999; Aan MYC is ph bioinformatics.ude Ms sites are s Ms sites are s potoget sites are s potoget sites are s potoget potoget sites are s potoget potoget sites are s potoget potoget sites are s potoget potoget sites are s potoget potoget sites are s source: potoget potoget sites are s source: potoget potoget sites are s sites are s source: potoget sites are s source: potoget sites are s are source: potoget sites are s sites are s potoget potoget sites are s are source: potoget sites are s sites are s are source: potoget sites are s are source: sites are s are source: sites are s are source: sites are s are source: are source: sites are s are source: sites are source: sites	Homo sapiens 18 enz (Human) Homo sapiens 6 enzy (Human) Cosphorylated or el.edu/iptmnet/entry/PC shown in yellow Source: PhosphoSitePlus,nextProt PMID: 145 Source: PhosphoSitePlus,nextPhosphoSitePlus,nextPhosphoSitePlus,nextPhosphoSit	PRIO Enzyme Role PPI Sites mes × 4 interactants 65 mes × 1 interactants 65 O-glycosylated 1106 in alignment t/align proteoforms across species 10051811 63837, 16023596, 10051811 63837, 16023596, 10051811 63837, 16023596, 10051811 63837, 16023596, 10051811 63837, 16023596, 10051811 63837, 16023596, 10051811 10051811 10051811 10051811 10051811 10051811 10051811 10051811 10051811 10050840, 15735756, 261576 PMID B PHID B PHID B PHID B PHID B PHID P PHID P PHID P PHID P P P P P P P P P P </td	