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Supporting Information

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# RNF219/α-catenin/LGALS3 axis Promotes Hepatocellular Carcinoma Bone Metastasis and Associated Skeletal Complications

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# Supporting Information

# RNF219/α-catenin/LGALS3 axis promotes hepatocellular carcinoma bone metastasis and associated skeletal complications

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These authors contributed equally: Shuxia Zhang, Yingru Xu, Chan Xie

# Supplementary Figures and Legends

## Figure S1

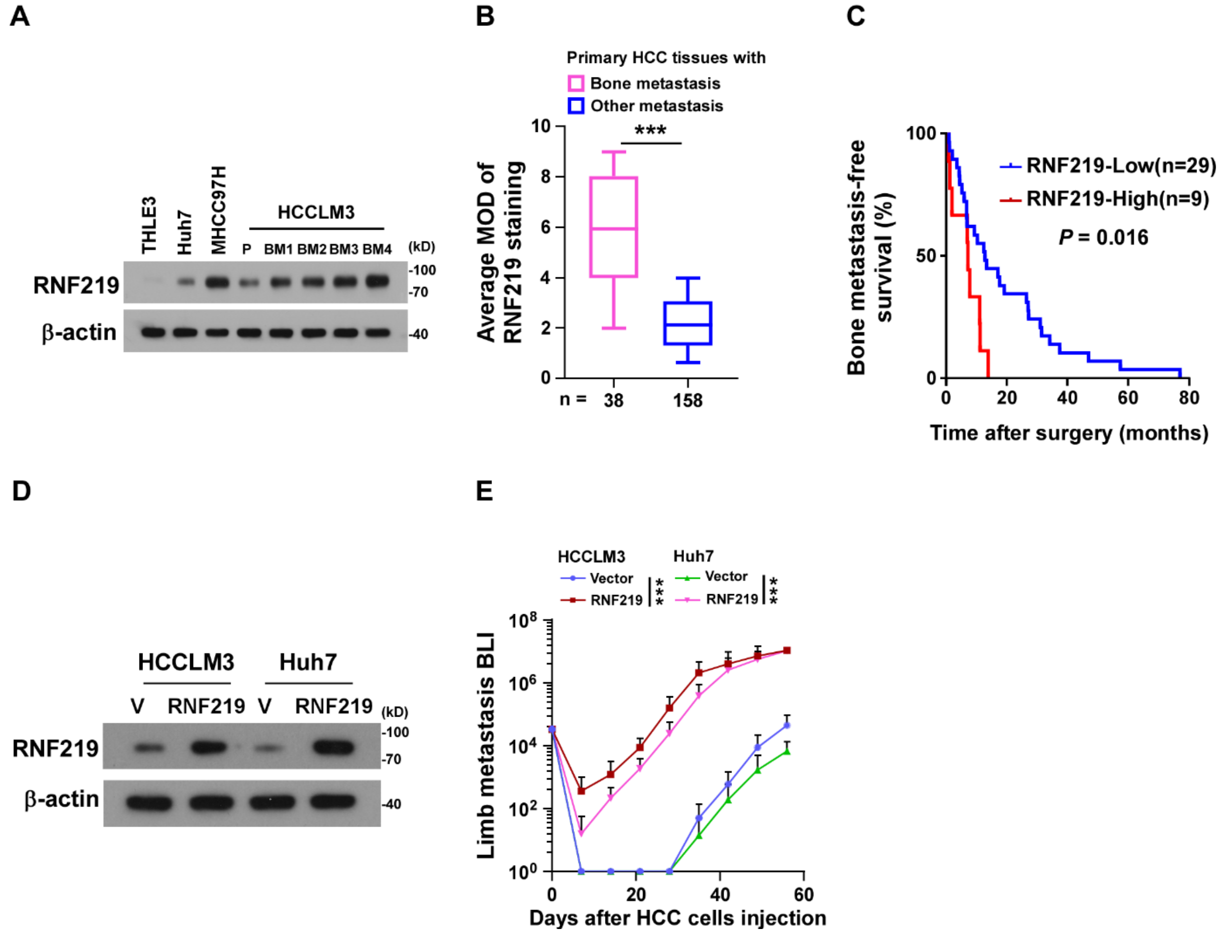

**Figure S1.** ***RNF219* overexpression promotes bone metastasis and SREs in HCC.** **(A)** IB analysis of RNF219 expression in immortalized normal liver epithelial cells THLE3, HCC cells (Huh7 and MHCC97H) and HCCLM3-derived cells (HCCLM3/BM1, HCCLM3/BM2, HCCLM3/BM3, HCCLM3/BM4). β-actin served as the loading control. **(B)** IHC statistical analysis of RNF219 expression in bone metastatic HCC tissues (n = 38) and other organ metastatic HCC tissues (n = 158). **(C)** Kaplan-Meier analysis of bone metastasis-free survival curves in HCC/BM with low vs high expression of RNF219 (n = 38; *P* = 0.016, log-rank test). **(D)** IB analysis of RNF219 expression in vector- and *RNF219*-transduced HCCLM3 and Huh7 cells. β-actin served as the loading control. **(E)** Normalized BLI signals of bone metastases in mice intracardially injected with the indicated cells from each experimental group. Each error bar in panels **B, E** represents the mean ± SD of independent experiments. Significant differences were determined by Student’s *t*-test (**B**). *** $P < 0.001$.

Figure S2

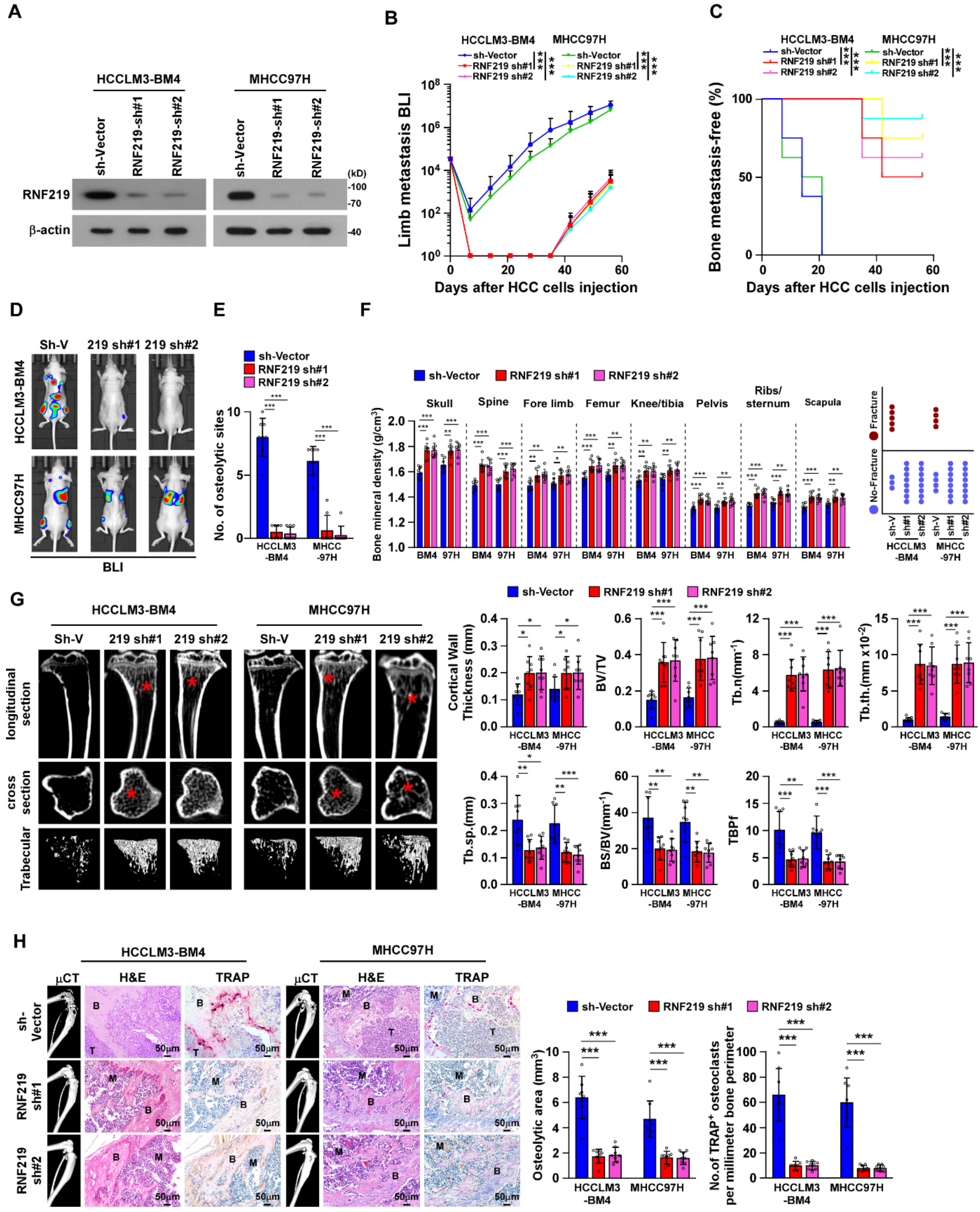

**Figure S2. Downregulation of RNF219 inhibits bone metastasis and SREs in HCC.**

**(A)** IB analysis of RNF219 expression in sh-vector- and *RNF219*-shRNA(s)-transduced HCCLM3/BM4 and MHCC97H cells. β-actin served as the loading control. **(B)**

Normalized BLI signals of bone metastases in mice intracardially injected with the indicated cells from each experimental group (n = 8/group). **(C)** Kaplan-Meier bone metastasis-free survival curve of mice from indicated experimental group (n = 8/group). **(D, E)** BLI images **(D)** and quantification **(E)** of osteolytic sites from representative mice (n = 8/group). **(F)** Quantification of BMD (left) and fracture frequency (right) of the indicated mice (n = 8/group) from experiments in **(D)**. **(G)** μCT images (left) and quantification (right) of bone parameters from representative mice. Left-upper, -middle and -lower: longitudinal, cross and trabecular section. Asterisks: trabecular structure (n = 8/group). BV/TV, bone volume/tissue volume ratio; BS/TV, bone surface/ tissue volume ratio; Tb. n, trabecular number; Tb. sp., trabecular separation; Tb. th., trabecular thickness; TBPf, trabecular bone pattern factor. **(H)** μCT and histological (H&E and TRAP) images (left) and quantification (right) of osteolytic area and TRAP$^+$-osteoclasts along the bone-tumor interface of metastases from representative mice. Scale bar, 50μm. Each error bar in panels **B** and **E-H** represents the mean ± SD of three independent experiments. Significant differences were determined by One-way ANOVA with Tukey's multiple comparison test (**B** and **E-H**). * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$.

Figure S3

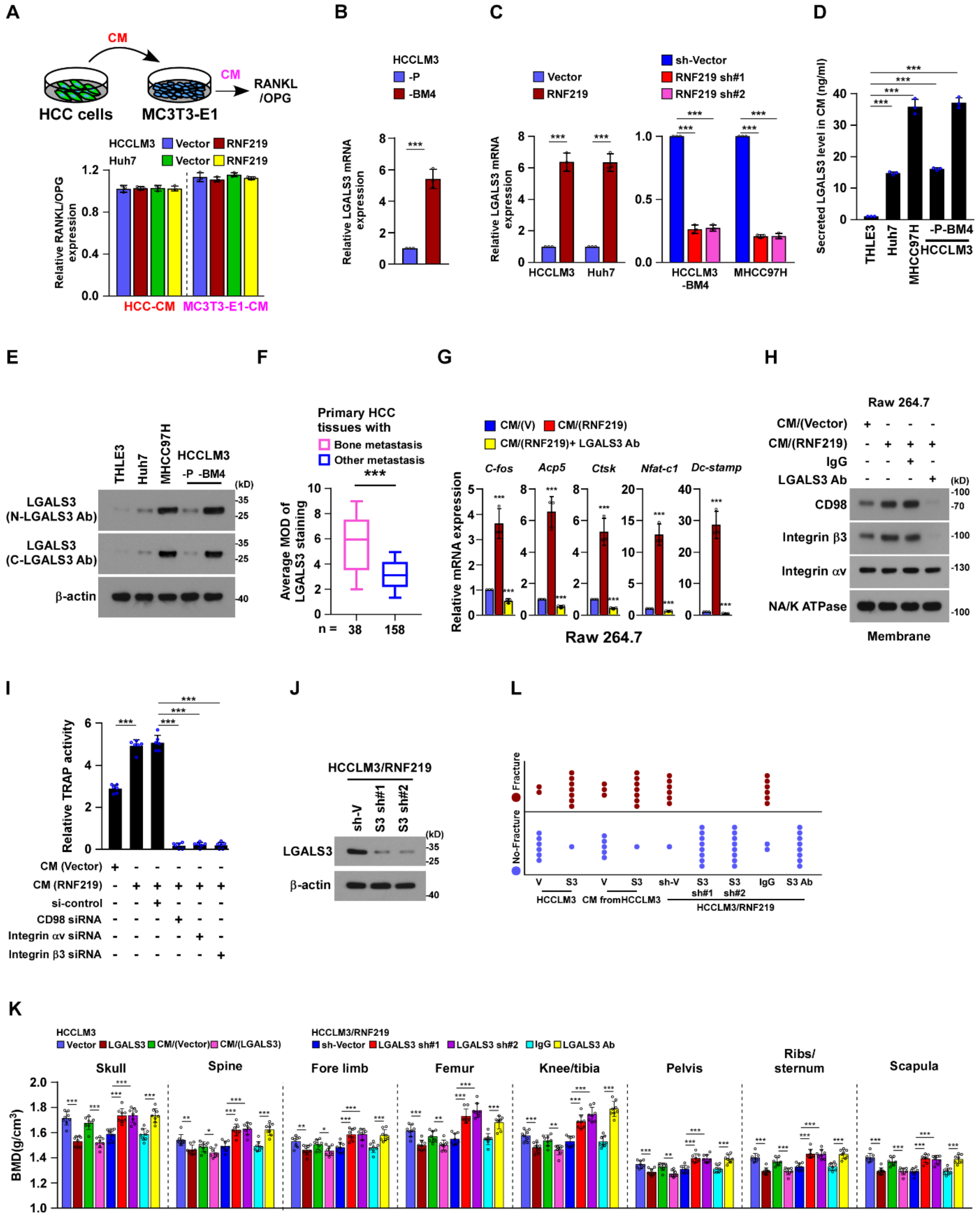

**Figure S3. RNF219 induced-LGALS3 promotes osteoclastogenesis *in vitro*.** **(A)** ELISA analysis of RANKL/OPG ratio in CM from osteoblast precursor cells MC3T3-E1 cells in the presence of CM from the indicated HCC cells. **(B, C)** Real-time PCR analysis of mRNA level of LGALS3 in the indicated HCC cells. *GAPDH* serve as a loading control. **(D)** ELISA analysis of secreted LGALS3 protein level in CM from the indicated HCC cells. **(E)** IB analysis of secreted LGALS3 protein using N- and C- LGALS3 antibodies in CM from the indicated HCC cells. β-actin served as the loading control. **(F)** IHC statistical analysis of LGALS3 expression in bone metastatic HCC tissues (n = 38) and other organ metastatic HCC tissues (n = 158). **(G)** Real-time PCR analysis of mRNA level of osteoclast differentiation markers, including C-fos, Acp5, Ctsk, Nfat-c1 and Dc-stamp, in RAW264.7 cells cultured with CM-HCCLM3/vector, or CM-HCCLM3/RNF219, or CM-HCCLM3/RNF219 added with LGALS3 Ab. *GAPDH* serve as a loading control. **(H)** IB analysis of expression of CD98, integrin αv and integrin β3 in the cytoplasmic membrane fraction of RAW264.7 cells cultured with CM-HCCLM3/V, or CM-HCCLM3/RNF219, or CM-HCCLM3/RNF219 added with LGALS3 Ab. Na/K ATPase served as a loading control. **(I)** Analysis of TRAP activity of RAW264.7 cells as indicated treatments. **(J)** IB analysis of LGALS3 expression in sh-vector- and *LGALS3*-shRNA(s)-transduced HCCLM3/RNF219 cells. β-actin served as the loading control. **(K, L)** Quantification of BMD **(K)** and fracture frequency **(L)** of the indicated mice (n = 8/group) from experiments in Figure 3**C**. Each error bar in panels **A-D F, G. I and K** represents the mean ± SD of three independent experiments. Significant differences were determined by (**B, F**) and One-way ANOVA with Tukey’s multiple comparison test (**A, D**, **G, I** and **K**). * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$.

Figure S4

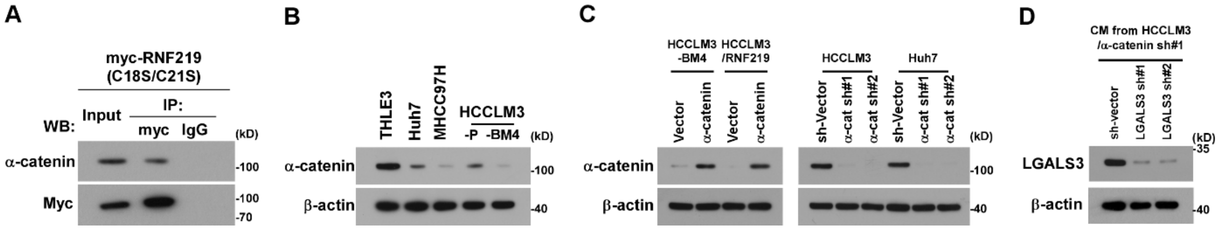

**Figure S4. RNF219-mediated α-catenin proteasomal degradation induced LGALS3 expression and bone metastasis.** **(A)** Co-IP using anti-myc-antibody and IB analyses of expression of α-catenin in RNF219 (C18S/C21S)-mu transfected HCCLM3 cells. **(B)** IB analysis of α-catenin expression in the indicated cells. β-actin served as a loading control. **(C)** IB analysis of α-catenin expression in the vector- or *α-catenin*-transduced cells (left) or sh-vector- or *α-catenin* shRNA(s)-transduced cells. β-actin served as a loading control. **(D)** IB analysis of LGALS3 expression in sh-vector- and *LGALS3*-shRNA(s)-transduced HCCLM3/α-catenin sh#1 cells. β-actin served as the loading control.

Figure S5

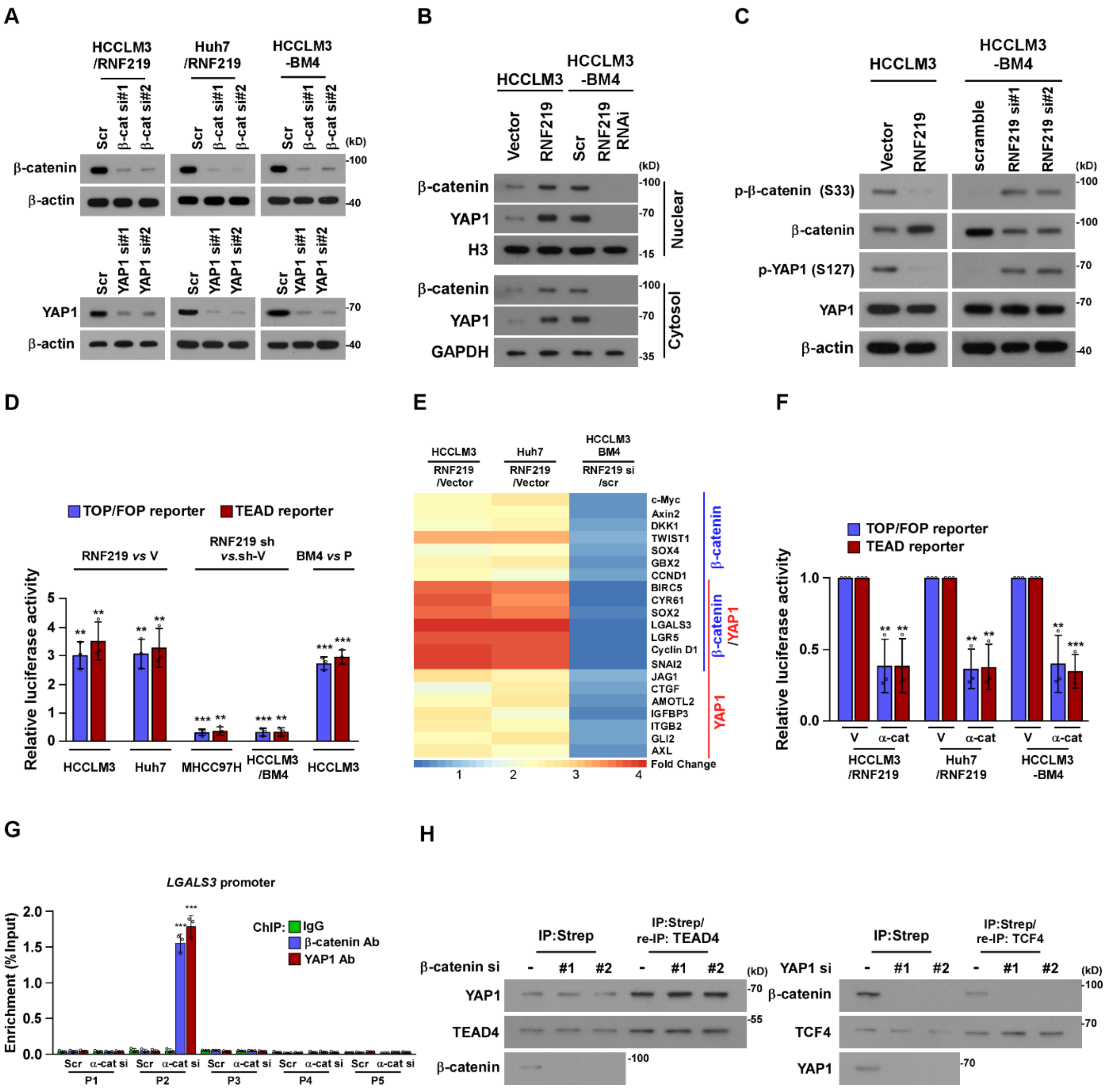

**Figure S5. RNF219-mediated α-catenin reduction activates Wnt/β-catenin and YAP1 pathways.** **(A)** IB analysis of expression of β-catenin and YAP1 in the indicated cells. β-actin served as the loading control. **(B)** IB analysis of expression of β-catenin and YAP1 in the nucleus (upper) and cytoplasm (lower) in the indicated cells. Histone (H3) was used as a nuclear loading control and GAPDH was used as a cytoplasmic loading control. **(C)** IB analysis of expression of phosphorylated-β-catenin (S33), total β-catenin, phosphorylated-YAP1 (S127), total YAP1 in the indicated cells. β-actin served as the loading control. **(D)** Relative TOPflash /FOPflash (blue square) or TEAD (red square) luciferase reporter activity was analyzed in the indicated cells. **(E)** Real-time PCR analysis indicating an apparent overlap between β-catenin-regulated gene expression and YAP1-regulated gene expression in the indicated cells. The pseudocolor represents the intensity scale of RNF219 versus the vector, or RNF219 si versus scramble, generated by a log2 transformation. *GAPDH* serve as a loading control. **(F)** Relative TOPflash/FOPflash (blue square) or TEAD (red square) luciferase reporter activity was analyzed in the vector- or *α-catenin*-transduced cells. **(G)** ChIP-qPCR analysis of the enrichment of β-catenin and YAP1 on the promoter regions of *LGALS3* in the scramble- or α-catenin si-transfected cells. **(H)** Re-co-IP assay, using CAPTURE-approached proteins, analyses of YAP1/TEAD4 interaction in the scramble- or β-catenin si-transfected cell (left) or β-catenin/TCF4 interaction in the scramble- or YAP1 si-transfected cell (right). Each error bar in panels **D, F and G** represents the mean ± SD of three independent experiments. Significant differences were determined by Student's *t*-test (**D, F**) and One-way ANOVA with Tukey's multiple comparison test (**G**). ** $P < 0.01$, *** $P < 0.001$.

**Figure S6**

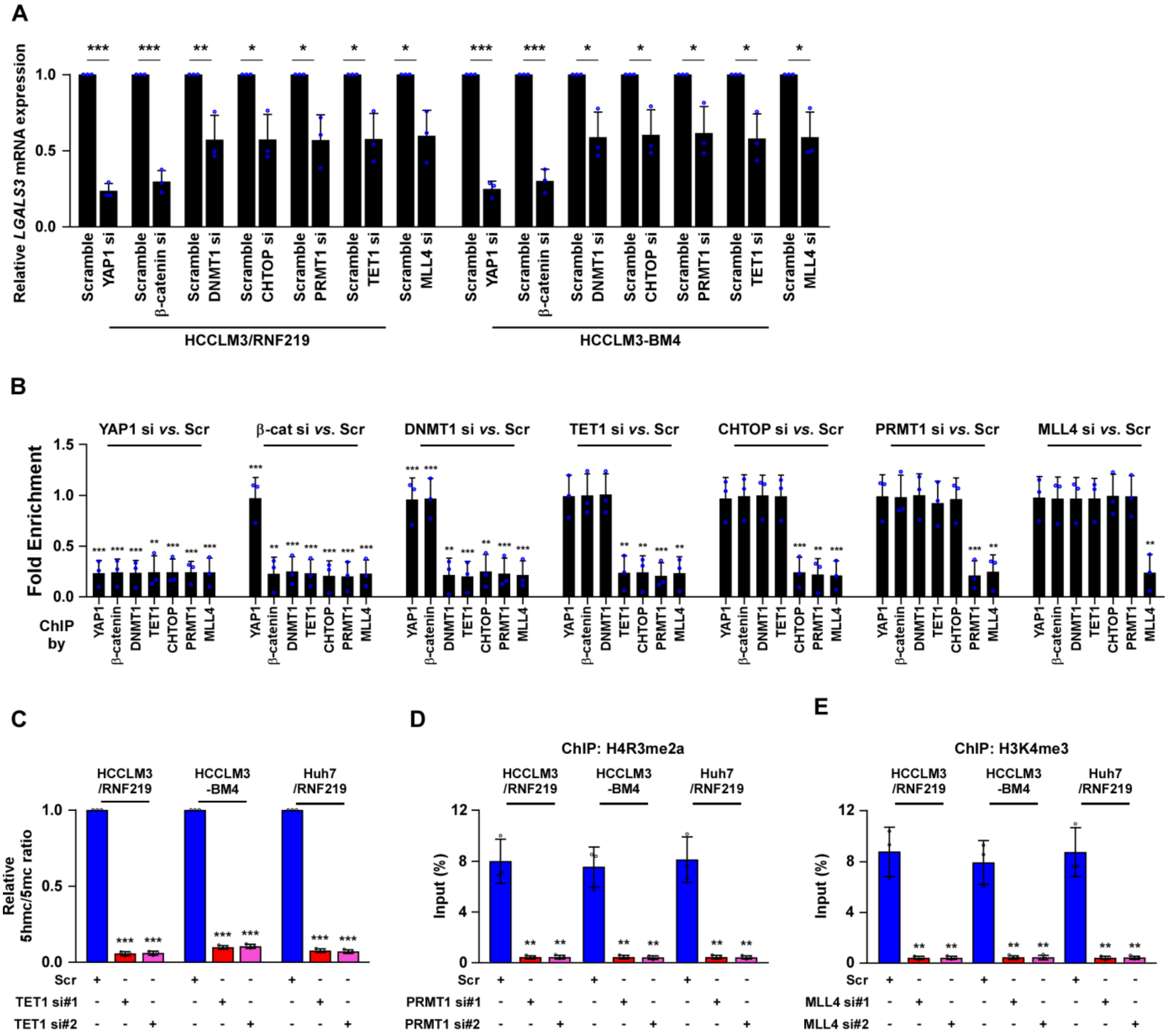

**Figure S6. RNF219/α-catenin/YAP1/β-catenin axis induces a succession of epigenetic modifications at *LGALS3* promoter.** **(A)** Relative mRNA expression of LGALS3, analyzed by real-time PCR assays, in YAP1 si-, or β-catenin si-, or DNMT1 si-, or CHTOP si-, or PRMT1 si-, or TET1 si-, or MLL4 si-transfected cells versus scramble-transfected cells. *GAPDH* serve as a loading control. **(B)** Relative enrichment of YAP1, or β-catenin, or DNMT1, or CHTOP, or PRMT1, or TET1, or MLL4 on the *LGALS3* promoter in the indicated gene silenced cells versus scramble-transfected cells analyzed by ChIP-qPCR assays. **(C)** Relative 5hmc/5mc ratio was examined in the scramble- and TET si(s)-transfected cells. **(D)** ChIP-qPCR analysis of the enrichment of H4R3me2a on the *LGALS3* promoter in the scramble- or PRMT1 si-transfected cells. **(E)** ChIP-qPCR analysis of the enrichment of H3K4me3 on the *LGALS3* promoter in the scramble- or MLL4 si-transfected cells. Each error bar in panels **A-E** represents the mean ± SD of three independent experiments. Significant differences were determined by Student's $t$-test (**A, B**) and One-way ANOVA with Tukey's multiple comparison test (**C-E**). * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$.

Figure S7

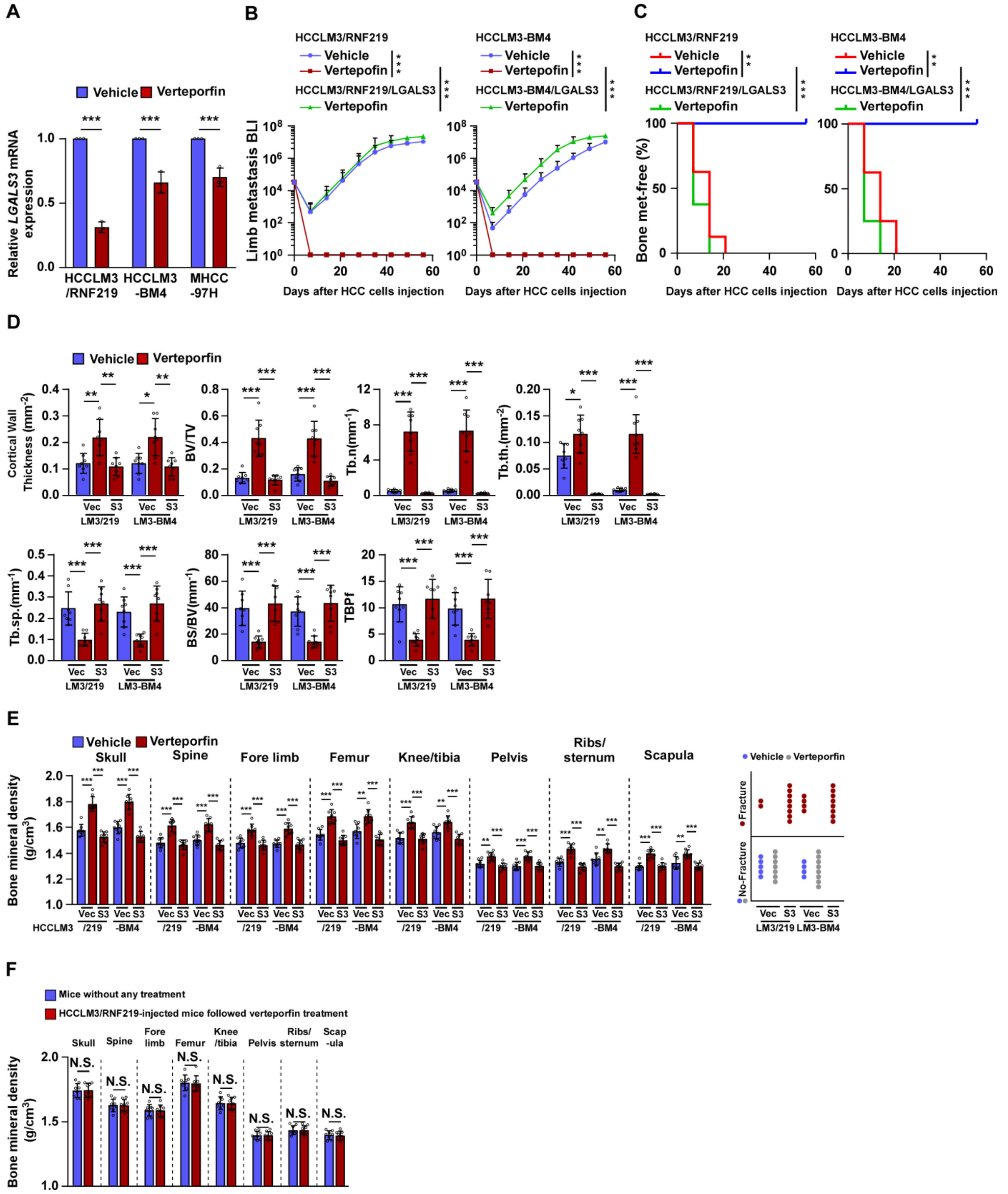

**Figure S7. Verteporfin treatment reduces LGALS3 expression and suppresses HCC bone-metastasis and SREs. (A)** Real-time PCR analysis of mRNA level of LGALS3 in the vehicle- or Verteporfin (10μM)-treated HCC cells. *GAPDH* serve as a loading control. **(B-C)** Normalized BLI signals of bone metastases (**B**) and Kaplan-Meier bone metastasis-free survival curve (**C**) of mice from experiments in Figure 8**A** (n = 8/group). **(D-F)** Quantification of bone parameters analyzed by μCT assay **(D)** and BMD **(E-F)** and fracture frequency of mice **(E)** in the representative mice from experiment in Figure 8**A**. Each error bar in panels **A-B and D-F** represents the mean ± SD of three independent experiments. Significant differences were determined by Student's *t*-test (**A and D-F**). * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$ and N.S.: not significant ($P > 0.05$).

**Figure S8**

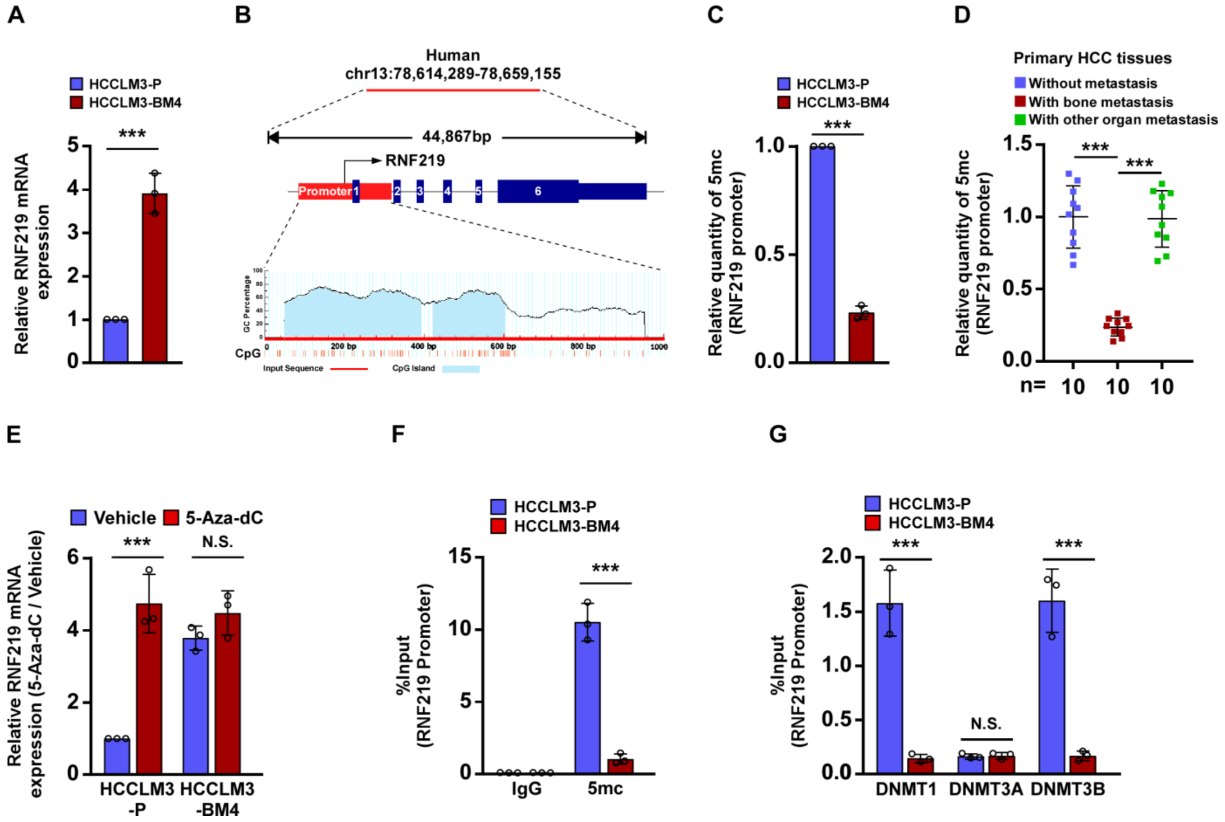

**Figure S8. Promoter hypomethylation-mediated RNF219 upregulation in bone metastatic HCC cells. (A)** Real-time PCR analysis of mRNA level of RNF219 in the HCCLM3-BM4 or HCCLM3-P cells. *GAPDH* serve as a loading control. **(B)** Schematic illustration of the predicted RNF219 promoter region contains high frequency of CpG sites. **(C-D)** Relative 5-methylcytosine (5mc) level was examined in RNF219 promoter in the indicated HCC cells (C) and indicated HCC tissues (n = 10/group). **(E)** Real-time PCR analysis of mRNA level of RNF219 in vehicle- or 5-Aza-dC treated HCC cells. *GAPDH* serve as a loading control. **(F, G)** ChIP-qPCR analysis of the enrichment of 5mc **(F)** and DNMTs, including DNMT1, DNMT3A and DNMT3B **(G)**, on the *RNF219* promoter in the indicated HCC cells. Each error bar in panels **A, and C-G** represents the mean ± SD of three independent experiments. Significant differences were determined by Student's *t*-test (**A, C**) and One-way ANOVA with Tukey's multiple comparison test (**D-G**). ** $P < 0.01$, *** $P < 0.001$ and N.S.: not significant ($P > 0.05$).

