



Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances		
										0hr	1hr	2hr
DLDGTNGEISYSLYYSSQEIDKPFELSSLGSEIR	19388	3.95	1	3912.8675	5		0		yes	2140.95	2012.31	1871.44

Tags
 Modification with Phosphoryl+STY

B2RDF2

Pescadillo homolog OS=Homo sapiens GN=PES1 PE=2 SV=1
1 peptide


Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances		
										0hr	1hr	2hr
VMATFEFYTTLLGFVNFR	5066	3.95	1	2256.0937	3		1		no	2.22e+004	2.18e+004	2.44e+004

Tags
 Modification with Phosphoryl+STY

B7Z3X3

cDNA FLJ56097_ highly similar to Homo sapiens dystrobrevin_ alpha (DTNA)_ transcript variant 2_ mRNA OS=Homo sapiens PE=2
SV=1
1 peptide


Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances		
										0hr	1hr	2hr
GHAGGSHSNQHQKEYTSWK	9488	3.86	1	2269.0267	3		0		yes	1.15e+004	1.01e+004	1.13e+004

Tags
 Modification with Phosphoryl+STY

A0A024R0X1

NEL-like 2 (Chicken)_ isoform CRA_b OS=Homo sapiens GN=NELL2 PE=4 SV=1
1 peptide

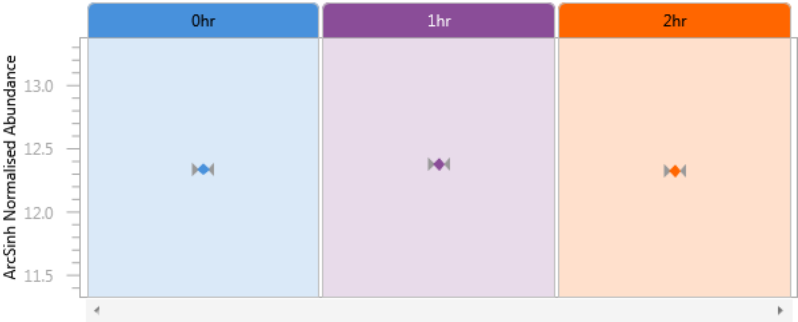
Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances		
										0hr	1hr	2hr
AN[C]INLPGWYH[C]E[CRDGYHDNGMFSPSGES[C]EDIDE[CGTGR	12420	3.84	1	4821.7854	4		0	Carbamidomethyl+C[3] Carbamidomethyl+C[12] Carbamidomethyl+C[14] Carbamidomethyl+C[31] Carbamidomethyl+C[37] Carbamidomethyl+C	yes	1.07e+004	9003.51	1.03e

Tags
 Modification with Phosphoryl+STY

Accession Q5T200 (+3)

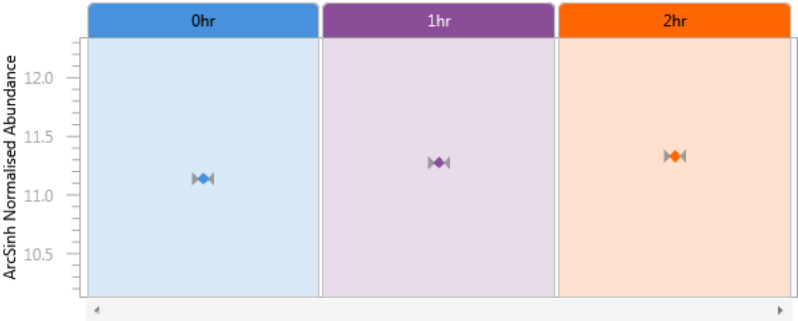
Description Zinc finger CCCH domain-containing protein 13 OS=Homo sapiens GN=ZC3H13 PE=1 SV=1
Peptides 56 (35)
Score 286.55
Anova ---
Fold 1.05

