

| Accession | Peptides | Score | Anova (p)* | Fold | Tags | Description | Average Normalised Abundances | | |
|----------------------------|----------|-------|------------|------|------|---|-------------------------------|-----------|-----------|
| | | | | | | | 0hr | 1hr | 2hr |
| Q13643 | 1 (0) | 4.03 | --- | --- | | Four and a half LIM domains protein 3 OS=Homo sapiens GN=FHL3 PE=1 SV=4 | --- | --- | --- |
| B4E153 | 1 (1) | 4.00 | --- | 1.31 | | cDNA FLJ61525_ highly similar to Thyroglobulin OS=Homo sapiens PE=2 SV=1 | 3233.09 | 3898.22 | 2980.79 |
| Q96BD5 | 1 (1) | 3.99 | --- | 1.23 | | PHD finger protein 21A OS=Homo sapiens GN=PHF21A PE=1 SV=1 | 9959.59 | 9093.99 | 8078.12 |
| A0A0A0MRU5 | 1 (1) | 3.99 | --- | 1.33 | | Ceroid-lipofuscinosis neuronal protein 5 OS=Homo sapiens GN=CLN5 PE=1 SV=1 | 7582.69 | 5696.11 | 6549.27 |
| D6RF86 | 1 (1) | 3.98 | --- | 1.19 | | Cadherin-6 OS=Homo sapiens GN=CDH6 PE=1 SV=1 | 1.14e+004 | 1.02e+004 | 1.21e+004 |
| Q9Y2X7 | 2 (2) | 3.97 | --- | 1.45 | | ARF GTPase-activating protein GIT1 OS=Homo sapiens GN=GIT1 PE=1 SV=2 | 4030.24 | 3239.40 | 4709.07 |
| Q5TCH6 | 1 (0) | 3.96 | --- | --- | | Meiotic recombination protein SPO11 (Fragment) OS=Homo sapiens GN=SPO11 PE=4 SV=2 | --- | --- | --- |
| B2R708 | 1 (1) | 3.95 | --- | 1.14 | | cDNA_ FLJ93213_ highly similar to Homo sapiens protocadherin beta 15 (PCDHB15)_ mRNA OS=Homo sapiens PE=2 SV=1 | 2140.95 | 2012.31 | 1871.44 |
| B2RDF2 | 1 (0) | 3.95 | --- | --- | | Pescadillo homolog OS=Homo sapiens GN=PES1 PE=2 SV=1 | --- | --- | --- |
| B7Z3X3 | 1 (1) | 3.86 | --- | 1.14 | | cDNA FLJ56097_ highly similar to Homo sapiens dystrobrevin alpha (DTNA)_ transcript variant 2_ mRNA OS=Homo sapiens PE=2 SV=1 | 1.15e+004 | 1.01e+004 | 1.13e+004 |
| A0A024R0X1 | 1 (1) | 3.84 | --- | 1.18 | | NEL-like 2 (Chicken)_ isoform CRA_b OS=Homo sapiens GN=NELL2 PE=4 SV=1 | 1.07e+004 | 9003.51 | 1.03e+004 |

Tags

Modification with Phosphoryl+STY

Max fold change ≥ 1.2

Q5T200

Zinc finger CCCH domain-containing protein 13 OS=Homo sapiens GN=ZC3H13 PE=1 SV=1
56 peptides