## Figure S9

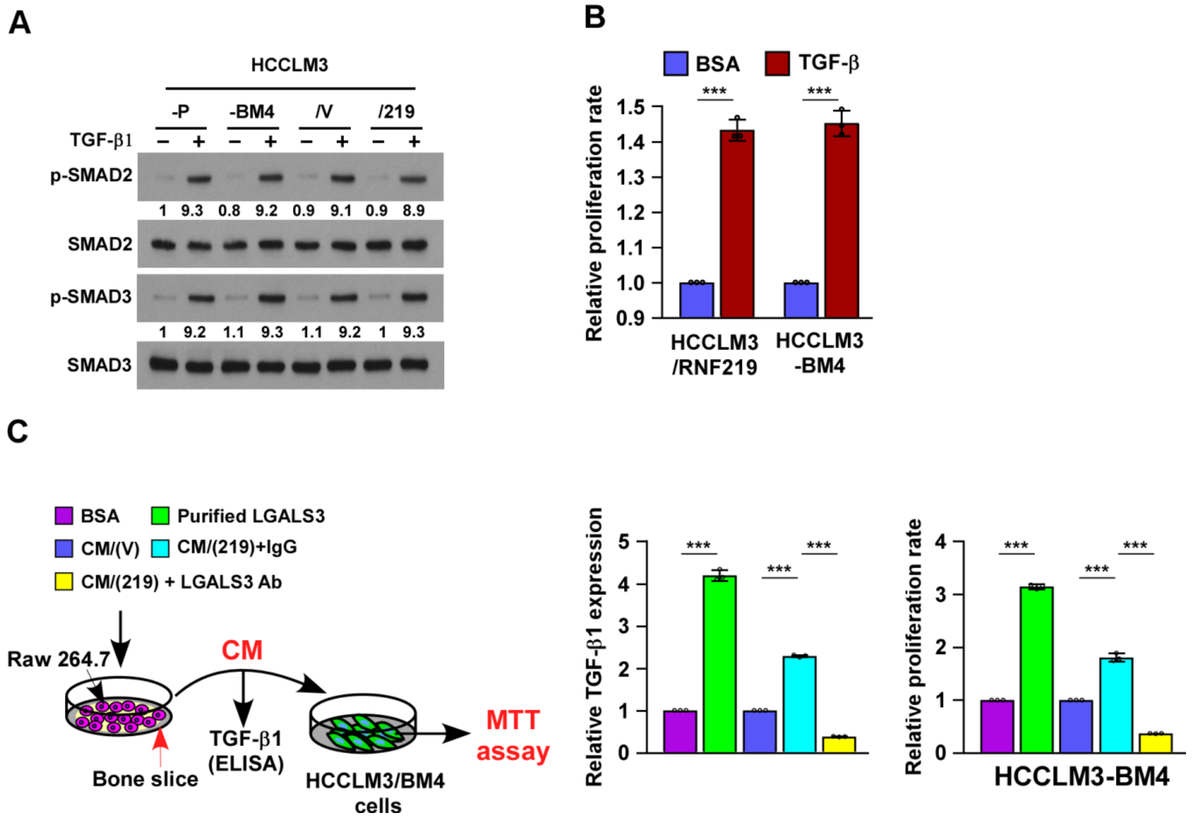

**Figure S9. TGF-β signaling contributes to HCC-BM by inducing osteolytic vicious cycle.** **(A)** IB analysis of the expression and phosphorylation level of SMAD2 and SMAD3 in the indicated cells treated with or without TGF-β (50 pM). **(B)** MTT assay analysis of proliferation rate of indicated cells treated with or without TGF-beta (50pM) in DMEM (1.0% FBS). **(C)** Left: Schematic illustration of LGALS3-induced “vicious cycle” between cancer cells and osteoclasts. Middle: ELISA analysis of TGF-β1 levels in CM from RAW 264.7 cells cultured onto the bone slice in the presence of indicated CM from HCC cells, or BSA, or purified LGALS3. Right： MTT assay analysis of proliferation rate of indicated cells from experiment in left panel. Each error bar in panels **B and C** represents the mean ± SD of independent experiments. Significant differences were determined by Student’s *t*-test (**B**) and One-way ANOVA with Tukey’s multiple comparison test (**C**). *** $P < 0.001$.

## Supplementary Materials and Methods

**Cell lines.** The HCCLM3, Huh7 and MHCC97H HCC cell lines, were obtained from the Sun Yat-sen University Cancer Center mouse osteoclast. Precursors Raw 264.7 cells and Human embryonic kidney cells (HEK) 293FT cells were purchased from American Type Culture Collection (ATCC, Manassas, VA). All the cell lines were grown in Dulbecco's modified Eagle's medium (DMEM) (Gibco, Grand Island, NY) supplemented with 10% fetal bovine serum (Gibco, Grand Island, NY). All the cell lines were tested for mycoplasma contamination and were authenticated by short tandem repeat (STR) fingerprinting at Medicine Lab of Forensic Medicine Department of Sun Yat-Sen University (China).

**Establishment of the HCC bone metastasis cell line.** To establish HCC bone metastasis cell line, the HCCLM3-parental cells that stably expressed firefly luciferase reporter were inoculated into the left cardiac ventricle of immunodeficient mice, and the formed bone metastatic tumors were monitored by bioluminescence signal. Then bone metastatic HCCLM3 cells (named as HCCLM3-BM1) were recovered from BLI-suspected bone sites, expanded in culture, and re-injected intracardially into mice for the next round. Total 4 round was performed.

To isolate cells from bone metastatic tumors, mice were euthanized, and bones from BLI-suspected sites were resected from the body at the joints with the surrounding soft tissue removed. Excised bone was minced into tissue volumes of 1 mm$^3$ and incubated in RBC lysis buffer followed by collagenase/hyaluronidase (Sigma-Aldrich, MO, USA) digesting solution on a rocking plate. Cells were collected via centrifugation and seeded onto a 12-well plate. Culturing medium was replaced after 24 h to eliminate non-adherent cells. Cells were maintained in 10 % FBS DMEM.

**Plasmids, retroviral infection and transfection.** The human RNF219, LGALS3, α-catenin and truncated-α-catenin fragments were cloned into pSin-EF2 vector. The RNF219-mu (C18S/C21S) was created using primers and a Stratagene mutagenesis kit according to the protocol recommended by the manufacturer (Stratagene, San Diego, CA, USA). ShRNAs targeting RNF219, α-catenin, LGALS3 and were cloned into the pSuper retro viral vector. The TCF/LEF1 reporter plasmids contain wild-type (CCTTTGATC; TOP flash) or mutated (CCTTTGGCC and FOP flash) binding site and TEAD reporter plasmid containing wild-type (ACATTCCA) TEAD binding sites). All primers and oligonucleotides used in plasmid construction are listed in Supplementary Table9. Transfection of short interfering RNAs (siRNAs) or plasmids was performed using the Lipofectamine 3000 reagent (Thermo Fisher Scientific, Waltham, MA, USA) according to the manufacturer's instructions. Stable cell lines expressing RNF219 or LGALS3 and RNF219 or LGALS3 shRNA(s) were generated via retroviral infection and selected for 10 days with 0.5 μg/mL puromycin 48 h after infection.

**RNA extraction, reverse transcription and real-time PCR.** Total RNA was extracted from the indicated cell using the Trizol (Life Technologies, Carlsbad, CA, USA) reagent according to the manufacturer's instruction. Real-time reverse transcription-polymerase chain reaction (PCR) primers and probes were designed with the assistance of the Primer Express v 2.0 software (Applied BioSystems, Foster City, CA, USA). Expression data were normalized to the geometric mean of housekeeping gene *GAPDH* to control the variability in expression levels and calculated as $2^{-[(C_{t}\text{ of gene}) - (C_{t}\text{ of }GAPDH)]}$, where $C_t$ represents the cycle threshold for each transcript. All primers are listed in Supplementary Table9.

**Chemical reagents.** Verteporfin (VP, S1786) was purchased from Selleck Chemicals (Houston, TX, USA). LGALS3 antagonist (GCS-100, also known as MCP) was purchased from La Jolla Pharmaceutical Company (San Diego, CA, USA). Human recombinant α-catenin protein (ab51443; Cambridge, MA, USA), recombinant human TGF beta 1 protein

(Active) (ab50036) and 5-Aza-2'-deoxycytidine (Decitabine) (ab120842) were purchased from Abcam. Sucrose, Lactose, Tecfidera and MG132, 3-MA (3-methyladenine), clasto-lactacystin β-lactone(cLL), leupeptin, and NH4Cl were purchased from Sigma Aldrich (St. Louis, MO, USA).

**Far-Western analysis.** Far-Immunoblotting were performed by using the proteins immunoprecipitated by anti-RNF219 antibody and human recombinant α-catenin protein. Briefly, the proteins were separated by SDS-PAGE, and were transferred onto a PVDF membrane. Membranes were then preincubated in 10% skimmed milk for 1 hour at 4°C. As indicated, recombinant α-catenin protein was added at 5μg/mL and incubated at 4°C for 18 hours. After extensive washing six times with TBST, the membrane was subjected to immunoblotting analysis using indicated antibodies.

**Co-immunoprecipitation (Co-IP) assay.** Cells grown in 100-mm culture dishes were lysed using 500 μL of lysis buffer [25 mmol/L HEPES (pH 7.4), 150 mmol/L NaCl, 1% NP-40, 1 mmol/L EDTA, 2% glycerol, and 1 mmol/L phenylmethylsulfonyl fluoride (PMSF)]. After being maintained on ice for 30 minutes, the lysates were clarified by microcentrifugation at 12,000 rpm for 10 minutes. To preclear the supernatants, the lysates were incubated with 20 mL of agarose beads (Calbiochem, San Diego, CA, USA) for 1 hour with rotation at 4°C. After centrifugation at 2,000 rpm for 1 minutes, the supernatants were incubated with 20 mL of antibody-cross-linked protein G-agarose beads overnight at 4°C. The agarose beads were then washed six times with wash buffer [25 mmol/L HEPES (pH 7.4), 150 mmol/L NaCl, 0.5% NP-40, 1 mmol/L EDTA, 2% glycerol, 1 mmol/L PMSF]. After removing all the liquid, the pelleted beads were resuspended in 30 mL of 1 M glycine (pH 3), after which, 10 μL 4 × sample buffer was added, the samples were denatured, and the sample components were electrophoretically separated on SDS-PAGE for immunoblot analysis.

**Luciferase assay.** The cells (1 × $10^3$) were seeded in triplicate in 48-well plates and allowed to settle for 24 h. One hundred nanograms of luciferase reporter plasmids or the control-luciferase plasmid, plus 5 ng of pRL-TK renilla plasmid (Promega, Madison, WI), were transfected into indicated cells using the Lipofectamine 3000 reagent (Invitrogen, Carlsbad, CA, USA) according to the manufacturer’s recommendation. Luciferase and renilla signals were measured at 48 h after transfection using the Dual Luciferase Reporter Assay Kit (Promega, Madison, WI) according to a protocol provided by the manufacturer.

**Chromatin Immunoprecipitation (ChIP) assay.** The entire procedure was performed with the chromatin immunoprecipitation (ChIPs) assay kit (Cell Signaling Technology, Danvers, MA, USA) according to the manufacturer's instructions. Briefly, indicated cells were grown to 70~80% confluence on 100-mm culture dish and were fixed with 1% formaldehyde to cross-link proteins to DNA. The cell lysates were sonicated to shear DNA into small uniform fragments. Equal aliquots of chromatin supernatants were then immunoprecipitated overnight at 4°C using anti-YAP1 (Cell Signaling Technology, Danvers, MA, USA (CST) #14074), anti-β-catenin (CST#8480), anti-DNMT1 (Abcam; ab13537), anti-CHTOP (CST#2895), anti-PRMT1 (ab3768), anti-TET1 (GeneTex Inc., Irvine, CA, USA; GTX124207), anti-MLL4 (Novus Biologicals, Centennial, CO, USA; NB600-254), anti-α-catenin (ab47105), anti-APC (CST# 2504), anti-LSD1 (ab17721), anti-H3K4me3 (ab12209), anti-H4R3me1(Diagenode, Valparaiso, Chile; C15410299), anti-H4R3me2a (Active Motif, Carlsbad, CA, USA; Cat.39705), anti-H3R2me1 (ab15584), anti-H3R2me2s (ab194684), anti-DNMT1 (#ab87656), anti-DNMT3A (#ab2850), anti-DNMT3B (#ab13604), anti-5mc (#15200081; Diagenode), anti-H3R8me2s (Epigentek, Farmingdale, NY, USA; A-3706-050), and anti-IgG antibodies (Millipore, Billerica, MA) with protein G magnetic beads. The cross-linked protein/DNA complexes were collected by magnetic pull down, and then were eluted from beads by elution buffer. After reverse cross-link of protein/DNA complexes to free DNA, PCR was performed using specific primers. All ChIP primers are listed as Supplementary Table9.

**Plasma Membrane Protein Extraction.** A plasma membrane protein extraction kit (ab65400; Abcam, Cambridge, MA, USA) was used to extract the plasma membrane protein according to the manufacturer's instructions.

**Mean optical density (MOD) analysis.** IHC staining for protein expression of RNF219 and LGALS3 in HCC samples with bone or other organ metastasis was quantitatively analyzed by using the AxioVision 4.6 computerized image analysis system assisted with an automatic measurement program (Carl Zeiss). The method of mean optical density (MOD) was used to determine the immunostaining intensity of each tested specimen. Briefly, the stained sections were evaluated at ×200 magnification, and 10 representative staining fields of each section were analyzed to verify the MOD, which represents the strength of staining signals as measured per positive pixels. The MOD data were statistically analyzed by using the t test to compare the average MOD difference between different groups of tissues, and $P < 0.05$ was considered significant.

**Immunoblotting analysis (IB).** IB was performed according to a standard protocol with the following antibodies: anti-integrin αv (AF1219) and anti-integrin β3 (AF2266) antibodies were purchased from BD company (Franklin lakes, NJ, USA); anti-c-SRC (ab16885), anti-p-SYK (ab58575), anti-SYK (ab40781), anti-p-VAV-3 (ab192590), anti-VAV-3 (ab203315), anti-RAC1(ab155938), anti-RNF219 (ab91464), anti-CD98 (ab2528), anti-H3 (ab1791), anti-p-YAP1(S127) (ab76252), anti-TCF4 (ab76151), anti-N-LGALS3(ab2785), anti-C-LGALS3(ab53082), anti-TEAD4 (ab58310), anti-$Na^+/K^+$-ATPase (ab58475), anti-APC (ab40778), anti-LSD1 (ab17721), anti-PRMT1(ab3768), anti-DNMT1(ab13537) and anti-CHTOP (ab222861) antibodies were purchased from Abcam (Cambridge, MA).

Anti-YAP1 (CST#14074), anti-β-catenin (CST#8480) and anti-β-actin (CST#3700), anti-p-SRC (CST#2101), anti-GAPDH (CST#97166), anti-α-tubulin (CST#2144) anti-Smad2 (CST#3122S) , anti-p-Smad2 (CST#18338), anti-Smad3 (CST#9523S) and anti-p-Smad3 (CST#9520S) antibodies were purchased from Cell Signaling technology (Danvers, MA). Anti-MLL4 (NB600-254) antibody was purchased from Novus Biologicals (Centennial, Colorado, USA). Anti-TET1 antibody (GTX124207) was purchased from GeneTex (San Diego, CA). Anti-α-catenin antibody (C2081), anti-β-catenin (pS33) (C2363), anti-Flag (F3165) and anti-HA (SAB1306169) antibodies purchased from Sigma-Aldrich (St. Louis, MO).

**Immunofluorescence (IF) staining.** The osteoclast precursors, Raw 264.7 cells were placed in 24-well clusters containing glass coverslips (Thermo Fisher Scientific) for 24 h and were treated with BSA or purified FLAG-tagged LGALS3 protein (100ng/ml) or conditioned media (CM) from HCC cells for 6 days. Cells were rinsed briefly with PBS and fixed in 4% (w/v) paraformaldehyde in PBS for 20 min at 37 °C. Aspirate fixation solution and wash cells 2-3 times in PBS. And followed by the antibody: anti-LGALS3 (ab2785, 1:200) antibody, anti-FLAG (Sigma MAB3118, 1:100) antibody, anti-CD98 (ab2528, 1:200) antibody, anti-αvβ3 (ab78289, 1: 500) antibody. The secondary antibody was goat anti-rabbit IgG (H + L) conjugated with Alexa Fluor 488 (Thermo Fisher Scientific), or added 1:1000 dilution of Phalloidin-iFluor 594 (ab176757) in 1% BSA at room temperature for 20-90 minutes. Rinse cells 2-3 times with PBS (5 min/wash). Then cells were mounted with Antifade Mountant with DAPI (Thermo Fisher Scientific). Observe the cells at Ex/Em 493/517 nm and the images were captured using the AxioVision Rel.4.6 computerized image analysis system (Carl Zeiss, Jena, Germany).

**Enzyme-linked immunosorbent assay (ELISA).** Serum samples were kept at room temperature for about 1.0 h to defrost completely before assays. The levels of mouse serum LGALS3 in supernatants were measured using a mouse LGALS3 enzyme-linked immunosorbent assay kits (ab203369, Abcam, Cambridge, MA.). The LGALS3 level in human serum and the culture medium from HCC cells were measured using a human LGALS3 enzyme-linked immunosorbent assay kits (ab188394, Abcam, Cambridge, MA.) and analyzed according to the manufacturer's instructions. The levels of TGF-β, RANKL and OPG in culture medium were measured using mouse TGF-β ELISA Kit (ab119557), human RANKL ELISA Kit (ab213841), mouse RANKL ELISA Kit (ab100749), human OPG ELISA Kit (ab100617) and mouse OPG ELISA Kit (ab203365), respectively. Data were read with the SpectraMax i3x Multi-Mode Microplate Reader (Molecular Devices) at 450 nm, the concentrations of LGALS3 in the samples were determined by extrapolating from the standard curve created by plotting the absorbance of the standards versus corresponding concentrations.

**Cell growth assay.** Cell growth was examined by 3-(4, 5-Dimethylthiazol-2-yl)-2, 5-diphenyltetrazolium bromide (MTT) assay. Briefly, cells were seeded at the density of 8000 cells/well into 96-well plate. At the time of assay, 0.5 mg/mL MTT in basic medium was added to each well and incubated for 4 h. After removing MTT, dimethyl sulfoxide (DMSO) was added and mixed vigorously. Absorbance was measured at 490 nm using the SpectraMax i3x Multi-Mode Microplate Reader (Molecular Devices).

**Osteoclastogenesis assay.** The RAW264.7 cells ($1 \times 10^5$) were cultured on 24-well clusters containing glass coverslips (Thermo Fisher Scientific) and grown in the conditioned media (CM) from indicated HCC cells treated with DMSO or Verteporfin (10 μM), or in medium containing purified LGALS3 protein (100 ng/ml) or BSA. Media were changed every other day. Osteoclasts were counted on day 6. The osteoclasts cultured on plastic dishes were fixed with 4% paraformaldehyde/PBS, and TRAP expression was examined by staining with a commercial kit (387A-1KT; Sigma-Aldrich). Osteoclasts were defined as TRAP-positive multinucleated cells containing more than 3 nuclei.

**Bone resorption pit assay.** To study the ability of osteoclasts to form resorption pits on bone slices (IDS PLC, catalog number: DT-1BON1000-96), RAW264.7 cells ($1 \times 10^5$) were seeded onto the bone slices. Then cells were cultured for 9 days in either conditioned media (CM) from HCC cells with indicated treatment or in medium containing 100 ng/ml LGALS3 protein or BSA. Media were changed every other day. After 9 days, bone slices were fixed with 2.5% glutaraldehyde, followed by the removal of cells by mechanical agitation and sonication. Resorption lacunae were visualized by scanning electron microscopy (SEM). Three fields were randomly selected for each bone slice for further analysis. Pit areas were quantified using ImageJ software.

**Xenografted tumor models.** All of the animal procedures were approved by the Sun Yat-sen University Animal Care Committee. Intracardiac injections of luciferase-expressing HCC cells ($1\times10^5$) were conducted in nu/nu nude mice (5 weeks old) for bone metastasis assays. Before cancer cell injection, mice were educated for 2 weeks by intraperitoneal injection of 300 μl of CM from indicated cells. Anti-LGALS3 antibody (abcam) or anti-rabbit IgG was administered intraperitoneally twice a week at 1 mg/kg, 2 days after implantation. Verteporfin (20 mg/kg) was injected intraperitoneally twice a week. The formation of bone metastases was observed and assessed weekly in mice injected with D-luciferin (75 mg/kg) by bioluminescence imaging using the IVIS Spectrum *In Vivo* Imager. At week 5, the osteolytic lesions in mice were observed using SIEMENS micro-CT system (Inveon). The bone of mice were harvested and prepared for further analyses.

**Micro-CT (μCT) analysis.** The hind limbs were removed from euthanized mice and fixed in either 4% paraformaldehyde solution or periodate-lysine-paraformaldehyde fixative. Fixed hind limbs were dissected free of tissue and scanned on a micro-CT scanner (SIEMENS, Munich, Germany). A standard trabecular volume of interest was chosen starting 0.1 mm from the growth plate and included all trabeculae in a 1 $mm^3$ region of bone. Trabecular volume and number were assessed in this region. Osteolytic lesions were measured through $360^o$ view of the bone on a three-dimensional model in a 3 mm length of cortical bone, starting at the growth plate.

***In vivo* quantification of osteoclast number.** Hind limbs were fixed in paraformaldehyde solution (4%), decalcified in 14.3% EDTA for 4 days at 37 $^oC$ with daily changes of EDTA, then embedded in paraffin wax. Sections were used by H&E stained with Mayer’s hematoxylin solution, or IHC stained using antibodies of RNF219 (ab224493), or stained with TRAP (a TRAP kit, 387A-1KT; Sigma-Aldrich) according to manufacturer’s protocols. The numbers of $TRAP^+$-osteoclasts were determined on a 3 mm length of endocortical surface and viewed on an optical microscope (Olympus, DP72, Tokyo, Japan).

**Alkaline phosphatase (ALP) staining.** Fourteen days after osteogenic induction, a TRAP/ALP Stain Kit (Wako, Richmond, VA, USA; 294-67001) was used to perform alkaline phosphatase (ALP) staining. The cells cultured in 24-well plates were rinsed three times by PBS and fixated for 30 min using pre-cold fixative. Next, ALP substrate solution was added and cells were cultivated (room temperature, 15-45min) in a darkroom. After that, cells with ddH2O were rinsed and filmed under an optical microscope. The absorbance at 405 nm of each well was measured with a microplate reader according to the manufacturer’s instruction.

**Preparation of nuclear and cytosol extracts.** Nuclear and cytosol fractions were isolated by using NE-PER™ Nuclear and Cytoplasmic Extraction Reagents (Thermo Fisher Scientific, Waltham, MA) according to the manufacturer’s instructions. The indicated Cells were treated with 0.25% trypsin-EDTA and subsequently harvested at centrifuge at 500 × g for 5 minutes. The cell pellet was washed 2-3 times with PBS (pH7.4) and then transferred to a 1.5mL microcentrifuge tube and centrifuged at 500 × g for 2-3 minutes. The cell pellet was resuspended in 200μl ice-cold CER I and vortexed the tube vigorously and incubated on ice for 10 min. The cells were added 11 μL ice-cold CER II to the tube, vortexed for 5 seconds and centrifuged for 5 minutes at 16,000 × g. The supernatant (cytoplasmic extract) was immediately transfer to a clean pre-chilled tube. The pelleted nuclei were resuspended in 100μl ice-cold NER, which contains nuclei and vortexed for seconds every 10 minutes, for a total of 40 minutes. The supernatant (nuclear extract) fraction was then centrifuged at ~16,000 × g for 10 minutes and then immediately transferred the to a clean pre-chilled tube. Store extracts at -80°C until use.

**Purification of LGALS3 Protein.** The plasmid encoding FLAG-tagged LGALS3 was transiently transfected into HCCLM3 cells ($1 \times 10^8$) and cultured for 2 days. The cell cultured media were harvested and centrifuged at 2,000 x g for 5 min at 4 °C, and the supernatant was transfer into an Amicon centrifuge filter unit and spined at 4,000 × *g* for 30-40 min. The concentrated conditioned media was incubated with FLAG-M2 beads for more than 2.0 h while rotating at 4 °C. The beads were washed with cold wash buffer for 4 times by spinning at 100 × *g* for 1 min. After the last wash, syringe needles were used to remove as much buffer as possible with minimal disruption of the beads. Then the beads were incubated with elution buffer for 1 h at room temperature and collected the purified FLAG-tagged LGALS3 after centrifugation for quantification.

## Supplemental Tables

**Table S1.** Incidence of metastasis (Number of metastasis mice/ total mice)

|  | **HCCLM3-Parental (n=8)** |  | **HCCLM3/RNF219 (n=8)** |  | **Huh7 (n=8)** |  | **Huh7/RNF219 (n=8)** |  |
|---|---|---|---|---|---|---|---|---|
| **Days** | **Bone Metastasis** | **Other Metastasis** | **Bone Metastasis** | **Other Metastasis** | **Bone Metastasis** | **Other Metastasis** | **Bone Metastasis** | **Other Metastasis** |
| **7** | 0/8 | 0/8 | 4/8 | 0/8 | 0/8 | 0/8 | 1/8 | 0/8 |
| **14** | 0/8 | 0/8 | 6/8 | 0/8 | 0/8 | 0/8 | 8/8 | 0/8 |
| **21** | 0/8 | 0/8 | 8/8 | 0/8 | 0/8 | 0/8 | 8/8 | 0/8 |
| **28** | 0/8 | 0/8 | 8/8 | 0/8 | 0/8 | 0/8 | 8/8 | 0/8 |
| **35** | 2/8 | 3/8 | 8/8 | 2/8 | 1/8 | 2/8 | 8/8 | 3/8 |
| **42** | 5/8 | 4/8 | 8/8 | 2/8 | 4/8 | 3/8 | 8/8 | 3/8 |
| **49** | 5/8 | 5/8 | 8/8 | 4/8 | 5/8 | 4/8 | 8/8 | 4/8 |
| **56** | 8/8 | 5/8 | 8/8 | 5/8 | 5/8 | 5/8 | 8/8 | 4/8 |

|  | **HCCLM3-BM4 (n=8)** |  | **HCCLM3-BM4-RNF219 sh#1(n=8)** |  | **HCCLM3-BM4-RNF219 sh#2(n=8)** |  |
|---|---|---|---|---|---|---|
| **Days** | **Bone Metastasis** | **Other Metastasis** | **Bone Metastasis** | **Other Metastasis** | **Bone Metastasis** | **Other Metastasis** |
| **7** | 2/8 | 0/8 | 0/8 | 0/8 | 0/8 | 0/8 |
| **14** | 5/8 | 0/8 | 0/8 | 0/8 | 0/8 | 0/8 |
| **21** | 8/8 | 0/8 | 0/8 | 0/8 | 0/8 | 0/8 |
| **28** | 8/8 | 0/8 | 0/8 | 0/8 | 0/8 | 0/8 |
| **35** | 8/8 | 0/8 | 0/8 | 0/8 | 0/8 | 0/8 |
| **42** | 8/8 | 0/8 | 2/8 | 0/8 | 3/8 | 0/8 |
| **49** | 8/8 | 0/8 | 4/8 | 0/8 | 3/8 | 1/8 |
| **56** | 8/8 | 0/8 | 4/8 | 1/8 | 3/8 | 1/8 |

|  | **MHCC97H (n=8)** |  | **MHCC97H-RNF219 sh#1(n=8)** |  | **MHCC97H-RNF219 sh#2(n=8)** |  |
|---|---|---|---|---|---|---|
| **Days** | **Bone Metastasis** | **Other Metastasis** | **Bone Metastasis** | **Other Metastasis** | **Bone Metastasis** | **Other Metastasis** |
| **7** | 3/8 | 2/8 | 0/8 | 2/8 | 0/8 | 1/8 |
| **14** | 4/8 | 4/8 | 0/8 | 3/8 | 0/8 | 4/8 |
| **21** | 8/8 | 5/8 | 0/8 | 5/8 | 0/8 | 6/8 |
| **28** | 8/8 | 8/8 | 0/8 | 8/8 | 0/8 | 8/8 |
| **35** | 8/8 | 8/8 | 0/8 | 8/8 | 0/8 | 8/8 |
| **42** | 8/8 | 8/8 | 2/8 | 8/8 | 1/8 | 8/8 |
| **49** | 8/8 | 8/8 | 2/8 | 8/8 | 1/8 | 8/8 |
| **56** | 8/8 | 8/8 | 2/8 | 8/8 | 1/8 | 8/8 |

**Table S2:** 94 proteins in Protein profiling of HCCLM3-BM4 vs. HCCLM3-parental cells

| **Accessions** | **Protein** | **Log2 Foldchange** | **P value** | **HCCLM3-P (113)** | **HCCLM3-P (114)** | **HCCLM3-BM4(115)** | **HCCLM3-BM4(116)** | **Gene Name** |
|---|---|---|---|---|---|---|---|---|
| Q5W0B1 | RN219 | 1.951231 | 8.57E-03 | 0.50519 | 0.46449 | 1.600121 | 1.4302052 | RING finger protein 219 OS=Homo sapiens GN=RNF219 PE=1 SV=1 |
| P00414 | COX3 | 1.789059 | 1.81E-04 | 0.49506 | 0.47138 | 1.6044651 | 1.4291039 | Cytochrome c oxidase subunit 3 OS=Homo sapiens GN=MT-CO3 PE=1 SV=2 |
| Q6N075 | MFSD5 | 1.483457 | 1.66E-03 | 0.55921 | 0.53796 | 1.5527312 | 1.3500966 | Molybdate-anion transporter OS=Homo sapiens GN=MFSD5 PE=1 SV=2 |
| Q9BTM1 | H2AJ | 1.463885 | 2.22E-04 | 0.55794 | 0.53829 | 1.5486696 | 1.3551051 | Histone H2A.J OS=Homo sapiens GN=H2AFJ PE=1 SV=1 |
| Q71UI9 | H2AV | 1.355801 | 1.13E-04 | 0.56856 | 0.54856 | 1.5390663 | 1.3438106 | Histone H2A.V OS=Homo sapiens GN=H2AFV PE=1 SV=3 |
| Q16864 | VATF | 1.284311 | 3.79E-04 | 0.60397 | 0.55814 | 1.4910116 | 1.3468835 | V-type proton ATPase subunit F OS=Homo sapiens GN=ATP6V1F PE=1 SV=2 |
| P17931 | LEG3 | 1.177207 | 1.40E-04 | 0.60421 | 0.5895 | 1.4669441 | 1.3393405 | Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=2 |
| P62807 | H2B1C | 1.164009 | 1.33E-02 | 0.62457 | 0.61643 | 1.3647417 | 1.3942573 | Histone H2B type 1-C/E/F/G/I OS=Homo sapiens GN=HIST1H2BC PE=1 SV=4 |
| O60906 | NSMA | 1.157004 | 1.51E-03 | 0.62161 | 0.58592 | 1.482915 | 1.3095514 | Sphingomyelin phosphodiesterase 2 OS=Homo sapiens GN=SMPD2 PE=1 SV=2 |
| O43653 | PSCA | 1.147658 | 5.52E-03 | 0.58476 | 0.62552 | 1.4790844 | 1.3106351 | Prostate stem cell antigen OS=Homo sapiens GN=PSCA PE=1 SV=1 |
| Q9NP84 | TNR12 | 1.12927 | 3.06E-03 | 0.60834 | 0.6056 | 1.4858819 | 1.3001721 | Tumor necrosis factor receptor superfamily member 12A OS=Homo sapiens GN=TNFRSF12A PE=1 SV=1 |
| Q96F44 | TRI11 | 1.084555 | 9.73E-04 | 0.63958 | 0.59205 | 1.46195 | 1.3064172 | E3 ubiquitin-protein ligase TRIM11 OS=Homo sapiens GN=TRIM11 PE=1 SV=2 |
| P47914 | RL29 | 1.060647 | 1.10E-03 | 0.65406 | 0.62272 | 1.3880932 | 1.3351278 | 60S ribosomal protein L29 OS=Homo sapiens GN=RPL29 PE=1 SV=2 |
| Q86T03 | TM55B | 0.993397 | 1.73E-03 | 0.64416 | 0.66219 | 1.4160597 | 1.2775839 | Type 1 phosphatidylinositol 4,5-bisphosphate 4-phosphatase OS=Homo sapiens GN=TMEM55B PE=1 SV=1 |
| P29966 | MARCS | 0.98084 | 1.18E-03 | 0.67987 | 0.6513 | 1.3542738 | 1.3145497 | Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCKS PE=1 SV=4 |
| P62750 | RL23A | 0.943285 | 4.33E-03 | 0.72512 | 0.63504 | 1.329166 | 1.310678 | 60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1 |
| Q9Y5Y0 | FLVC1 | 0.927284 | 1.16E-03 | 0.71309 | 0.65784 | 1.3769905 | 1.2520803 | Feline leukemia virus subgroup C receptor-related protein 1 OS=Homo sapiens GN=FLVCR1 PE=1 SV=1 |
| P35790 | CHKA | 0.922426 | 2.47E-03 | 0.69958 | 0.68242 | 1.3891898 | 1.2288054 | Choline kinase alpha OS=Homo sapiens GN=CHKA PE=1 SV=3 |
| Q6DN03 | H2B2C | 0.905013 | 6.62E-03 | 0.70942 | 0.68849 | 1.2835703 | 1.3185155 | Putative histone H2B type 2-C OS=Homo sapiens GN=HIST2H2BC PE=5 SV=3 |
| Q6PI78 | TMM65 | 0.836854 | 4.90E-04 | 0.72412 | 0.70994 | 1.3377645 | 1.2281771 | Transmembrane protein 65 OS=Homo sapiens GN=TMEM65 PE=1 SV=2 |
| Q99717 | SMAD5 | 0.825497 | 5.61E-04 | 0.72643 | 0.71086 | 1.3239545 | 1.2387532 | Mothers against decapentaplegic homolog 5 OS=Homo sapiens GN=SMAD5 PE=1 SV=1 |
| Q12894 | IFRD2 | 0.824141 | 7.52E-03 | 0.75006 | 0.67579 | 1.3607981 | 1.2133486 | Interferon-related developmental regulator 2 OS=Homo sapiens GN=IFRD2 PE=1 SV=3 |
| P62899 | RL31 | 0.817736 | 5.52E-03 | 0.72054 | 0.72099 | 1.2742541 | 1.2842144 | 60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=1 SV=1 |
| O14521 | DHSD | 0.813883 | 8.36E-04 | 0.72926 | 0.71038 | 1.3423761 | 1.2179861 | Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial OS=Homo sapiens GN=SDHD PE=1 SV=1 |
| Q92820 | GGH | 0.80005 | 6.02E-03 | 0.7455 | 0.69298 | 1.3557817 | 1.2057386 | Gamma-glutamyl hydrolase OS=Homo sapiens GN=GGH PE=1 SV=2 |
| P16989 | YBOX3 | 0.784363 | 6.42E-03 | 0.72183 | 0.74512 | 1.2914142 | 1.2416394 | Y-box-binding protein 3 OS=Homo sapiens GN=YBX3 PE=1 SV=4 |
| P62805 | H4 | 0.782766 | 2.73E-04 | 0.73585 | 0.7178 | 1.3180284 | 1.2283179 | Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2 |
| Q9NSU2 | TREX1 | 0.782036 | 3.20E-03 | 0.72735 | 0.72992 | 1.3254927 | 1.2172329 | Three-prime repair exonuclease 1 OS=Homo sapiens GN=TREX1 PE=1 SV=1 |
| Q92804 | RBP56 | 0.779653 | 8.80E-03 | 0.78367 | 0.68403 | 1.3009145 | 1.2313901 | TATA-binding protein-associated factor 2N OS=Homo sapiens GN=TAF15 PE=1 SV=1 |
| Q9NV92 | NFIP2 | 0.776018 | 1.91E-03 | 0.73795 | 0.72507 | 1.2825591 | 1.2544205 | NEDD4 family-interacting protein 2 OS=Homo sapiens GN=NDFIP2 PE=1 SV=2 |
| P68402 | PA1B2 | 0.764968 | 1.56E-02 | 0.70933 | 0.77109 | 1.284836 | 1.2347442 | Platelet-activating factor acetylhydrolase IB subunit beta OS=Homo sapiens GN=PAFAH1B2 PE=1 SV=1 |
| P67809 | YBOX1 | 0.764158 | 6.34E-04 | 0.74026 | 0.72666 | 1.2923635 | 1.2407146 | Nuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=YBX1 PE=1 SV=3 |
| Q9H300 | PARL | 0.759599 | 2.69E-03 | 0.73437 | 0.73757 | 1.3016435 | 1.2264162 | Presenilins-associated rhomboid-like protein, mitochondrial OS=Homo sapiens GN=PARL PE=1 SV=2 |
| Q9Y3U8 | RL36 | 0.751962 | 1.24E-03 | 0.75662 | 0.71476 | 1.3139966 | 1.2146271 | 60S ribosomal protein L36 OS=Homo sapiens GN=RPL36 PE=1 SV=3 |
| Q8NBQ5 | DHB11 | 0.748791 | 4.07E-03 | 0.75473 | 0.7247 | 1.250308 | 1.270257 | Estradiol 17-beta-dehydrogenase 11 OS=Homo sapiens GN=HSD17B11 PE=1 SV=3 |
| O95159 | ZFPL1 | 0.748366 | 1.25E-02 | 0.77927 | 0.69716 | 1.3520792 | 1.1714848 | Zinc finger protein-like 1 OS=Homo sapiens GN=ZFPL1 PE=1 SV=2 |
| Q5T440 | CAF17 | 0.727921 | 6.02E-04 | 0.75251 | 0.73094 | 1.3028128 | 1.2137441 | Putative transferase CAF17, mitochondrial OS=Homo sapiens GN=IBA57 PE=1 SV=1 |
| P0CW18 | PRS56 | 0.723205 | 1.50E-03 | 0.76866 | 0.72236 | 1.3035537 | 1.2054232 | Serine protease 56 OS=Homo sapiens GN=PRSS56 PE=1 SV=1 |
| P62273 | RS29 | 0.664116 | 5.50E-03 | 0.78236 | 0.76451 | 1.2181274 | 1.2350082 | 40S ribosomal protein S29 OS=Homo sapiens GN=RPS29 PE=1 SV=2 |
| Q15185 | TEBP | 0.643312 | 1.20E-03 | 0.78796 | 0.76546 | 1.2306475 | 1.2159305 | Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 |
| Q9UG56 | PISD | 0.637388 | 4.51E-03 | 0.79698 | 0.7519 | 1.2880317 | 1.1630859 | Phosphatidylserine decarboxylase proenzyme, mitochondrial OS=Homo sapiens GN=PISD PE=2 SV=4 |
| P62854 | RS26 | 0.631754 | 5.55E-03 | 0.81384 | 0.73468 | 1.2750016 | 1.176474 | 40S ribosomal protein S26 OS=Homo sapiens GN=RPS26 PE=1 SV=3 |
| Q8NC51 | PAIRB | 0.62665 | 6.90E-03 | 0.82459 | 0.73356 | 1.2333271 | 1.2085276 | Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2 |
| Q9UIS9 | MBD1 | 0.622151 | 4.46E-02 | 0.77778 | 0.81151 | 1.1180738 | 1.2926444 | Methyl-CpG-binding domain protein 1 OS=Homo sapiens GN=MBD1 PE=1 SV=2 |
| Q5BJH7 | YIF1B | 0.621127 | 5.77E-03 | 0.77804 | 0.79911 | 1.2099057 | 1.2129388 | Protein YIF1B OS=Homo sapiens GN=YIF1B PE=1 SV=1 |
| P23528 | COF1 | 0.61724 | 2.27E-03 | 0.8125 | 0.7555 | 1.2227411 | 1.2092553 | Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 |

| Names | Sequence | Area 113 | Area 114 | Area 115 | Area 116 |
|---|---|---|---|---|---|
| RING finger protein 219 | ESSVVQAGGSK | 12.82 | 9.96 | 98.69 | 123.32 |
| RING finger protein 219 | PLTLVQGNQNEDKHLVTDNPSK | 667.11 | 261.48 | 2492.45 | 2908.78 |