● Modification with Phosphoryl+STY



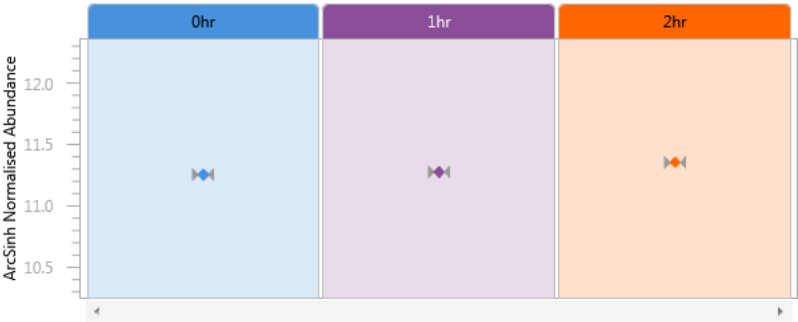
Accession P55287 (+4)

Description Cadherin-11 OS=Homo sapiens GN=CDH11 PE=2 SV=2
Peptides 3 (2)
Score 14.42
Anova ---
Fold 1.21



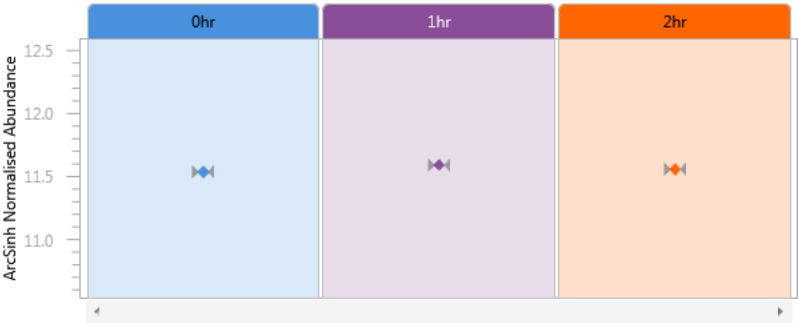
Accession Q5TON1 (+2)

Description Cilia- and flagella-associated protein 70 OS=Homo sapiens GN=CFAP70 PE=2 SV=3
Peptides 3 (2)
Score 13.23
Anova ---
Fold 1.11



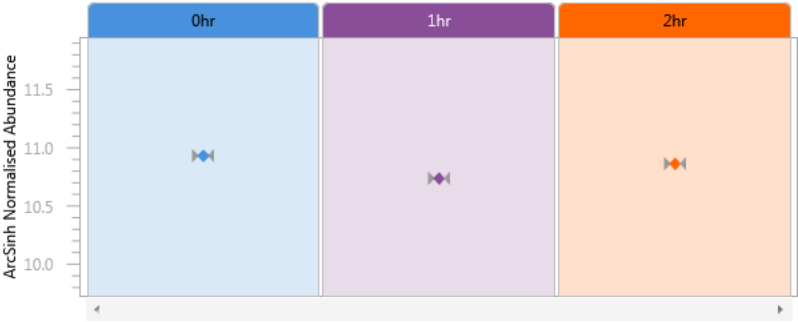
Accession O00629

Description Importin subunit alpha-3 OS=Homo sapiens GN=KPNA4 PE=1 SV=1
Peptides 3 (2)
Score 13.20
Anova ---
Fold 1.06



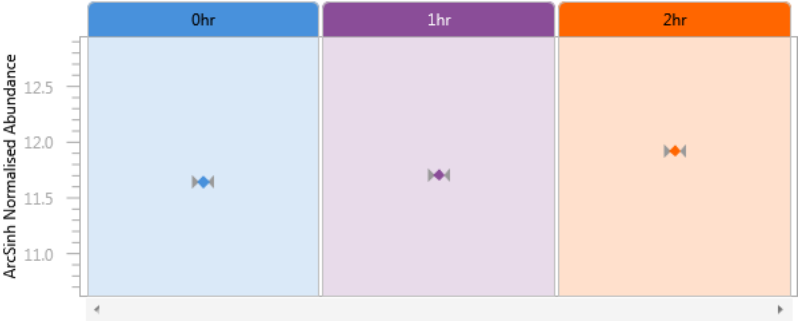
Accession AOA024R0F1 (+1)