| Sequence | Peptide lon | Score | Hits | Mass | Charge | Tags | Conflicts | Modifications | In quantitation | Average Normalised Abundances | | |
|----------------------------------|-------------|-------|------|-----------|--------|------|-----------|---------------------|-----------------|-------------------------------|-----------|-----------|
| | | | | | | | | | | 0hr | 1hr | 2hr |
| AQDIIGHQSEDR | 5720 | 4.56 | 1 | 1504.7127 | 2 | | 0 | | no | 1.61e+004 | 1.24e+004 | 3.21e+004 |
| ARERDRERDRERERERERDREREKER | 23793 | 5.06 | 1 | 4167.1040 | 4 | | 0 | | no | 1744.90 | 1583.21 | 952.98 |
| AREREREREKERDRERDRDR | 17276 | 4.65 | 1 | 2741.4063 | 3 | | 0 | | no | 2414.51 | 1682.18 | 1793.97 |
| DADNLFELHFGALNMAALLR | 1284 | 4.91 | 1 | 2212.0845 | 3 | | 0 | | no | 5.66e+004 | 6.07e+004 | 6.68e+004 |
| DADNLFELHFGALNMAALLR | 3895 | --- | --- | 2212.2568 | 2 | | 0 | | no | 2.62e+004 | 3.19e+004 | 3.05e+004 |
| DAHDYRDREGDRDTHR | 17686 | 5.12 | 1 | 1897.8799 | 3 | | 0 | | no | 5105.88 | 4567.75 | 4009.15 |
| DGHDER | 13002 | 4.97 | 1 | 727.2721 | 2 | | 0 | | no | 3827.66 | 2825.88 | 1655.25 |
| DMRDSREMRDYSRDTK | 14118 | 5.14 | 1 | 2059.9075 | 3 | | 0 | | no | 3532.49 | 2613.26 | 2591.76 |
| DMRDSREMRDYSRDTKESR | 2365 | 5.34 | 1 | 2432.0671 | 4 | | 0 | | no | 2.63e+004 | 1.93e+004 | 2.39e+004 |
| DRDHREREREREREREKEREREREERERERER | 17286 | 5.06 | 1 | 4891.3269 | 5 | | 0 | | no | 5458.47 | 7111.98 | 4516.35 |
| DRDRDHRERERERER | 2977 | 5.45 | 1 | 2224.0559 | 3 | | 1 | | no | 3.87e+004 | 3.46e+004 | 3.94e+004 |
| DREKEREREERERER | 588 | 5.40 | 1 | 2101.0659 | 3 | | 0 | | yes | 1.58e+005 | 1.54e+005 | 1.59e+005 |
| DREKEREREERERERERER | 18188 | 5.08 | 1 | 2671.2960 | 4 | | 1 | | no | 5066.21 | 4804.83 | 4122.34 |
| DRERDRDRDHRERER | 18781 | 4.62 | 1 | 2210.0611 | 3 | | 0 | | no | 3010.28 | 2109.72 | 2630.97 |
| DRGRDFERQR | 941 | 5.85 | 1 | 1333.6595 | 2 | | 0 | | no | 5.64e+004 | 8.24e+004 | 5.61e+004 |
| DRYEHDR | 15645 | 5.87 | 1 | 989.4221 | 2 | | 0 | | no | 2770.05 | 2610.18 | 2488.79 |
| DYSRDTKESRDPDRSR | 11187 | 4.87 | 1 | 1981.9134 | 3 | | 0 | | no | 3.65e+004 | 3.41e+004 | 3.73e+004 |
| DYSRDTKESRDPDRSR | 24321 | 5.05 | 1 | 1981.9375 | 3 | | 0 | | no | 1329.07 | 1394.07 | 1241.63 |
| EDIKITKER | 15710 | 4.98 | 1 | 1130.6148 | 2 | | 2 | | no | 5.83e+004 | 5.71e+004 | 8.32e+004 |
| EKERDRERDRDRDHR | 8451 | 4.74 | 1 | 2182.0336 | 3 | | 0 | | no | 2.92e+004 | 2.78e+004 | 3.09e+004 |
| EKEREREEREERERER | 12313 | 5.60 | 2 | 2115.0499 | 3 | | 0 | | no | 1.19e+004 | 1.29e+004 | 1.38e+004 |
| EKEREREEREERERERERERERERERERERER | 4023 | --- | --- | 4111.3043 | 3 | | 1 | | no | 5.19e+004 | 3.96e+004 | 5.16e+004 |
| EKEREREEREERERERERERERERERERERER | 6785 | 5.06 | 1 | 4111.0577 | 4 | | 1 | | no | 2.30e+004 | 1.76e+004 | 2.36e+004 |
| ELRDSRDMRDSREMRDYSR | 4873 | 5.00 | 1 | 2472.1579 | 3 | | 1 | | no | 5.03e+004 | 3.94e+004 | 4.72e+004 |
| EMRDYSRDTK | 1937 | 4.45 | 1 | 1299.6115 | 2 | | 1 | | no | 1.08e+005 | 8.63e+004 | 1.08e+005 |
| EMRDYSRDTKESRDPDR | 3830 | 4.74 | 1 | 2039.9610 | 3 | | 2 | | no | 6.36e+004 | 5.82e+004 | 6.85e+004 |
| EPGAALLKFTPGAVMLR | 1905 | 5.19 | 1 | 1785.9825 | 2 | | 2 | [15] Oxidation+M | no | 6.60e+004 | 5.82e+004 | 6.66e+004 |
| EPGAALLKFTPGAVMLR | 399 | --- | --- | 1785.8069 | 3 | | 2 | [15] Oxidation+M | no | 1.30e+005 | 1.24e+005 | 1.50e+005 |