(Continued on next page)

**Continued**

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| P62829 | RL23 | 0.615076 | 1.51E-04 | 0.80209 | 0.76467 | 1.2454541 | 1.1877863 | 60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1 |
| O76095 | JTB | 0.607557 | 8.77E-03 | 0.77293 | 0.81015 | 1.2579218 | 1.1590016 | Protein JTB OS=Homo sapiens GN=JTB PE=1 SV=1 |
| Q96S97 | MYADM | 0.604585 | 6.55E-03 | 0.79603 | 0.77559 | 1.2788987 | 1.1494788 | Myeloid-associated differentiation marker OS=Homo sapiens GN=MYADM PE=1 SV=2 |
| P35637 | FUS | 0.604297 | 1.21E-02 | 0.83422 | 0.73445 | 1.2674598 | 1.1638658 | RNA-binding protein FUS OS=Homo sapiens GN=FUS PE=1 SV=1 |
| P62633 | CNBP | 0.601353 | 2.37E-02 | 0.78032 | 0.79754 | 1.3131105 | 1.1090318 | Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP PE=1 SV=1 |
| P61927 | RL37 | 0.593791 | 2.89E-04 | 0.80694 | 0.77982 | 1.2180567 | 1.1951763 | 60S ribosomal protein L37 OS=Homo sapiens GN=RPL37 PE=1 SV=2 |
| O75391 | SPAG7 | 0.59018 | 1.23E-02 | 0.79797 | 0.81227 | 1.1685565 | 1.2212053 | Sperm-associated antigen 7 OS=Homo sapiens GN=SPAG7 PE=1 SV=2 |
| Q6PML9 | ZNT9 | -0.59411 | 3.96E-03 | 1.18869 | 1.20312 | 0.8116055 | 0.7965892 | Zinc transporter 9 OS=Homo sapiens GN=SLC30A9 PE=1 SV=1 |
| Q15119 | PDK2 | -0.60113 | 1.85E-02 | 1.16385 | 1.22986 | 0.7920959 | 0.8141893 | [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial OS=Homo sapiens GN=PDK2 PE=1 SV=2 |
| Q9H1E5 | TMX4 | -0.60144 | 2.35E-02 | 1.17035 | 1.21719 | 0.7884671 | 0.8239853 | Thioredoxin-related transmembrane protein 4 OS=Homo sapiens GN=TMX4 PE=1 SV=1 |
| Q9Y3B6 | EMC9 | -0.60364 | 1.79E-02 | 1.16903 | 1.22565 | 0.7906697 | 0.8146489 | ER membrane protein complex subunit 9 OS=Homo sapiens GN=EMC9 PE=1 SV=3 |
| O00180 | KCNK1 | -0.6186 | 3.48E-02 | 1.32527 | 1.10312 | 0.813472 | 0.7581363 | Potassium channel subfamily K member 1 OS=Homo sapiens GN=KCNK1 PE=1 SV=1 |
| Q8NFX7 | STXB6 | -0.62489 | 1.48E-02 | 1.25332 | 1.16377 | 0.778261 | 0.8046533 | Syntaxin-binding protein 6 OS=Homo sapiens GN=STXBP6 PE=1 SV=2 |
| Q9H773 | DCTP1 | -0.62569 | 2.53E-02 | 1.18736 | 1.22879 | 0.8492898 | 0.7345599 | dCTP pyrophosphatase 1 OS=Homo sapiens GN=DCTPP1 PE=1 SV=1 |
| P40692 | MLH1 | -0.62581 | 5.20E-03 | 1.22372 | 1.18977 | 0.7897879 | 0.7967307 | DNA mismatch repair protein Mlh1 OS=Homo sapiens GN=MLH1 PE=1 SV=1 |
| O75351 | VPS4B | -0.62647 | 2.53E-03 | 1.2063 | 1.20645 | 0.7992039 | 0.7880401 | Vacuolar protein sorting-associated protein 4B OS=Homo sapiens GN=VPS4B PE=1 SV=2 |
| Q9UN37 | VPS4A | -0.64506 | 5.06E-03 | 1.19433 | 1.22821 | 0.7986288 | 0.7788326 | Vacuolar protein sorting-associated protein 4A OS=Homo sapiens GN=VPS4A PE=1 SV=1 |
| Q9UPT5 | EXOC7 | -0.6826 | 1.12E-02 | 1.21204 | 1.23061 | 0.7659152 | 0.7914357 | Exocyst complex component 7 OS=Homo sapiens GN=EXOC7 PE=1 SV=3 |
| Q5W0Z9 | ZDH20 | -0.68732 | 8.41E-03 | 1.30736 | 1.15885 | 0.7813449 | 0.7524514 | Probable palmitoyltransferase ZDHHC20 OS=Homo sapiens GN=ZDHHC20 PE=1 SV=1 |
| P52895 | AK1C2 | -0.69148 | 1.35E-03 | 1.23702 | 1.21299 | 0.7872556 | 0.7627341 | Aldo-keto reductase family 1 member C2 OS=Homo sapiens GN=AKR1C2 PE=1 SV=3 |
| Q9BV23 | ABHD6 | -0.69211 | 5.82E-03 | 1.20735 | 1.24445 | 0.7910231 | 0.7571746 | Monoacylglycerol lipase ABHD6 OS=Homo sapiens GN=ABHD6 PE=1 SV=1 |
| O95167 | NDUA3 | -0.72079 | 7.50E-05 | 1.27161 | 1.20105 | 0.7849357 | 0.7423961 | NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3 OS=Homo sapiens GN=NDUFA3 PE=1 SV=1 |
| O43242 | PSMD3 | -0.73087 | 4.58E-03 | 1.22253 | 1.25248 | 0.7828453 | 0.7421517 | 26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens GN=PSMD3 PE=1 SV=2 |
| Q15006 | EMC2 | -0.75579 | 1.21E-02 | 1.22498 | 1.28478 | 0.7967742 | 0.6934717 | ER membrane protein complex subunit 2 OS=Homo sapiens GN=EMC2 PE=1 SV=1 |
| P32929 | CGL | -0.76746 | 4.45E-03 | 1.28597 | 1.23474 | 0.7911612 | 0.6881283 | Cystathionine gamma-lyase OS=Homo sapiens GN=CTH PE=1 SV=3 |
| O43760 | SNG2 | -0.77741 | 7.58E-03 | 1.27294 | 1.25709 | 0.7946226 | 0.675352 | Synaptogyrin-2 OS=Homo sapiens GN=SYNGR2 PE=1 SV=1 |
| Q9UK23 | NAGPA | -0.79099 | 1.04E-02 | 1.21552 | 1.3196 | 0.768717 | 0.6961603 | N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase OS=Homo sapiens GN=NAGPA PE=1 SV=2 |
| Q00059 | TFAM | -0.79882 | 5.12E-03 | 1.31125 | 1.21618 | 0.7273952 | 0.7451779 | Transcription factor A, mitochondrial OS=Homo sapiens GN=TFAM PE=1 SV=1 |
| P15121 | ALDR | -0.80789 | 9.57E-04 | 1.28994 | 1.24311 | 0.7442526 | 0.7227039 | Aldose reductase OS=Homo sapiens GN=AKR1B1 PE=1 SV=3 |
| Q15527 | SURF2 | -0.82321 | 1.52E-02 | 1.33944 | 1.20666 | 0.7943177 | 0.6595798 | Surfeit locus protein 2 OS=Homo sapiens GN=SURF2 PE=1 SV=3 |
| Q7KZI7 | MARK2 | -0.82757 | 2.06E-02 | 1.25941 | 1.25983 | 0.71611 | 0.7646443 | Serine/threonine-protein kinase MARK2 OS=Homo sapiens GN=MARK2 PE=1 SV=2 |
| Q9BVT8 | TMUB1 | -0.86246 | 1.15E-02 | 1.24554 | 1.30843 | 0.7180145 | 0.7280086 | Transmembrane and ubiquitin-like domain-containing protein 1 OS=Homo sapiens GN=TMUB1 PE=1 SV=1 |
| Q9NWT6 | HIF1N | -0.87545 | 3.52E-04 | 1.33265 | 1.24946 | 0.7381229 | 0.6797711 | Hypoxia-inducible factor 1-alpha inhibitor OS=Homo sapiens GN=HIF1AN PE=1 SV=2 |
| P04004 | VTNC | -0.87942 | 2.92E-02 | 1.4577 | 1.14497 | 0.7244956 | 0.6728264 | Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1 |
| Q6UW56 | ARAID | -0.88804 | 5.40E-03 | 1.26653 | 1.32894 | 0.7442468 | 0.6602777 | All-trans retinoic acid-induced differentiation factor OS=Homo sapiens GN=ATRAID PE=1 SV=2 |
| Q9UK97 | FBX9 | -0.94648 | 5.07E-03 | 1.29673 | 1.31869 | 0.7128471 | 0.6717293 | F-box only protein 9 OS=Homo sapiens GN=FBXO9 PE=1 SV=1 |
| P37268 | FDFT | -1.0228 | 3.74E-03 | 1.33251 | 1.3372 | 0.6703285 | 0.6599552 | Squalene synthase OS=Homo sapiens GN=FDFT1 PE=1 SV=1 |
| Q9NVR2 | INT10 | -1.03843 | 4.94E-03 | 1.29509 | 1.34798 | 0.7150775 | 0.6418567 | Integrator complex subunit 10 OS=Homo sapiens GN=INTS10 PE=1 SV=2 |
| Q96PY5 | FMNL2 | -1.04387 | 1.57E-03 | 1.34168 | 1.30429 | 0.7161243 | 0.637905 | Formin-like protein 2 OS=Homo sapiens GN=FMNL2 PE=1 SV=3 |
| P51151 | RAB9A | -1.07663 | 6.01E-03 | 1.31473 | 1.38485 | 0.6560985 | 0.644318 | Ras-related protein Rab-9A OS=Homo sapiens GN=RAB9A PE=1 SV=1 |
| O75608 | LYPA1 | -1.11467 | 2.45E-03 | 1.34498 | 1.37264 | 0.6391517 | 0.6432274 | Acyl-protein thioesterase 1 OS=Homo sapiens GN=LYPLA1 PE=1 SV=1 |
| Q9Y2W2 | WBP11 | -1.12351 | 9.51E-05 | 1.38753 | 1.32482 | 0.6505823 | 0.637067 | WW domain-binding protein 11 OS=Homo sapiens GN=WBP11 PE=1 SV=1 |
| P40616 | ARL1 | -1.15289 | 1.02E-02 | 1.34635 | 1.3833 | 0.6116957 | 0.6586542 | ADP-ribosylation factor-like protein 1 OS=Homo sapiens GN=ARL1 PE=1 SV=1 |
| P27448 | MARK3 | -1.28438 | 2.89E-03 | 1.41379 | 1.39689 | 0.5810361 | 0.6082859 | MAP/microtubule affinity-regulating kinase 3 OS=Homo sapiens GN=MARK3 PE=1 SV=4 |
| Q8NCQ2 | CNAS1 | -1.45656 | 3.36E-03 | 1.61696 | 1.34192 | 0.5266036 | 0.5145202 | Uncharacterized protein CSNK1G2-AS1 OS=Homo sapiens GN=CSNK1G2-AS1 PE=2 SV=2 |
| Q14145 | KEAP1 | -1.48529 | 4.44E-03 | 1.56636 | 1.40857 | 0.4695892 | 0.5554795 | Kelch-like ECH-associated protein 1 OS=Homo sapiens GN=KEAP1 PE=1 SV=2 |
| Q99969 | RARR2 | -1.5285 | 1.01E-02 | 1.47351 | 1.49357 | 0.4727995 | 0.5601275 | Retinoic acid receptor responder protein 2 OS=Homo sapiens GN=RARRES2 PE=1 SV=1 |
| Q8IWV1 | LAX1 | -1.91047 | 5.74E-03 | 2.00386 | 1.27831 | 0.413466 | 0.3043688 | Lymphocyte transmembrane adapter 1 OS=Homo sapiens GN=LAX1 PE=1 SV=1 |

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|---|---|---|---|---|---|
| RING finger protein 219 | FAVAALQSK | 1296.99 | 1434.54 | 5346.49 | 5340.23 |
| RING finger protein 219 | LDVTDTSMDTYLER | 667.11 | 261.48 | 2492.45 | 2908.78 |
| RING finger protein 219 | NLSLESQIK | 3314.76 | 3998.01 | 22099.16 | 20825.3 |
| RING finger protein 219 | SLDLDGLSK | 3659.85 | 3414.84 | 18140.3 | 21295.9 |
| RING finger protein 219 | EIIGGTSESEPMLSH | 332.65 | 326.7 | 492.06 | 841.9 |
| RING finger protein 219 | LKLENGGLVR | 196.22 | 188.4 | 226.96 | 250.42 |
| RING finger protein 219 | KIQSSLSSASPSK | 75.78 | 172.69 | 115.6 | 69.95 |
| RING finger protein 219 | DVTDTSMDTYLER | 38.42 | 34.38 | 73.22 | 60.13 |
| Cytochrome c oxidase subunit 3 | ESTYQGHHTPPVQK | 114.29 | 91.82 | 251.84 | 241.08 |
| Cytochrome c oxidase subunit 3 | ITIL | 114.69 | 158.48 | 37.77 | 113.82 |
| Cytochrome c oxidase subunit 3 | LGLL | 1296.99 | 1434.54 | 5346.49 | 5340.23 |
| Cytochrome c oxidase subunit 3 | LGLL | 667.11 | 261.48 | 2492.45 | 2908.78 |
| Cytochrome c oxidase subunit 3 | LGLL | 3314.76 | 3998.01 | 22099.16 | 20825.3 |
| Cytochrome c oxidase subunit 3 | LGLL | 3659.85 | 3414.84 | 18140.3 | 21295.9 |
| Cytochrome c oxidase subunit 3 | LGLL | 332.65 | 326.7 | 492.06 | 841.9 |
| Molybdate-anion transporter | VPSPTEEPYAPEL | 1229.65 | 1172.35 | 3403.93 | 4897.02 |
| Molybdate-anion transporter | LAVL | 4384.27 | 4183.51 | 14747.8 | 17040.8 |
| Molybdate-anion transporter | LGLL | 2105.29 | 1682.61 | 3410.78 | 4449.91 |
| Molybdate-anion transporter | LGLL | 1505.25 | 1603.39 | 2879.59 | 2988.3 |
| Molybdate-anion transporter | LGLL | 1057.77 | 1452.14 | 2799.67 | 2329.69 |
| Molybdate-anion transporter | LGLL | 1179.78 | 1206.45 | 2644.64 | 2135.2 |
| Molybdate-anion transporter | LGLL | 893.03 | 813.09 | 2037.03 | 1522 |
| Molybdate-anion transporter | LLAL | 3427.6 | 4552.18 | 19059.3 | 19150.2 |
| Molybdate-anion transporter | LLAL | 11917.0 | 10813.6 | 45916.9 | 50894.3 |
| Molybdate-anion transporter | VPSPTEEPYAPEL | 1558.4 | 1564.95 | 8416.24 | 7153.81 |
| Histone H2A.J | NDEELNKLLGK | 3095.22 | 2922.24 | 10321.92 | 12424.92 |
| Histone H2A.J | AGLQFPVGR | 735.36 | 539.74 | 1137.2 | 1255.8 |
| Histone H2A.J | AGLQFPVGR | 7391.74 | 7902.96 | 31114.53 | 37885.3 |
| Histone H2A.J | AGLQFPVGR | 3719.2 | 3082.61 | 12229.63 | 15352.61 |
| Histone H2A.J | AGLQFPVGR | 4353.16 | 3002.59 | 18013.83 | 16481.37 |
| Histone H2A.J | AGLQFPVGR | 3005.12 | 3845.47 | 14662.96 | 15630.89 |
| Histone H2A.J | AGLQFPVGR | 2346.47 | 1790.98 | 6527.64 | 5785.87 |
| Histone H2A.J | AGLQFPVGR | 1232.46 | 1639.57 | 5706.37 | 6792.3 |
| Histone H2A.J | AGLQFPVGR | 1543.28 | 1463.39 | 4984.86 | 3335.49 |
| Histone H2A.J | AGLQFPVGR | 1229.65 | 1172.35 | 3403.93 | 4897.02 |
| Histone H2A.J | AGLQFPVGR | 4384.27 | 4183.51 | 14747.87 | 17040.89 |
| Histone H2A.J | AGLQFPVGR | 2105.29 | 1682.61 | 3410.78 | 4449.91 |
| Histone H2A.J | AGLQFPVGR | 1505.25 | 1603.39 | 2879.59 | 2988.3 |
| Histone H2A.J | AGLQFPVGR | 1057.77 | 1452.14 | 2799.67 | 2329.69 |
| Histone H2A.J | AGLQFPVGR | 1179.78 | 1206.45 | 2644.64 | 2135.2 |
| Histone H2A.J | AGLQFPVGR | 893.03 | 813.09 | 2037.03 | 1522 |
| Histone H2A.J | AGLQFPVGR | 3427.6 | 4552.18 | 19059.3 | 19150.29 |
| Histone H2A.J | AGLQFPVGR | 11917.04 | 10813.63 | 45916.92 | 50894.32 |
| Histone H2A.J | AGLQFPVGR | 1558.4 | 1564.95 | 8416.24 | 7153.81 |
| Histone H2A.J | AGLQFPVGR | 1930.54 | 968.73 | 2663.15 | 3057.85 |
| Histone H2A.J | AGLQFPVGR | 3083.15 | 3902.41 | 10017.74 | 10807.33 |
| Histone H2A.J | AGLQFPVGR | 1605.11 | 1524.98 | 3253.99 | 2625.91 |
| Histone H2A.J | AGLQFPVGR | 1586.56 | 1230.13 | 6418.46 | 4920.93 |
| Histone H2A.J | AGLQFPVGR | 7803.66 | 6567.92 | 31816.9 | 34752.98 |
| Histone H2A.J | AGLQFPVGR | 1567.22 | 1119.55 | 2757.29 | 4205.61 |
| Histone H2A.J | AGLQFPVGR | 2736.28 | 2852.93 | 8417.13 | 8692.62 |
| Histone H2A.J | AGLQFPVGR | 5666.01 | 5635.96 | 19796.31 | 21829.52 |
| Histone H2A.J | AGLQFPVGR | 706.08 | 772.74 | 2590.48 | 2318.32 |
| Histone H2A.J | AGLQFPVGR | 1682.07 | 1368.73 | 6871.55 | 6293.89 |
| Histone H2A.J | AGLQFPVGR | 1364.82 | 2073.96 | 5169.37 | 6334.01 |
| Histone H2A.J | AGLQFPVGR | 7356.34 | 7571.09 | 38671.86 | 39202.02 |
| Histone H2A.J | AGLQFPVGR | 808.66 | 850.58 | 2566.07 | 1891.6 |
| Histone H2A.J | AGLQFPVGR | 1076.3 | 1004.63 | 1730.47 | 1973.07 |
| Histone H2A.J | AGLQFPVGR | 5221.48 | 4873.95 | 19067.57 | 19826.8 |
| Histone H2A.J | AGLQFPVGR | 5211.96 | 4750.17 | 19959.64 | 23151.88 |
| Histone H2A.J | AGLQFPVGR | 1975.77 | 2138.09 | 8959.97 | 8677.1 |
| Histone H2A.J | AGLQFPVGR | 1265.45 | 1571.74 | 5217.66 | 5867.18 |
| Histone H2A.J | AGLQFPVGR | 1474.02 | 1922.84 | 4478.49 | 5591.33 |
| Histone H2A.J | AGLQFPVGR | 1088.92 | 1353.18 | 2102.07 | 2730.95 |

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|---|---|---|---|---|---|
| Histone H2A.J | AGLQFPVGR | 734.61 | 826.28 | 2656.6 | 3038.88 |
| Histone H2A.J | AGLQFPVGR | 1115.46 | 752.24 | 2104.38 | 2955.29 |
| Histone H2A.J | AGLQFPVGR | 844.59 | 705.34 | 1321.23 | 1843.46 |
| Histone H2A.J | AGLQFPVGR | 989.68 | 731.88 | 2136.19 | 2097.21 |
| Histone H2A.J | AGLQFPVGR | 1056.54 | 1042.06 | 4313.21 | 4131.46 |
| Histone H2A.J | AGLQFPVGR | 2156.06 | 1985.76 | 3015.43 | 3427.61 |
| Histone H2A.J | AGLQFPVGR | 2783.63 | 2962.21 | 12465.42 | 12932.62 |
| Histone H2A.J | AGLQFPVGR | 995.36 | 1022.58 | 2309.6 | 2467.86 |
| Histone H2A.J | AGLQFPVGR | 965.41 | 1108.98 | 1390.06 | 1732.83 |
| Histone H2A.J | AGLQFPVGR | 9080.93 | 9738.21 | 42648.28 | 47032.29 |
| Histone H2A.J | AGLQFPVGR | 801.65 | 479.34 | 2817.88 | 2014.33 |
| Histone H2A.J | AGLQFPVGR | 946.89 | 598.13 | 1303.19 | 1877.72 |
| Histone H2A.J | AGLQFPVGR | 12921.42 | 13072.49 | 56983.82 | 62024.65 |
| Histone H2A.J | AGLQFPVGR | 973.93 | 692.24 | 1016.59 | 1318.97 |
| Histone H2A.J | AGLQFPVGR | 906.98 | 1350.04 | 1381.44 | 1763.9 |
| Histone H2A.J | AGLQFPVGR | 780.34 | 776.35 | 2192.85 | 1573.82 |
| Histone H2A.J | AGLQFPVGR | 913.85 | 670.53 | 715.07 | 970.42 |
| Histone H2A.J | AGLQFPVGR | 1451.42 | 1283.56 | 6770.79 | 6163.01 |
| Histone H2A.J | AGLQFPVGR | 2052.99 | 1955.73 | 5889.32 | 5656.88 |
| Histone H2A.J | AGLQFPVGR | 973.28 | 969.46 | 1454.53 | 1594.17 |
| Histone H2A.J | AGLQFPVGR | 846.83 | 483.9 | 2214.39 | 1892.43 |
| Histone H2A.J | AGLQFPVGR | 460.6 | 450.89 | 1486.04 | 1116.19 |
| Histone H2A.J | AGLQFPVGR | 875.51 | 1161.33 | 3012.76 | 3331.16 |
| Histone H2A.J | AGLQFPVGR | 411.83 | 163.42 | 619.25 | 875.38 |
| Histone H2A.J | AGLQFPVGR | 1027.49 | 1251.77 | 2183.95 | 2801.88 |
| Histone H2A.J | AGLQFPVGR | 9789.6 | 8978.43 | 47210.65 | 48156.78 |
| Histone H2A.J | AGLQFPVGR | 7337.1 | 6812.75 | 30936.86 | 32724.84 |
| Histone H2A.J | AGLQFPVGR | 2191.89 | 1743.8 | 8310.88 | 6655.3 |
| Histone H2A.J | AGLQFPVGR | 381.79 | 578.16 | 532.32 | 470.78 |
| Histone H2A.J | AGLQFPVGR | 770.94 | 853.63 | 1649.32 | 2090.21 |
| Histone H2A.J | AGLQFPVGR | 2561.86 | 2745.08 | 9923.76 | 11767.1 |
| Histone H2A.J | AGLQFPVGR | 1072.29 | 1081.21 | 2372.08 | 1835.76 |
| Histone H2A.J | AGLQFPVGR | 681.56 | 960.87 | 1884.51 | 1837.95 |
| Histone H2A.J | AGLQFPVGR | 11781.22 | 10827.76 | 63002.79 | 65067.61 |
| Histone H2A.J | AGLQFPVGR | 634.06 | 653.99 | 2292.9 | 1868.72 |
| Histone H2A.J | AGLQFPVGR | 829.97 | 766.59 | 3823.66 | 4723.98 |
| Histone H2A.J | AGLQFPVGR | 1583.64 | 1837.12 | 6030.03 | 6618.06 |
| Histone H2A.J | AGLQFPVGR | 1463.63 | 1779.87 | 1801.83 | 2111.98 |
| Histone H2A.J | AGLQFPVGR | 1990.11 | 2530.31 | 7270.88 | 5859.88 |
| Histone H2A.J | AGLQFPVGR | 1177.54 | 1108.01 | 1724.2 | 1887.06 |
| Histone H2A.J | AGLQFPVGR | 807.81 | 934.77 | 1702.29 | 1692.95 |
| Histone H2A.J | AGLQFPVGR | 1191.31 | 1024.77 | 1802.28 | 1715.42 |
| Histone H2A.J | AGLQFPVGR | 15580.76 | 14908.89 | 71607.21 | 74831.87 |
| Histone H2A.J | AGLQFPVGR | 770.96 | 533.16 | 1331.88 | 1680.9 |
| Histone H2A.J | AGLQFPVGR | 800.46 | 384.67 | 1016.38 | 1345.14 |
| Histone H2A.J | AGLQFPVGR | 728.49 | 1217.84 | 1820.1 | 2499.85 |
| Histone H2A.J | AGLQFPVGR | 5500.73 | 6113.81 | 22880.82 | 28990.17 |
| Histone H2A.J | AGLQFPVGR | 13342.21 | 14477.4 | 69294.52 | 77085.73 |
| Histone H2A.J | AGLQFPVGR | 963.56 | 866.55 | 1421.16 | 1210.32 |
| Histone H2A.J | AGLQFPVGR | 659.15 | 515.27 | 924.45 | 1211.15 |
| Histone H2A.J | AGLQFPVGR | 1169.19 | 1720.32 | 4390.78 | 5177.26 |
| Histone H2A.J | AGLQFPVGR | 1835.38 | 1965.98 | 5807.36 | 7331.35 |
| Histone H2A.J | AGLQFPVGR | 750.79 | 717.55 | 2390.72 | 1899.98 |
| Histone H2A.J | AGLQFPVGR | 4341.52 | 3939.4 | 16395.2 | 19115.57 |
| Histone H2A.J | AGLQFPVGR | 3840.33 | 2711.39 | 13979.03 | 14060.98 |
| Histone H2A.J | AGLQFPVGR | 13267.3 | 12410.55 | 64418.72 | 68188.72 |
| Histone H2A.J | AGLQFPVGR | 1669.13 | 2646.7 | 5934.27 | 9711.38 |
| Histone H2A.J | AGLQFPVGR | 1256.66 | 845.09 | 3589.58 | 3030.78 |
| Histone H2A.J | AGLQFPVGR | 22173.4 | 23357.7 | 113914.5 | 117779.3 |
| Histone H2A.J | AGLQFPVGR | 615.78 | 1290.12 | 2115.03 | 2124.18 |
| Histone H2A.J | AGLQFPVGR | 4396.96 | 3355.39 | 8858.52 | 9554.16 |
| Histone H2A.J | AGLQFPVGR | 2323.51 | 2144.22 | 7595.02 | 5547.48 |
| Histone H2A.J | AGLQFPVGR | 771.65 | 783.48 | 1818.86 | 1461.33 |
| Histone H2A.J | AGLQFPVGR | 755.07 | 613.21 | 1845.28 | 1443.02 |

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|---|---|---|---|---|---|
| Histone H2A.J | AGLQFPVGR | 1337.63 | 1462.02 | 1498.03 | 2430.35 |
| Histone H2A.J | AGLQFPVGR | 1787.99 | 1648.17 | 2500.27 | 2807.22 |
| Histone H2A.J | AGLQFPVGR | 1206.66 | 891.01 | 1926.46 | 1862.94 |
| Histone H2A.J | AGLQFPVGR | 15965.26 | 17347.55 | 82594.47 | 85498.15 |
| Histone H2A.J | AGLQFPVGR | 2950.12 | 2896.52 | 7923.98 | 8552.25 |
| Histone H2A.J | AGLQFPVGR | 1914.91 | 1768.74 | 3092.14 | 3497.98 |
| Histone H2A.J | AGLQFPVGR | 25003.83 | 27547.2 | 133263 | 132321.3 |
| Histone H2A.J | AGLQFPVGR | 776.19 | 335.35 | 1311.11 | 830.06 |
| Histone H2A.J | AGLQFPVGR | 1078.53 | 890.24 | 1530.31 | 1802.05 |
| Histone H2A.J | AGLQFPVGR | 621.31 | 530.86 | 664.59 | 649.84 |
| Histone H2A.J | AGLQFPVGR | 974.47 | 1596.7 | 3559.94 | 2425.87 |
| Histone H2A.J | AGLQFPVGR | 1512.85 | 1810.52 | 8615.78 | 8315.48 |
| Histone H2A.J | AGLQFPVGR | 18520.47 | 21280.89 | 94612.43 | 100476.7 |
| Histone H2A.J | AGLQFPVGR | 688.78 | 673.05 | 1096.26 | 1126.67 |
| Histone H2A.J | AGLQFPVGR | 461.72 | 340.39 | 618.4 | 920.2 |
| Histone H2A.J | AGLQFPVGR | 1259.02 | 1143.55 | 2220.91 | 2744.3 |
| Histone H2A.J | AGLQFPVGR | 2654.47 | 3382.38 | 4919.8 | 5595.68 |
| Histone H2A.J | AGLQFPVGR | 357.04 | 469.41 | 1002.77 | 1192.24 |
| Histone H2A.J | AGLQFPVGR | 1270.08 | 901.76 | 1428.42 | 1014.2 |
| Histone H2A.J | AGLQFPVGR | 21202.08 | 18045.75 | 97054.73 | 97989.67 |
| Histone H2A.J | AGLQFPVGR | 1022 | 624.66 | 1789.91 | 1699.53 |
| Histone H2A.J | AGLQFPVGR | 6274.58 | 6892.98 | 33468.67 | 34576.11 |
| Histone H2A.J | AGLQFPVGR | 1949.98 | 1814.34 | 5335.88 | 4130.09 |
| Histone H2A.J | AGLQFPVGR | 408.49 | 493.33 | 854.2 | 937.65 |
| Histone H2A.J | AGLQFPVGR | 953.99 | 748.01 | 1948.09 | 1932.83 |
| Histone H2A.J | AGLQFPVGR | 7506.25 | 6802.85 | 15275.03 | 16186.78 |
| Histone H2A.J | AGLQFPVGR | 25508.24 | 26861.2 | 137211.1 | 150031.6 |
| Histone H2A.J | AGLQFPVGR | 839.08 | 1142.89 | 2037.25 | 2143.55 |
| Histone H2A.J | AGLQFPVGR | 204.16 | 254.95 | 1958.89 | 898.18 |
| Histone H2A.J | AGLQFPVGR | 9390.52 | 9364.29 | 40276.81 | 43372.96 |
| Histone H2A.J | AGLQFPVGR | 781.62 | 755.91 | 1178.04 | 1225.45 |
| Histone H2A.J | AGLQFPVGR | 359.77 | 199.84 | 285.26 | 343.68 |
| Histone H2A.J | AGLQFPVGR | 1064.99 | 845.5 | 2463.35 | 2116.21 |
| Histone H2A.J | AGLQFPVGR | 12898.72 | 12549.22 | 60824.75 | 66481.3 |
| Histone H2A.J | AGLQFPVGR | 717.32 | 938.89 | 1776.93 | 1638.44 |
| Histone H2A.J | AGLQFPVGR | 1512.12 | 1244.2 | 2112.28 | 2589.62 |
| Histone H2A.J | AGLQFPVGR | 3754.24 | 4727.03 | 5169.87 | 7731.69 |
| Histone H2A.J | AGLQFPVGR | 730.17 | 946.19 | 2379.41 | 2757.84 |
| Histone H2A.J | AGLQFPVGR | 1010.57 | 1328.08 | 1981.97 | 1578.95 |
| Histone H2A.J | AGLQFPVGR | 594.64 | 931.85 | 1298.1 | 1376.65 |
| Histone H2A.J | AGLQFPVGR | 5684.85 | 6008.46 | 10502.22 | 14303.33 |
| Histone H2A.J | AGLQFPVGR | 1499.12 | 2103.35 | 6733.66 | 4358.06 |
| Histone H2A.J | AGLQFPVGR | 10952.99 | 11591.67 | 47877.18 | 49740.2 |
| Histone H2A.J | AGLQFPVGR | 1930.09 | 2821.77 | 2753.96 | 2318.96 |
| Histone H2A.J | AGLQFPVGR | 32037.25 | 35319.58 | 180394.8 | 177293.2 |
| Histone H2A.J | AGLQFPVGR | 6193.2 | 8550.31 | 11781.76 | 14807.87 |
| Histone H2A.J | AGLQFPVGR | 1314.71 | 1279.9 | 2718.63 | 2826.48 |
| Histone H2A.J | AGLQFPVGR | 1116.67 | 1696.97 | 685.15 | 644.61 |
| Histone H2A.J | AGLQFPVGR | 8329.98 | 7760.7 | 12479.6 | 16636.78 |
| Histone H2A.J | AGLQFPVGR | 881.92 | 1484.84 | 1720.03 | 2290.7 |
| Histone H2A.J | AGLQFPVGR | 778.46 | 536.83 | 1495.14 | 1886.07 |
| Histone H2A.J | AGLQFPVGR | 459.93 | 198.27 | 1272.39 | 1253.57 |
| Histone H2A.J | AGLQFPVGR | 17775.7 | 16564.34 | 95128.73 | 90015.13 |
| Histone H2A.J | AGLQFPVGR | 538.35 | 429.01 | 1059.91 | 969.96 |
| Histone H2A.J | AGLQFPVGR | 959.21 | 1828.02 | 2811.16 | 3161.15 |
| Histone H2A.J | AGLQFPVGR | 307.29 | 278.98 | 392.5 | 897.91 |
| Histone H2A.J | AGLQFPVGR | 509.98 | 785.59 | 1929.15 | 706.56 |
| Histone H2A.J | AGLQFPVGR | 278.74 | 546.54 | 1197.66 | 1129.15 |
| Histone H2A.J | AGLQFPVGR | 1255.47 | 2664.7 | 10602.54 | 2080.34 |
| Histone H2A.J | AGLQFPVGR | 883.09 | 837.78 | 692.62 | 1080.91 |
| Histone H2A.J | AGLQFPVGR | 8340.85 | 9878.16 | 12958.73 | 17024.35 |
| Histone H2A.J | AGLQFPVGR | 7429.04 | 9324.5 | 12678.39 | 16348.85 |
| Histone H2A.J | AGLQFPVGR | 436.23 | 305.23 | 1174.46 | 967.27 |
| Histone H2A.J | AGLQFPVGR | 1440.41 | 1413.68 | 3246.5 | 2125.68 |