Description Transcription termination factor_ RNA polymerase II_ isoform CRA_a OS=Homo sapiens GN=TTF2 PE=4 SV=1
Peptides 3 (3)
Score 13.63
Anova ---
Fold 1.22



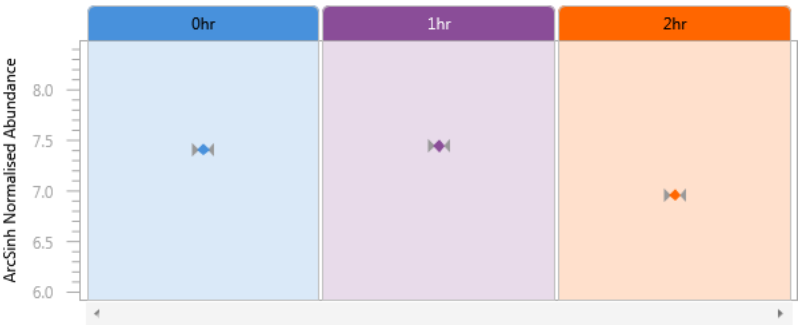
Accession Q05DH4

Description Protein FAM160A1 OS=Homo sapiens GN=FAM160A1 PE=2 SV=2
Peptides 3 (2)
Score 12.62
Anova ---
Fold 1.33



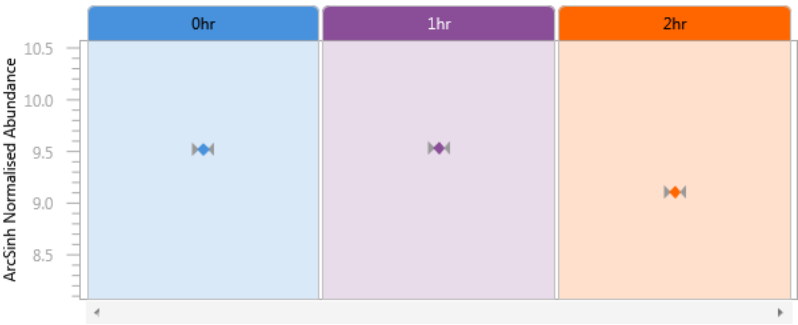
Accession AOA024R1I2 (+5)

Description Myotubularin related protein 3_ isoform CRA_d OS=Homo sapiens GN=MTMR3 PE=3 SV=1
Peptides 3 (1)
Score 13.92
Anova ---
Fold 1.62



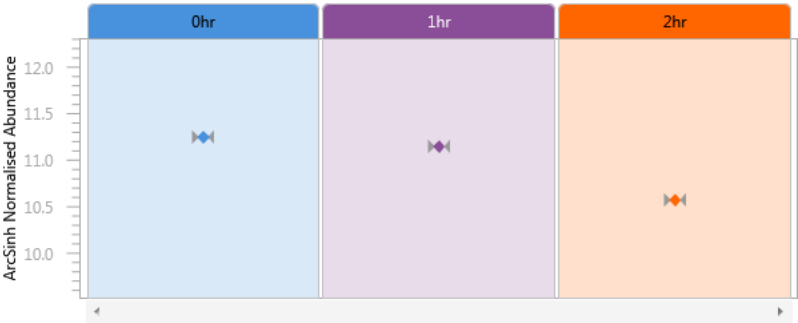
Accession P52179 (+2)

Description Myomesin-1 OS=Homo sapiens GN=MYOM1 PE=1 SV=2
Peptides 3 (2)
Score 15.45
Anova ---
Fold 1.54



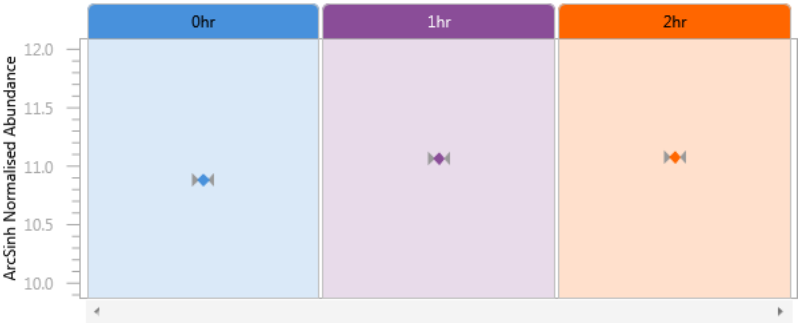
Accession Q9UPQ9 (+3)

