

# Illuminating the World of Protein Post Translational Modifications

Evaluate modification site assignment confidence using Ascore and Ascore-derived probabilities

**Motif:** All Modification Types

Modification	Motif	Score	# Matches	Enzyme	Enzyme Type
Phosphorylation	...SP...	67.46	11		
Phosphorylation	...[R]P...	59.95	17	Growth associated histone ...	kinase
Phosphorylation	...[R]R...	56.76	21	Growth associated histone ...	kinase
Phosphorylation	...[R]...	56.76	29	Growth associated histone ...	kinase
Phosphorylation	...R...P...	54.81	14		
Phosphorylation	...S...P...	50.78	23		
Phosphorylation	...S...P...	45.75	23		
Phosphorylation	...[P]...K...	41.53	12		
Phosphorylation	...S...E...	38.94	30		
Phosphorylation	...[P]...P...	36.08	26		
Phosphorylation	...[E]D...	34.62	26		
Phosphorylation	...[R]...S...	30.26	26	HSPK3/CK1 kinase subunit...	kinase
Phosphorylation	...[P]...K...	30.19	21	Growth associated histone ...	kinase
Phosphorylation	...[P]...	26.05	65	WW domain binding motif	binding
Phosphorylation	...[P]...	24.68	13		
Phosphorylation	...S...E...	24.40	20		
Phosphorylation	...[R]...[Y]...	22.80	12	Phosphorylase kinase subs...	kinase
Phosphorylation	...[E]E...	20.83	17		
Phosphorylation	...S...E...	19.45	27		
Phosphorylation	...[P]...	9.22	149	WW domain binding motif	binding
Phosphorylation	...S...E...	7.94	121	Casein kinase II substrate ...	kinase

**Sequences:**

Modification	Surrounding Sequence	Accession	Name
Phosphorylation	THQRRI-SDSVAE	spn-PA	SpH ends [AAF51535.2.2]
Phosphorylation	DELYAD-SAGEDE	Spn-PA	Spnophilin [AAF49622]
Phosphorylation	KVALQH-LEAEKT	RUGAP7E-PA	Dmel_CG2149 [AAF49]
Phosphorylation	QSGRR-RRPDS	kuk-PA	kuglelem [AAN13753.1]
Phosphorylation	KKKVVE-SCEPEP	CC226-PA	Dmel_CG226 [AAF520]
Phosphorylation	SSSES-PEKTSK	Usp4E-FA	UbiAin-specific protea
Phosphorylation	DNDIEDY-PKKSIVQ	Or21-PA	Orign receptor comp
Phosphorylation	LNLGSS-GADIER	Spn-PA	Dmel_CG8594 [AAF533]
Phosphorylation	ADVVA-IDSEDT	CC226-FA	Dmel_CG226 [AAF520]
Phosphorylation	DSQVAI-PRRRRQ	CG14897-FB	D [AAF53320.1]
Phosphorylation	CTPBRV-LATAVQ	2nd-PA	2nd homolog [AAF46]
Phosphorylation	RSKGG-PKNSPP	Spn-PA	Spnophilin [AAF4957]
Phosphorylation	LESAS-NZSKQ	CG1703-PA	Dmel_CG1703 [AAF480]
Phosphorylation	DYSLNE-RKSTTE	CG14897-FB	D [AAF53320.1]
Phosphorylation	KANLQY-SDADEE	Spn-PA	Dmel_CG9594 [AAF533]
Phosphorylation	RTRRPP-NKSNAN	BRW03-PA	Dmel_CG11132 [AAF56]
Phosphorylation	RRIKLT-PRLLPF	CG14897-FB	D [AAF53320.1]
Phosphorylation	PVVEE-SQPKVE	CG1246-FB	Dmel_CG1246 [AAF480]
Phosphorylation	EEDDD-DSGDKP	CG8877-PA	Dmel_CG8877 [AAF539]
Phosphorylation	SKAKDQ-ESDQDA	CG828-PA	Dmel_CG828 [AAF487]
Phosphorylation	SVTSSP-PMAPLK	muc59-FA	mu59 sensitive 209
Phosphorylation	SDAFPI-PRRRFE	CG14896-FA	D [AAF53319.2]

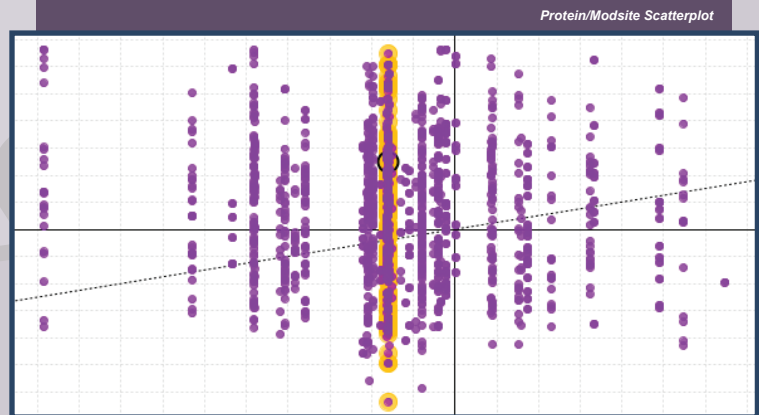
Quantitation: (IP100759596) Isoform 4 of Heterogeneous nuclear ... Display Options: Log2 Ratio

Site	Modification	Best Ascore	Localization Probability	Reference	Treatment 1	Treatment 2
				Quant 1	Quant 2	Quant 3
M195	Oxidation	1,000.00	100%	0.13	-0.76	0.127
S197	Phosphorylation	1,000.00	100%	0.04	-0.58	0.121
S204	Phosphorylation	1,000.00	100%	0.11	-0.73	0.0117

Assess the significance of differences between modified and unmodified intensities using statistical testing

Annotate motifs reported in the literature and associate specific enzymes and kinases with PTM sites

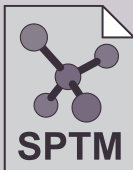
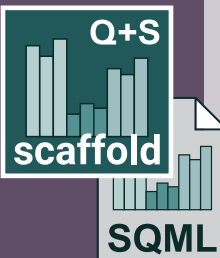
Compare samples with modified spectra using differential expression



Import Scaffold Q+S data from unenriched samples to get background protein levels

Adjust quantitative values in enriched samples to properly reflect differential modification

Export quantitative data from Scaffold Q+S and analyze it at the modsite level in Scaffold PTM



Share results with the free Scaffold PTM viewer