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|---|---|---|---|---|---|
| Histone H2A.J | AGLQFPVGR | 769.75 | 758.75 | 2889.53 | 693.74 |
| Histone H2A.J | AGLQFPVGR | 765.55 | 1173.51 | 2653.85 | 1286.41 |
| Histone H2A.J | AGLQFPVGR | 799.88 | 1505.24 | 2341.31 | 1378.18 |
| Histone H2A.J | AGLQFPVGR | 9134.02 | 11195.56 | 41371.96 | 53640.86 |
| Histone H2A.J | AGLQFPVGR | 358.62 | 313.44 | 1052.6 | 581.51 |
| Histone H2A.J | AGLQFPVGR | 658.77 | 1191.15 | 3183.2 | 1092.5 |
| Histone H2A.J | AGLQFPVGR | 425.61 | 290.65 | 658.22 | 350.91 |
| Histone H2A.J | AGLQFPVGR | 438.12 | 118.68 | 183.07 | 477.05 |
| Histone H2A.J | AGLQFPVGR | 535.37 | 830.33 | 1005.83 | 960.25 |
| Histone H2A.J | AGLQFPVGR | 397.55 | 510.46 | 1270.11 | 1211.33 |
| Histone H2A.J | AGLQFPVGR | 24910.02 | 28091.79 | 141081.8 | 137110 |
| Histone H2A.J | AGLQFPVGR | 7062.89 | 9223.16 | 15097.36 | 16468.32 |
| Histone H2A.J | AGLQFPVGR | 968.2 | 620.37 | 709.89 | 709.61 |
| Histone H2A.J | AGLQFPVGR | 2521.6 | 3743.75 | 13966.48 | 16544.49 |
| Histone H2A.J | AGLQFPVGR | 2521.6 | 3743.75 | 13966.48 | 16544.49 |
| Histone H2A.J | AGLQFPVGR | 406.9 | 543.67 | 1082.3 | 818.21 |
| Histone H2A.J | AGLQFPVGR | 840.21 | 1031.86 | 3057.41 | 3192.68 |
| Histone H2A.J | AGLQFPVGR | 668.36 | 350.57 | 421.08 | 623.23 |
| Histone H2A.J | AGLQFPVGR | 1418.3 | 1683.46 | 1098.86 | 958.1 |
| Histone H2A.J | AGLQFPVGR | 2912.07 | 3038.75 | 1133.96 | 1269.9 |
| Histone H2A.J | AGLQFPVGR | 178.05 | 281.42 | 745.2 | 320.37 |
| Histone H2A.J | AGLQFPVGR | 852.94 | 1156.96 | 5918.07 | 700.19 |
| Histone H2A.J | AGLQFPVGR | 16367.95 | 19583.16 | 72920.64 | 82336.19 |
| Histone H2A.J | AGLQFPVGR | 488.76 | 541.34 | 685.19 | 1306.41 |
| Histone H2A.J | AGLQFPVGR | 23470.75 | 25820.33 | 120423.2 | 119929.1 |
| Histone H2A.J | AGLQFPVGR | 509.98 | 785.59 | 1929.15 | 706.56 |
| Histone H2A.J | AGLQFPVGR | 888.88 | 691.45 | 2165.07 | 2089.24 |
| Histone H2A.J | AGLQFPVGR | 769.75 | 758.75 | 2889.53 | 693.74 |
| Histone H2A.J | AGLQFPVGR | 28765.71 | 27264.85 | 157592.2 | 146114.7 |
| Histone H2A.J | AGLQFPVGR | 1207.97 | 1080.54 | 5737.75 | 6853.03 |
| Histone H2A.J | AGLQFPVGR | 4045.77 | 4648.2 | 2469.06 | 2154.7 |
| Histone H2A.J | AGLQFPVGR | 31596.32 | 30159.57 | 175405.2 | 170862.1 |
| Histone H2A.J | AGLQFPVGR | 31384.23 | 39943.32 | 198050.1 | 194084.3 |
| Histone H2A.J | AGLQFPVGR | 333.11 | 281.33 | 181.56 | 196.3 |
| Histone H2A.J | AGLQFPVGR | 658.77 | 1191.15 | 3183.2 | 1092.5 |
| Histone H2A.J | AGLQFPVGR | 26360.24 | 26302.61 | 145444.1 | 146949.2 |
| Histone H2A.J | AGLQFPVGR | 28568.85 | 31075.36 | 159389.5 | 154730 |
| Histone H2A.J | AGLQFPVGR | 30331.6 | 30643.17 | 171915 | 166589.2 |
| Histone H2A.J | AGLQFPVGR | 769.12 | 501.57 | 1093.09 | 1370.01 |
| Histone H2A.J | AGLQFPVGR | 33743.25 | 33579.08 | 190507.8 | 186818.8 |
| Histone H2A.J | AGLQFPVGR | 30236.94 | 30207.49 | 160197.4 | 157297.6 |
| Histone H2A.J | AGLQFPVGR | 52526.38 | 52207.16 | 281929.4 | 304593.4 |
| Histone H2A.J | AGLQFPVGR | 1354.4 | 1932.75 | 3841.77 | 2597.42 |
| Histone H2A.J | AGLQFPVGR | 58565.43 | 53434.29 | 298827.4 | 324923.5 |
| Histone H2A.J | AGLQFPVGR | 958.12 | 552.94 | 1210.06 | 859.72 |
| Histone H2A.J | AGLQFPVGR | 486.55 | 334.21 | 460.71 | 960.71 |
| Histone H2A.J | AGLQFPVGR | 1193.06 | 2128.14 | 5086.7 | 2653.11 |
| Histone H2A.J | AGLQFPVGR | 1195.6 | 1983.61 | 4354.74 | 3935.23 |
| Histone H2A.J | AGLQFPVGR | 179.5 | 138.09 | 170.7 | 16.57 |
| Histone H2A.J | AGLQFPVGR | 571.42 | 566.22 | 3034.2 | 2546.55 |
| Histone H2A.J | AGLQFPVGR | 31542.75 | 30133.07 | 179465.5 | 172668.1 |
| Histone H2A.J | AGLQFPVGR | 5621.18 | 6022.58 | 28229.04 | 26278.96 |
| Histone H2A.J | AGLQFPVGR | 231.27 | 129.64 | 398.74 | 159.37 |
| Histone H2A.J | AGLQFPVGR | 408.3 | 512.34 | 1191.24 | 1045.61 |
| Histone H2A.J | AGLQFPVGR | 59862.48 | 57948.53 | 352305.3 | 381336.6 |
| Histone H2A.J | AGLQFPVGR | 561.55 | 584.14 | 1333.07 | 1520.52 |
| Histone H2A.J | AGLQFPVGR | 256.34 | 206.44 | 337.55 | 314.07 |
| Histone H2A.J | AGLQFPVGR | 789.17 | 967.8 | 2796.5 | 2654.17 |
| Histone H2A.J | AGLQFPVGR | 5621.18 | 6022.58 | 28229.04 | 26278.96 |
| Histone H2A.J | AGLQFPVGR | 305.85 | 421.07 | 1028.26 | 706.26 |
| Histone H2A.J | AGLQFPVGR | 33825.63 | 35865.82 | 195702.3 | 183745.3 |
| Histone H2A.J | AGLQFPVGR | 356.25 | 547.45 | 868.27 | 1357.04 |
| Histone H2A.J | AGLQFPVGR | 958.12 | 552.94 | 1210.06 | 859.72 |
| Histone H2A.J | AGLQFPVGR | 30350.76 | 33111.27 | 186082.3 | 169240.5 |

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| Histone H2A.J | AGLQFPVGR | 956.41 | 934.7 | 2065.4 | 2277.84 |
| Histone H2A.J | AGLQFPVGR | 872.12 | 1708.26 | 4692.79 | 5115.06 |
| Histone H2A.J | AGLQFPVGR | 614.01 | 613.72 | 688.21 | 1293.43 |
| Histone H2A.J | AGLQFPVGR | 381.98 | 558.93 | 685.14 | 924.91 |
| Histone H2A.J | AGLQFPVGR | 204.06 | 265.09 | 181.36 | 247.95 |
| Histone H2A.J | AGLQFPVGR | 799.88 | 1505.24 | 2341.31 | 1378.18 |
| Histone H2A.J | AGLQFPVGR | 408.02 | 433.59 | 1311.1 | 1082.41 |
| Histone H2A.J | AGLQFPVGR | 1207.97 | 1080.54 | 5737.75 | 6853.03 |
| Histone H2A.J | AGLQFPVGR | 506.73 | 362.05 | 871.03 | 1321.75 |
| Histone H2A.J | AGLQFPVGR | 756.81 | 866.76 | 1424.1 | 987.71 |
| Histone H2A.J | AGLQFPVGR | 496.18 | 340.55 | 484.39 | 1051.85 |
| Histone H2A.J | AGLQFPVGR | 669.57 | 337.37 | 1175.99 | 1326.11 |
| Histone H2A.J | AGLQFPVGR | 305.24 | 480.89 | 571.52 | 414.08 |
| Histone H2A.J | AGLQFPVGR | 505.84 | 1088.23 | 909.13 | 1098.16 |
| Histone H2A.J | AGLQFPVGR | 1001.85 | 487.22 | 1056.17 | 1783.61 |
| Histone H2A.J | AGLQFPVGR | 1416.92 | 1075.45 | 1659.77 | 2608.41 |
| Histone H2A.J | AGLQFPVGR | 1932.74 | 2879.5 | 1164.89 | 1161.08 |
| Histone H2A.J | AGLQFPVGR | 3013.27 | 3785.06 | 12302.32 | 13726.99 |
| Histone H2A.J | AGLQFPVGR | 953.46 | 1332.51 | 2184.47 | 2191.61 |
| Histone H2A.J | AGLQFPVGR | 153.13 | 190.41 | 232.33 | 427.19 |
| Histone H2A.J | AGLQFPVGR | 304.28 | 575.71 | 937.6 | 823.44 |
| Histone H2A.J | AGLQFPVGR | 1255.47 | 2664.7 | 10602.54 | 2080.34 |
| Histone H2A.J | AGLQFPVGR | 4884.28 | 5422.52 | 2794.05 | 2499.44 |
| Histone H2A.J | AGLQFPVGR | 3013.27 | 3785.06 | 12302.32 | 13726.99 |
| Histone H2A.J | AGLQFPVGR | 1833.78 | 1698.45 | 3409.3 | 3955.73 |
| Histone H2A.J | AGLQFPVGR | 535.03 | 438.15 | 726.65 | 1141.12 |
| Histone H2A.J | AGLQFPVGR | 409.55 | 388.09 | 1003.16 | 813.93 |
| Histone H2A.J | AGLQFPVGR | 651.37 | 645.75 | 1306.89 | 1501.44 |
| Histone H2A.J | AGLQFPVGR | 506.73 | 362.05 | 871.03 | 1321.75 |
| Histone H2A.J | AGLQFPVGR | 496.18 | 340.55 | 484.39 | 1051.85 |
| Histone H2A.J | AGLQFPVGR | 230.21 | 234.19 | 337.37 | 264.51 |
| Histone H2A.J | AGLQFPVGR | 1663.44 | 2571.04 | 6027.59 | 9178.14 |
| Histone H2A.J | AGLQFPVGR | 523.28 | 535.42 | 1170.39 | 1428.15 |
| Histone H2A.J | AGLQFPVGR | 334.77 | 116.6 | 664.71 | 792.52 |
| Histone H2A.J | AGLQFPVGR | 383.11 | 447.31 | 723.55 | 706.98 |
| Histone H2A.J | AGLQFPVGR | 12694.93 | 12683.01 | 52399.88 | 61492.76 |
| Histone H2A.J | GLQFPVGR | 5465.72 | 3615.26 | 4160.52 | 5161 |
| Histone H2A.J | GLQFPVGR | 3623.58 | 3806.48 | 8633.53 | 11317.45 |
| Histone H2A.J | GLQFPVGR | 5458.29 | 4774.93 | 13576.62 | 15270.13 |
| Histone H2A.J | HLQLAIR | 3406.51 | 2805.59 | 9845.33 | 9587 |
| Histone H2A.J | HLQLAIR | 4891.35 | 6532.1 | 17241.07 | 18515.23 |
| Histone H2A.J | HLQLAIR | 2459.32 | 2024.44 | 4086.24 | 6509.23 |
| Histone H2A.J | HLQLAIR | 7413.79 | 6682.28 | 19822.83 | 25349.53 |
| Histone H2A.J | HLQLAIR | 495.22 | 434.72 | 935.64 | 881.85 |
| Histone H2A.J | HLQLAIR | 282 | 224.26 | 638.52 | 477.65 |
| Histone H2A.J | HLQLAIR | 1530.69 | 1537.48 | 3653.3 | 3427 |
| Histone H2A.J | HLQLAIR | 3931.58 | 4653.8 | 12025.64 | 13178.84 |
| Histone H2A.J | HLQLAIR | 1002.23 | 982.03 | 3598.64 | 4772.14 |
| Histone H2A.J | HLQLAIR | 1935.65 | 1740.56 | 4303.7 | 3262.49 |
| Histone H2A.J | HLQLAIR | 15328.33 | 16445.01 | 49841.69 | 56921.78 |
| Histone H2A.J | HLQLAIR | 563.83 | 465.08 | 405.85 | 895.7 |
| Histone H2A.J | HLQLAIR | 1388.91 | 1608.16 | 3389.16 | 3857.72 |
| Histone H2A.J | HLQLAIR | 10528.26 | 9191.79 | 30012.6 | 33431.36 |
| Histone H2A.J | HLQLAIR | 669.97 | 723.28 | 808.02 | 1712.34 |
| Histone H2A.J | HLQLAIR | 559.96 | 634.81 | 853.33 | 941.75 |
| Histone H2A.J | HLQLAIR | 384.9 | 270.38 | 533.4 | 793.71 |
| Histone H2A.J | HLQLAIR | 1740.16 | 1160.57 | 2860.4 | 3819.71 |
| Histone H2A.J | HLQLAIR | 781.09 | 489.86 | 936.67 | 1419 |
| Histone H2A.J | HLQLAIR | 887.97 | 781.1 | 765.9 | 1651.08 |
| Histone H2A.J | HLQLAIR | 2482.4 | 1978.24 | 3467.88 | 4010.84 |
| Histone H2A.J | HLQLAIR | 610.06 | 791.49 | 1430.07 | 2167.54 |
| Histone H2A.J | HLQLAIR | 14199.58 | 13601.52 | 47619.1 | 56553.43 |
| Histone H2A.J | HLQLAIR | 963.2 | 1540.38 | 2557.8 | 2904.39 |
| Histone H2A.J | HLQLAIR | 690.08 | 758.18 | 1082.08 | 919.83 |

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|---|---|---|---|---|---|
| Histone H2A.J | HLQLAIR | 631.41 | 916.33 | 1080.23 | 1045.42 |
| Histone H2A.J | HLQLAIR | 308.12 | 196.69 | 630.41 | 589.88 |
| Histone H2A.J | HLQLAIR | 513.5 | 330.95 | 895.5 | 1183.96 |
| Histone H2A.J | HLQLAIR | 573.38 | 585.5 | 743.35 | 562.86 |
| Histone H2A.J | HLQLAIR | 537.34 | 528.6 | 658.33 | 1329.39 |
| Histone H2A.J | IIPR | 640.2 | 366.14 | 1243.74 | 910.95 |
| Histone H2A.J | IQAVLLPK | 1305.23 | 1258.8 | 2254.8 | 2691.81 |
| Histone H2A.J | IQAVLLPK | 559.15 | 821.1 | 1109.19 | 1145.08 |
| Histone H2A.J | KGNYAER | 254.49 | 282.79 | 1142.13 | 1352.36 |
| Histone H2A.J | KGNYAER | 206.92 | 195 | 871.88 | 1031.79 |
| Histone H2A.J | LLGK | 3497.2 | 4271.32 | 5463.79 | 5805.31 |
| Histone H2A.J | LLGK | 6358.35 | 8191.63 | 19930.68 | 27872.12 |
| Histone H2A.J | LLGK | 5627.84 | 5364.58 | 18307.75 | 21015.58 |
| Histone H2A.J | LLGK | 4093.22 | 3045.08 | 7609.02 | 8332.05 |
| Histone H2A.J | LLGK | 2955.88 | 3816.51 | 8510.03 | 11071 |
| Histone H2A.J | LLGK | 1741.15 | 1701.46 | 2482.79 | 3844.17 |
| Histone H2A.J | LLPK | 4819.23 | 6635.9 | 9232.09 | 9789.93 |
| Histone H2A.J | LLPK | 1534.23 | 1613.26 | 2604.07 | 4192.49 |
| Histone H2A.J | LLPK | 2978.85 | 3887.58 | 5122.53 | 5474.69 |
| Histone H2A.J | NDEELNKLLGK | 902.6 | 1143.99 | 3824.53 | 7125.37 |
| Histone H2A.J | NDEELNKLLGK | 2901.36 | 2500.87 | 8951.51 | 11805.43 |
| Histone H2A.J | NDEELNKLLGK | 5623.4 | 5164.91 | 26073.44 | 32967.19 |
| Histone H2A.J | NDEELNKLLGK | 5021.62 | 6321.13 | 25444.44 | 37838.48 |
| Histone H2A.J | NDEELNKLLGK | 2420.32 | 1940.94 | 5912.96 | 8101.84 |
| Histone H2A.J | NDEELNKLLGK | 5596.52 | 5054.19 | 21755.51 | 30486.4 |
| Histone H2A.J | NDEELNKLLGK | 4912.7 | 5593.56 | 26197.29 | 35994.03 |
| Histone H2A.J | NDEELNKLLGK | 792.81 | 820.98 | 2492.88 | 2953 |
| Histone H2A.J | NDEELNKLLGK | 1539.82 | 1911.76 | 3615.23 | 3935.66 |
| Histone H2A.J | NDEELNKLLGK | 1737.71 | 2147.31 | 3950.68 | 4334.55 |
| Histone H2A.J | NDEELNKLLGK | 2453.13 | 3274.67 | 10666.68 | 15847.08 |
| Histone H2A.J | NDEELNKLLGK | 1345.14 | 1252.22 | 2486.98 | 2554.85 |
| Histone H2A.J | RAGLQFPVGR | 842.15 | 2329.3 | 10836.33 | 1053.15 |
| Histone H2A.J | RAGLQFPVGR | 571.41 | 779.52 | 993.43 | 409.63 |
| Histone H2A.J | TRIIPRHLQLAIR | 2335.79 | 2101.65 | 3804.97 | 3910.23 |
| Histone H2A.J | TRIIPRHLQLAIR | 2184.26 | 1965.37 | 2697.14 | 3301.59 |
| Histone H2A.J | VLLPK | 1406.89 | 1640.91 | 2820.39 | 2781.79 |
| Histone H2A.J | VLLPK | 1770.34 | 1689.95 | 2306.96 | 3430.99 |
| Histone H2A.J | VLLPK | 3943.06 | 3199.82 | 5823.9 | 7006.84 |
| Histone H2A.J | VLLPK | 1595.46 | 1839.56 | 2887.4 | 3401.13 |
| Histone H2A.J | VTIAQGGVLP | 1190.82 | 115.51 | 134.33 | 328.03 |
| Histone H2A.J | VTIAQGGVLPN | 511.18 | 454.14 | 1139.99 | 865.66 |
| Histone H2A.J | VTIAQGGVLPN | 253.1 | 526.63 | 680.64 | 369.69 |
| Histone H2A.J | VTIAQGGVLPN | 356.55 | 517.88 | 681.32 | 784.42 |
| Histone H2A.J | VTIAQGGVLPN | 231.79 | 78.64 | 366.84 | 467.48 |
| Histone H2A.J | VTIAQGGVLPN | 436.65 | 264.08 | 655.15 | 612.14 |
| Histone H2A.J | VTIAQGGVLPNIQ | 76.07 | 144.29 | 242.94 | 179.99 |
| Histone H2A.J | VTIAQGGVLPNIQA | 25.76 | 7.85 | 49.11 | 61.88 |
| Histone H2A.J | VTIAQGGVLPNIQA | 102.94 | 42.08 | 94.08 | 200.44 |
| Histone H2A.J | VTIAQGGVLPNIQA | 38.54 | 22.48 | 23.51 | 24.08 |
| Histone H2A.J | VTIAQGGVLPNIQA | 76.95 | 57.39 | 70.48 | 99.39 |
| Histone H2A.J | VTIAQGGVLPNIQAV | 25.52 | 31.73 | 38.86 | 66.68 |
| Histone H2A.V | ATIAGGGVIPHIHK | 1502.26 | 1686.15 | 3956.14 | 4213.9 |
| Histone H2A.V | GDEELDSLIK | 357.64 | 410.52 | 1360.14 | 1677.5 |
| Histone H2A.V | ATIAGGGVIPH | 1559.96 | 1411.51 | 1692.45 | 2161.21 |
| Histone H2A.V | AGGK | 112.85 | 127.66 | 292.73 | 305.06 |
| Histone H2A.V | AGLQFPVGR | 735.36 | 539.74 | 1137.2 | 1255.8 |
| Histone H2A.V | AGLQFPVGR | 7391.74 | 7902.96 | 31114.53 | 37885.3 |
| Histone H2A.V | AGLQFPVGR | 3719.2 | 3082.61 | 12229.63 | 15352.61 |
| Histone H2A.V | AGLQFPVGR | 4353.16 | 3002.59 | 18013.83 | 16481.37 |
| Histone H2A.V | AGLQFPVGR | 3005.12 | 3845.47 | 14662.96 | 15630.89 |
| Histone H2A.V | AGLQFPVGR | 2346.47 | 1790.98 | 6527.64 | 5785.87 |
| Histone H2A.V | AGLQFPVGR | 1232.46 | 1639.57 | 5706.37 | 6792.3 |
| Histone H2A.V | AGLQFPVGR | 1543.28 | 1463.39 | 4984.86 | 3335.49 |
| Histone H2A.V | AGLQFPVGR | 1229.65 | 1172.35 | 3403.93 | 4897.02 |

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| Histone H2A.V | AGLQFPVGR | 4384.27 | 4183.51 | 14747.87 | 17040.89 |
| Histone H2A.V | AGLQFPVGR | 2105.29 | 1682.61 | 3410.78 | 4449.91 |
| Histone H2A.V | AGLQFPVGR | 1505.25 | 1603.39 | 2879.59 | 2988.3 |
| Histone H2A.V | AGLQFPVGR | 1057.77 | 1452.14 | 2799.67 | 2329.69 |
| Histone H2A.V | AGLQFPVGR | 1179.78 | 1206.45 | 2644.64 | 2135.2 |
| Histone H2A.V | AGLQFPVGR | 893.03 | 813.09 | 2037.03 | 1522 |
| Histone H2A.V | AGLQFPVGR | 3427.6 | 4552.18 | 19059.3 | 19150.29 |
| Histone H2A.V | AGLQFPVGR | 11917.04 | 10813.63 | 45916.92 | 50894.32 |
| Histone H2A.V | AGLQFPVGR | 1558.4 | 1564.95 | 8416.24 | 7153.81 |
| Histone H2A.V | AGLQFPVGR | 1930.54 | 968.73 | 2663.15 | 3057.85 |
| Histone H2A.V | AGLQFPVGR | 3083.15 | 3902.41 | 10017.74 | 10807.33 |
| Histone H2A.V | AGLQFPVGR | 1605.11 | 1524.98 | 3253.99 | 2625.91 |
| Histone H2A.V | AGLQFPVGR | 1586.56 | 1230.13 | 6418.46 | 4920.93 |
| Histone H2A.V | AGLQFPVGR | 7803.66 | 6567.92 | 31816.9 | 34752.98 |
| Histone H2A.V | AGLQFPVGR | 1567.22 | 1119.55 | 2757.29 | 4205.61 |
| Histone H2A.V | AGLQFPVGR | 2736.28 | 2852.93 | 8417.13 | 8692.62 |
| Histone H2A.V | AGLQFPVGR | 5666.01 | 5635.96 | 19796.31 | 21829.52 |
| Histone H2A.V | AGLQFPVGR | 706.08 | 772.74 | 2590.48 | 2318.32 |
| Histone H2A.V | AGLQFPVGR | 1682.07 | 1368.73 | 6871.55 | 6293.89 |
| Histone H2A.V | AGLQFPVGR | 1364.82 | 2073.96 | 5169.37 | 6334.01 |
| Histone H2A.V | AGLQFPVGR | 7356.34 | 7571.09 | 38671.86 | 39202.02 |
| Histone H2A.V | AGLQFPVGR | 808.66 | 850.58 | 2566.07 | 1891.6 |
| Histone H2A.V | AGLQFPVGR | 1076.3 | 1004.63 | 1730.47 | 1973.07 |
| Histone H2A.V | AGLQFPVGR | 5221.48 | 4873.95 | 19067.57 | 19826.8 |
| Histone H2A.V | AGLQFPVGR | 5211.96 | 4750.17 | 19959.64 | 23151.88 |
| Histone H2A.V | AGLQFPVGR | 1975.77 | 2138.09 | 8959.97 | 8677.1 |
| Histone H2A.V | AGLQFPVGR | 1265.45 | 1571.74 | 5217.66 | 5867.18 |
| Histone H2A.V | AGLQFPVGR | 1474.02 | 1922.84 | 4478.49 | 5591.33 |
| Histone H2A.V | AGLQFPVGR | 1088.92 | 1353.18 | 2102.07 | 2730.95 |
| Histone H2A.V | AGLQFPVGR | 734.61 | 826.28 | 2656.6 | 3038.88 |
| Histone H2A.V | AGLQFPVGR | 1115.46 | 752.24 | 2104.38 | 2955.29 |
| Histone H2A.V | AGLQFPVGR | 844.59 | 705.34 | 1321.23 | 1843.46 |
| Histone H2A.V | AGLQFPVGR | 989.68 | 731.88 | 2136.19 | 2097.21 |
| Histone H2A.V | AGLQFPVGR | 1056.54 | 1042.06 | 4313.21 | 4131.46 |
| Histone H2A.V | AGLQFPVGR | 2156.06 | 1985.76 | 3015.43 | 3427.61 |
| Histone H2A.V | AGLQFPVGR | 2783.63 | 2962.21 | 12465.42 | 12932.62 |
| Histone H2A.V | AGLQFPVGR | 995.36 | 1022.58 | 2309.6 | 2467.86 |
| Histone H2A.V | AGLQFPVGR | 965.41 | 1108.98 | 1390.06 | 1732.83 |
| Histone H2A.V | AGLQFPVGR | 9080.93 | 9738.21 | 42648.28 | 47032.29 |
| Histone H2A.V | AGLQFPVGR | 801.65 | 479.34 | 2817.88 | 2014.33 |
| Histone H2A.V | AGLQFPVGR | 946.89 | 598.13 | 1303.19 | 1877.72 |
| Histone H2A.V | AGLQFPVGR | 12921.42 | 13072.49 | 56983.82 | 62024.65 |
| Histone H2A.V | AGLQFPVGR | 973.93 | 692.24 | 1016.59 | 1318.97 |
| Histone H2A.V | AGLQFPVGR | 906.98 | 1350.04 | 1381.44 | 1763.9 |
| Histone H2A.V | AGLQFPVGR | 780.34 | 776.35 | 2192.85 | 1573.82 |
| Histone H2A.V | AGLQFPVGR | 913.85 | 670.53 | 715.07 | 970.42 |
| Histone H2A.V | AGLQFPVGR | 1451.42 | 1283.56 | 6770.79 | 6163.01 |
| Histone H2A.V | AGLQFPVGR | 2052.99 | 1955.73 | 5889.32 | 5656.88 |
| Histone H2A.V | AGLQFPVGR | 973.28 | 969.46 | 1454.53 | 1594.17 |
| Histone H2A.V | AGLQFPVGR | 846.83 | 483.9 | 2214.39 | 1892.43 |
| Histone H2A.V | AGLQFPVGR | 460.6 | 450.89 | 1486.04 | 1116.19 |
| Histone H2A.V | AGLQFPVGR | 875.51 | 1161.33 | 3012.76 | 3331.16 |
| Histone H2A.V | AGLQFPVGR | 411.83 | 163.42 | 619.25 | 875.38 |
| Histone H2A.V | AGLQFPVGR | 1027.49 | 1251.77 | 2183.95 | 2801.88 |
| Histone H2A.V | AGLQFPVGR | 9789.6 | 8978.43 | 47210.65 | 48156.78 |
| Histone H2A.V | AGLQFPVGR | 7337.1 | 6812.75 | 30936.86 | 32724.84 |
| Histone H2A.V | AGLQFPVGR | 2191.89 | 1743.8 | 8310.88 | 6655.3 |
| Histone H2A.V | AGLQFPVGR | 381.79 | 578.16 | 532.32 | 470.78 |
| Histone H2A.V | AGLQFPVGR | 770.94 | 853.63 | 1649.32 | 2090.21 |
| Histone H2A.V | AGLQFPVGR | 2561.86 | 2745.08 | 9923.76 | 11767.1 |
| Histone H2A.V | AGLQFPVGR | 1072.29 | 1081.21 | 2372.08 | 1835.76 |
| Histone H2A.V | AGLQFPVGR | 681.56 | 960.87 | 1884.51 | 1837.95 |
| Histone H2A.V | AGLQFPVGR | 11781.22 | 10827.76 | 63002.79 | 65067.61 |
| Histone H2A.V | AGLQFPVGR | 634.06 | 653.99 | 2292.9 | 1868.72 |

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|---|---|---|---|---|---|
| Histone H2A.V | AGLQFPVGR | 829.97 | 766.59 | 3823.66 | 4723.98 |
| Histone H2A.V | AGLQFPVGR | 1583.64 | 1837.12 | 6030.03 | 6618.06 |
| Histone H2A.V | AGLQFPVGR | 1463.63 | 1779.87 | 1801.83 | 2111.98 |
| Histone H2A.V | AGLQFPVGR | 1990.11 | 2530.31 | 7270.88 | 5859.88 |
| Histone H2A.V | AGLQFPVGR | 1177.54 | 1108.01 | 1724.2 | 1887.06 |
| Histone H2A.V | AGLQFPVGR | 807.81 | 934.77 | 1702.29 | 1692.95 |
| Histone H2A.V | AGLQFPVGR | 1191.31 | 1024.77 | 1802.28 | 1715.42 |
| Histone H2A.V | AGLQFPVGR | 15580.76 | 14908.89 | 71607.21 | 74831.87 |
| Histone H2A.V | AGLQFPVGR | 770.96 | 533.16 | 1331.88 | 1680.9 |
| Histone H2A.V | AGLQFPVGR | 800.46 | 384.67 | 1016.38 | 1345.14 |
| Histone H2A.V | AGLQFPVGR | 728.49 | 1217.84 | 1820.1 | 2499.85 |
| Histone H2A.V | AGLQFPVGR | 5500.73 | 6113.81 | 22880.82 | 28990.17 |
| Histone H2A.V | AGLQFPVGR | 13342.21 | 14477.4 | 69294.52 | 77085.73 |
| Histone H2A.V | AGLQFPVGR | 963.56 | 866.55 | 1421.16 | 1210.32 |
| Histone H2A.V | AGLQFPVGR | 659.15 | 515.27 | 924.45 | 1211.15 |
| Histone H2A.V | AGLQFPVGR | 1169.19 | 1720.32 | 4390.78 | 5177.26 |
| Histone H2A.V | AGLQFPVGR | 1835.38 | 1965.98 | 5807.36 | 7331.35 |
| Histone H2A.V | AGLQFPVGR | 750.79 | 717.55 | 2390.72 | 1899.98 |
| Histone H2A.V | AGLQFPVGR | 4341.52 | 3939.4 | 16395.2 | 19115.57 |
| Histone H2A.V | AGLQFPVGR | 3840.33 | 2711.39 | 13979.03 | 14060.98 |
| Histone H2A.V | AGLQFPVGR | 13267.3 | 12410.55 | 64418.72 | 68188.72 |
| Histone H2A.V | AGLQFPVGR | 1669.13 | 2646.7 | 5934.27 | 9711.38 |
| Histone H2A.V | AGLQFPVGR | 1256.66 | 845.09 | 3589.58 | 3030.78 |
| Histone H2A.V | AGLQFPVGR | 22173.4 | 23357.7 | 113914.5 | 117779.3 |
| Histone H2A.V | AGLQFPVGR | 615.78 | 1290.12 | 2115.03 | 2124.18 |
| Histone H2A.V | AGLQFPVGR | 4396.96 | 3355.39 | 8858.52 | 9554.16 |
| Histone H2A.V | AGLQFPVGR | 2323.51 | 2144.22 | 7595.02 | 5547.48 |
| Histone H2A.V | AGLQFPVGR | 771.65 | 783.48 | 1818.86 | 1461.33 |
| Histone H2A.V | AGLQFPVGR | 755.07 | 613.21 | 1845.28 | 1443.02 |
| Histone H2A.V | AGLQFPVGR | 1337.63 | 1462.02 | 1498.03 | 2430.35 |
| Histone H2A.V | AGLQFPVGR | 1787.99 | 1648.17 | 2500.27 | 2807.22 |
| Histone H2A.V | AGLQFPVGR | 1206.66 | 891.01 | 1926.46 | 1862.94 |
| Histone H2A.V | AGLQFPVGR | 15965.26 | 17347.55 | 82594.47 | 85498.15 |
| Histone H2A.V | AGLQFPVGR | 2950.12 | 2896.52 | 7923.98 | 8552.25 |
| Histone H2A.V | AGLQFPVGR | 1914.91 | 1768.74 | 3092.14 | 3497.98 |
| Histone H2A.V | AGLQFPVGR | 25003.83 | 27547.2 | 133263 | 132321.3 |
| Histone H2A.V | AGLQFPVGR | 776.19 | 335.35 | 1311.11 | 830.06 |
| Histone H2A.V | AGLQFPVGR | 1078.53 | 890.24 | 1530.31 | 1802.05 |
| Histone H2A.V | AGLQFPVGR | 621.31 | 530.86 | 664.59 | 649.84 |
| Histone H2A.V | AGLQFPVGR | 974.47 | 1596.7 | 3559.94 | 2425.87 |
| Histone H2A.V | AGLQFPVGR | 1512.85 | 1810.52 | 8615.78 | 8315.48 |
| Histone H2A.V | AGLQFPVGR | 18520.47 | 21280.89 | 94612.43 | 100476.7 |
| Histone H2A.V | AGLQFPVGR | 688.78 | 673.05 | 1096.26 | 1126.67 |
| Histone H2A.V | AGLQFPVGR | 461.72 | 340.39 | 618.4 | 920.2 |
| Histone H2A.V | AGLQFPVGR | 1259.02 | 1143.55 | 2220.91 | 2744.3 |
| Histone H2A.V | AGLQFPVGR | 2654.47 | 3382.38 | 4919.8 | 5595.68 |
| Histone H2A.V | AGLQFPVGR | 357.04 | 469.41 | 1002.77 | 1192.24 |
| Histone H2A.V | AGLQFPVGR | 1270.08 | 901.76 | 1428.42 | 1014.2 |
| Histone H2A.V | AGLQFPVGR | 21202.08 | 18045.75 | 97054.73 | 97989.67 |
| Histone H2A.V | AGLQFPVGR | 1022 | 624.66 | 1789.91 | 1699.53 |
| Histone H2A.V | AGLQFPVGR | 6274.58 | 6892.98 | 33468.67 | 34576.11 |
| Histone H2A.V | AGLQFPVGR | 1949.98 | 1814.34 | 5335.88 | 4130.09 |
| Histone H2A.V | AGLQFPVGR | 408.49 | 493.33 | 854.2 | 937.65 |
| Histone H2A.V | AGLQFPVGR | 953.99 | 748.01 | 1948.09 | 1932.83 |
| Histone H2A.V | AGLQFPVGR | 7506.25 | 6802.85 | 15275.03 | 16186.78 |
| Histone H2A.V | AGLQFPVGR | 25508.24 | 26861.2 | 137211.1 | 150031.6 |
| Histone H2A.V | AGLQFPVGR | 839.08 | 1142.89 | 2037.25 | 2143.55 |
| Histone H2A.V | AGLQFPVGR | 204.16 | 254.95 | 1958.89 | 898.18 |
| Histone H2A.V | AGLQFPVGR | 9390.52 | 9364.29 | 40276.81 | 43372.96 |
| Histone H2A.V | AGLQFPVGR | 781.62 | 755.91 | 1178.04 | 1225.45 |
| Histone H2A.V | AGLQFPVGR | 359.77 | 199.84 | 285.26 | 343.68 |
| Histone H2A.V | AGLQFPVGR | 1064.99 | 845.5 | 2463.35 | 2116.21 |
| Histone H2A.V | AGLQFPVGR | 12898.72 | 12549.22 | 60824.75 | 66481.3 |
| Histone H2A.V | AGLQFPVGR | 717.32 | 938.89 | 1776.93 | 1638.44 |

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| Histone H2A.V | AGLQFPVGR | 1512.12 | 1244.2 | 2112.28 | 2589.62 |
| Histone H2A.V | AGLQFPVGR | 3754.24 | 4727.03 | 5169.87 | 7731.69 |
| Histone H2A.V | AGLQFPVGR | 730.17 | 946.19 | 2379.41 | 2757.84 |
| Histone H2A.V | AGLQFPVGR | 1010.57 | 1328.08 | 1981.97 | 1578.95 |
| Histone H2A.V | AGLQFPVGR | 594.64 | 931.85 | 1298.1 | 1376.65 |
| Histone H2A.V | AGLQFPVGR | 5684.85 | 6008.46 | 10502.22 | 14303.33 |
| Histone H2A.V | AGLQFPVGR | 1499.12 | 2103.35 | 6733.66 | 4358.06 |
| Histone H2A.V | AGLQFPVGR | 10952.99 | 11591.67 | 47877.18 | 49740.2 |
| Histone H2A.V | AGLQFPVGR | 1930.09 | 2821.77 | 2753.96 | 2318.96 |
| Histone H2A.V | AGLQFPVGR | 32037.25 | 35319.58 | 180394.8 | 177293.2 |
| Histone H2A.V | AGLQFPVGR | 6193.2 | 8550.31 | 11781.76 | 14807.87 |
| Histone H2A.V | AGLQFPVGR | 1314.71 | 1279.9 | 2718.63 | 2826.48 |
| Histone H2A.V | AGLQFPVGR | 1116.67 | 1696.97 | 685.15 | 644.61 |
| Histone H2A.V | AGLQFPVGR | 8329.98 | 7760.7 | 12479.6 | 16636.78 |
| Histone H2A.V | AGLQFPVGR | 881.92 | 1484.84 | 1720.03 | 2290.7 |
| Histone H2A.V | AGLQFPVGR | 778.46 | 536.83 | 1495.14 | 1886.07 |
| Histone H2A.V | AGLQFPVGR | 459.93 | 198.27 | 1272.39 | 1253.57 |
| Histone H2A.V | AGLQFPVGR | 17775.7 | 16564.34 | 95128.73 | 90015.13 |
| Histone H2A.V | AGLQFPVGR | 538.35 | 429.01 | 1059.91 | 969.96 |
| Histone H2A.V | AGLQFPVGR | 959.21 | 1828.02 | 2811.16 | 3161.15 |
| Histone H2A.V | AGLQFPVGR | 307.29 | 278.98 | 392.5 | 897.91 |
| Histone H2A.V | AGLQFPVGR | 509.98 | 785.59 | 1929.15 | 706.56 |
| Histone H2A.V | AGLQFPVGR | 278.74 | 546.54 | 1197.66 | 1129.15 |
| Histone H2A.V | AGLQFPVGR | 1255.47 | 2664.7 | 10602.54 | 2080.34 |
| Histone H2A.V | AGLQFPVGR | 883.09 | 837.78 | 692.62 | 1080.91 |
| Histone H2A.V | AGLQFPVGR | 8340.85 | 9878.16 | 12958.73 | 17024.35 |
| Histone H2A.V | AGLQFPVGR | 7429.04 | 9324.5 | 12678.39 | 16348.85 |
| Histone H2A.V | AGLQFPVGR | 436.23 | 305.23 | 1174.46 | 967.27 |
| Histone H2A.V | AGLQFPVGR | 1440.41 | 1413.68 | 3246.5 | 2125.68 |
| Histone H2A.V | AGLQFPVGR | 769.75 | 758.75 | 2889.53 | 693.74 |
| Histone H2A.V | AGLQFPVGR | 765.55 | 1173.51 | 2653.85 | 1286.41 |
| Histone H2A.V | AGLQFPVGR | 799.88 | 1505.24 | 2341.31 | 1378.18 |
| Histone H2A.V | AGLQFPVGR | 9134.02 | 11195.56 | 41371.96 | 53640.86 |
| Histone H2A.V | AGLQFPVGR | 358.62 | 313.44 | 1052.6 | 581.51 |
| Histone H2A.V | AGLQFPVGR | 658.77 | 1191.15 | 3183.2 | 1092.5 |
| Histone H2A.V | AGLQFPVGR | 425.61 | 290.65 | 658.22 | 350.91 |
| Histone H2A.V | AGLQFPVGR | 438.12 | 118.68 | 183.07 | 477.05 |
| Histone H2A.V | AGLQFPVGR | 535.37 | 830.33 | 1005.83 | 960.25 |
| Histone H2A.V | AGLQFPVGR | 397.55 | 510.46 | 1270.11 | 1211.33 |
| Histone H2A.V | AGLQFPVGR | 24910.02 | 28091.79 | 141081.8 | 137110 |
| Histone H2A.V | AGLQFPVGR | 7062.89 | 9223.16 | 15097.36 | 16468.32 |
| Histone H2A.V | AGLQFPVGR | 968.2 | 620.37 | 709.89 | 709.61 |
| Histone H2A.V | AGLQFPVGR | 2521.6 | 3743.75 | 13966.48 | 16544.49 |
| Histone H2A.V | AGLQFPVGR | 2521.6 | 3743.75 | 13966.48 | 16544.49 |
| Histone H2A.V | AGLQFPVGR | 406.9 | 543.67 | 1082.3 | 818.21 |
| Histone H2A.V | AGLQFPVGR | 840.21 | 1031.86 | 3057.41 | 3192.68 |
| Histone H2A.V | AGLQFPVGR | 668.36 | 350.57 | 421.08 | 623.23 |
| Histone H2A.V | AGLQFPVGR | 1418.3 | 1683.46 | 1098.86 | 958.1 |
| Histone H2A.V | AGLQFPVGR | 2912.07 | 3038.75 | 1133.96 | 1269.9 |
| Histone H2A.V | AGLQFPVGR | 178.05 | 281.42 | 745.2 | 320.37 |
| Histone H2A.V | AGLQFPVGR | 852.94 | 1156.96 | 5918.07 | 700.19 |
| Histone H2A.V | AGLQFPVGR | 16367.95 | 19583.16 | 72920.64 | 82336.19 |
| Histone H2A.V | AGLQFPVGR | 488.76 | 541.34 | 685.19 | 1306.41 |
| Histone H2A.V | AGLQFPVGR | 23470.75 | 25820.33 | 120423.2 | 119929.1 |
| Histone H2A.V | AGLQFPVGR | 509.98 | 785.59 | 1929.15 | 706.56 |
| Histone H2A.V | AGLQFPVGR | 888.88 | 691.45 | 2165.07 | 2089.24 |
| Histone H2A.V | AGLQFPVGR | 769.75 | 758.75 | 2889.53 | 693.74 |
| Histone H2A.V | AGLQFPVGR | 28765.71 | 27264.85 | 157592.2 | 146114.7 |
| Histone H2A.V | AGLQFPVGR | 1207.97 | 1080.54 | 5737.75 | 6853.03 |
| Histone H2A.V | AGLQFPVGR | 4045.77 | 4648.2 | 2469.06 | 2154.7 |
| Histone H2A.V | AGLQFPVGR | 31596.32 | 30159.57 | 175405.2 | 170862.1 |
| Histone H2A.V | AGLQFPVGR | 31384.23 | 39943.32 | 198050.1 | 194084.3 |
| Histone H2A.V | AGLQFPVGR | 333.11 | 281.33 | 181.56 | 196.3 |
| Histone H2A.V | AGLQFPVGR | 658.77 | 1191.15 | 3183.2 | 1092.5 |