Description Trinucleotide repeat-containing gene 6B protein OS=Homo sapiens GN=TNRC6B PE=1 SV=4
Peptides 3 (2)
Score 13.99
Anova ---
Fold 1.96



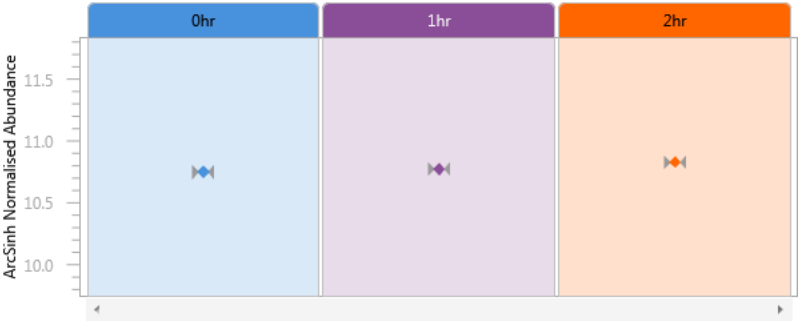
Accession Q86T13

Description C-type lectin domain family 14 member A OS=Homo sapiens GN=CLEC14A PE=1 SV=1
Peptides 3 (2)
Score 13.44
Anova ---
Fold 1.21



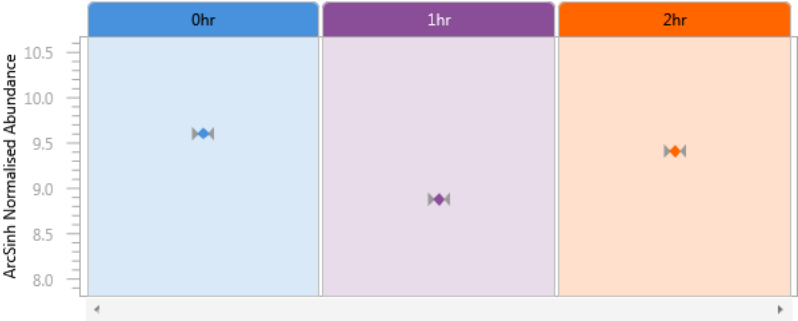
Accession Q9Y2A7 (+1)

Description Nck-associated protein 1 OS=Homo sapiens GN=NCKAP1 PE=1 SV=1
Peptides 3 (3)
Score 11.91
Anova ---
Fold 1.09



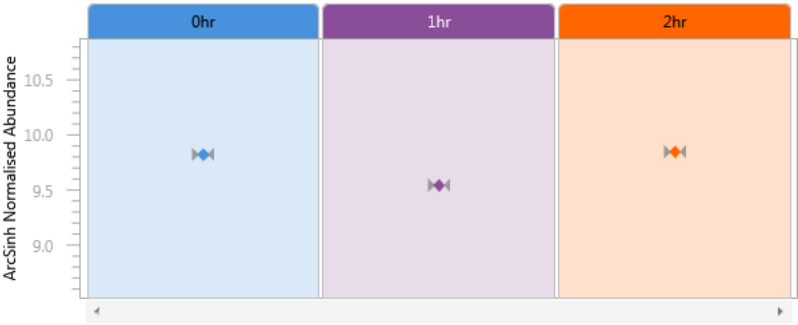
Accession Q58EX2

Description Protein sidekick-2 OS=Homo sapiens GN=SDK2 PE=1 SV=3
Peptides 3 (1)
Score 13.57
Anova ---
Fold 2.08



