

Illuminating the World of Protein Post Translational Modifications

Evaluate modification site assignment confidence using Ascore and Ascore derived probabilities

Modification	Motif	Score	# Matches	Enzyme	Enzyme Type
Phosphorylation	[SP]	67.46	11		kinase
Phosphorylation	[SP]	59.56	17	Growth associated histone...	kinase
Phosphorylation	[SP]	56.76	21	Growth associated histone...	kinase
Phosphorylation	[SP]	56.76	29	Growth associated histone...	kinase
Phosphorylation	[S.P]	54.81	14		
Phosphorylation	[S.P]	50.78	33		
Phosphorylation	[S.P]	49.73	23		
Phosphorylation	[S.P]	41.53	12		
Phosphorylation	[S.P]	38.94	30		
Phosphorylation	[S.P]	36.08	26		
Phosphorylation	[S.P]	34.62	26		
Phosphorylation	[S.P]	31.03	26	MAPKAP1 kinase substrat...	kinase
Phosphorylation	[S.P]	30.19	21	Growth associated histone...	kinase
Phosphorylation	[S.P]	26.05	63	WW domain binding motif	binding
Phosphorylation	[S.P]	24.68	13		
Phosphorylation	[S.P]	24.40	28		
Phosphorylation	[S.P]	22.60	12	Phosphorase kinase subs...	kinase
Phosphorylation	[S.P]	20.83	17		
Phosphorylation	[S.P]	19.45	27		
Phosphorylation	[S.P]	9.22	140	WW domain binding motif	binding
Phosphorylation	[S.P]	7.94	121	Casoin Kinase II substrate...	kinase

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

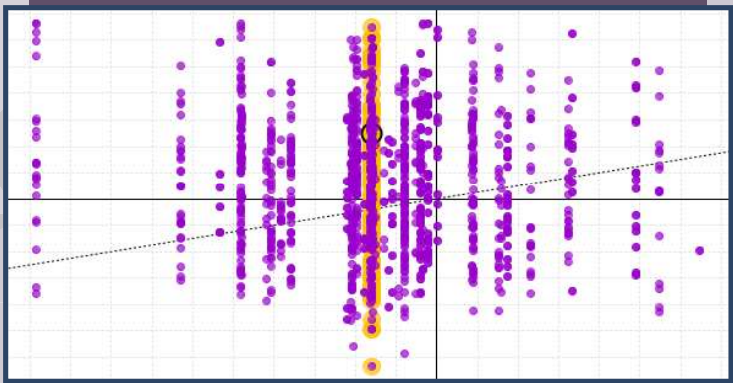
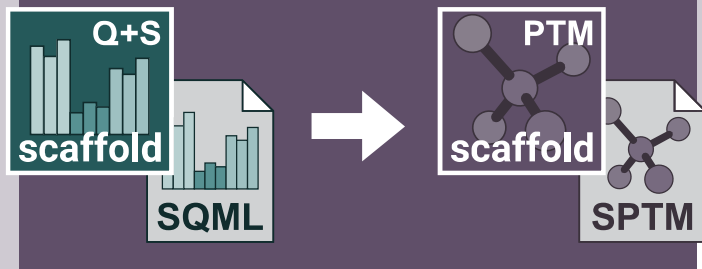
Site	Modification	Best Ascore	Localization Probability	Reference	Treatment 1	Treatment 2
				Quant 1	Quant 2	Quant 3
M195	Oxidation	1,000.00	100%	0.13	-0.76	0.127
S197	Phosphorylation	1,000.00	100%	0.04	-0.58	0.121
S204	Phosphorylation	1,000.00	100%	0.11	-0.73	0.05

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

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



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

Adjust quantitative values in enriched samples to properly reflect differential modification