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| Histone H2A.V | AGLQFPVGR | 26360.24 | 26302.61 | 145444.1 | 146949.2 |
| Histone H2A.V | AGLQFPVGR | 28568.85 | 31075.36 | 159389.5 | 154730 |
| Histone H2A.V | AGLQFPVGR | 30331.6 | 30643.17 | 171915 | 166589.2 |
| Histone H2A.V | AGLQFPVGR | 769.12 | 501.57 | 1093.09 | 1370.01 |
| Histone H2A.V | AGLQFPVGR | 33743.25 | 33579.08 | 190507.8 | 186818.8 |
| Histone H2A.V | AGLQFPVGR | 30236.94 | 30207.49 | 160197.4 | 157297.6 |
| Histone H2A.V | AGLQFPVGR | 52526.38 | 52207.16 | 281929.4 | 304593.4 |
| Histone H2A.V | AGLQFPVGR | 1354.4 | 1932.75 | 3841.77 | 2597.42 |
| Histone H2A.V | AGLQFPVGR | 58565.43 | 53434.29 | 298827.4 | 324923.5 |
| Histone H2A.V | AGLQFPVGR | 958.12 | 552.94 | 1210.06 | 859.72 |
| Histone H2A.V | AGLQFPVGR | 486.55 | 334.21 | 460.71 | 960.71 |
| Histone H2A.V | AGLQFPVGR | 1193.06 | 2128.14 | 5086.7 | 2653.11 |
| Histone H2A.V | AGLQFPVGR | 1195.6 | 1983.61 | 4354.74 | 3935.23 |
| Histone H2A.V | AGLQFPVGR | 179.5 | 138.09 | 170.7 | 16.57 |
| Histone H2A.V | AGLQFPVGR | 571.42 | 566.22 | 3034.2 | 2546.55 |
| Histone H2A.V | AGLQFPVGR | 31542.75 | 30133.07 | 179465.5 | 172668.1 |
| Histone H2A.V | AGLQFPVGR | 5621.18 | 6022.58 | 28229.04 | 26278.96 |
| Histone H2A.V | AGLQFPVGR | 231.27 | 129.64 | 398.74 | 159.37 |
| Histone H2A.V | AGLQFPVGR | 408.3 | 512.34 | 1191.24 | 1045.61 |
| Histone H2A.V | AGLQFPVGR | 59862.48 | 57948.53 | 352305.3 | 381336.6 |
| Histone H2A.V | AGLQFPVGR | 561.55 | 584.14 | 1333.07 | 1520.52 |
| Histone H2A.V | AGLQFPVGR | 256.34 | 206.44 | 337.55 | 314.07 |
| Histone H2A.V | AGLQFPVGR | 789.17 | 967.8 | 2796.5 | 2654.17 |
| Histone H2A.V | AGLQFPVGR | 5621.18 | 6022.58 | 28229.04 | 26278.96 |
| Histone H2A.V | AGLQFPVGR | 305.85 | 421.07 | 1028.26 | 706.26 |
| Histone H2A.V | AGLQFPVGR | 33825.63 | 35865.82 | 195702.3 | 183745.3 |
| Histone H2A.V | AGLQFPVGR | 356.25 | 547.45 | 868.27 | 1357.04 |
| Histone H2A.V | AGLQFPVGR | 958.12 | 552.94 | 1210.06 | 859.72 |
| Histone H2A.V | AGLQFPVGR | 30350.76 | 33111.27 | 186082.3 | 169240.5 |
| Histone H2A.V | AGLQFPVGR | 956.41 | 934.7 | 2065.4 | 2277.84 |
| Histone H2A.V | AGLQFPVGR | 872.12 | 1708.26 | 4692.79 | 5115.06 |
| Histone H2A.V | AGLQFPVGR | 614.01 | 613.72 | 688.21 | 1293.43 |
| Histone H2A.V | AGLQFPVGR | 381.98 | 558.93 | 685.14 | 924.91 |
| Histone H2A.V | AGLQFPVGR | 204.06 | 265.09 | 181.36 | 247.95 |
| Histone H2A.V | AGLQFPVGR | 799.88 | 1505.24 | 2341.31 | 1378.18 |
| Histone H2A.V | AGLQFPVGR | 408.02 | 433.59 | 1311.1 | 1082.41 |
| Histone H2A.V | AGLQFPVGR | 1207.97 | 1080.54 | 5737.75 | 6853.03 |
| Histone H2A.V | AGLQFPVGR | 506.73 | 362.05 | 871.03 | 1321.75 |
| Histone H2A.V | AGLQFPVGR | 756.81 | 866.76 | 1424.1 | 987.71 |
| Histone H2A.V | AGLQFPVGR | 496.18 | 340.55 | 484.39 | 1051.85 |
| Histone H2A.V | AGLQFPVGR | 669.57 | 337.37 | 1175.99 | 1326.11 |
| Histone H2A.V | AGLQFPVGR | 305.24 | 480.89 | 571.52 | 414.08 |
| Histone H2A.V | AGLQFPVGR | 505.84 | 1088.23 | 909.13 | 1098.16 |
| Histone H2A.V | AGLQFPVGR | 1001.85 | 487.22 | 1056.17 | 1783.61 |
| Histone H2A.V | AGLQFPVGR | 1416.92 | 1075.45 | 1659.77 | 2608.41 |
| Histone H2A.V | AGLQFPVGR | 1932.74 | 2879.5 | 1164.89 | 1161.08 |
| Histone H2A.V | AGLQFPVGR | 3013.27 | 3785.06 | 12302.32 | 13726.99 |
| Histone H2A.V | AGLQFPVGR | 953.46 | 1332.51 | 2184.47 | 2191.61 |
| Histone H2A.V | AGLQFPVGR | 153.13 | 190.41 | 232.33 | 427.19 |
| Histone H2A.V | AGLQFPVGR | 304.28 | 575.71 | 937.6 | 823.44 |
| Histone H2A.V | AGLQFPVGR | 1255.47 | 2664.7 | 10602.54 | 2080.34 |
| Histone H2A.V | AGLQFPVGR | 4884.28 | 5422.52 | 2794.05 | 2499.44 |
| Histone H2A.V | AGLQFPVGR | 3013.27 | 3785.06 | 12302.32 | 13726.99 |
| Histone H2A.V | AGLQFPVGR | 1833.78 | 1698.45 | 3409.3 | 3955.73 |
| Histone H2A.V | AGLQFPVGR | 535.03 | 438.15 | 726.65 | 1141.12 |
| Histone H2A.V | AGLQFPVGR | 409.55 | 388.09 | 1003.16 | 813.93 |
| Histone H2A.V | AGLQFPVGR | 651.37 | 645.75 | 1306.89 | 1501.44 |
| Histone H2A.V | AGLQFPVGR | 506.73 | 362.05 | 871.03 | 1321.75 |
| Histone H2A.V | AGLQFPVGR | 496.18 | 340.55 | 484.39 | 1051.85 |
| Histone H2A.V | AGLQFPVGR | 230.21 | 234.19 | 337.37 | 264.51 |
| Histone H2A.V | AGLQFPVGR | 1663.44 | 2571.04 | 6027.59 | 9178.14 |
| Histone H2A.V | AGLQFPVGR | 523.28 | 535.42 | 1170.39 | 1428.15 |
| Histone H2A.V | AGLQFPVGR | 334.77 | 116.6 | 664.71 | 792.52 |
| Histone H2A.V | AGLQFPVGR | 383.11 | 447.31 | 723.55 | 706.98 |

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|---|---|---|---|---|---|
| Histone H2A.V | AGLQFPVGR | 12694.93 | 12683.01 | 52399.88 | 61492.76 |
| Histone H2A.V | ATIAGGGVIPHIHK | 625.74 | 1156.62 | 2671.66 | 2176.83 |
| Histone H2A.V | ATIAGGGVIPHIHK | 3192.06 | 2716.31 | 9037.32 | 10270.15 |
| Histone H2A.V | ATIAGGGVIPHIHK | 1600.38 | 1885.77 | 3721.58 | 3521.86 |
| Histone H2A.V | ATIAGGGVIPHIHK | 2144.65 | 1516.99 | 3799.51 | 4263.05 |
| Histone H2A.V | ATIAGGGVIPHIHK | 5047.6 | 5350.32 | 8745.87 | 10039.22 |
| Histone H2A.V | ATIAGGGVIPHIHK | 2037.63 | 1665.66 | 3911.89 | 3687.03 |
| Histone H2A.V | ATIAGGGVIPHIHK | 2690.86 | 2446.24 | 3329.36 | 3115 |
| Histone H2A.V | ATIAGGGVIPHIHK | 1945.45 | 2261.97 | 3900.53 | 3785.59 |
| Histone H2A.V | ATIAGGGVIPHIHK | 6336.7 | 4692.18 | 11471.79 | 9511.1 |
| Histone H2A.V | ATIAGGGVIPHIHK | 1991.83 | 1616.08 | 2915.23 | 3374.47 |
| Histone H2A.V | ATIAGGGVIPHIHK | 3064.41 | 2774.8 | 5920.01 | 6741.72 |
| Histone H2A.V | DSLIK | 1116.61 | 1064.15 | 1511.15 | 2352 |
| Histone H2A.V | GDEELDSLIK | 601.43 | 474.07 | 1099.92 | 1500.78 |
| Histone H2A.V | GDEELDSLIK | 2412.05 | 3184.35 | 7306.71 | 7992.74 |
| Histone H2A.V | GDEELDSLIK | 5741.47 | 5520.86 | 17660.19 | 22177.41 |
| Histone H2A.V | GDEELDSLIK | 5569.36 | 5290.75 | 14567.5 | 17206.21 |
| Histone H2A.V | GDEELDSLIK | 2784.9 | 2624.22 | 4446.49 | 5985.54 |
| Histone H2A.V | GDEELDSLIK | 1469.74 | 1601.77 | 2398.24 | 3466.03 |
| Histone H2A.V | GDEELDSLIK | 6912.77 | 7778.19 | 30318.64 | 33961.05 |
| Histone H2A.V | GDEELDSLIK | 1706.38 | 2051.76 | 3632.49 | 3055.51 |
| Histone H2A.V | GLQFPVGR | 5465.72 | 3615.26 | 4160.52 | 5161 |
| Histone H2A.V | GLQFPVGR | 3623.58 | 3806.48 | 8633.53 | 11317.45 |
| Histone H2A.V | GLQFPVGR | 5458.29 | 4774.93 | 13576.62 | 15270.13 |
| Histone H2A.V | HLQLAIR | 3406.51 | 2805.59 | 9845.33 | 9587 |
| Histone H2A.V | HLQLAIR | 4891.35 | 6532.1 | 17241.07 | 18515.23 |
| Histone H2A.V | HLQLAIR | 2459.32 | 2024.44 | 4086.24 | 6509.23 |
| Histone H2A.V | HLQLAIR | 7413.79 | 6682.28 | 19822.83 | 25349.53 |
| Histone H2A.V | HLQLAIR | 495.22 | 434.72 | 935.64 | 881.85 |
| Histone H2A.V | HLQLAIR | 282 | 224.26 | 638.52 | 477.65 |
| Histone H2A.V | HLQLAIR | 1530.69 | 1537.48 | 3653.3 | 3427 |
| Histone H2A.V | HLQLAIR | 3931.58 | 4653.8 | 12025.64 | 13178.84 |
| Histone H2A.V | HLQLAIR | 1002.23 | 982.03 | 3598.64 | 4772.14 |
| Histone H2A.V | HLQLAIR | 1935.65 | 1740.56 | 4303.7 | 3262.49 |
| Histone H2A.V | HLQLAIR | 15328.33 | 16445.01 | 49841.69 | 56921.78 |
| Histone H2A.V | HLQLAIR | 563.83 | 465.08 | 405.85 | 895.7 |
| Histone H2A.V | HLQLAIR | 1388.91 | 1608.16 | 3389.16 | 3857.72 |
| Histone H2A.V | HLQLAIR | 10528.26 | 9191.79 | 30012.6 | 33431.36 |
| Histone H2A.V | HLQLAIR | 669.97 | 723.28 | 808.02 | 1712.34 |
| Histone H2A.V | HLQLAIR | 559.96 | 634.81 | 853.33 | 941.75 |
| Histone H2A.V | HLQLAIR | 384.9 | 270.38 | 533.4 | 793.71 |
| Histone H2A.V | HLQLAIR | 1740.16 | 1160.57 | 2860.4 | 3819.71 |
| Histone H2A.V | HLQLAIR | 781.09 | 489.86 | 936.67 | 1419 |
| Histone H2A.V | HLQLAIR | 887.97 | 781.1 | 765.9 | 1651.08 |
| Histone H2A.V | HLQLAIR | 2482.4 | 1978.24 | 3467.88 | 4010.84 |
| Histone H2A.V | HLQLAIR | 610.06 | 791.49 | 1430.07 | 2167.54 |
| Histone H2A.V | HLQLAIR | 14199.58 | 13601.52 | 47619.1 | 56553.43 |
| Histone H2A.V | HLQLAIR | 963.2 | 1540.38 | 2557.8 | 2904.39 |
| Histone H2A.V | HLQLAIR | 690.08 | 758.18 | 1082.08 | 919.83 |
| Histone H2A.V | HLQLAIR | 631.41 | 916.33 | 1080.23 | 1045.42 |
| Histone H2A.V | HLQLAIR | 308.12 | 196.69 | 630.41 | 589.88 |
| Histone H2A.V | HLQLAIR | 513.5 | 330.95 | 895.5 | 1183.96 |
| Histone H2A.V | HLQLAIR | 573.38 | 585.5 | 743.35 | 562.86 |
| Histone H2A.V | HLQLAIR | 537.34 | 528.6 | 658.33 | 1329.39 |
| Histone H2A.V | LDSL | 357.3 | 444.42 | 376.14 | 235.28 |
| Histone H2A.V | LDSL | 382.05 | 658.05 | 515.6 | 643.4 |
| Histone H2A.V | LIGK | 3497.2 | 4271.32 | 5463.79 | 5805.31 |
| Histone H2A.V | LIGK | 6358.35 | 8191.63 | 19930.68 | 27872.12 |
| Histone H2A.V | LIGK | 5627.84 | 5364.58 | 18307.75 | 21015.58 |
| Histone H2A.V | LIGK | 4093.22 | 3045.08 | 7609.02 | 8332.05 |
| Histone H2A.V | LIGK | 2955.88 | 3816.51 | 8510.03 | 11071 |
| Histone H2A.V | LIGK | 1741.15 | 1701.46 | 2482.79 | 3844.17 |
| Histone H2A.V | LIKA | 1307.15 | 1601.51 | 2368.98 | 4199.33 |
| Histone H2A.V | LIKA | 2139.52 | 2555.78 | 5516.39 | 5965.56 |

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|---|---|---|---|---|---|
| Histone H2A.V | LIKA | 2452.19 | 2516.46 | 6687.89 | 7159.26 |
| Histone H2A.V | LIKA | 2478.27 | 3662.86 | 5467.4 | 7682.72 |
| Histone H2A.V | RAGLQFPVGR | 842.15 | 2329.3 | 10836.33 | 1053.15 |
| Histone H2A.V | RAGLQFPVGR | 571.41 | 779.52 | 993.43 | 409.63 |
| Histone H2A.V | RITPRHLQLAIR | 661.13 | 851.58 | 1834.17 | 962.91 |
| Histone H2A.V | RITPRHLQLAIR | 661.13 | 851.58 | 1834.17 | 962.91 |
| Histone H2A.V | SLIGK | 4603.28 | 5738 | 8909.5 | 12586.64 |
| Histone H2A.V | SLIGK | 3379.39 | 3676.75 | 10520.34 | 15298.75 |
| Histone H2A.V | SLIGK | 2271.88 | 2883.21 | 5749 | 8369.79 |
| Histone H2A.V | SLIGK | 2753.12 | 2998.01 | 8093.61 | 9673.51 |
| Histone H2A.V | SLIGK | 2456.19 | 2227.74 | 4360.39 | 4192.61 |
| Histone H2A.V | SLIGK | 9655.84 | 9109.04 | 17994.91 | 21970.2 |
| Histone H2A.V | SLIGK | 676.71 | 801.94 | 1519.87 | 1799.44 |
| Histone H2A.V | SLIGK | 5495.46 | 5251.42 | 8433.31 | 10103.3 |
| Histone H2A.V | SLIGK | 6026.24 | 7598.65 | 18193.98 | 25070.11 |
| Histone H2A.V | SLIGK | 4421.56 | 4329.99 | 4652.49 | 5512.69 |
| Histone H2A.V | SLIGK | 6330.68 | 5924.92 | 12161.75 | 14789.7 |
| Histone H2A.V | SLIGK | 280.05 | 416.73 | 1284.15 | 1378.46 |
| Histone H2A.V | SLIGK | 1788.66 | 2220.59 | 4075.22 | 4606.11 |
| V-type proton ATPase subunit F | GMFTAEDLR | 1030.94 | 911.18 | 1998.24 | 1595.68 |
| V-type proton ATPase subunit F | AEDLR | 691.52 | 508.75 | 383.74 | 673.37 |
| V-type proton ATPase subunit F | EIPSK | 437.91 | 139.9 | 410.94 | 566.14 |
| V-type proton ATPase subunit F | GMFTAEDLR | 2324.43 | 2797.9 | 3978.49 | 5194.1 |
| V-type proton ATPase subunit F | GMFTAEDLR | 685.19 | 496.38 | 1231.77 | 1313.25 |
| V-type proton ATPase subunit F | IGII | 1296.99 | 1434.54 | 5346.49 | 5340.23 |
| V-type proton ATPase subunit F | IGII | 667.11 | 261.48 | 2492.45 | 2908.78 |
| V-type proton ATPase subunit F | IGII | 3314.76 | 3998.01 | 22099.16 | 20825.3 |
| V-type proton ATPase subunit F | IGII | 3659.85 | 3414.84 | 18140.3 | 21295.9 |
| V-type proton ATPase subunit F | IGII | 332.65 | 326.7 | 492.06 | 841.9 |
| Galectin-3 | GNDVAFHFNPR | 1707.37 | 1953.65 | 3269.34 | 2840.6 |
| Galectin-3 | IALDFQR | 1938.24 | 1697.66 | 3225.27 | 4037.03 |
| Galectin-3 | VAVNDAHLLQYNHR | 636.23 | 865.42 | 2357.7 | 3225.41 |
| Galectin-3 | VIVCNTK | 732.96 | 1202.26 | 925.53 | 1114.38 |
| Galectin-3 | LDNNWGR | 2340.04 | 2851.25 | 3409.78 | 4893.78 |
| Galectin-3 | LDNNWGREER | 1188.41 | 1310.91 | 2764.69 | 2458.5 |
| Galectin-3 | LNEISK | 2852.15 | 2043.94 | 3809.84 | 3855.56 |
| Galectin-3 | GNDVAFHFNPR | 2371.69 | 2490.81 | 4209.46 | 5156.65 |
| Galectin-3 | GNDVAFHFNPR | 1989.42 | 1853.54 | 2879.42 | 3102 |
| Galectin-3 | GNDVAFHFNPR | 811.51 | 887.89 | 1508.12 | 1677.37 |
| Galectin-3 | GNDVAFHFNPR | 6064.74 | 6561.63 | 12543.78 | 16612.59 |
| Galectin-3 | GNDVAFHFNPR | 663.75 | 699.31 | 2335.51 | 1465.46 |
| Galectin-3 | GNDVAFHFNPR | 4372.89 | 4776.73 | 8529.38 | 9403.49 |
| Galectin-3 | GNDVAFHFNPR | 1543.45 | 1234.26 | 2329.38 | 2636.31 |
| Galectin-3 | GNDVAFHFNPR | 3884.62 | 3867.07 | 6594.42 | 7510.22 |
| Galectin-3 | GNDVAFHFNPR | 986.58 | 1464.19 | 2145.31 | 2254.33 |
| Galectin-3 | GNDVAFHFNPR | 534.85 | 1200.24 | 1272.8 | 873.63 |
| Galectin-3 | GNDVAFHFNPR | 1106.53 | 2166.97 | 2897.74 | 3196.91 |
| Galectin-3 | GNDVAFHFNPR | 9031.67 | 9392.73 | 11780.77 | 12799.15 |
| Galectin-3 | GNDVAFHFNPR | 1109.83 | 1308.15 | 1593.17 | 1933.53 |
| Galectin-3 | GNDVAFHFNPR | 788.34 | 943.42 | 1133.03 | 1396.13 |
| Galectin-3 | IALDFQR | 809.74 | 1276.11 | 2097.21 | 2900.03 |
| Galectin-3 | IALDFQR | 12119.15 | 13717.63 | 29925.46 | 35107.63 |
| Galectin-3 | IALDFQR | 330.7 | 518.84 | 834.67 | 970.75 |
| Galectin-3 | IALDFQR | 1306.64 | 1651.25 | 4271.6 | 4668.96 |
| Galectin-3 | IALDFQR | 1024.44 | 915.56 | 2603.35 | 3342.54 |
| Galectin-3 | IALDFQR | 1788.76 | 1572.19 | 2586.24 | 2785.72 |
| Galectin-3 | IALDFQR | 934 | 807.55 | 2001.12 | 2861.66 |
| Galectin-3 | IALDFQR | 1533.36 | 1485.61 | 2272.88 | 2736.62 |
| Galectin-3 | IALDFQR | 410.84 | 686.76 | 1170.37 | 2363.95 |
| Galectin-3 | IALDFQR | 356.77 | 496.3 | 949.94 | 683.25 |
| Galectin-3 | IALDFQR | 3180.76 | 2875.63 | 5931.5 | 7776.64 |
| Galectin-3 | IALDFQR | 406.63 | 677.37 | 905.93 | 1292.5 |
| Galectin-3 | IALDFQR | 848.17 | 1415.81 | 2013.62 | 1818.77 |
| Galectin-3 | IALDFQR | 6994.54 | 4911.56 | 10496.01 | 12038.38 |

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|---|---|---|---|---|---|
| Galectin-3 | IALDFQR | 2022.17 | 2448.42 | 4076.71 | 5581.75 |
| Galectin-3 | IALDFQR | 4032.78 | 4335.85 | 8287.53 | 8728.16 |
| Galectin-3 | IALDFQR | 301.12 | 249.77 | 583.48 | 433.13 |
| Galectin-3 | ITIL | 114.69 | 158.48 | 37.77 | 113.82 |
| Galectin-3 | LDNNWGR | 1303.11 | 1467.84 | 2932.35 | 4309.26 |
| Galectin-3 | LDNNWGREER | 1414.05 | 614.08 | 2046.89 | 2067.62 |
| Galectin-3 | LNEISK | 1090.18 | 803.57 | 2529.94 | 2521.15 |
| Galectin-3 | LNEISK | 2426.77 | 2687.23 | 3918.57 | 4949.16 |
| Galectin-3 | LNEISK | 2504.78 | 2533.09 | 5300.13 | 8087.77 |
| Galectin-3 | LNEISK | 3733.46 | 4120.62 | 5722.84 | 6837.65 |
| Galectin-3 | VAVNDAHLLQYNHR | 2616.18 | 3335.3 | 5899.82 | 5991.57 |
| Galectin-3 | VIVCNTK | 1704.6 | 2333.86 | 3088.54 | 3478.04 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSFVNDIFER | 26.57 | 34.56 | 54.85 | 29.13 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 931.14 | 1409.25 | 4427.87 | 4055 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYKVLK | 410.41 | 302.95 | 1381.96 | 1108.93 |
| Histone H2B type 1-C/E/F/G/I | HAVSEGTK | 310.93 | 344.41 | 1503.84 | 1827.56 |
| Histone H2B type 1-C/E/F/G/I | IAGEASR | 165.44 | 144.04 | 353.21 | 503.41 |
| Histone H2B type 1-C/E/F/G/I | KESYSVYVYK | 660.98 | 1079.41 | 2479.03 | 3840.86 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 489.85 | 326.94 | 1180.36 | 1360.34 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 4048 | 3789.63 | 14453.91 | 15354.33 |
| Histone H2B type 1-C/E/F/G/I | STITSR | 420.06 | 413.54 | 1088.58 | 1343.96 |
| Histone H2B type 1-C/E/F/G/I | SAPAPK | 223.19 | 289.49 | 978.76 | 1133.44 |
| Histone H2B type 1-C/E/F/G/I | EIQTAVR | 938.21 | 498.52 | 783.88 | 1574.28 |
| Histone H2B type 1-C/E/F/G/I | PEPAKSAPAPK | 665.2 | 875.41 | 2395.74 | 3114.4 |
| Histone H2B type 1-C/E/F/G/I | LAHYNK | 471.05 | 695.36 | 1375.76 | 2331.67 |
| Histone H2B type 1-C/E/F/G/I | SFVNDIFER | 277.81 | 637.9 | 724.07 | 654.02 |
| Histone H2B type 1-C/E/F/G/I | AVTKYTSSK | 402.55 | 441.78 | 926.07 | 516.03 |
| Histone H2B type 1-C/E/F/G/I | SRKESYSVYVYK | 277.97 | 622.59 | 1001.96 | 694.44 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSF | 195.49 | 47.46 | 127.29 | 113.32 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVY | 552.51 | 626.35 | 873.58 | 821.48 |
| Histone H2B type 1-C/E/F/G/I | IAGEASRL | 846.05 | 666.97 | 1033.18 | 1010.71 |
| Histone H2B type 1-C/E/F/G/I | LLLPGEL | 49.28 | 24.75 | 84.59 | 58.53 |
| Histone H2B type 1-C/E/F/G/I | PGELAK | 359.32 | 244.38 | 636.56 | 848.48 |
| Histone H2B type 1-C/E/F/G/I | SVYVYK | 3918.57 | 5619.97 | 7470.13 | 8961.18 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSF | 214.49 | 85.76 | 184.4 | 273.87 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSF | 188.54 | 96.31 | 289.39 | 332.57 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSF | 150.04 | 69.84 | 144.38 | 251.1 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSFVNDIFER | 60.95 | 42.44 | 70.82 | 49.81 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSFVNDIFER | 473.02 | 181.24 | 790.04 | 831.92 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSFVNDIFER | 231.03 | 153.67 | 487.6 | 436.28 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSFVNDIFER | 230.24 | 231.61 | 465.05 | 309.39 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSFVNDIFER | 384.36 | 323.61 | 455.5 | 809.47 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSFVNDIFER | 358.47 | 328.24 | 320.97 | 599.4 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSFVNDIFER | 203.85 | 285.58 | 445.2 | 855.16 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSFVNDIFER | 282.97 | 127.9 | 295.49 | 162.69 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSFVNDIFER | 589.82 | 344.54 | 1326.65 | 950.75 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSFVNDIFER | 333.41 | 250.87 | 410.41 | 361.69 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSFVNDIFER | 306.45 | 361.49 | 143.72 | 429.24 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSFVNDIFER | 86.6 | 60.72 | 29.96 | 81.93 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSFVNDIFER | 90.01 | 43.6 | 66.43 | 47.8 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSFVNDIFER | 461.87 | 431.99 | 341.72 | 537 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSFVNDIFER | 102.44 | 91.98 | 180.87 | 209.04 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSFVNDIFER | 77.12 | 39.8 | 301.59 | 163.74 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSFVNDIFER | 178.47 | 239.63 | 257.83 | 331.22 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSFVNDIFER | 152.87 | 215.67 | 260.51 | 295.43 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSFVNDIFER | 230.99 | 157.56 | 295.28 | 113.15 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSFVNDIFER | 256.83 | 157.88 | 184.93 | 349.02 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSFVNDIFER | 788.19 | 639.04 | 1350.44 | 1342.32 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSFVNDIFER | 127.02 | 216.62 | 308.25 | 420.83 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSFVNDIFER | 25.17 | 66.2 | 37.2 | 49.52 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSFVNDIFER | 101.76 | 159.5 | 35.01 | 203.7 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSFVNDIFER | 115.63 | 65.35 | 173.52 | 81.04 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSFVNDIFER | 179.78 | 110.08 | 278.62 | 162.06 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSFVNDIFER | 788.19 | 639.04 | 1350.44 | 1342.32 |

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|---|---|---|---|---|---|
| Histone H2B type 1-C/E/F/G/I | AMGIMNSFVNDIFER | 754.6 | 660.11 | 1441.77 | 1510.51 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSFVNDIFER | 153.41 | 162.44 | 338.24 | 391.47 |
| Histone H2B type 1-C/E/F/G/I | AMGIMNSFVNDIFER | 754.6 | 660.11 | 1441.77 | 1510.51 |
| Histone H2B type 1-C/E/F/G/I | AVTK | 148.31 | 134.21 | 477.05 | 549.01 |
| Histone H2B type 1-C/E/F/G/I | AVTKYTSSK | 654.17 | 582.49 | 968.61 | 960.45 |
| Histone H2B type 1-C/E/F/G/I | AVTKYTSSK | 843.45 | 817.51 | 1202.25 | 1390.58 |
| Histone H2B type 1-C/E/F/G/I | AVTKYTSSK | 331.18 | 472.06 | 912.86 | 822.99 |
| Histone H2B type 1-C/E/F/G/I | AVTKYTSSK | 473.37 | 359.48 | 907.7 | 1077.01 |
| Histone H2B type 1-C/E/F/G/I | DIFER | 1593.21 | 2487.58 | 2488.22 | 3345.97 |
| Histone H2B type 1-C/E/F/G/I | EIQTAVR | 604.17 | 628.08 | 1449.76 | 2002.3 |
| Histone H2B type 1-C/E/F/G/I | EIQTAVR | 560.64 | 461.38 | 653.58 | 630.16 |
| Histone H2B type 1-C/E/F/G/I | EIQTAVR | 411.04 | 241.48 | 590.79 | 801.46 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVY | 775.93 | 680.09 | 960.49 | 835.08 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 1076.52 | 663.49 | 2062.75 | 2565.5 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 382.29 | 528.07 | 1837.97 | 1716.51 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 733.98 | 463.23 | 1256.51 | 1199.2 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 7323.28 | 8177.34 | 19069.2 | 22569.74 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 3424.66 | 3672.25 | 7545.23 | 9604.92 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 2352.45 | 2689.5 | 5036.46 | 6547.51 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 177.28 | 357.57 | 811.03 | 965.94 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 4040.11 | 5739 | 11296.05 | 14499.39 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 5149.31 | 4131.55 | 11376.26 | 14479.84 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 3890.58 | 3917.3 | 10417.68 | 10759.36 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 9540.3 | 11374.57 | 32570.53 | 38824.03 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 1689.37 | 1817.03 | 3551.49 | 3672.69 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 2546.99 | 1660.43 | 3899.39 | 3464.57 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 500.03 | 491.69 | 1823.41 | 1979.59 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 3560.21 | 3471.82 | 6218.5 | 9255.4 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 306.26 | 380.87 | 1472.71 | 1682.19 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 3524.13 | 4483.05 | 9306.06 | 11674.98 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 381.36 | 620.34 | 894.12 | 561.38 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 2094.24 | 2029.32 | 4970.16 | 5638.48 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 1164.41 | 1448.5 | 3386.67 | 4044.16 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 487.37 | 359.78 | 841.96 | 726.99 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 2780.75 | 1757.51 | 6113.09 | 5254.13 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 3277.69 | 3405.68 | 7494.11 | 7046.67 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 1574.9 | 1318.05 | 4026.75 | 5168.07 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 1007 | 829.58 | 2611.98 | 3024.25 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 48785.91 | 53034.17 | 184887 | 227413.7 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 4839.98 | 7139.82 | 14122.17 | 18183.23 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 1695.36 | 1331.49 | 2335.42 | 4239.5 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 2355.47 | 1753.02 | 3159.73 | 4062.06 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 1303.11 | 936.45 | 2889.18 | 2878.31 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 5778.92 | 4054.68 | 12073.42 | 13224.38 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 1366.56 | 1156.68 | 3411.37 | 2759.1 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 1171.57 | 1591.35 | 2623.64 | 3334.11 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 4705.24 | 3643.23 | 7638.75 | 11296.71 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 1849.69 | 1509.84 | 3106.62 | 3992.1 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 1007 | 829.58 | 2611.98 | 3024.25 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 5001.6 | 3831.47 | 8889.42 | 9568.49 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 41229.34 | 43012.36 | 144883.2 | 183573.4 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 8098.13 | 8964.59 | 17551.38 | 22549.53 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 56713.13 | 61118.64 | 230964.2 | 294623 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 1867.16 | 2017.82 | 3924.43 | 3966.87 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 2018.1 | 2318.57 | 3227.77 | 5624.49 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 1218.36 | 1437.11 | 1996.9 | 2262.72 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 5902.44 | 6957.63 | 13283.21 | 16096.88 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 487.13 | 383.27 | 957.38 | 1157.11 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 501.85 | 630.92 | 1365.24 | 1212.6 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 1012.29 | 945.65 | 2382.69 | 3580.91 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 3004.17 | 2131.04 | 5113.95 | 7018.25 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 898.49 | 1124.39 | 1990.05 | 2069.79 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 2780.75 | 1757.51 | 6113.09 | 5254.13 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 500.03 | 491.69 | 1823.41 | 1979.59 |