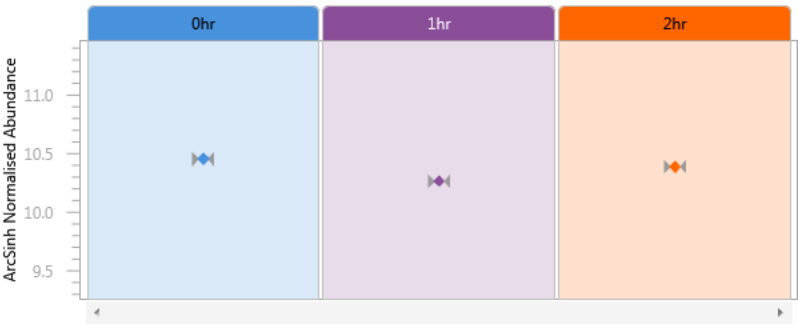
Accession G3V256 (+4)

Description Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1
Peptides 3 (1)
Score 13.08
Anova ---
Fold 1.36



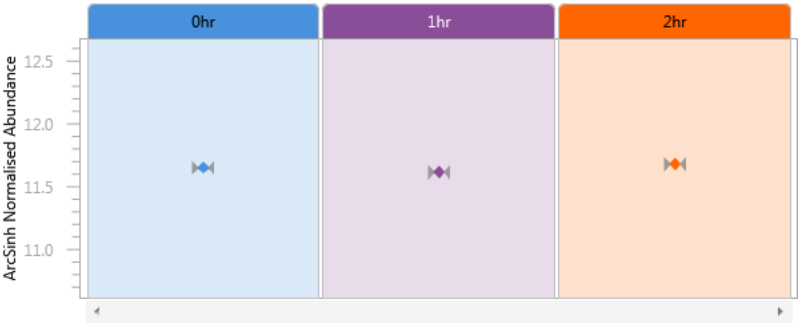
Accession B7Z855 (+5)

Description cDNA FLJ50427_ highly similar to Ubiquitin carboxyl-terminal hydrolase 7 (EC3.1.2.15) OS=Homo sapiens PE=2 SV=1
Peptides 3 (2)
Score 12.11
Anova ---
Fold 1.20



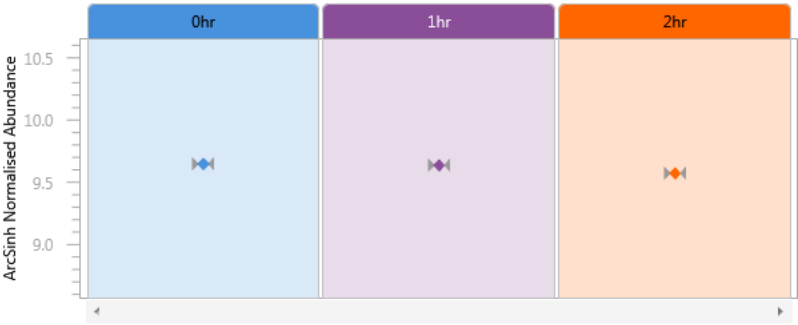
Accession O00519

Description Fatty-acid amide hydrolase 1 OS=Homo sapiens GN=FAAH PE=1 SV=2
Peptides 3 (2)
Score 14.56
Anova ---
Fold 1.07



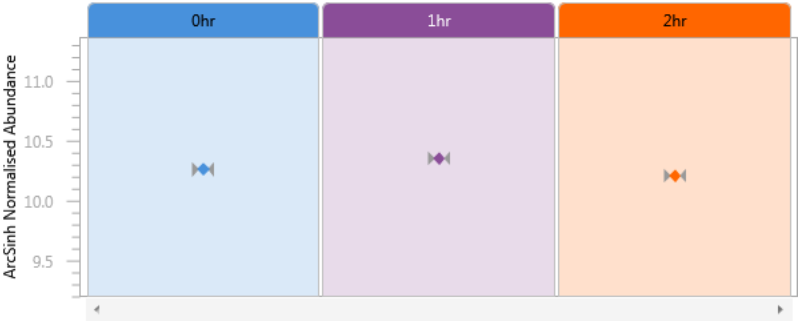
Accession Q05BV3

Description Echinoderm microtubule-associated protein-like 5 OS=Homo sapiens GN=EML5 PE=2 SV=3
Peptides 3 (3)
Score 13.22
Anova ---
Fold 1.08



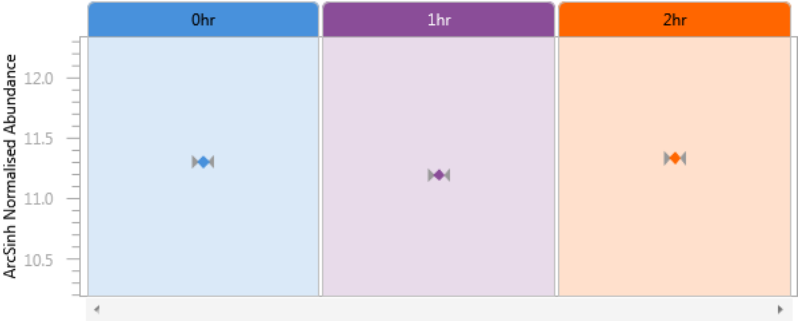
Accession B3KUQ8

Description Transmembrane channel-like protein OS=Homo sapiens PE=2 SV=1
Peptides 3 (3)
Score 12.86
Anova ---
Fold 1.15



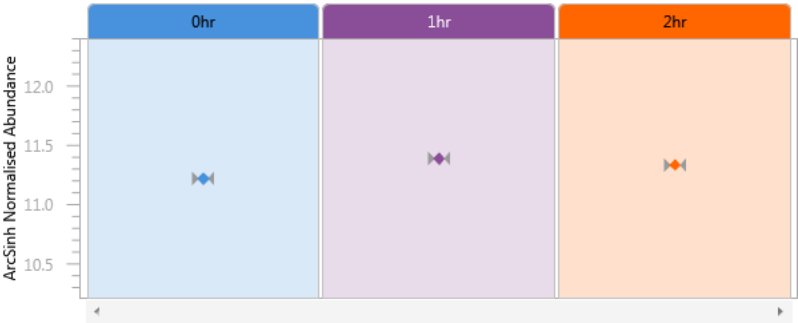
Accession AOA024R125 (+4)

Description Protein kinase_ AMP-activated_ gamma 1 non-catalytic subunit_ isoform CRA_a OS=Homo sapiens GN=PRKAG1 PE=4 SV=1
Peptides 3 (2)
Score 13.00
Anova ---
Fold 1.15



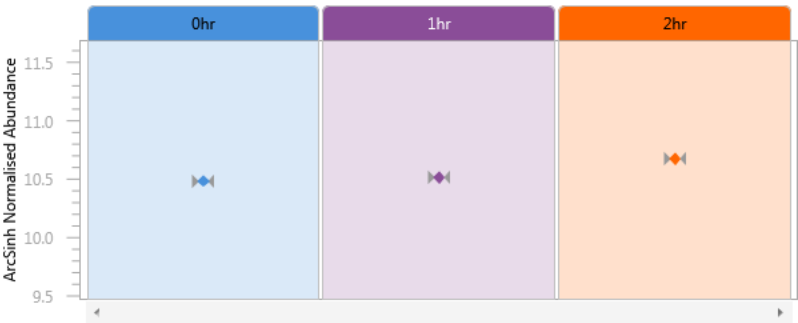
Accession P14784

Description Interleukin-2 receptor subunit beta OS=Homo sapiens GN=IL2RB PE=1 SV=1
Peptides 3 (1)
Score 15.24
Anova ---
Fold 1.18



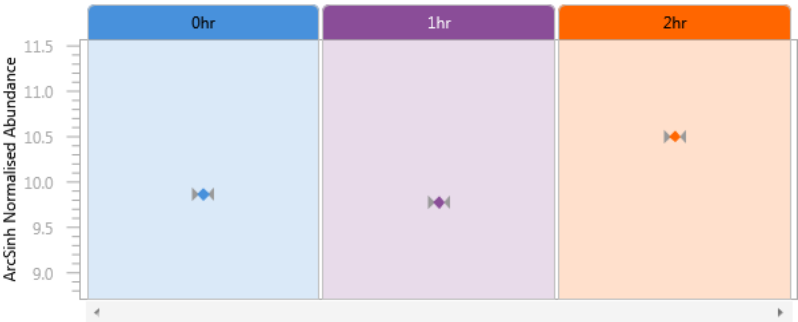
Accession AOA024R2K6 (+7)