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| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 3311.48 | 3471.36 | 5716.58 | 6666.04 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 1448.13 | 1608.55 | 3259.34 | 3066.17 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 306.26 | 380.87 | 1472.71 | 1682.19 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 1985.16 | 2062.1 | 4812.21 | 5328.35 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 1076.35 | 574.21 | 2543.68 | 2194.12 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 1218.36 | 1437.11 | 1996.9 | 2262.72 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 2018.1 | 2318.57 | 3227.77 | 5624.49 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 1861.82 | 1694.81 | 2635.39 | 3914.55 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 1012.29 | 945.65 | 2382.69 | 3580.91 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 1012.29 | 945.65 | 2382.69 | 3580.91 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 3004.17 | 2131.04 | 5113.95 | 7018.25 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 1277.18 | 1264.06 | 2256.91 | 1761.06 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 1007 | 829.58 | 2611.98 | 3024.25 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 739.76 | 637.12 | 1888.77 | 1977.07 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 5408.01 | 4636.25 | 7323.39 | 7229.91 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 1076.35 | 574.21 | 2543.68 | 2194.12 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 5857.07 | 6547.1 | 12640.76 | 14807.32 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 153.94 | 110.7 | 342.81 | 350.38 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 2780.75 | 1757.51 | 6113.09 | 5254.13 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 3697.5 | 3524.72 | 6609.07 | 8509.17 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 530.06 | 78.47 | 558.49 | 532.59 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYK | 3004.17 | 2131.04 | 5113.95 | 7018.25 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYKVLK | 485.46 | 548.44 | 1515.95 | 1803.44 |
| Histone H2B type 1-C/E/F/G/I | ESYSVYVYKVLK | 334.2 | 172.88 | 435.9 | 534.6 |
| Histone H2B type 1-C/E/F/G/I | GELAK | 1457.89 | 1389.09 | 2058.59 | 2290.22 |
| Histone H2B type 1-C/E/F/G/I | GELAK | 1348.31 | 1470.66 | 1669.66 | 3162.87 |
| Histone H2B type 1-C/E/F/G/I | GELAK | 773.77 | 893.62 | 1469.23 | 1073.26 |
| Histone H2B type 1-C/E/F/G/I | GELAK | 1903.96 | 1679.84 | 2583.27 | 3006.86 |
| Histone H2B type 1-C/E/F/G/I | GELAK | 824.81 | 851.06 | 1366.22 | 1404.52 |
| Histone H2B type 1-C/E/F/G/I | GELAK | 1256.84 | 933 | 1952.88 | 2320.18 |
| Histone H2B type 1-C/E/F/G/I | GELAK | 840.61 | 991.82 | 1153.9 | 1309.03 |
| Histone H2B type 1-C/E/F/G/I | GELAK | 1529.98 | 1394.42 | 1583.48 | 1682.39 |
| Histone H2B type 1-C/E/F/G/I | GELAK | 1387.51 | 1108.72 | 1664.47 | 2564.02 |
| Histone H2B type 1-C/E/F/G/I | GELAK | 1744.6 | 1572.91 | 2978.2 | 2970.08 |
| Histone H2B type 1-C/E/F/G/I | GELAK | 596.94 | 1130.41 | 1467.6 | 1142.85 |
| Histone H2B type 1-C/E/F/G/I | GELAK | 1511.1 | 1450.81 | 1629.16 | 2542.72 |
| Histone H2B type 1-C/E/F/G/I | HAVSEGTK | 277.5 | 243.61 | 974.78 | 1249.78 |
| Histone H2B type 1-C/E/F/G/I | KESYSVYVYK | 3554.9 | 4315.54 | 11468.69 | 15257.32 |
| Histone H2B type 1-C/E/F/G/I | KESYSVYVYK | 1738.93 | 2133.46 | 6227.21 | 8229.1 |
| Histone H2B type 1-C/E/F/G/I | KESYSVYVYK | 358.57 | 318.32 | 811.28 | 1130.39 |
| Histone H2B type 1-C/E/F/G/I | KESYSVYVYK | 937.13 | 1137.3 | 2752.4 | 3071.97 |
| Histone H2B type 1-C/E/F/G/I | KESYSVYVYK | 959.89 | 696.93 | 2325.44 | 3125.34 |
| Histone H2B type 1-C/E/F/G/I | KESYSVYVYK | 7109.95 | 6701.05 | 16762.98 | 23363.76 |
| Histone H2B type 1-C/E/F/G/I | KESYSVYVYK | 1023.16 | 722.51 | 2051.75 | 2386.53 |
| Histone H2B type 1-C/E/F/G/I | KESYSVYVYK | 2804.55 | 3235.95 | 7996.56 | 11950.12 |
| Histone H2B type 1-C/E/F/G/I | KESYSVYVYK | 5963.9 | 6417.74 | 21946.35 | 25978.26 |
| Histone H2B type 1-C/E/F/G/I | KESYSVYVYK | 887.79 | 1224.71 | 2332.73 | 3201.64 |
| Histone H2B type 1-C/E/F/G/I | KESYSVYVYK | 648.17 | 429.85 | 1945.56 | 2991.1 |
| Histone H2B type 1-C/E/F/G/I | LAHYNK | 2471.12 | 2985.83 | 10846.92 | 12348.12 |
| Histone H2B type 1-C/E/F/G/I | LAHYNK | 617.8 | 345.73 | 1058.58 | 1359.2 |
| Histone H2B type 1-C/E/F/G/I | LAHYNK | 539.66 | 299.56 | 1075.88 | 1173.62 |
| Histone H2B type 1-C/E/F/G/I | LAHYNK | 1469.56 | 2150.93 | 5392.58 | 5677.07 |
| Histone H2B type 1-C/E/F/G/I | LAHYNK | 4115.62 | 2853.34 | 9352.38 | 12624.02 |
| Histone H2B type 1-C/E/F/G/I | LAHYNK | 128.09 | 110.61 | 441.69 | 491.54 |
| Histone H2B type 1-C/E/F/G/I | LAHYNK | 253.54 | 375.86 | 743.47 | 774.99 |
| Histone H2B type 1-C/E/F/G/I | LAHYNK | 366.53 | 595.67 | 838.74 | 1024.38 |
| Histone H2B type 1-C/E/F/G/I | LAHYNK | 252.83 | 553.31 | 638.49 | 712.57 |
| Histone H2B type 1-C/E/F/G/I | LLLPGEL | 174.61 | 88.91 | 68.23 | 99.09 |
| Histone H2B type 1-C/E/F/G/I | LLLPGEL | 77.27 | 25.39 | 56.51 | 130.88 |
| Histone H2B type 1-C/E/F/G/I | LLLPGEL | 245.2 | 30.46 | 147.64 | 146.41 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELA | 59.67 | 62.31 | 103.08 | 148.53 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 3118.23 | 3734.01 | 11091.76 | 15233.83 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 1039.37 | 1142.45 | 1857.06 | 2403.43 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 1618.24 | 2355.68 | 6421.5 | 6540.6 |

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| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 794.73 | 631.66 | 2595.77 | 2258.86 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 666.66 | 624.4 | 2413.44 | 2912.42 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 2401.33 | 3391.82 | 8997.65 | 14025.22 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 593.91 | 578.67 | 1219.16 | 1493.28 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 2236.58 | 3818.04 | 9793.53 | 13528.25 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 1343.91 | 1905.47 | 3793.6 | 5132.07 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 537.5 | 512.93 | 1060.53 | 1094.38 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 371.53 | 208.2 | 519.86 | 770.54 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 406.7 | 669.84 | 958.67 | 1622.88 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 2807.67 | 2394.98 | 9107.28 | 11461.73 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 807.31 | 984.45 | 2810.32 | 3653.83 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 8914.86 | 11465.29 | 36066.34 | 47495.6 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 752.07 | 803.27 | 3411.88 | 4242.67 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 2414.16 | 2443.86 | 7759.3 | 8630.15 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 767.64 | 648.14 | 1454.45 | 2290.05 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 1036.08 | 1254.15 | 3949.86 | 4804.5 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 494.18 | 325.18 | 1251.89 | 1414.49 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 484.51 | 642.31 | 971.99 | 1588.89 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 2519.26 | 1846.93 | 8764.65 | 8841.66 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 279.7 | 451.76 | 776.26 | 1161.18 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 1865.12 | 2007.05 | 5369.04 | 7283.45 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 1903.63 | 3627.87 | 11751.3 | 7073.72 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 332.43 | 348.19 | 706.47 | 1127.23 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 1131.41 | 1198.17 | 3869.64 | 4297.46 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 921.28 | 1426.3 | 4631.29 | 2444.01 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 2814.92 | 2849.21 | 11238.57 | 12761.31 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 3666.33 | 3093.06 | 12013.12 | 15002.3 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 177.33 | 352.86 | 1043.82 | 1480.29 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 1701.65 | 1455.38 | 4109.02 | 4200.89 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 2151.55 | 2112.26 | 6934.03 | 7809.12 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 483.33 | 758.44 | 1560.89 | 2147.81 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 3551.05 | 4376.92 | 13074.34 | 17459.77 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 1121.8 | 1402.88 | 5214.17 | 5607.28 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 30.4 | 82.05 | 138.21 | 190.53 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 9182.82 | 9352.88 | 27613.06 | 37228.57 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 6498.58 | 6357.97 | 21507.41 | 26017.28 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 2275.72 | 2716.48 | 3078.4 | 4492.22 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 1172.59 | 1491.49 | 4102.13 | 3343.25 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 1994.95 | 1945.77 | 6328.86 | 6984.73 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 145.55 | 88.02 | 219 | 266.7 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 6223.82 | 5951.17 | 21786.56 | 25861.08 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 179.33 | 154.97 | 612.66 | 777.82 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 5933.46 | 6871.68 | 21091.49 | 25176.14 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 359.25 | 251.06 | 306.26 | 394.04 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 1574.17 | 1603.44 | 5550.22 | 6852.2 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 2768.83 | 2083.76 | 7304.7 | 9668.31 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 1016.43 | 961.54 | 3017.87 | 2748.96 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 282.63 | 161.9 | 1168.04 | 995.8 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 2971.21 | 3897.72 | 7574.76 | 8478 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 5031.62 | 5333.15 | 17313.57 | 23369.74 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 5442.24 | 6467.29 | 22576.94 | 27520.45 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 1638.11 | 1456.21 | 3981.75 | 4054.66 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 615.03 | 513.24 | 1612.08 | 1136.32 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 890.91 | 703.71 | 1019.71 | 1340.11 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 729.53 | 1008.84 | 3271.78 | 1099.75 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 411.55 | 191.07 | 529.38 | 808.11 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 1897.31 | 1698.78 | 5872.86 | 6434.08 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 1192.42 | 595.61 | 1964.05 | 1989.15 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 1783.99 | 3638.79 | 6915.31 | 7886.89 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 480.34 | 309.21 | 815.79 | 1452.68 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 332.63 | 328.77 | 389.72 | 634.68 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 435.55 | 372.7 | 392.64 | 684.85 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 21558.18 | 22970.01 | 84709.3 | 100086.6 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 2433.83 | 2521 | 7275.45 | 6787.92 |

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| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 2813.87 | 2633.72 | 6530.23 | 7513.52 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 1660.52 | 1263.61 | 2576.05 | 2291.27 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 828.49 | 1870.8 | 3354.73 | 662.9 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 5611.71 | 6320.03 | 19559.82 | 29360.41 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 360.09 | 168.98 | 534.2 | 663.89 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 203.1 | 359.26 | 632.65 | 325.1 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 3383.03 | 3317.13 | 8350 | 12691.89 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 155.02 | 110.33 | 144.3 | 203.94 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 1065.82 | 1507.85 | 3152.39 | 3756.56 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 1131.2 | 898.98 | 2447.26 | 1928.78 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 510.71 | 287.75 | 489.58 | 528.36 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 469.44 | 641.17 | 1455.69 | 1718.37 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 71637.41 | 77802.4 | 271380.3 | 335139 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 1780.25 | 1455.69 | 4443.98 | 4454.83 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 281.97 | 227.06 | 500.52 | 383.88 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 2574.82 | 2953.29 | 8193.59 | 6726.86 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 882.28 | 1024.07 | 1427.12 | 1576.26 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 37046.08 | 39713.57 | 133930.9 | 177706.6 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 588.57 | 255.22 | 536.63 | 384.05 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 280.67 | 355.34 | 542.16 | 442.7 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 52962.66 | 58678.16 | 211020.7 | 256683.5 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 2959.02 | 3718.83 | 8224.17 | 11460.16 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 295.42 | 174.48 | 179.74 | 447.7 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 282.76 | 149.08 | 525.39 | 435.49 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 255.09 | 329.34 | 645.54 | 170.93 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 121.71 | 102.52 | 227.06 | 362.24 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 411.56 | 189.89 | 587.55 | 663.02 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 117258.5 | 120428.4 | 479013 | 579883.8 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 466.04 | 126.8 | 423.51 | 248.12 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 338.38 | 79.77 | 186.22 | 357.18 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 3085.96 | 2773.44 | 7557.54 | 7742.94 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 54292.88 | 60659.47 | 220208.2 | 270141.6 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 526.54 | 425.81 | 1261.82 | 1652.57 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 358.78 | 298.46 | 516.53 | 798.79 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 811.75 | 971.29 | 2487.96 | 2266.3 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 2689.15 | 1551.33 | 2286.24 | 2835.94 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 1197.02 | 885.85 | 2376.66 | 2153 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 116793.6 | 129230 | 493195.1 | 601644.1 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 357.61 | 413.84 | 398.39 | 416.85 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 1752.32 | 65.54 | 548.46 | 432.18 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 256.09 | 231.23 | 389.12 | 261.97 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 90979.78 | 95646.55 | 400063.9 | 479092.8 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 280.88 | 334.36 | 302.72 | 344.64 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 1089.71 | 530.93 | 1657.29 | 1765.8 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 95.04 | 78.26 | 88.77 | 123.94 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 359.56 | 221.4 | 495.88 | 152.01 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 828.49 | 1870.8 | 3354.73 | 662.9 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 864.21 | 362.28 | 613.43 | 896.84 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 145.73 | 70.64 | 120.65 | 288.5 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 1268.26 | 975.55 | 3369.84 | 4412.23 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 581.09 | 355.43 | 713.65 | 674.5 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 729.53 | 1008.84 | 3271.78 | 1099.75 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 729.53 | 1008.84 | 3271.78 | 1099.75 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 154.54 | 50.63 | 120.39 | 160.83 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 141.21 | 91.13 | 80.69 | 111.67 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 380.66 | 689.66 | 552.84 | 623.18 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 585.43 | 884.46 | 1282.76 | 1236.83 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 926.29 | 824.79 | 2240.42 | 2365.7 |
| Histone H2B type 1-C/E/F/G/I | LLLPGELAK | 119.42 | 116.92 | 161.32 | 162.56 |
| Histone H2B type 1-C/E/F/G/I | LLPGELAK | 60.02 | 27.75 | 109.43 | 11.39 |
| Histone H2B type 1-C/E/F/G/I | NSFVNDIFER | 596.57 | 102.43 | 406.28 | 786.68 |
| Histone H2B type 1-C/E/F/G/I | PEPAKSAPAPK | 1919.95 | 1802.57 | 2836.57 | 3816.66 |
| Histone H2B type 1-C/E/F/G/I | PGELAK | 557.17 | 590.73 | 1448.34 | 1954.02 |
| Histone H2B type 1-C/E/F/G/I | PGELAK | 489.62 | 137.57 | 336.64 | 467.89 |

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| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 379.86 | 768.59 | 1491.64 | 1658.16 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 140.61 | 150.6 | 332.41 | 362.73 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 154.73 | 31.77 | 414.7 | 552.06 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 2443.89 | 3761.5 | 10766.94 | 13051.1 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 295.73 | 250.46 | 781.52 | 1019.24 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 38.81 | 0 | 86.25 | 136.89 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 511 | 472.12 | 1527.91 | 1174.12 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 139.82 | 441.57 | 1527.01 | 342.36 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 186.85 | 262.76 | 625.54 | 515.49 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 584.76 | 417.97 | 1063.81 | 1181.41 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 616.06 | 624.17 | 1706.2 | 2797.51 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 383.67 | 285.48 | 854.94 | 1032.22 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 178.49 | 237.83 | 718.91 | 747.61 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 1096.22 | 1057.18 | 3579.36 | 4322.77 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 465.8 | 362.77 | 2049.28 | 2417.69 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 816.45 | 1039.08 | 2734.3 | 3987.61 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 167.34 | 62.46 | 764.92 | 659.35 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 165.2 | 274.32 | 452.19 | 614.85 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 3475.91 | 3609.26 | 11005.28 | 14347.75 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 102.56 | 80.32 | 119.03 | 147.92 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 69.07 | 90.73 | 205.49 | 288.3 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 69.07 | 90.73 | 205.49 | 288.3 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 76.98 | 53.94 | 240.85 | 331.69 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 1559.63 | 805.28 | 4555.08 | 3439.98 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 25.1 | 73.67 | 93.44 | 162.6 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 25.1 | 73.67 | 93.44 | 162.6 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 3253.38 | 3572.93 | 11756.11 | 13585.31 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 649.38 | 735.91 | 1588.29 | 2517.2 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 141.56 | 162.83 | 255.98 | 343.08 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 626.55 | 757.5 | 710.37 | 1069.79 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 704.41 | 830.85 | 2062.74 | 2178.74 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 1366.71 | 1355.07 | 4181.62 | 3928.41 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 208.94 | 207.8 | 603.49 | 754.37 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 823.83 | 1160.99 | 2846.69 | 3889.25 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 728.14 | 933.21 | 1007.91 | 1012.69 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 628.49 | 459.44 | 1192.58 | 1410.75 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 200.6 | 393.96 | 733.99 | 842.76 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 628.38 | 683.28 | 1822.09 | 2391.75 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 724.46 | 765.43 | 1661.54 | 2052.16 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 51.9 | 84.69 | 141.77 | 172.36 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 1449.92 | 1644.33 | 4035.69 | 5830.76 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 114.74 | 153.15 | 301.4 | 320.25 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 372.47 | 434.36 | 924.64 | 1434.78 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 128.54 | 66.01 | 93.27 | 175.52 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 1494.85 | 1673.42 | 5144.98 | 6228.82 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 542.31 | 463.43 | 1257.76 | 1812.53 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 0 | 37.81 | 45.72 | 113.16 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 945.16 | 1088.17 | 3930.02 | 4606.16 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 229.83 | 378.7 | 1009.41 | 927.45 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 502.69 | 442.05 | 1556.21 | 1970.14 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 129.89 | 358.67 | 930.32 | 574.94 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 1871.73 | 2843.05 | 8670.33 | 11042.9 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 45.64 | 171.67 | 436.43 | 331.76 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 208.94 | 207.8 | 603.49 | 754.37 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 127.52 | 166.89 | 213.23 | 258.27 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 3489.25 | 3461.14 | 9932.71 | 14329.38 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 1311.8 | 1886.19 | 4333.22 | 6577.8 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 50.21 | 146.14 | 246.45 | 61.03 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 408.16 | 525.68 | 1542.45 | 1939.5 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 704.41 | 830.85 | 2062.74 | 2178.74 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 577.22 | 631.1 | 867.52 | 1190.3 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 683.56 | 763.94 | 2948.66 | 2499.52 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 381.81 | 575.92 | 802.6 | 875.73 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 1726.62 | 2605.05 | 6454.36 | 8010.2 |

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| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 660.21 | 411.13 | 1444.79 | 948.62 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 9744.27 | 9839.75 | 42109.06 | 46383.64 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 93.52 | 122.25 | 311.84 | 467.2 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 407 | 639.99 | 679.14 | 846.6 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 726.92 | 629 | 1593.06 | 1868.92 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 176.6 | 105.94 | 175.82 | 340.65 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 307.36 | 272.24 | 725.65 | 654.57 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 134.52 | 326.5 | 483.2 | 441.9 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 162.7 | 201.69 | 330.72 | 309.64 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 2475.98 | 2718.65 | 9311.93 | 10968.72 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 11194.18 | 11166.58 | 48393.93 | 56122.98 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 1619.86 | 1238.21 | 2492.3 | 2774.98 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 112.83 | 128.83 | 234.65 | 270.03 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 366.25 | 304.36 | 622.73 | 540.72 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 215.25 | 223.25 | 294.92 | 449.98 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 372.47 | 434.36 | 924.64 | 1434.78 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 628.38 | 683.28 | 1822.09 | 2391.75 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 668.97 | 502.48 | 1255.36 | 1302.39 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 668.97 | 502.48 | 1255.36 | 1302.39 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 704.41 | 830.85 | 2062.74 | 2178.74 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 184.1 | 215.86 | 508.84 | 779.88 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 139.82 | 441.57 | 1527.01 | 342.36 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 93.52 | 122.25 | 311.84 | 467.2 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 1626.49 | 1327.99 | 3186.63 | 3806.67 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 138.51 | 145.51 | 326.35 | 361.2 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 138.51 | 145.51 | 326.35 | 361.2 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 348 | 405.16 | 809.63 | 826.98 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 1449.92 | 1644.33 | 4035.69 | 5830.76 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 549.27 | 414.25 | 1590.63 | 1810.18 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 76.62 | 89.54 | 396.22 | 339.24 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 162.31 | 134.55 | 408.68 | 428.88 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 465.25 | 417.32 | 1214.53 | 1214.44 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 184.1 | 215.86 | 508.84 | 779.88 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 76.62 | 89.54 | 396.22 | 339.24 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 208.94 | 207.8 | 603.49 | 754.37 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 3489.25 | 3461.14 | 9932.71 | 14329.38 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 0 | 37.81 | 45.72 | 113.16 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 1726.62 | 2605.05 | 6454.36 | 8010.2 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 138.51 | 145.51 | 326.35 | 361.2 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 944.31 | 639.97 | 2062.09 | 1727.19 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 1449.92 | 1644.33 | 4035.69 | 5830.76 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 317.13 | 476.3 | 754.95 | 890.57 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 51.9 | 84.69 | 141.77 | 172.36 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 15209.35 | 15752.49 | 59960.52 | 73533.41 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 421.36 | 392.27 | 912.72 | 704.8 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 279.61 | 460.02 | 633.63 | 890.77 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 214.96 | 464.46 | 651.04 | 490.5 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 314.44 | 210.69 | 552.98 | 420.37 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 717.95 | 1195.61 | 1362.5 | 1629.39 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 408.16 | 525.68 | 1542.45 | 1939.5 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 93.52 | 122.25 | 311.84 | 467.2 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 439.08 | 449.94 | 973.82 | 658.43 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 549.27 | 414.25 | 1590.63 | 1810.18 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 421.2 | 407.33 | 806.74 | 1016.64 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 679.79 | 710.15 | 1314.88 | 1310.9 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 372.47 | 434.36 | 924.64 | 1434.78 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 628.38 | 683.28 | 1822.09 | 2391.75 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 310.42 | 394.85 | 819.37 | 1169.3 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 76.33 | 117.98 | 266.9 | 295.26 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 76.33 | 117.98 | 266.9 | 295.26 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 140.34 | 177.57 | 275.87 | 294.26 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 51.9 | 84.69 | 141.77 | 172.36 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 437.23 | 207.13 | 917.3 | 1118.55 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 149.28 | 145.26 | 352.16 | 323.52 |

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|---|---|---|---|---|---|
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 387.86 | 403.29 | 1447.72 | 1916.54 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 324.38 | 505.56 | 876.69 | 1241.13 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 5744.36 | 7681.94 | 27925.91 | 30255.76 |
| Histone H2B type 1-C/E/F/G/I | QVHPDTGISSK | 16258.34 | 14881.07 | 65978.89 | 69315.01 |
| Histone H2B type 1-C/E/F/G/I | RLLLPGELAK | 330.49 | 539.6 | 1457.48 | 360.85 |
| Histone H2B type 1-C/E/F/G/I | RLLLPGELAK | 575.39 | 706.01 | 1689.55 | 625.7 |
| Histone H2B type 1-C/E/F/G/I | RLLLPGELAK | 947.02 | 1224.01 | 2735.03 | 1086.69 |
| Histone H2B type 1-C/E/F/G/I | SFVNDIFER | 636.63 | 719.77 | 465.32 | 944.88 |
| Histone H2B type 1-C/E/F/G/I | SFVNDIFER | 645.71 | 992.13 | 1001.56 | 1640.46 |
| Histone H2B type 1-C/E/F/G/I | SFVNDIFER | 153.17 | 186.35 | 433.11 | 613.19 |
| Histone H2B type 1-C/E/F/G/I | SFVNDIFER | 255.86 | 253.61 | 559.14 | 557.09 |
| Histone H2B type 1-C/E/F/G/I | SFVNDIFER | 3668.94 | 4218.2 | 9749.35 | 10874.69 |
| Histone H2B type 1-C/E/F/G/I | SFVNDIFER | 306.79 | 327.73 | 535.69 | 428.05 |
| Histone H2B type 1-C/E/F/G/I | SFVNDIFER | 612.59 | 541.46 | 757.42 | 718.08 |
| Histone H2B type 1-C/E/F/G/I | STITSR | 150.13 | 167.65 | 411.62 | 405.42 |
| Histone H2B type 1-C/E/F/G/I | VHPDTGISSK | 173.14 | 234.29 | 169.33 | 215.43 |
| Histone H2B type 1-C/E/F/G/I | VLKQVHPDTGISSK | 724.06 | 698.4 | 2159.61 | 3122.19 |
| Histone H2B type 1-C/E/F/G/I | VLKQVHPDTGISSK | 5107.65 | 6013.14 | 14567.1 | 18404.69 |
| Histone H2B type 1-C/E/F/G/I | VLKQVHPDTGISSK | 1913.83 | 2088.29 | 4310.21 | 7676.46 |
| Sphingomyelin phosphodiesterase 2 | AQAELQHVLGR | 2004.27 | 2089 | 3252.15 | 2641.25 |
| Sphingomyelin phosphodiesterase 2 | AQAELQHVLGR | 2944.88 | 2882.39 | 5557.33 | 5812.39 |
| Sphingomyelin phosphodiesterase 2 | AQAR | 206.2 | 53.15 | 444.83 | 501 |
| Sphingomyelin phosphodiesterase 2 | LGLL | 1296.99 | 1434.54 | 5346.49 | 5340.23 |
| Sphingomyelin phosphodiesterase 2 | LGLL | 667.11 | 261.48 | 2492.45 | 2908.78 |
| Sphingomyelin phosphodiesterase 2 | LGLL | 3314.76 | 3998.01 | 22099.16 | 20825.3 |
| Sphingomyelin phosphodiesterase 2 | LGLL | 3659.85 | 3414.84 | 18140.3 | 21295.9 |
| Sphingomyelin phosphodiesterase 2 | LGLL | 332.65 | 326.7 | 492.06 | 841.9 |
| Sphingomyelin phosphodiesterase 2 | LLAL | 196.22 | 188.4 | 226.96 | 250.42 |
| Sphingomyelin phosphodiesterase 2 | LLAL | 75.78 | 172.69 | 115.6 | 69.95 |
| Sphingomyelin phosphodiesterase 2 | VFSK | 1080.67 | 1104.39 | 1567.12 | 2017.99 |
| Prostate stem cell antigen | AVGLLTVISK | 128.32 | 88.3 | 267.91 | 461.39 |
| Prostate stem cell antigen | AVGLLTVISK | 90.37 | 114.64 | 221.22 | 213.32 |
| Prostate stem cell antigen | ILAL | 196.22 | 188.4 | 226.96 | 250.42 |
| Prostate stem cell antigen | ILAL | 75.78 | 172.69 | 115.6 | 69.95 |
| Prostate stem cell antigen | LGLL | 1296.99 | 1434.54 | 5346.49 | 5340.23 |
| Prostate stem cell antigen | LGLL | 667.11 | 261.48 | 2492.45 | 2908.78 |
| Prostate stem cell antigen | LGLL | 3314.76 | 3998.01 | 22099.16 | 20825.3 |
| Prostate stem cell antigen | LGLL | 3659.85 | 3414.84 | 18140.3 | 21295.9 |
| Prostate stem cell antigen | LGLL | 332.65 | 326.7 | 492.06 | 841.9 |
| Prostate stem cell antigen | LLAL | 196.22 | 188.4 | 226.96 | 250.42 |
| Prostate stem cell antigen | LLAL | 75.78 | 172.69 | 115.6 | 69.95 |
| Prostate stem cell antigen | TVISK | 4782.88 | 6610.31 | 9727.15 | 9915.58 |
| Tumor necrosis factor receptor superfamily member 12A | GSSWSADLDK | 2271.1 | 2109.02 | 2985.78 | 2758.18 |
| Tumor necrosis factor receptor superfamily member 12A | MARGSLR | 2321.88 | 3049.72 | 3180.05 | 3235.44 |
| Tumor necrosis factor receptor superfamily member 12A | GSSWSADLDK | 1667.09 | 1784.67 | 2254.8 | 2090.29 |
| Tumor necrosis factor receptor superfamily member 12A | LALLR | 1010.67 | 892.3 | 1517.21 | 956.09 |
| Tumor necrosis factor receptor superfamily member 12A | LALLR | 562.37 | 502.42 | 1117.23 | 1193.58 |
| Tumor necrosis factor receptor superfamily member 12A | LGLL | 1296.99 | 1434.54 | 5346.49 | 5340.23 |
| Tumor necrosis factor receptor superfamily member 12A | LGLL | 667.11 | 261.48 | 2492.45 | 2908.78 |
| Tumor necrosis factor receptor superfamily member 12A | LGLL | 3314.76 | 3998.01 | 22099.16 | 20825.3 |
| Tumor necrosis factor receptor superfamily member 12A | LGLL | 3659.85 | 3414.84 | 18140.3 | 21295.9 |
| Tumor necrosis factor receptor superfamily member 12A | LGLL | 332.65 | 326.7 | 492.06 | 841.9 |
| Tumor necrosis factor receptor superfamily member 12A | LLRL | 912.1 | 950.18 | 1143.27 | 1280.65 |
| Tumor necrosis factor receptor superfamily member 12A | LLRL | 556.67 | 959.36 | 927.48 | 1147.92 |
| Tumor necrosis factor receptor superfamily member 12A | LVWR | 830.07 | 969.55 | 1123.99 | 997.82 |
| Tumor necrosis factor receptor superfamily member 12A | SGFLVWR | 229.67 | 287.62 | 249.59 | 498 |
| Tumor necrosis factor receptor superfamily member 12A | SGFLVWR | 256.11 | 229.14 | 492.3 | 334.79 |
| Tumor necrosis factor receptor superfamily member 12A | VALI | 1296.99 | 1434.54 | 5346.49 | 5340.23 |
| Tumor necrosis factor receptor superfamily member 12A | VALI | 3314.76 | 3998.01 | 22099.16 | 20825.3 |
| Tumor necrosis factor receptor superfamily member 12A | VALI | 3659.85 | 3414.84 | 18140.3 | 21295.9 |
| E3 ubiquitin-protein ligase TRIM11 | LQPPEVVPMELR | 383.84 | 375.75 | 431.26 | 259.53 |
| E3 ubiquitin-protein ligase TRIM11 | EPLAAFCGDELR | 398.33 | 220.18 | 414.47 | 287.32 |
| E3 ubiquitin-protein ligase TRIM11 | FDPGPCVLGQER | 1569.13 | 1356.07 | 2646.03 | 3122.82 |
| E3 ubiquitin-protein ligase TRIM11 | ILVF | 143.35 | 92.25 | 124.04 | 131.39 |

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|---|---|---|---|---|---|
| E3 ubiquitin-protein ligase TRIM11 | LGLL | 1296.99 | 1434.54 | 5346.49 | 5340.23 |
| E3 ubiquitin-protein ligase TRIM11 | LGLL | 667.11 | 261.48 | 2492.45 | 2908.78 |
| E3 ubiquitin-protein ligase TRIM11 | LGLL | 3314.76 | 3998.01 | 22099.16 | 20825.3 |
| E3 ubiquitin-protein ligase TRIM11 | LGLL | 3659.85 | 3414.84 | 18140.3 | 21295.9 |
| E3 ubiquitin-protein ligase TRIM11 | LGLL | 332.65 | 326.7 | 492.06 | 841.9 |
| E3 ubiquitin-protein ligase TRIM11 | LQDIK | 538.29 | 435.34 | 640.67 | 971.58 |
| E3 ubiquitin-protein ligase TRIM11 | LQDIK | 1460.7 | 1855.93 | 2358.64 | 2539.25 |
| E3 ubiquitin-protein ligase TRIM11 | LQDIK | 1346.76 | 1517.15 | 1981.63 | 2159.87 |
| E3 ubiquitin-protein ligase TRIM11 | LSEDRR | 493.79 | 363.06 | 655.72 | 665.62 |
| E3 ubiquitin-protein ligase TRIM11 | RLLAEEEQQLLQR | 462.39 | 274.74 | 459.06 | 362.28 |
| 60S ribosomal protein L29 | AQAAAPASVPAQAPK | 2334.67 | 1680.29 | 6195.06 | 7280.77 |
| 60S ribosomal protein L29 | LAYIAHPK | 1091.7 | 1609.98 | 2154.12 | 2037.67 |
| 60S ribosomal protein L29 | AEAIK | 510.45 | 632.33 | 838.51 | 1051.07 |
| 60S ribosomal protein L29 | AEAIK | 735 | 1000.94 | 1249.24 | 1590.88 |
| 60S ribosomal protein L29 | AEAIK | 459.3 | 580.02 | 1060.27 | 1537.12 |
| 60S ribosomal protein L29 | AEAIK | 510.3 | 541.23 | 664.54 | 1100.17 |
| 60S ribosomal protein L29 | AEAIK | 230.24 | 231.67 | 462.05 | 513.79 |
| 60S ribosomal protein L29 | AEAIK | 691.04 | 450.48 | 608.72 | 1129.16 |
| 60S ribosomal protein L29 | AQAAAPASVPAQAPK | 140.07 | 203.78 | 363.53 | 394.3 |
| 60S ribosomal protein L29 | AQAAAPASVPAQAPK | 101.68 | 166.56 | 324.25 | 496.34 |
| 60S ribosomal protein L29 | AQAAAPASVPAQAPK | 453.21 | 329.94 | 2017.32 | 2868.21 |
| 60S ribosomal protein L29 | AQAAAPASVPAQAPK | 1621.38 | 1513.32 | 7548.06 | 8973.84 |
| 60S ribosomal protein L29 | AQAAAPASVPAQAPK | 1627.28 | 930.07 | 10367.83 | 12292.14 |
| 60S ribosomal protein L29 | AQAAAPASVPAQAPK | 1568.39 | 897.37 | 3637.37 | 4152.4 |
| 60S ribosomal protein L29 | AQAAAPASVPAQAPK | 980.84 | 1606.14 | 2910.22 | 2757.99 |
| 60S ribosomal protein L29 | AQAAAPASVPAQAPK | 345.36 | 347.45 | 748.76 | 759.1 |
| 60S ribosomal protein L29 | AQAAAPASVPAQAPK | 750.98 | 1124.4 | 1306.93 | 1306.04 |
| 60S ribosomal protein L29 | AQAAAPASVPAQAPK | 1153.05 | 1187.72 | 1435.06 | 1410.06 |
| 60S ribosomal protein L29 | AQAAAPASVPAQAPK | 657.96 | 1271.69 | 3723.19 | 4623.08 |
| 60S ribosomal protein L29 | AQAAAPASVPAQAPK | 1532.64 | 1557.34 | 2876.51 | 2545.81 |
| 60S ribosomal protein L29 | AQAAAPASVPAQAPK | 1973.91 | 2428.95 | 4684.92 | 4836.07 |
| 60S ribosomal protein L29 | AQAAAPASVPAQAPK | 513.28 | 353.13 | 1075.53 | 900.39 |
| 60S ribosomal protein L29 | AQAAAPASVPAQAPK | 634.62 | 705.59 | 1227.59 | 1089.49 |
| 60S ribosomal protein L29 | AQAAAPASVPAQAPK | 308.11 | 197.92 | 569.32 | 760.66 |
| 60S ribosomal protein L29 | AQAAAPASVPAQAPK | 1422.06 | 1418.12 | 1870.73 | 2336.71 |
| 60S ribosomal protein L29 | AQAAAPASVPAQAPK | 750.98 | 1124.4 | 1306.93 | 1306.04 |
| 60S ribosomal protein L29 | AQAAAPASVPAQAPK | 872.61 | 808.97 | 1358.11 | 1114.87 |
| 60S ribosomal protein L29 | LAYIAHPK | 2819.61 | 1854.19 | 9751.83 | 9282.65 |
| 60S ribosomal protein L29 | LAYIAHPK | 1004.74 | 947.02 | 4204.44 | 3493.62 |
| 60S ribosomal protein L29 | LAYIAHPK | 1707.08 | 1237.81 | 7671.41 | 10647.88 |
| 60S ribosomal protein L29 | LAYIAHPK | 1351.45 | 1054.18 | 3377.67 | 3661.6 |
| 60S ribosomal protein L29 | LAYIAHPK | 2719.23 | 2835.62 | 16516.98 | 21085.3 |
| 60S ribosomal protein L29 | LAYIAHPK | 1903.72 | 2554.39 | 9641.19 | 8533.61 |
| 60S ribosomal protein L29 | LAYIAHPK | 668.96 | 1249.03 | 5548.61 | 7579.1 |
| 60S ribosomal protein L29 | LAYIAHPK | 1251.21 | 851.16 | 3256.02 | 5664.15 |
| 60S ribosomal protein L29 | LAYIAHPK | 484.48 | 644.77 | 1488.64 | 1756.34 |
| 60S ribosomal protein L29 | LAYIAHPK | 1097.13 | 1180.38 | 5779.56 | 6660.22 |
| 60S ribosomal protein L29 | LAYIAHPK | 943.04 | 766.28 | 5499.29 | 5092.58 |
| 60S ribosomal protein L29 | LAYIAHPK | 1271.06 | 2400.96 | 2953.93 | 3174.46 |
| 60S ribosomal protein L29 | LAYIAHPK | 664.72 | 496.93 | 3460.61 | 4664.11 |
| 60S ribosomal protein L29 | LAYIAHPK | 577.41 | 506.36 | 2090.31 | 2065.44 |
| 60S ribosomal protein L29 | LAYIAHPK | 945.67 | 825.18 | 4384.32 | 4870.69 |
| 60S ribosomal protein L29 | LAYIAHPK | 2296.14 | 2508.37 | 5372.94 | 5504.61 |
| 60S ribosomal protein L29 | LAYIAHPK | 585.81 | 1059.02 | 1050.31 | 1207.89 |
| 60S ribosomal protein L29 | LAYIAHPK | 860.33 | 639.39 | 2930.23 | 4239.33 |
| 60S ribosomal protein L29 | LAYIAHPK | 711.75 | 744.74 | 2252.98 | 3594.46 |
| 60S ribosomal protein L29 | LAYIAHPK | 1269.33 | 443.59 | 1542.61 | 2421.21 |
| 60S ribosomal protein L29 | LAYIAHPK | 703.31 | 620.73 | 2407.84 | 2572.93 |
| 60S ribosomal protein L29 | LAYIAHPK | 658.97 | 533.95 | 2447.84 | 2961.15 |
| 60S ribosomal protein L29 | LAYIAHPK | 306.9 | 317.33 | 1422.07 | 1819.36 |
| 60S ribosomal protein L29 | LAYIAHPK | 2984.78 | 2238.1 | 5580.58 | 5606.15 |
| 60S ribosomal protein L29 | YESLK | 1538.24 | 1535.58 | 5953.25 | 5531.07 |
| 60S ribosomal protein L29 | YESLK | 969.39 | 1673.58 | 4669.1 | 6246.91 |
| 60S ribosomal protein L29 | YESLK | 4095.43 | 4529.43 | 17577.63 | 21368.12 |