Description Calcium-transporting ATPase OS=Homo sapiens GN=ATP2B2 PE=3 SV=1
Peptides 3 (2)
Score 14.31
Anova ---
Fold 1.21



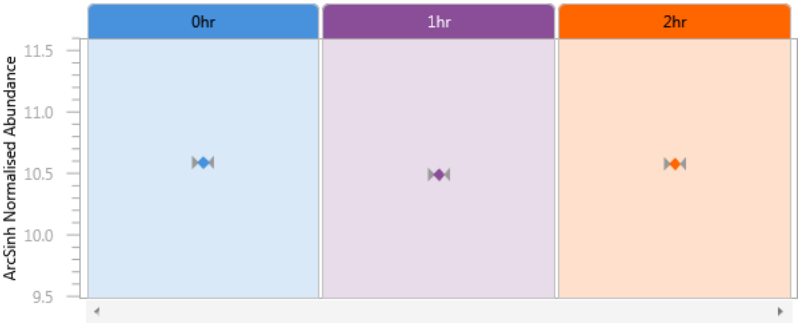
Accession Q6ZSY0 (+4)

Description cDNA FLJ45137 fis_ clone BRAWH3038827_ highly similar to Homo sapiens leucine-zipper-like transcriptional regulator_ 1 (LZTR1)
OS=Homo sapiens PE=2 SV=1
Peptides 3 (3)
Score 15.30
Anova ---
Fold 2.07
● Max fold change ≥ 1.2
● Modification with Phosphoryl+STY



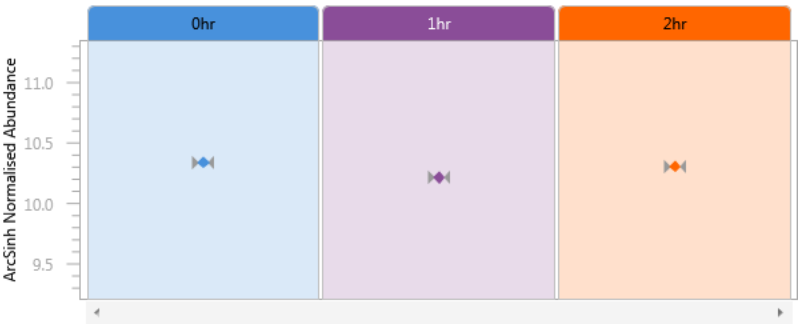
Accession Q9UKP4

Description A disintegrin and metalloproteinase with thrombospondin motifs 7 OS=Homo sapiens GN=ADAMTS7 PE=1 SV=2
Peptides 3 (2)
Score 12.10
Anova ---
Fold 1.11
● Modification with Phosphoryl+STY



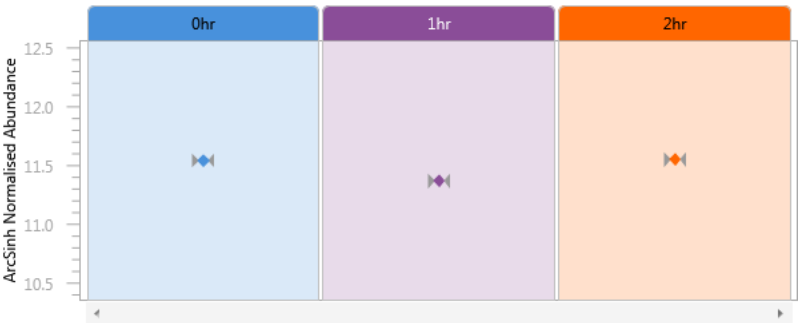
Accession AOA024RBC7 (+1)

Description Calcium-transporting ATPase OS=Homo sapiens GN=ATP2B1 PE=3 SV=1
Peptides 3 (1)
Score 12.78
Anova ---
Fold 1.13



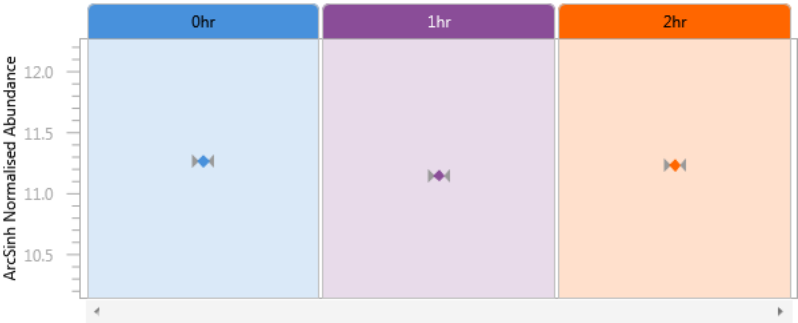
Accession Q14696

Description LDLR chaperone MESD OS=Homo sapiens GN=MESDC2 PE=1 SV=2
Peptides 3 (2)
Score 13.35
Anova ---
Fold 1.20



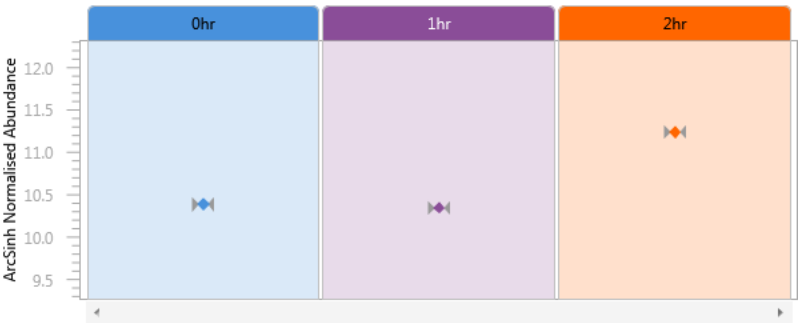
Accession Q16799 (+4)

Description Reticulon-1 OS=Homo sapiens GN=RTN1 PE=1 SV=1
Peptides 3 (3)
Score 9.99
Anova ---
Fold 1.12
● Modification with Phosphoryl+STY



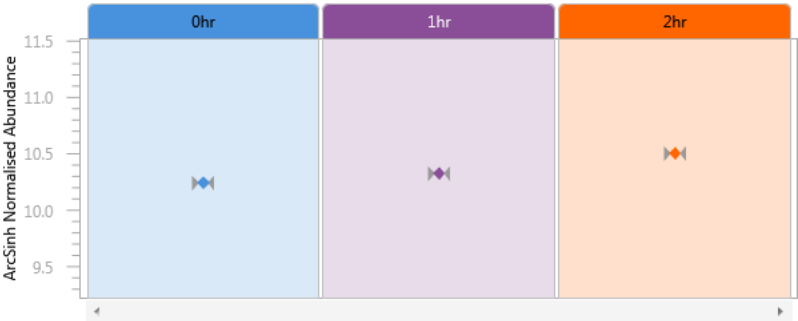
Accession F5GXT3 (+2)

Description Anoctamin OS=Homo sapiens GN=ANO2 PE=1 SV=2
Peptides 3 (2)
Score 14.74
Anova ---
Fold 2.43



Accession V9H1F4

Description Endogenous retrovirus ERV9 protein OS=Homo sapiens GN=endogenous retrovirus ERV9 PE=2 SV=1
Peptides 3 (3)
Score 13.63
Anova ---
Fold 1.30



Accession AOA024R2K4 (+2)

Description Leucine rich repeat (In FLII) interacting protein 2_ isoform CRA_b OS=Homo sapiens GN=LRRFIP2 PE=4 SV=1
Peptides 3 (3)
Score 14.35
Anova ---
Fold 1.78