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|---|---|---|---|---|---|
| 60S ribosomal protein L29 | YESLK | 3082.65 | 4164.64 | 11409.07 | 13751.92 |
| 60S ribosomal protein L29 | YESLK | 1453.92 | 1568.73 | 7707.87 | 7208.38 |
| 60S ribosomal protein L29 | YESLK | 1297.12 | 1527.93 | 6311.22 | 6729.36 |
| 60S ribosomal protein L29 | YESLK | 1182.42 | 1051.88 | 4642.53 | 3828.26 |
| 60S ribosomal protein L29 | YESLK | 2927.21 | 2712.91 | 7250.63 | 7875.29 |
| 60S ribosomal protein L29 | YESLK | 1050.57 | 567.91 | 1567.04 | 2012.29 |
| Type 1 phosphatidylinositol 4,5-bisphosphate 4-phosphatase | VCQSLINVEGK | 1681.33 | 1654.32 | 2853.37 | 2563.92 |
| Type 1 phosphatidylinositol 4,5-bisphosphate 4-phosphatase | LAVL | 667.11 | 261.48 | 2492.45 | 2908.78 |
| Type 1 phosphatidylinositol 4,5-bisphosphate 4-phosphatase | LGLL | 1296.99 | 1434.54 | 5346.49 | 5340.23 |
| Type 1 phosphatidylinositol 4,5-bisphosphate 4-phosphatase | LGLL | 667.11 | 261.48 | 2492.45 | 2908.78 |
| Type 1 phosphatidylinositol 4,5-bisphosphate 4-phosphatase | LGLL | 3314.76 | 3998.01 | 22099.16 | 20825.3 |
| Type 1 phosphatidylinositol 4,5-bisphosphate 4-phosphatase | LGLL | 3659.85 | 3414.84 | 18140.3 | 21295.9 |
| Type 1 phosphatidylinositol 4,5-bisphosphate 4-phosphatase | LGLL | 332.65 | 326.7 | 492.06 | 841.9 |
| Type 1 phosphatidylinositol 4,5-bisphosphate 4-phosphatase | LICK | 1603.37 | 2122.18 | 1643.54 | 2818.13 |
| Type 1 phosphatidylinositol 4,5-bisphosphate 4-phosphatase | VCQSLINVEGK | 2048.69 | 1955.4 | 4166.09 | 3094.09 |
| Type 1 phosphatidylinositol 4,5-bisphosphate 4-phosphatase | VEGK | 1478.35 | 2133.56 | 2017.74 | 3214.35 |
| Type 1 phosphatidylinositol 4,5-bisphosphate 4-phosphatase | VLCL | 611.67 | 738.6 | 636.02 | 731.71 |
| Type 1 phosphatidylinositol 4,5-bisphosphate 4-phosphatase | VLCL | 526.88 | 1349.68 | 824.39 | 1044.25 |
| Type 1 phosphatidylinositol 4,5-bisphosphate 4-phosphatase | VLCL | 280.74 | 348.72 | 178.21 | 170.57 |
| Choline kinase alpha | LEQFIPSR | 358.98 | 278.5 | 226.9 | 404.76 |
| Choline kinase alpha | AQAR | 206.2 | 53.15 | 444.83 | 501 |
| Choline kinase alpha | IFPQGR | 333.91 | 202.2 | 262.98 | 226.54 |
| Choline kinase alpha | LGLL | 1296.99 | 1434.54 | 5346.49 | 5340.23 |
| Choline kinase alpha | LGLL | 667.11 | 261.48 | 2492.45 | 2908.78 |
| Choline kinase alpha | LGLL | 3314.76 | 3998.01 | 22099.16 | 20825.3 |
| Choline kinase alpha | LGLL | 3659.85 | 3414.84 | 18140.3 | 21295.9 |
| Choline kinase alpha | LGLL | 332.65 | 326.7 | 492.06 | 841.9 |
| Choline kinase alpha | LLEV | 538.71 | 180.42 | 590.2 | 407.12 |
| Choline kinase alpha | LLEV | 581.57 | 945.93 | 1022.29 | 951.69 |
| Choline kinase alpha | LLRL | 912.1 | 950.18 | 1143.27 | 1280.65 |
| Choline kinase alpha | LLRL | 556.67 | 959.36 | 927.48 | 1147.92 |
| Choline kinase alpha | LRIK | 3814.3 | 3262.06 | 4759.66 | 4438.43 |
| Choline kinase alpha | MPFNK | 3074.2 | 4254.47 | 3964.41 | 4320.72 |
| Putative histone H2B type 2-C | ESYSIYVYK | 7359.69 | 8622.83 | 20940.72 | 29384.54 |
| Putative histone H2B type 2-C | KESYSIYVYK | 789.86 | 686.94 | 2698.18 | 2518.95 |
| Putative histone H2B type 2-C | AHNTK | 306.98 | 309.66 | 152.47 | 248.5 |
| Putative histone H2B type 2-C | VHPDTGIWCK | 128.82 | 39.12 | 145.83 | 197.73 |
| Putative histone H2B type 2-C | FAPAPK | 98.6 | 471.68 | 560.73 | 807 |
| Putative histone H2B type 2-C | SIYVYK | 777.71 | 717.09 | 1198.1 | 1706.9 |
| Putative histone H2B type 2-C | AMGIMNSF | 195.49 | 47.46 | 127.29 | 113.32 |
| Putative histone H2B type 2-C | AMGIMNSF | 214.49 | 85.76 | 184.4 | 273.87 |
| Putative histone H2B type 2-C | AMGIMNSF | 188.54 | 96.31 | 289.39 | 332.57 |
| Putative histone H2B type 2-C | AMGIMNSF | 150.04 | 69.84 | 144.38 | 251.1 |
| Putative histone H2B type 2-C | AVTK | 148.31 | 134.21 | 477.05 | 549.01 |
| Putative histone H2B type 2-C | DIFER | 1593.21 | 2487.58 | 2488.22 | 3345.97 |
| Putative histone H2B type 2-C | ESYSIY | 518.32 | 706.43 | 1186.45 | 1567.91 |
| Putative histone H2B type 2-C | ESYSIYVY | 385.11 | 249.72 | 278.09 | 474.99 |
| Putative histone H2B type 2-C | ESYSIYVYK | 2407.35 | 2584.54 | 4708.27 | 7602 |
| Putative histone H2B type 2-C | ESYSIYVYK | 1492.24 | 1506.08 | 2953.59 | 4650.42 |
| Putative histone H2B type 2-C | ESYSIYVYK | 2492.72 | 2341.78 | 6297.51 | 8283.88 |
| Putative histone H2B type 2-C | ESYSIYVYK | 2447.35 | 2994.17 | 7542.64 | 7935.67 |
| Putative histone H2B type 2-C | ESYSIYVYK | 2877.15 | 1595.05 | 5232.34 | 5730.78 |
| Putative histone H2B type 2-C | ESYSIYVYK | 2351.57 | 2776.72 | 6203.39 | 7197.23 |
| Putative histone H2B type 2-C | ESYSIYVYK | 1840.84 | 1746.13 | 4535.6 | 4535.71 |
| Putative histone H2B type 2-C | ESYSIYVYK | 2395.5 | 2159.53 | 4711.91 | 6033.31 |
| Putative histone H2B type 2-C | ESYSIYVYK | 2745.17 | 2399.89 | 5423.25 | 6049.48 |
| Putative histone H2B type 2-C | ESYSIYVYK | 1826.93 | 1524.67 | 4690.38 | 5744.3 |
| Putative histone H2B type 2-C | ESYSIYVYK | 332.09 | 381.88 | 955.68 | 946.51 |
| Putative histone H2B type 2-C | ESYSIYVYK | 1685.23 | 1375.38 | 3924.65 | 4511.28 |
| Putative histone H2B type 2-C | ESYSIYVYK | 10924.99 | 10528.04 | 24797.36 | 28806.99 |
| Putative histone H2B type 2-C | ESYSIYVYK | 1713.97 | 1195.27 | 1080.05 | 1900.41 |
| Putative histone H2B type 2-C | ESYSIYVYK | 3430.56 | 4472.62 | 10590.55 | 5635.34 |

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|---|---|---|---|---|---|
| Putative histone H2B type 2-C | ESYSIYVYK | 1393.64 | 1247.78 | 1730.82 | 2776.3 |
| Putative histone H2B type 2-C | ESYSIYVYK | 28382.45 | 27044.79 | 107648.8 | 136501 |
| Putative histone H2B type 2-C | ESYSIYVYK | 8105.2 | 10819.34 | 27051.29 | 38427.75 |
| Putative histone H2B type 2-C | ESYSIYVYK | 30458.38 | 31521.15 | 113710.2 | 130986.3 |
| Putative histone H2B type 2-C | ESYSIYVYK | 24313.56 | 26382.4 | 85487.27 | 101571.4 |
| Putative histone H2B type 2-C | ESYSIYVYK | 927.29 | 939.27 | 2105.59 | 1582.47 |
| Putative histone H2B type 2-C | ESYSIYVYK | 512.21 | 458.73 | 855.9 | 1407.22 |
| Putative histone H2B type 2-C | ESYSIYVYK | 2742.94 | 2088.44 | 4987.17 | 6139.46 |
| Putative histone H2B type 2-C | ESYSIYVYK | 3980.45 | 3442.25 | 6460.54 | 8976.7 |
| Putative histone H2B type 2-C | ESYSIYVYK | 3217.36 | 2450.42 | 4225.16 | 4439.98 |
| Putative histone H2B type 2-C | ESYSIYVYK | 1665.3 | 1322.53 | 2356.93 | 2561.51 |
| Putative histone H2B type 2-C | ESYSIYVYK | 1359.01 | 1477.84 | 1647.73 | 2062.43 |
| Putative histone H2B type 2-C | ESYSIYVYK | 909.45 | 1212.11 | 1866.02 | 3003.51 |
| Putative histone H2B type 2-C | ESYSIYVYK | 512.21 | 458.73 | 855.9 | 1407.22 |
| Putative histone H2B type 2-C | ESYSIYVYK | 512.21 | 458.73 | 855.9 | 1407.22 |
| Putative histone H2B type 2-C | ESYSIYVYK | 3275.47 | 3624.15 | 7971.1 | 7434.94 |
| Putative histone H2B type 2-C | ESYSIYVYK | 3081.45 | 3537.7 | 4022.62 | 5567.5 |
| Putative histone H2B type 2-C | ESYSIYVYK | 2455.09 | 2016.49 | 4548.33 | 5916.35 |
| Putative histone H2B type 2-C | ESYSIYVYK | 1776.53 | 1929.09 | 2901.41 | 4401.92 |
| Putative histone H2B type 2-C | ESYSIYVYK | 3336.2 | 4326.61 | 5127.11 | 5899.32 |
| Putative histone H2B type 2-C | ESYSIYVYK | 1570.78 | 1512.88 | 3819.04 | 3607.31 |
| Putative histone H2B type 2-C | IAGEASR | 165.44 | 144.04 | 353.21 | 503.41 |
| Putative histone H2B type 2-C | IAGEASRL | 846.05 | 666.97 | 1033.18 | 1010.71 |
| Putative histone H2B type 2-C | KESYSIYVYK | 2461.09 | 2488.12 | 8802.06 | 10451.9 |
| Putative histone H2B type 2-C | KESYSIYVYK | 9107.13 | 8639.05 | 24797.96 | 30946.26 |
| Putative histone H2B type 2-C | KESYSIYVYK | 1132.86 | 735.3 | 1336.04 | 1442.95 |
| Putative histone H2B type 2-C | KESYSIYVYK | 6623.38 | 9028.73 | 24730.19 | 34352.63 |
| Putative histone H2B type 2-C | KESYSIYVYK | 435.58 | 370.09 | 521.59 | 1042.49 |
| Putative histone H2B type 2-C | LAHYNK | 471.05 | 695.36 | 1375.76 | 2331.67 |
| Putative histone H2B type 2-C | LAHYNK | 2471.12 | 2985.83 | 10846.92 | 12348.12 |
| Putative histone H2B type 2-C | LAHYNK | 617.8 | 345.73 | 1058.58 | 1359.2 |
| Putative histone H2B type 2-C | LAHYNK | 539.66 | 299.56 | 1075.88 | 1173.62 |
| Putative histone H2B type 2-C | LAHYNK | 1469.56 | 2150.93 | 5392.58 | 5677.07 |
| Putative histone H2B type 2-C | LAHYNK | 4115.62 | 2853.34 | 9352.38 | 12624.02 |
| Putative histone H2B type 2-C | LAHYNK | 128.09 | 110.61 | 441.69 | 491.54 |
| Putative histone H2B type 2-C | LAHYNK | 253.54 | 375.86 | 743.47 | 774.99 |
| Putative histone H2B type 2-C | LAHYNK | 366.53 | 595.67 | 838.74 | 1024.38 |
| Putative histone H2B type 2-C | LAHYNK | 252.83 | 553.31 | 638.49 | 712.57 |
| Putative histone H2B type 2-C | LNDIFER | 819.97 | 1116.49 | 2189.56 | 2278.42 |
| Putative histone H2B type 2-C | LNDIFER | 2050.07 | 2563.82 | 5819.06 | 4224.69 |
| Putative histone H2B type 2-C | LNDIFER | 4086.88 | 5905.96 | 6854.98 | 9693.13 |
| Putative histone H2B type 2-C | SIYVYK | 550.75 | 587.45 | 995.94 | 1652.17 |
| Putative histone H2B type 2-C | STITSR | 420.06 | 413.54 | 1088.58 | 1343.96 |
| Putative histone H2B type 2-C | STITSR | 150.13 | 167.65 | 411.62 | 405.42 |
| Transmembrane protein 65 | DFIYSLHSTER | 1477.14 | 1401.75 | 1946.74 | 2017.84 |
| Transmembrane protein 65 | KEPMEALNTAQGAR | 504.11 | 620.85 | 897.84 | 1031.93 |
| Transmembrane protein 65 | QVDMWQTR | 1721.91 | 1794.1 | 3609.03 | 3413.87 |
| Transmembrane protein 65 | IGII | 1296.99 | 1434.54 | 5346.49 | 5340.23 |
| Transmembrane protein 65 | IGII | 667.11 | 261.48 | 2492.45 | 2908.78 |
| Transmembrane protein 65 | IGII | 3314.76 | 3998.01 | 22099.16 | 20825.3 |
| Transmembrane protein 65 | IGII | 3659.85 | 3414.84 | 18140.3 | 21295.9 |
| Transmembrane protein 65 | IGII | 332.65 | 326.7 | 492.06 | 841.9 |
| Transmembrane protein 65 | KEPMEALNTAQGAR | 539.28 | 443.73 | 1605.18 | 2047.13 |
| Transmembrane protein 65 | KEPMEALNTAQGAR | 563.81 | 679.61 | 963.86 | 1453.82 |
| Transmembrane protein 65 | KEPMEALNTAQGAR | 408.73 | 469.07 | 829.82 | 1192.68 |
| Transmembrane protein 65 | LLAL | 196.22 | 188.4 | 226.96 | 250.42 |
| Transmembrane protein 65 | LLAL | 75.78 | 172.69 | 115.6 | 69.95 |
| Transmembrane protein 65 | LPLLR | 2878.52 | 2629.2 | 4548.76 | 4509.69 |
| Transmembrane protein 65 | LPLLR | 2910.98 | 2507.35 | 3967.9 | 4971.32 |
| Transmembrane protein 65 | LPLLR | 2091.52 | 3149.96 | 3906.01 | 4705.2 |
| Transmembrane protein 65 | LPLLR | 3488.74 | 3936.48 | 5409.66 | 6450.34 |
| Mothers against decapentaplegic homolog 5 | VESPVLPPVLVPR | 191.22 | 256.95 | 577.7 | 439.96 |
| Mothers against decapentaplegic homolog 5 | DVQPVAYEEPK | 728.76 | 978.85 | 822.35 | 1086.91 |
| Mothers against decapentaplegic homolog 5 | ALSSPGQPSK | 627.44 | 775.97 | 1016.92 | 1694.25 |

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|---|---|---|---|---|---|
| Mothers against decapentaplegic homolog 5 | EVCINPYHYK | 1828.29 | 2240.81 | 2238.26 | 2732.97 |
| Mothers against decapentaplegic homolog 5 | ALSSPGQPSK | 449.79 | 349.32 | 592.7 | 758.18 |
| Mothers against decapentaplegic homolog 5 | ALSSPGQPSK | 460.03 | 401.12 | 652.43 | 519.67 |
| Mothers against decapentaplegic homolog 5 | AVDALVK | 1221.87 | 1090.2 | 1910.8 | 2284.54 |
| Mothers against decapentaplegic homolog 5 | AVDALVK | 1585.64 | 1321.28 | 3987.36 | 3270.08 |
| Mothers against decapentaplegic homolog 5 | DALVK | 728.04 | 730.32 | 1416.93 | 1299.98 |
| Mothers against decapentaplegic homolog 5 | DALVK | 281.16 | 307.2 | 368.8 | 771.11 |
| Mothers against decapentaplegic homolog 5 | DALVK | 330.72 | 516.99 | 979.64 | 830.05 |
| Mothers against decapentaplegic homolog 5 | DALVK | 541.46 | 973.28 | 1092.56 | 951.76 |
| Mothers against decapentaplegic homolog 5 | FCLGLLSNVNR | 255.79 | 260.79 | 204.22 | 347.81 |
| Mothers against decapentaplegic homolog 5 | FCLGLLSNVNR | 232.28 | 30.42 | 196.97 | 220.67 |
| Mothers against decapentaplegic homolog 5 | GLPHVIYCR | 3024.81 | 3176.33 | 4659.81 | 6743.55 |
| Mothers against decapentaplegic homolog 5 | LGLL | 1296.99 | 1434.54 | 5346.49 | 5340.23 |
| Mothers against decapentaplegic homolog 5 | LGLL | 667.11 | 261.48 | 2492.45 | 2908.78 |
| Mothers against decapentaplegic homolog 5 | LGLL | 3314.76 | 3998.01 | 22099.16 | 20825.3 |
| Mothers against decapentaplegic homolog 5 | LGLL | 3659.85 | 3414.84 | 18140.3 | 21295.9 |
| Mothers against decapentaplegic homolog 5 | LGLL | 332.65 | 326.7 | 492.06 | 841.9 |
| Mothers against decapentaplegic homolog 5 | LLGWK | 1541.18 | 2095.95 | 2849.91 | 3434.84 |
| Mothers against decapentaplegic homolog 5 | LLGWK | 2032.78 | 1824.89 | 2595.5 | 3920.65 |
| Mothers against decapentaplegic homolog 5 | MSFVK | 633.47 | 606.02 | 838.1 | 1358.43 |
| Mothers against decapentaplegic homolog 5 | VESPVLPPVLVPR | 257.37 | 104.51 | 270.03 | 204.42 |
| Interferon-related developmental regulator 2 | LLPDFLLER | 214.48 | 193.2 | 295.09 | 365.08 |
| Interferon-related developmental regulator 2 | QGALESLR | 1333.42 | 2303.09 | 1609.46 | 1920.18 |
| Interferon-related developmental regulator 2 | LPQLLSSESVNLR | 89.24 | 119.79 | 130.25 | 121.38 |
| Interferon-related developmental regulator 2 | AVLHSVEGGECEEEIVR | 384.49 | 311.29 | 1064.11 | 950.5 |
| Interferon-related developmental regulator 2 | EIVR | 334.17 | 388.86 | 709.55 | 798.59 |
| Interferon-related developmental regulator 2 | EIVR | 153.27 | 176.51 | 174.96 | 329.95 |
| Interferon-related developmental regulator 2 | EIVR | 180.45 | 257.22 | 444.12 | 348.36 |
| Interferon-related developmental regulator 2 | FLLER | 1360.38 | 810.33 | 1843.89 | 1805.08 |
| Interferon-related developmental regulator 2 | FLLER | 1038.48 | 1229.85 | 2004.81 | 1668.97 |
| Interferon-related developmental regulator 2 | FLLER | 4006.63 | 3302.59 | 4549.6 | 5389.65 |
| Interferon-related developmental regulator 2 | LFELAR | 102.71 | 64.79 | 248.31 | 166.5 |
| Interferon-related developmental regulator 2 | LGLL | 1296.99 | 1434.54 | 5346.49 | 5340.23 |
| Interferon-related developmental regulator 2 | LGLL | 667.11 | 261.48 | 2492.45 | 2908.78 |
| Interferon-related developmental regulator 2 | LGLL | 3314.76 | 3998.01 | 22099.16 | 20825.3 |
| Interferon-related developmental regulator 2 | LGLL | 3659.85 | 3414.84 | 18140.3 | 21295.9 |
| Interferon-related developmental regulator 2 | LGLL | 332.65 | 326.7 | 492.06 | 841.9 |
| Interferon-related developmental regulator 2 | LPQLLSSESVNLR | 599.46 | 30.08 | 144.79 | 211.13 |
| Interferon-related developmental regulator 2 | QGALESLR | 702.07 | 849.83 | 919.42 | 1099.1 |
| Interferon-related developmental regulator 2 | QGALESLR | 2605.93 | 2114.26 | 1712.46 | 1675.56 |
| 60S ribosomal protein L31 | NLQTVNVDEN | 357.19 | 454.97 | 439.69 | 667.22 |
| 60S ribosomal protein L31 | SAINEVVTR | 821.83 | 826.53 | 781.92 | 1919.87 |
| 60S ribosomal protein L31 | IHGVGFK | 4115.55 | 4243.2 | 11343.92 | 13274.84 |
| 60S ribosomal protein L31 | EYTINIHK | 3562.01 | 4357.69 | 11432.17 | 12187.15 |
| 60S ribosomal protein L31 | EYTINIHKR | 1159.17 | 1433.47 | 4309.04 | 6492.08 |
| 60S ribosomal protein L31 | FAMKEMGTPDVR | 1015.13 | 1303.17 | 1601.8 | 2555.19 |
| 60S ribosomal protein L31 | EYTINIH | 1473.86 | 1194.66 | 2787.92 | 2651.19 |
| 60S ribosomal protein L31 | AVWAK | 2053.7 | 2524.3 | 8558.8 | 10216.96 |
| 60S ribosomal protein L31 | AVWAK | 2421.55 | 3095.95 | 8878.76 | 8634.07 |
| 60S ribosomal protein L31 | AVWAK | 693.84 | 1130.47 | 2013.71 | 3172.17 |
| 60S ribosomal protein L31 | AVWAK | 6860.86 | 8863.8 | 19731.35 | 24183.16 |
| 60S ribosomal protein L31 | AVWAK | 7516.36 | 8250.38 | 25067.54 | 29906.85 |
| 60S ribosomal protein L31 | AVWAK | 1996.27 | 2879.13 | 3769.59 | 4752.48 |
| 60S ribosomal protein L31 | AVWAK | 3263.9 | 2852.91 | 6271.94 | 7391.23 |
| 60S ribosomal protein L31 | AVWAK | 1803.44 | 2780.97 | 4172.58 | 4117.48 |
| 60S ribosomal protein L31 | AVWAK | 674.75 | 889.53 | 2566.28 | 2206.24 |
| 60S ribosomal protein L31 | AVWAK | 11592.78 | 13912.97 | 25010.45 | 34096.6 |
| 60S ribosomal protein L31 | AVWAK | 1224.3 | 1275.69 | 2194.35 | 2602.54 |
| 60S ribosomal protein L31 | AVWAK | 1130.76 | 1368.28 | 2318.7 | 2319.53 |
| 60S ribosomal protein L31 | AVWAK | 12429.93 | 11949.28 | 37327.15 | 43216.64 |
| 60S ribosomal protein L31 | AVWAK | 7576.4 | 9127.25 | 23917.18 | 30152.94 |
| 60S ribosomal protein L31 | EYTINIHK | 5198.11 | 4416.31 | 16685.11 | 20881.51 |
| 60S ribosomal protein L31 | EYTINIHK | 894.55 | 982.31 | 2437.25 | 2526.95 |
| 60S ribosomal protein L31 | EYTINIHK | 4104.43 | 4810.42 | 10718.61 | 11776.48 |

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|---|---|---|---|---|---|
| 60S ribosomal protein L31 | EYTINIHK | 2044.79 | 2447.03 | 5232.91 | 5239.33 |
| 60S ribosomal protein L31 | EYTINIHK | 18286.22 | 18360.55 | 75200.23 | 92285.68 |
| 60S ribosomal protein L31 | EYTINIHK | 1644.06 | 1719.09 | 4147.17 | 5062.23 |
| 60S ribosomal protein L31 | EYTINIHK | 1148.34 | 1546.65 | 4335.01 | 4793.68 |
| 60S ribosomal protein L31 | EYTINIHK | 1666.3 | 1011.05 | 4676.16 | 6170.3 |
| 60S ribosomal protein L31 | EYTINIHK | 2506.66 | 2560.27 | 7938.38 | 9454.02 |
| 60S ribosomal protein L31 | EYTINIHK | 882.85 | 1180.32 | 2791.07 | 2735.79 |
| 60S ribosomal protein L31 | EYTINIHK | 1120.51 | 1424.04 | 2150.98 | 3628.63 |
| 60S ribosomal protein L31 | EYTINIHK | 6500.92 | 6659.46 | 23127.24 | 28455.17 |
| 60S ribosomal protein L31 | EYTINIHK | 4163 | 3810.43 | 9759.24 | 10881.79 |
| 60S ribosomal protein L31 | EYTINIHK | 877.12 | 788.84 | 2177.73 | 2673.1 |
| 60S ribosomal protein L31 | EYTINIHKR | 1022.43 | 901.18 | 2311.44 | 3685.78 |
| 60S ribosomal protein L31 | FAMK | 3007.55 | 3711.17 | 9382.64 | 10454.26 |
| 60S ribosomal protein L31 | FAMK | 1285.38 | 1836.7 | 3420.35 | 5620.44 |
| 60S ribosomal protein L31 | FAMK | 3003.9 | 3327.02 | 8186.22 | 10407.54 |
| 60S ribosomal protein L31 | FAMK | 2988.79 | 3969.03 | 5738.11 | 9092.73 |
| 60S ribosomal protein L31 | FAMK | 1494.31 | 1833.07 | 3100.39 | 4688.25 |
| 60S ribosomal protein L31 | FAMK | 3849.62 | 4453.29 | 8255.63 | 11007.05 |
| 60S ribosomal protein L31 | FAMK | 1137.72 | 1425.27 | 2824.93 | 3427.63 |
| 60S ribosomal protein L31 | FAMK | 4737.05 | 3585.63 | 8722.35 | 13012.68 |
| 60S ribosomal protein L31 | IHGVGFK | 968.97 | 544.13 | 2137.9 | 1656.79 |
| 60S ribosomal protein L31 | IHGVGFK | 1529.87 | 1617.59 | 5331.55 | 6177.91 |
| 60S ribosomal protein L31 | IHGVGFK | 1493.85 | 1878.63 | 4784.64 | 5641.07 |
| 60S ribosomal protein L31 | IHGVGFK | 1898.81 | 2189.13 | 5866.26 | 6687.39 |
| 60S ribosomal protein L31 | IHGVGFK | 1063.63 | 1724.36 | 2662.87 | 3545.57 |
| 60S ribosomal protein L31 | IHGVGFK | 3497.63 | 4334.75 | 7962.56 | 10961.42 |
| 60S ribosomal protein L31 | NLQTVNVDEN | 1242.2 | 1528.4 | 3829.98 | 3130.88 |
| 60S ribosomal protein L31 | NLQTVNVDEN | 639.11 | 474.62 | 934.64 | 1317.24 |
| 60S ribosomal protein L31 | NLQTVNVDEN | 329.69 | 618.49 | 1281.14 | 1017.07 |
| 60S ribosomal protein L31 | SAINEVVTR | 6716.56 | 6311.35 | 26152.61 | 28579.54 |
| 60S ribosomal protein L31 | SAINEVVTR | 2215.39 | 1974.97 | 5778.45 | 6287.37 |
| 60S ribosomal protein L31 | SAINEVVTR | 2306.3 | 2781.12 | 6045.39 | 6873.25 |
| 60S ribosomal protein L31 | SAINEVVTR | 9779.9 | 8340.9 | 32347.39 | 41619.07 |
| 60S ribosomal protein L31 | SAINEVVTR | 1883.61 | 2095.13 | 4880.27 | 6536.26 |
| 60S ribosomal protein L31 | SAINEVVTR | 1090.26 | 1433.15 | 1917.49 | 2598.53 |
| 60S ribosomal protein L31 | SAINEVVTR | 2782.22 | 2250.57 | 6450.92 | 8420.08 |
| 60S ribosomal protein L31 | SAINEVVTR | 1819.59 | 1824.44 | 6164.9 | 5716.81 |
| 60S ribosomal protein L31 | SAINEVVTR | 2407.49 | 2463.87 | 4240.74 | 4320 |
| 60S ribosomal protein L31 | SAINEVVTR | 1678.21 | 2175.2 | 3161.46 | 3606.64 |
| 60S ribosomal protein L31 | SAINEVVTR | 6950.61 | 7230.98 | 18419.75 | 20828.69 |
| 60S ribosomal protein L31 | SAINEVVTR | 1305.54 | 909.3 | 2946.87 | 3013.04 |
| 60S ribosomal protein L31 | SAINEVVTR | 2842.01 | 2619.23 | 5122.62 | 4162.81 |
| 60S ribosomal protein L31 | SAINEVVTR | 428.9 | 710.6 | 1095.42 | 920.33 |
| 60S ribosomal protein L31 | SAINEVVTR | 2264.72 | 1570.12 | 2167.59 | 1786.85 |
| 60S ribosomal protein L31 | SAINEVVTR | 4076.5 | 4484.17 | 8130.15 | 7974.31 |
| 60S ribosomal protein L31 | SAINEVVTR | 482.56 | 515.22 | 1042.44 | 1054.43 |
| 60S ribosomal protein L31 | SAINEVVTR | 1415.95 | 1490.57 | 2351.65 | 2401.79 |
| 60S ribosomal protein L31 | SAINEVVTR | 4661.06 | 5560.58 | 11835.64 | 12284.95 |
| 60S ribosomal protein L31 | SAINEVVTR | 1702.47 | 1480.49 | 3130 | 3364.4 |
| 60S ribosomal protein L31 | SAINEVVTR | 1958.81 | 1899.57 | 3480.72 | 2587.66 |
| Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial | AVAMLWK | 663.66 | 708.83 | 1014.16 | 1068.66 |
| Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial | ALLLR | 2985.64 | 3641.8 | 8639.29 | 10643.07 |
| Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial | ALLLR | 807.23 | 1311.26 | 2069.48 | 2004.08 |
| Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial | AVAMLWK | 2142.79 | 1488.38 | 1764.28 | 2062.66 |
| Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial | AVAMLWK | 537.21 | 541.71 | 542.48 | 764.85 |
| Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial | AVAMLWK | 652.4 | 438.14 | 775.34 | 694.66 |
| Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial | AVAMLWK | 461.68 | 344.77 | 401.72 | 442.53 |
| Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial | AVAMLWK | 329.31 | 656.17 | 695.4 | 1203.58 |
| Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial | AVAMLWK | 538.74 | 816.02 | 1275.65 | 1124.36 |
| Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial | AVAMLWK | 851.35 | 569.11 | 589 | 635.4 |
| Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial | GLLP | 206.92 | 0 | 95.22 | 278.73 |
| Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial | LAAAL | 360.02 | 175.04 | 234.41 | 373.2 |

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| Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial | LGLL | 1296.99 | 1434.54 | 5346.49 | 5340.23 |
| Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial | LGLL | 667.11 | 261.48 | 2492.45 | 2908.78 |
| Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial | LGLL | 3314.76 | 3998.01 | 22099.16 | 20825.3 |
| Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial | LGLL | 3659.85 | 3414.84 | 18140.3 | 21295.9 |
| Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial | LGLL | 332.65 | 326.7 | 492.06 | 841.9 |
| Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial | LLAL | 196.22 | 188.4 | 226.96 | 250.42 |
| Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial | LLAL | 75.78 | 172.69 | 115.6 | 69.95 |
| Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial | LLLR | 386.99 | 489.76 | 684.01 | 680.12 |
| Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial | LLLR | 769.62 | 771.66 | 1081.49 | 1259.46 |
| Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial | LLLR | 864.03 | 699.71 | 1475.57 | 835.82 |
| Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial | LLLR | 912.1 | 950.18 | 1143.27 | 1280.65 |
| Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial | LLLR | 556.67 | 959.36 | 927.48 | 1147.92 |
| Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial | LLLR | 1415.65 | 1626.01 | 1823.04 | 1846.6 |
| Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial | LLLR | 279.39 | 481.67 | 627.51 | 552.92 |
| Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial | LLLR | 487.03 | 393.55 | 449.11 | 438.94 |
| Gamma-glutamyl hydrolase | NLDGISHAPNAVK | 407.77 | 563.8 | 774.94 | 997.54 |
| Gamma-glutamyl hydrolase | YYIAASYVK | 611.99 | 494.2 | 1288.7 | 898.75 |
| Gamma-glutamyl hydrolase | ILFK | 2470.97 | 2256.62 | 2983.58 | 3778.41 |
| Gamma-glutamyl hydrolase | ILFK | 2258.5 | 2184.3 | 3616.36 | 2876.62 |
| Gamma-glutamyl hydrolase | ILFK | 2361.06 | 3115.46 | 4624.91 | 5380.97 |
| Gamma-glutamyl hydrolase | ILFK | 1293.11 | 2456.52 | 2411.93 | 2123.8 |
| Gamma-glutamyl hydrolase | ILFK | 3623.08 | 1834.68 | 3835.96 | 5244.06 |
| Gamma-glutamyl hydrolase | LDLTEK | 1098.04 | 1090.06 | 2158.79 | 1517.13 |
| Gamma-glutamyl hydrolase | LGLL | 1296.99 | 1434.54 | 5346.49 | 5340.23 |
| Gamma-glutamyl hydrolase | LGLL | 667.11 | 261.48 | 2492.45 | 2908.78 |
| Gamma-glutamyl hydrolase | LGLL | 3314.76 | 3998.01 | 22099.16 | 20825.3 |
| Gamma-glutamyl hydrolase | LGLL | 3659.85 | 3414.84 | 18140.3 | 21295.9 |
| Gamma-glutamyl hydrolase | LGLL | 332.65 | 326.7 | 492.06 | 841.9 |
| Gamma-glutamyl hydrolase | NLDGISHAPNAVK | 1442.1 | 1247.07 | 2652.48 | 2549.56 |
| Gamma-glutamyl hydrolase | YYIAASYVK | 427.49 | 318.34 | 557.89 | 839.59 |
| Gamma-glutamyl hydrolase | YYIAASYVK | 459.02 | 607.57 | 762.61 | 812.23 |
| Y-box-binding protein 3 | DGVPEGAQLQGPVHR | 425.78 | 699.7 | 528.67 | 1432.7 |
| Y-box-binding protein 3 | GAEAANVTGPDGVPVEGSR | 954.42 | 918.53 | 904.65 | 1139.46 |
| Y-box-binding protein 3 | IQAGEIGEMKDGVPEGAQLQGPVHR | 483.24 | 767.17 | 969.97 | 1574.84 |
| Y-box-binding protein 3 | DGVPEGAQLQGPVHR | 558.3 | 585.36 | 858.98 | 1321.85 |
| Y-box-binding protein 3 | DGVPEGAQLQGPVHR | 380.39 | 716.05 | 737.23 | 1253.87 |
| Y-box-binding protein 3 | EDVFVHQTAIK | 332.94 | 297.58 | 654.88 | 631.44 |
| Y-box-binding protein 3 | EDVFVHQTAIK | 201.82 | 486.55 | 723.59 | 496.48 |
| Y-box-binding protein 3 | EDVFVHQTAIK | 432.47 | 783.41 | 938.01 | 1002.68 |
| Y-box-binding protein 3 | GAEAANVTGPDGVPVEGSR | 954.21 | 832.06 | 1618.96 | 2908.72 |
| Y-box-binding protein 3 | GAEAANVTGPDGVPVEGSR | 1014.91 | 473.35 | 896.88 | 832.2 |
| Y-box-binding protein 3 | GAEAANVTGPDGVPVEGSR | 828.04 | 1276.37 | 1698.29 | 1887.1 |
| Y-box-binding protein 3 | GAEAANVTGPDGVPVEGSR | 202.63 | 405.91 | 879.98 | 677.42 |
| Y-box-binding protein 3 | GAEAANVTGPDGVPVEGSR | 536.5 | 612.16 | 730.18 | 1121.32 |
| Y-box-binding protein 3 | GAEAANVTGPDGVPVEGSR | 849.46 | 756.06 | 1932.69 | 1796.01 |
| Y-box-binding protein 3 | GAEAANVTGPDGVPVEGSR | 849.46 | 756.06 | 1932.69 | 1796.01 |
| Y-box-binding protein 3 | GAEAANVTGPDGVPVEGSR | 849.46 | 756.06 | 1932.69 | 1796.01 |
| Y-box-binding protein 3 | NDTKEDVFVHQTAIK | 788.95 | 670.31 | 1662.17 | 1267.71 |
| Y-box-binding protein 3 | NDTKEDVFVHQTAIK | 1199.14 | 996 | 3994.87 | 4159.1 |
| Y-box-binding protein 3 | NGYGFINR | 2010.85 | 3140.89 | 7788.62 | 7482.09 |
| Y-box-binding protein 3 | NGYGFINR | 4012.75 | 4612.61 | 18393.51 | 21172.73 |
| Y-box-binding protein 3 | NGYGFINR | 3176.86 | 3260.67 | 7005.02 | 8186.4 |
| Y-box-binding protein 3 | NGYGFINR | 2645.23 | 4294.92 | 7843.94 | 7870.42 |
| Y-box-binding protein 3 | NGYGFINR | 3889.74 | 4531.72 | 9441.4 | 9869.68 |
| Y-box-binding protein 3 | NGYGFINR | 4061.56 | 3513.59 | 8857.19 | 10039.02 |
| Y-box-binding protein 3 | VLGTVK | 2175.54 | 1870.04 | 8402.6 | 9538.78 |
| Y-box-binding protein 3 | VLGTVK | 1904.25 | 2183.47 | 8998.43 | 11036.44 |
| Y-box-binding protein 3 | VLGTVK | 2813.16 | 2810.19 | 10409.63 | 12165.63 |
| Y-box-binding protein 3 | VLGTVK | 2173.26 | 2094.91 | 7233.67 | 7950.31 |
| Y-box-binding protein 3 | VLGTVK | 3072.44 | 3683.1 | 10746.22 | 12183.84 |
| Y-box-binding protein 3 | VLGTVK | 1474.8 | 1739.5 | 3226.15 | 3037.44 |

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| Y-box-binding protein 3 | VLGTVK | 2893.78 | 2505.13 | 8130.23 | 9659.56 |
| Y-box-binding protein 3 | VLGTVK | 1138.28 | 1050.68 | 2789.36 | 3717.21 |
| Y-box-binding protein 3 | VLGTVK | 1456.23 | 1978.69 | 2259.74 | 2606.42 |
| Y-box-binding protein 3 | VLGTVK | 720.88 | 586.78 | 1788.71 | 2517.57 |
| Y-box-binding protein 3 | WFNVR | 2035.79 | 2485.23 | 4971.8 | 6900.76 |
| Histone H4 | DAVTYTEHAK | 460.95 | 416.95 | 663.64 | 861.77 |
| Histone H4 | DNIQGITKPAIR | 4922.63 | 4506.15 | 16016.59 | 15522.26 |
| Histone H4 | ISGLIYEETR | 967.21 | 1356.5 | 1320.11 | 1286.92 |
| Histone H4 | KTVTAMDVVYALK | 1108.02 | 1062.31 | 4239.85 | 4593.03 |
| Histone H4 | RISGLIYEETR | 2867.89 | 2722.21 | 3550.37 | 4549.44 |
| Histone H4 | TVTAMDVVYALK | 212.02 | 117.1 | 292.18 | 336.98 |
| Histone H4 | TVTAMDVVYALKR | 368.44 | 407.26 | 1109.68 | 1693.77 |
| Histone H4 | VFLENVIR | 1403.72 | 1102.22 | 3681.63 | 4300.5 |
| Histone H4 | TLYGFGG | 1611.12 | 2100.96 | 4473.44 | 4447.47 |
| Histone H4 | DAVTYTEHAKR | 906.86 | 829.78 | 2756.65 | 2939.61 |
| Histone H4 | TVTAMDVVY | 359.14 | 262.77 | 1004.3 | 510.99 |
| Histone H4 | DNIQGITKPAIRR | 1410.94 | 2197.67 | 2072.02 | 2740.09 |
| Histone H4 | DNIQGITK | 1490.72 | 1336.71 | 2880.42 | 3271.52 |
| Histone H4 | TLYGF | 538 | 357.37 | 775.58 | 900.08 |
| Histone H4 | SGLIYEETR | 592.87 | 574.6 | 1264.52 | 850.08 |
| Histone H4 | KTVTAMDVVY | 1528.96 | 1601.9 | 3185.72 | 4193.07 |
| Histone H4 | ISGLIYEETRGV | 619.9 | 1201.96 | 1833.19 | 1792.92 |
| Histone H4 | TVTAMDVVYA | 231.53 | 104.4 | 369.85 | 314.79 |
| Histone H4 | DAVTYTEHAK | 228.42 | 411.16 | 685.04 | 576.95 |
| Histone H4 | DAVTYTEHAK | 1293.31 | 1692.14 | 6180.8 | 7217.49 |
| Histone H4 | DAVTYTEHAK | 2230.34 | 1988.05 | 8374.44 | 8726.53 |
| Histone H4 | DAVTYTEHAK | 331.2 | 469.86 | 1074.88 | 762.75 |
| Histone H4 | DAVTYTEHAK | 152.37 | 264.96 | 377.22 | 593.54 |
| Histone H4 | DAVTYTEHAK | 294.49 | 479.92 | 605.33 | 754.44 |
| Histone H4 | DAVTYTEHAK | 610.45 | 539.73 | 1116.47 | 1276.32 |
| Histone H4 | DAVTYTEHAK | 459.11 | 385.45 | 792.68 | 850.8 |
| Histone H4 | DAVTYTEHAK | 222.29 | 165.93 | 551.54 | 570.42 |
| Histone H4 | DAVTYTEHAK | 25.54 | 30.07 | 333.77 | 402.61 |
| Histone H4 | DAVTYTEHAK | 1063.2 | 1340.66 | 2389.92 | 4212.07 |
| Histone H4 | DAVTYTEHAK | 860.01 | 1309.72 | 3282.36 | 3161.97 |
| Histone H4 | DAVTYTEHAK | 201.4 | 527.52 | 719.73 | 679.19 |
| Histone H4 | DAVTYTEHAK | 324.83 | 1098.96 | 1999.42 | 2181.08 |
| Histone H4 | DAVTYTEHAK | 397.85 | 693.74 | 766.33 | 939.75 |
| Histone H4 | DAVTYTEHAK | 504.43 | 482.89 | 1338.05 | 1286.74 |
| Histone H4 | DAVTYTEHAK | 989.45 | 967.6 | 3295.66 | 3850.01 |
| Histone H4 | DAVTYTEHAK | 570 | 706.97 | 1023.91 | 2180.3 |
| Histone H4 | DAVTYTEHAK | 510.32 | 326.5 | 648.81 | 756.32 |
| Histone H4 | DAVTYTEHAK | 457.15 | 791.95 | 903.44 | 1626.65 |
| Histone H4 | DAVTYTEHAK | 1664 | 3260.23 | 7198.88 | 8230.62 |
| Histone H4 | DAVTYTEHAK | 285.1 | 343.54 | 1003.44 | 270.16 |
| Histone H4 | DAVTYTEHAK | 7121.58 | 8104.95 | 27751.19 | 33434.08 |
| Histone H4 | DAVTYTEHAK | 355.94 | 578.63 | 1614.36 | 1015.84 |
| Histone H4 | DAVTYTEHAK | 206.01 | 72.11 | 784.11 | 215.52 |
| Histone H4 | DAVTYTEHAK | 593.29 | 426.29 | 514.59 | 609.69 |
| Histone H4 | DAVTYTEHAK | 7632.55 | 9005.43 | 31173.71 | 39230.44 |
| Histone H4 | DAVTYTEHAK | 1891 | 1683.45 | 4952.19 | 5164.98 |
| Histone H4 | DAVTYTEHAK | 563.98 | 450.37 | 1133.03 | 1702.69 |
| Histone H4 | DAVTYTEHAK | 892.86 | 1148.9 | 3032.13 | 2111.56 |
| Histone H4 | DAVTYTEHAK | 597.7 | 629.18 | 993.52 | 931.24 |
| Histone H4 | DAVTYTEHAK | 38.29 | 46.85 | 95.53 | 147.56 |
| Histone H4 | DAVTYTEHAK | 2192.38 | 3184.81 | 7504.02 | 9114.84 |
| Histone H4 | DAVTYTEHAK | 230.56 | 199.86 | 757.58 | 786.33 |
| Histone H4 | DAVTYTEHAK | 440.51 | 414.93 | 997.91 | 1638.26 |
| Histone H4 | DAVTYTEHAK | 357.84 | 390.67 | 1064.75 | 870.89 |
| Histone H4 | DAVTYTEHAK | 680.89 | 814.57 | 1092.56 | 1555.45 |
| Histone H4 | DAVTYTEHAK | 153.8 | 123.66 | 340.27 | 265.07 |
| Histone H4 | DAVTYTEHAK | 892.86 | 1148.9 | 3032.13 | 2111.56 |
| Histone H4 | DAVTYTEHAK | 788.37 | 621.78 | 1086.63 | 941.37 |
| Histone H4 | DAVTYTEHAK | 716.67 | 364.79 | 1030.21 | 1433.7 |

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| Histone H4 | DAVTYTEHAK | 153.8 | 123.66 | 340.27 | 265.07 |
| Histone H4 | DAVTYTEHAK | 2073.94 | 2120.65 | 7228.98 | 8626.74 |
| Histone H4 | DAVTYTEHAK | 382.85 | 472.71 | 744.53 | 704.82 |
| Histone H4 | DAVTYTEHAK | 4076.22 | 4193.14 | 14921.88 | 18354.12 |
| Histone H4 | DAVTYTEHAK | 1379.41 | 1270.51 | 5658.57 | 7637.76 |
| Histone H4 | DAVTYTEHAK | 563.98 | 450.37 | 1133.03 | 1702.69 |
| Histone H4 | DAVTYTEHAK | 510.32 | 326.5 | 648.81 | 756.32 |
| Histone H4 | DAVTYTEHAK | 357.48 | 426.89 | 1827.81 | 1450.68 |
| Histone H4 | DAVTYTEHAK | 153.8 | 123.66 | 340.27 | 265.07 |
| Histone H4 | DAVTYTEHAK | 487.44 | 352.11 | 1220.87 | 786.41 |
| Histone H4 | DAVTYTEHAK | 140.46 | 165.71 | 224.22 | 322.17 |
| Histone H4 | DAVTYTEHAK | 563.98 | 450.37 | 1133.03 | 1702.69 |
| Histone H4 | DAVTYTEHAK | 383.84 | 375.23 | 456.82 | 727.68 |
| Histone H4 | DAVTYTEHAK | 808.4 | 663.55 | 1818.96 | 2379.31 |
| Histone H4 | DAVTYTEHAK | 345 | 595.53 | 711.84 | 785.85 |
| Histone H4 | DAVTYTEHAK | 776.41 | 1058.6 | 1702.33 | 2036.64 |
| Histone H4 | DAVTYTEHAK | 1094.35 | 816.54 | 2192.2 | 3150.44 |
| Histone H4 | DAVTYTEHAK | 3546.09 | 3590.44 | 10402.51 | 12794.54 |
| Histone H4 | DAVTYTEHAK | 1891 | 1683.45 | 4952.19 | 5164.98 |
| Histone H4 | DAVTYTEHAK | 801.97 | 766.67 | 2007.68 | 1783.5 |
| Histone H4 | DAVTYTEHAK | 1117.06 | 807.18 | 2838.28 | 2826.3 |
| Histone H4 | DAVTYTEHAK | 366.89 | 348.1 | 584.3 | 831.76 |
| Histone H4 | DAVTYTEHAK | 776.41 | 1058.6 | 1702.33 | 2036.64 |
| Histone H4 | DAVTYTEHAK | 153.8 | 123.66 | 340.27 | 265.07 |
| Histone H4 | DAVTYTEHAK | 9012.78 | 10833.43 | 36273.07 | 44679.3 |
| Histone H4 | DAVTYTEHAK | 337.81 | 241.71 | 794.42 | 998.16 |
| Histone H4 | DAVTYTEHAK | 202.12 | 137.55 | 539.99 | 551.71 |
| Histone H4 | DAVTYTEHAK | 140.46 | 165.71 | 224.22 | 322.17 |
| Histone H4 | DAVTYTEHAKR | 692.67 | 714.61 | 2164.26 | 2653.41 |
| Histone H4 | DNIQGITK | 3273.18 | 3106.14 | 5147.02 | 5957.24 |
| Histone H4 | DNIQGITK | 307.57 | 250.74 | 511.87 | 382.21 |
| Histone H4 | DNIQGITK | 1580.46 | 1939.18 | 4822.8 | 5240.22 |
| Histone H4 | DNIQGITK | 1849.32 | 1440.43 | 2392.87 | 3059.47 |
| Histone H4 | DNIQGITK | 7139.57 | 6647.18 | 16713.2 | 18168.82 |
| Histone H4 | DNIQGITK | 179.32 | 155.97 | 563.43 | 627.99 |
| Histone H4 | DNIQGITK | 256.15 | 225.17 | 688.34 | 819.96 |
| Histone H4 | DNIQGITK | 6513.32 | 9051.19 | 13330.95 | 17462.74 |
| Histone H4 | DNIQGITK | 7429.96 | 7744.65 | 12742.3 | 14629.75 |
| Histone H4 | DNIQGITK | 2989.85 | 3545.25 | 5101.93 | 5695.82 |
| Histone H4 | DNIQGITKPAIR | 1003.05 | 794.62 | 2281.76 | 3650.81 |
| Histone H4 | DNIQGITKPAIR | 1968.5 | 5197.35 | 14406.2 | 7746.2 |
| Histone H4 | DNIQGITKPAIR | 2585.84 | 4843.53 | 17252.81 | 9938.51 |
| Histone H4 | DNIQGITKPAIR | 787.12 | 957.28 | 2898.62 | 2424.27 |
| Histone H4 | DNIQGITKPAIR | 1994.96 | 3221.71 | 7731.97 | 8793.85 |
| Histone H4 | DNIQGITKPAIR | 1658.3 | 950.96 | 3422.81 | 3956.04 |
| Histone H4 | DNIQGITKPAIR | 955.18 | 1161.75 | 1795.75 | 2799.92 |
| Histone H4 | DNIQGITKPAIR | 1094.74 | 1309.83 | 2044.35 | 3523.84 |
| Histone H4 | DNIQGITKPAIR | 890.32 | 868.48 | 1753.83 | 2779.12 |
| Histone H4 | DNIQGITKPAIR | 1089.96 | 1144.1 | 2281.29 | 3459 |
| Histone H4 | DNIQGITKPAIR | 3217.32 | 3411.96 | 9000.03 | 9223.78 |
| Histone H4 | DNIQGITKPAIR | 891.34 | 980.2 | 1382.92 | 2100.83 |
| Histone H4 | DNIQGITKPAIR | 705.74 | 700.15 | 1502.09 | 2101.43 |
| Histone H4 | DNIQGITKPAIR | 2051.27 | 2019.74 | 7091.13 | 7257.52 |
| Histone H4 | DNIQGITKPAIR | 1948.07 | 1576.96 | 5862.07 | 7036.92 |
| Histone H4 | DNIQGITKPAIR | 1718.38 | 1184.97 | 2690.61 | 3134.55 |
| Histone H4 | DNIQGITKPAIR | 702.77 | 567.65 | 2375.74 | 3246.5 |
| Histone H4 | DNIQGITKPAIR | 1128.29 | 973.79 | 2480.43 | 3224.49 |
| Histone H4 | DNIQGITKPAIR | 830.95 | 776.31 | 1743.4 | 2472.43 |
| Histone H4 | DNIQGITKPAIR | 1538.87 | 1898.72 | 2348.92 | 2444.05 |
| Histone H4 | DNIQGITKPAIR | 1934.23 | 1242.26 | 3108.12 | 3285.57 |
| Histone H4 | DNIQGITKPAIR | 535.68 | 586.22 | 792.98 | 1407.15 |
| Histone H4 | DNIQGITKPAIR | 457.64 | 530.69 | 1325.99 | 1269.61 |
| Histone H4 | DNIQGITKPAIR | 5083.26 | 4487.31 | 11093.72 | 10944.07 |
| Histone H4 | DNIQGITKPAIR | 539.52 | 419.8 | 926.37 | 894.31 |

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| Histone H4 | DNIQGITKPAIR | 457.46 | 1080.93 | 1873.37 | 1760 |
| Histone H4 | DNIQGITKPAIR | 3160.81 | 2825.07 | 6697.11 | 10656.38 |
| Histone H4 | DNIQGITKPAIR | 980.98 | 1060.22 | 1830.09 | 1731.28 |
| Histone H4 | DNIQGITKPAIR | 539.3 | 548.03 | 1338.99 | 1435.49 |
| Histone H4 | DNIQGITKPAIR | 892.25 | 996.8 | 1196.75 | 1795.71 |
| Histone H4 | DNIQGITKPAIR | 3296.59 | 3346.84 | 8314.25 | 9304.78 |
| Histone H4 | DNIQGITKPAIR | 14096.2 | 14984.59 | 51867.17 | 64125.11 |
| Histone H4 | DNIQGITKPAIR | 3630.08 | 4121.47 | 11538.48 | 15265.72 |
| Histone H4 | DNIQGITKPAIR | 5174.58 | 4188.45 | 11394.45 | 12155.1 |
| Histone H4 | DNIQGITKPAIR | 597.7 | 523.25 | 2457.48 | 2388 |
| Histone H4 | DNIQGITKPAIR | 534.8 | 673.97 | 1295.67 | 1575 |
| Histone H4 | DNIQGITKPAIR | 3764.33 | 3518.12 | 7169.34 | 7598.84 |
| Histone H4 | DNIQGITKPAIR | 16789.32 | 20293.36 | 54435.57 | 72800.74 |
| Histone H4 | DNIQGITKPAIR | 6249.22 | 5037.36 | 12855.57 | 12610.84 |
| Histone H4 | DNIQGITKPAIR | 774.33 | 945.01 | 2169.81 | 1165.3 |
| Histone H4 | DNIQGITKPAIR | 1195.33 | 733.32 | 1577.12 | 1213.06 |
| Histone H4 | DNIQGITKPAIR | 5309.26 | 6839.52 | 20395.7 | 23523.11 |
| Histone H4 | DNIQGITKPAIR | 3866.14 | 4629.73 | 11487.89 | 10003.77 |
| Histone H4 | DNIQGITKPAIR | 481.03 | 879.38 | 1810.18 | 1146.86 |
| Histone H4 | DNIQGITKPAIR | 3869.02 | 5302.23 | 13156.85 | 16352.93 |
| Histone H4 | DNIQGITKPAIR | 4442.47 | 3965.78 | 8602.99 | 9300.03 |
| Histone H4 | DNIQGITKPAIR | 1239.5 | 1263.62 | 2044.07 | 3440.17 |
| Histone H4 | DNIQGITKPAIR | 1480.12 | 2384.77 | 3733.29 | 4054.34 |
| Histone H4 | DNIQGITKPAIR | 382.68 | 489.7 | 596.34 | 739.48 |
| Histone H4 | DNIQGITKPAIR | 3764.33 | 3518.12 | 7169.34 | 7598.84 |
| Histone H4 | DNIQGITKPAIR | 2493.33 | 2706.81 | 5950.71 | 7162.52 |
| Histone H4 | DNIQGITKPAIR | 1326.83 | 3060.47 | 10177.83 | 1191.86 |
| Histone H4 | DNIQGITKPAIR | 176.53 | 431.36 | 993.16 | 717.75 |
| Histone H4 | DNIQGITKPAIR | 1554.21 | 1873.29 | 2327.57 | 2598.83 |
| Histone H4 | DNIQGITKPAIR | 7183.93 | 8541.03 | 24833.65 | 23891.31 |
| Histone H4 | DNIQGITKPAIR | 2201.2 | 2313.53 | 4508.39 | 4355.41 |
| Histone H4 | DNIQGITKPAIR | 4952.8 | 8014.37 | 18797.28 | 13841.14 |
| Histone H4 | DNIQGITKPAIR | 5475.11 | 5772.92 | 14784.5 | 14492.76 |
| Histone H4 | DNIQGITKPAIR | 1199.43 | 1179.77 | 3413.54 | 2863.29 |
| Histone H4 | DNIQGITKPAIR | 4503.65 | 7069.78 | 18606.64 | 12319.48 |
| Histone H4 | DNIQGITKPAIR | 1412.67 | 1920.99 | 3145.91 | 4318.24 |
| Histone H4 | DNIQGITKPAIR | 1684.48 | 1449.65 | 3551.2 | 3070.27 |
| Histone H4 | DNIQGITKPAIR | 3230.01 | 5350.09 | 10524.73 | 7551.36 |
| Histone H4 | DNIQGITKPAIR | 8004.32 | 10679.77 | 28687.1 | 32990.99 |
| Histone H4 | DNIQGITKPAIR | 4391.8 | 6099.47 | 13558.37 | 11632.42 |
| Histone H4 | DNIQGITKPAIR | 27609.3 | 28323.27 | 99844.62 | 113320.4 |
| Histone H4 | DNIQGITKPAIR | 1326.83 | 3060.47 | 10177.83 | 1191.86 |
| Histone H4 | DNIQGITKPAIR | 2542.09 | 2463.76 | 4923.15 | 4929.32 |
| Histone H4 | DNIQGITKPAIR | 2173.09 | 2218.66 | 5740.31 | 6361.11 |
| Histone H4 | DNIQGITKPAIR | 9651.96 | 11194.05 | 34336.01 | 44633.75 |
| Histone H4 | DNIQGITKPAIR | 459.58 | 445.66 | 844.46 | 1356.25 |
| Histone H4 | DNIQGITKPAIR | 2173.09 | 2218.66 | 5740.31 | 6361.11 |
| Histone H4 | DNIQGITKPAIR | 8084.43 | 8829.01 | 25585.22 | 34200.88 |
| Histone H4 | DNIQGITKPAIR | 1310.58 | 1368.95 | 3541.15 | 2963.53 |
| Histone H4 | DNIQGITKPAIR | 461.99 | 314.3 | 631.64 | 927.1 |
| Histone H4 | DNIQGITKPAIR | 5010.18 | 4579.79 | 15191 | 15841.33 |
| Histone H4 | DNIQGITKPAIR | 10493.49 | 10393.25 | 31929.51 | 41229.09 |
| Histone H4 | DNIQGITKPAIR | 11801 | 11958.16 | 24192.52 | 29003.18 |
| Histone H4 | DNIQGITKPAIR | 1326.83 | 3060.47 | 10177.83 | 1191.86 |
| Histone H4 | DNIQGITKPAIR | 4259.6 | 5011.29 | 9681.35 | 11838.49 |
| Histone H4 | DNIQGITKPAIR | 4101.47 | 4783.39 | 9886.15 | 10453.87 |
| Histone H4 | DNIQGITKPAIR | 5010.18 | 4579.79 | 15191 | 15841.33 |
| Histone H4 | DNIQGITKPAIR | 750.68 | 515.59 | 1584.23 | 1509.52 |
| Histone H4 | DNIQGITKPAIR | 4805.93 | 4759.27 | 8603.78 | 11556.6 |
| Histone H4 | DNIQGITKPAIR | 1198.25 | 1403.06 | 3222.92 | 3371.67 |
| Histone H4 | DNIQGITKPAIR | 3399.33 | 2983.66 | 11062.83 | 10922.17 |
| Histone H4 | DNIQGITKPAIR | 1850.34 | 1339.16 | 3409.16 | 4218.22 |
| Histone H4 | DNIQGITKPAIR | 457.88 | 720.06 | 1212.51 | 1749.09 |
| Histone H4 | DNIQGITKPAIR | 1688.67 | 1673.29 | 2419.92 | 3183.26 |

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|---|---|---|---|---|---|
| Histone H4 | DNIQGITKPAIR | 3431.08 | 3144.36 | 6613.81 | 4411.7 |
| Histone H4 | DNIQGITKPAIR | 5132.5 | 5047.34 | 11826.62 | 13718.17 |
| Histone H4 | DNIQGITKPAIR | 3296.59 | 3346.84 | 8314.25 | 9304.78 |
| Histone H4 | DNIQGITKPAIR | 331.37 | 453.28 | 618.09 | 914.81 |
| Histone H4 | DNIQGITKPAIR | 604.82 | 670.13 | 963.24 | 1524.86 |
| Histone H4 | DNIQGITKPAIR | 12624.28 | 14024.72 | 33255.01 | 36173.29 |
| Histone H4 | DNIQGITKPAIR | 1808.15 | 2209.39 | 5355.4 | 4159.78 |
| Histone H4 | DNIQGITKPAIR | 1497.35 | 2171.39 | 3321.14 | 3921.96 |
| Histone H4 | DNIQGITKPAIR | 600.21 | 594.18 | 1492.67 | 798.5 |
| Histone H4 | DNIQGITKPAIR | 1116.73 | 1477.59 | 2175.28 | 2497.05 |
| Histone H4 | DNIQGITKPAIR | 822.08 | 801.26 | 1605.67 | 1223.3 |
| Histone H4 | DNIQGITKPAIR | 999.08 | 1611.92 | 1599.77 | 1615.33 |
| Histone H4 | DNIQGITKPAIR | 1311.51 | 1063.9 | 1766.47 | 2450.39 |
| Histone H4 | DNIQGITKPAIR | 592.21 | 852.63 | 1130.53 | 1613.53 |
| Histone H4 | DNIQGITKPAIR | 2226.93 | 2111.59 | 3711.84 | 4773.17 |
| Histone H4 | DNIQGITKPAIR | 18758.08 | 20784.43 | 58353.54 | 77052.05 |
| Histone H4 | DNIQGITKPAIRR | 2352.21 | 2393.95 | 2104.42 | 2882.84 |
| Histone H4 | DNIQGITKPAIRR | 1700.74 | 2182.85 | 2115.16 | 2352.15 |
| Histone H4 | DNIQGITKPAIRR | 3495.89 | 4400.84 | 6295.35 | 7329.65 |
| Histone H4 | DNIQGITKPAIRR | 3496.7 | 3788.55 | 5570.69 | 6013.07 |
| Histone H4 | DNIQGITKPAIRR | 2090.64 | 1853.2 | 1887.27 | 1665.81 |
| Histone H4 | DNIQGITKPAIRR | 305.11 | 493.82 | 1155.7 | 988.56 |
| Histone H4 | DNIQGITKPAIRR | 1153.96 | 1203.67 | 1387.16 | 2032.29 |
| Histone H4 | DNIQGITKPAIRR | 3311.39 | 4118.24 | 5100.01 | 7622.97 |
| Histone H4 | DNIQGITKPAIRR | 3083.95 | 4141.82 | 4607.74 | 5967.51 |
| Histone H4 | DVVYALK | 2336.17 | 2276.24 | 4687.94 | 4165.44 |
| Histone H4 | DVVYALK | 2366.66 | 2561.91 | 3795.63 | 4131.2 |
| Histone H4 | GGAK | 216.55 | 307.68 | 954 | 707.01 |
| Histone H4 | GGAK | 91.68 | 90.7 | 336.75 | 278.3 |
| Histone H4 | GGAK | 255.36 | 302.47 | 590.89 | 932.43 |
| Histone H4 | GLGK | 314.32 | 435.35 | 609.97 | 798.82 |
| Histone H4 | GLGK | 272.38 | 216.83 | 403.38 | 919.32 |
| Histone H4 | ISGLIYEETR | 2156.8 | 1486.72 | 2273.73 | 2367.04 |
| Histone H4 | ISGLIYEETR | 517.63 | 455.28 | 1006.8 | 1431.55 |
| Histone H4 | ISGLIYEETR | 2678.95 | 1708.39 | 6149.84 | 6880.7 |
| Histone H4 | ISGLIYEETR | 8446.71 | 8887.17 | 21859.31 | 26695.22 |
| Histone H4 | ISGLIYEETR | 894.97 | 834.53 | 1661.04 | 1871.64 |
| Histone H4 | ISGLIYEETR | 8611.9 | 8418.08 | 19884.27 | 24760.31 |
| Histone H4 | ISGLIYEETR | 1112.2 | 967.82 | 1717.83 | 1472.91 |
| Histone H4 | ISGLIYEETR | 408.13 | 528.74 | 380.26 | 735.67 |
| Histone H4 | ISGLIYEETR | 10617.03 | 12442.75 | 31634.65 | 34579.53 |
| Histone H4 | ISGLIYEETR | 10789.69 | 10597.16 | 27937.95 | 29464.33 |
| Histone H4 | ISGLIYEETR | 23066.08 | 19312.08 | 57101.7 | 68794.46 |
| Histone H4 | ISGLIYEETR | 346.88 | 196.7 | 487.79 | 437.41 |
| Histone H4 | ISGLIYEETR | 1308.36 | 1374.82 | 1610.05 | 2213.99 |
| Histone H4 | ISGLIYEETR | 2949.28 | 3085.11 | 4874.81 | 5868.43 |
| Histone H4 | ISGLIYEETR | 46299.8 | 53975.5 | 153177 | 168432.1 |
| Histone H4 | ISGLIYEETR | 583.11 | 900.18 | 1843.53 | 1052.73 |
| Histone H4 | ISGLIYEETR | 3269.56 | 3251.47 | 4939.39 | 6411.69 |
| Histone H4 | ISGLIYEETR | 1602.46 | 1467.88 | 2152.28 | 3198.96 |
| Histone H4 | ISGLIYEETR | 1465.46 | 1385.64 | 2148.29 | 3128.14 |
| Histone H4 | ISGLIYEETR | 179.75 | 113.06 | 131.23 | 95.63 |
| Histone H4 | ISGLIYEETR | 790.12 | 554.63 | 465.79 | 413.03 |
| Histone H4 | ISGLIYEETR | 128.09 | 111.41 | 402.35 | 369.88 |
| Histone H4 | ISGLIYEETR | 110.07 | 83.16 | 110.36 | 144.11 |
| Histone H4 | ISGLIYEETR | 116 | 28.78 | 66.14 | 86.23 |
| Histone H4 | ISGLIYEETR | 72.71 | 50.72 | 43.44 | 119.83 |
| Histone H4 | ISGLIYEETR | 306.83 | 324.41 | 699.85 | 546.25 |
| Histone H4 | ISGLIYEETR | 290.19 | 53.08 | 140.61 | 43.75 |
| Histone H4 | ISGLIYEETR | 1677.69 | 843.68 | 1477.78 | 1384.67 |
| Histone H4 | ISGLIYEETR | 552.4 | 424.42 | 1235.45 | 606.21 |
| Histone H4 | ISGLIYEETR | 359.76 | 200.88 | 233.55 | 347.61 |
| Histone H4 | ISGLIYEETR | 879.06 | 385.06 | 442.96 | 627.48 |
| Histone H4 | KTVTAMDVVYALK | 178.01 | 285.46 | 758.48 | 794.19 |

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|---|---|---|---|---|---|
| Histone H4 | KTVTAMDVVYALK | 381.6 | 596.3 | 1390.93 | 1194.97 |
| Histone H4 | KTVTAMDVVYALK | 307.39 | 268.61 | 904.98 | 1087.94 |
| Histone H4 | LENVIR | 1329.32 | 1325.13 | 1225.56 | 2319.11 |
| Histone H4 | LENVIR | 1682.15 | 1785.71 | 2414.36 | 2775.06 |
| Histone H4 | LYGFGG | 1642.73 | 1212.21 | 450.08 | 333.24 |
| Histone H4 | LYGFGG | 496.74 | 923.42 | 318.79 | 264.54 |
| Histone H4 | LYGFGG | 1359.64 | 1628.18 | 271.84 | 797.62 |
| Histone H4 | LYGFGG | 940.94 | 547.56 | 262.48 | 319.56 |
| Histone H4 | LYGFGG | 1958.2 | 2066.16 | 507.94 | 864 |
| Histone H4 | RDNIQGITKPAIR | 1146.57 | 2998.17 | 8015.96 | 1871.12 |
| Histone H4 | RDNIQGITKPAIR | 1341.32 | 3012.14 | 8100.69 | 1938.45 |
| Histone H4 | RISGLIYEETR | 3005.31 | 2549.88 | 5029.15 | 5359.45 |
| Histone H4 | RISGLIYEETR | 1776.42 | 1834.01 | 2870.92 | 2872.48 |
| Histone H4 | RISGLIYEETR | 1827.58 | 1992.09 | 4065.58 | 3802.21 |
| Histone H4 | RISGLIYEETR | 487.38 | 358.08 | 925.83 | 622.42 |
| Histone H4 | RISGLIYEETR | 307.56 | 252.17 | 440.9 | 204.32 |
| Histone H4 | RISGLIYEETR | 1048.88 | 1054.09 | 1618.74 | 1095.36 |
| Histone H4 | RISGLIYEETR | 835.23 | 566.35 | 1263.04 | 1535.3 |
| Histone H4 | RISGLIYEETR | 473.8 | 423.47 | 294.24 | 421.38 |
| Histone H4 | RISGLIYEETR | 473.8 | 423.47 | 294.24 | 421.38 |
| Histone H4 | SGLIYEETR | 653.72 | 520.12 | 811.15 | 859.8 |
| Histone H4 | SGLIYEETR | 389.18 | 592.86 | 894.9 | 657.94 |
| Histone H4 | TLYGF | 488.85 | 213.67 | 404.65 | 581.32 |
| Histone H4 | TLYGF | 411.04 | 240.98 | 615.24 | 457.28 |
| Histone H4 | TLYGFGG | 1014.59 | 824.05 | 1900.61 | 2451.06 |
| Histone H4 | TLYGFGG | 4807.53 | 5983.26 | 14698.57 | 17769.06 |
| Histone H4 | TLYGFGG | 2816.33 | 2071.66 | 4644.32 | 6356.28 |
| Histone H4 | TLYGFGG | 2531.08 | 2381.08 | 6074.76 | 6968.55 |
| Histone H4 | TLYGFGG | 153.65 | 138.61 | 239.58 | 296.68 |
| Histone H4 | TLYGFGG | 965.5 | 781.01 | 1975.28 | 2740.5 |
| Histone H4 | TLYGFGG | 25.11 | 72.71 | 140.85 | 300.98 |
| Histone H4 | TLYGFGG | 492.63 | 158.56 | 563.74 | 408.53 |
| Histone H4 | TLYGFGG | 101.41 | 193.75 | 256.62 | 474.09 |
| Histone H4 | TLYGFGG | 101.93 | 141.94 | 264.55 | 320.26 |
| Histone H4 | TLYGFGG | 67.95 | 94.91 | 162.24 | 76.24 |
| Histone H4 | TLYGFGG | 1052.49 | 1016.15 | 1301.39 | 2294.13 |
| Histone H4 | TLYGFGG | 179.5 | 137.85 | 182.49 | 478.12 |
| Histone H4 | TLYGFGG | 229.15 | 339.62 | 232.11 | 116.16 |
| Histone H4 | TLYGFGG | 73.47 | 400.81 | 63.18 | 47.6 |
| Histone H4 | TLYGFGG | 257.37 | 103.98 | 296.26 | 190.57 |
| Histone H4 | TLYGFGG | 204.89 | 183.23 | 398.04 | 497.86 |
| Histone H4 | TLYGFGG | 63.25 | 133.86 | 167.76 | 132.28 |
| Histone H4 | TLYGFGG | 64.55 | 5.49 | 23.74 | 50.33 |
| Histone H4 | TLYGFGG | 102.96 | 40.55 | 170.09 | 245.77 |
| Histone H4 | TLYGFGG | 42.41 | 65.27 | 20.01 | 50.11 |
| Histone H4 | TLYGFGG | 723.16 | 787.85 | 1621.2 | 2130.57 |
| Histone H4 | TLYGFGG | 1364.16 | 969 | 1534 | 2238.98 |
| Histone H4 | TLYGFGG | 671.11 | 930.08 | 1903.33 | 2769.95 |
| Histone H4 | TLYGFGG | 205.09 | 162.79 | 131.53 | 405.47 |
| Histone H4 | TLYGFGG | 358.08 | 367.57 | 930.48 | 922.11 |
| Histone H4 | TLYGFGG | 205.12 | 159.7 | 284.31 | 472.87 |
| Histone H4 | TLYGFGG | 76.57 | 95.11 | 120.9 | 57.52 |
| Histone H4 | TLYGFGG | 18472.24 | 16258.2 | 51762.74 | 57833.91 |
| Histone H4 | TLYGFGG | 128.61 | 59.85 | 397.97 | 339 |
| Histone H4 | TLYGFGG | 427.99 | 1120.21 | 1155.23 | 1778.31 |
| Histone H4 | TLYGFGG | 977.9 | 726.01 | 2788.8 | 1308.25 |
| Histone H4 | TLYGFGG | 48.93 | 271.82 | 416.81 | 131.31 |
| Histone H4 | TLYGFGG | 154.19 | 85.36 | 318.86 | 342.08 |
| Histone H4 | TLYGFGG | 128.11 | 109.23 | 510.23 | 358.8 |
| Histone H4 | TLYGFGG | 696.43 | 342.91 | 910.04 | 730.85 |
| Histone H4 | TLYGFGG | 231.53 | 104.37 | 371.4 | 263.99 |
| Histone H4 | TLYGFGG | 76.82 | 70.35 | 68.1 | 150.61 |
| Histone H4 | TLYGFGG | 304.28 | 576.01 | 816.11 | 1430.54 |
| Histone H4 | TLYGFGG | 384.77 | 283.43 | 1005.39 | 1209.47 |

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|---|---|---|---|---|---|
| Histone H4 | TLYGFGG | 155.68 | 44.99 | 182.71 | 135.77 |
| Histone H4 | TLYGFGG | 521.01 | 333.44 | 1117.32 | 908.97 |
| Histone H4 | TLYGFGG | 1255.3 | 1830.07 | 3273.87 | 4164.25 |
| Histone H4 | TLYGFGG | 1604.63 | 1572.36 | 3465.41 | 3806.55 |
| Histone H4 | TLYGFGG | 76.87 | 64.75 | 25.82 | 69.2 |
| Histone H4 | TLYGFGG | 879.35 | 568.85 | 1988.37 | 2010.64 |
| Histone H4 | TLYGFGG | 1059.27 | 665.84 | 1158.86 | 1950.94 |
| Histone H4 | TLYGFGG | 154.66 | 38.69 | 72.25 | 73.51 |
| Histone H4 | TLYGFGG | 41.71 | 28.19 | 48.43 | 75.64 |
| Histone H4 | TLYGFGG | 348.11 | 75.69 | 86.36 | 80.6 |
| Histone H4 | TLYGFGG | 1067.09 | 1063.28 | 1894.98 | 1847.97 |
| Histone H4 | TLYGFGG | 306.79 | 327.9 | 527.28 | 776.68 |
| Histone H4 | TLYGFGG | 382.09 | 548.6 | 823.35 | 885.45 |
| Histone H4 | TLYGFGG | 510.49 | 416.17 | 1797.33 | 1721.05 |
| Histone H4 | TLYGFGG | 1336.12 | 866.81 | 1319.6 | 1234.92 |
| Histone H4 | TLYGFGG | 705.27 | 640.3 | 2974.67 | 3243.95 |
| Histone H4 | TLYGFGG | 433.58 | 567.07 | 1476.33 | 698.46 |
| Histone H4 | TLYGFGG | 77.01 | 50.8 | 77.35 | 99.01 |
| Histone H4 | TLYGFGG | 103.21 | 15.4 | 136.44 | 134.65 |
| Histone H4 | TLYGFGG | 232.27 | 30.87 | 175.02 | 93.91 |
| Histone H4 | TLYGFGG | 17201.03 | 17170.37 | 46031.98 | 53595.04 |
| Histone H4 | TLYGFGG | 124.57 | 458.69 | 44.52 | 112.93 |
| Histone H4 | TLYGFGG | 50.19 | 147.82 | 163.38 | 249.09 |
| Histone H4 | TLYGFGG | 1591.97 | 1333.41 | 2566.1 | 2586.11 |
| Histone H4 | TLYGFGG | 167.74 | 23.25 | 149.85 | 95.27 |
| Histone H4 | TLYGFGG | 51.35 | 32.91 | 98.69 | 72.13 |
| Histone H4 | TVTAMDVVY | 947.92 | 1241.28 | 1505.31 | 2754 |
| Histone H4 | TVTAMDVVY | 1470.9 | 1167.6 | 4031.22 | 2719.88 |
| Histone H4 | TVTAMDVVY | 434.79 | 448.23 | 488.9 | 538.93 |
| Histone H4 | TVTAMDVVY | 282.99 | 125.95 | 391.82 | 391.05 |
| Histone H4 | TVTAMDVVY | 475.66 | 240.13 | 420.63 | 815.95 |
| Histone H4 | TVTAMDVVY | 179.25 | 162.6 | 235.66 | 373.16 |
| Histone H4 | TVTAMDVVY | 178.52 | 235.42 | 465.9 | 490.92 |
| Histone H4 | TVTAMDVVY | 102.97 | 39.91 | 201.37 | 66.74 |
| Histone H4 | TVTAMDVVY | 434.79 | 448 | 500.3 | 697.25 |
| Histone H4 | TVTAMDVVY | 475.66 | 240.13 | 420.63 | 815.95 |
| Histone H4 | TVTAMDVVYALK | 2139.93 | 2302.7 | 6651.33 | 8734.72 |
| Histone H4 | TVTAMDVVYALK | 211.31 | 186.39 | 590.47 | 803.18 |
| Histone H4 | TVTAMDVVYALK | 394.08 | 640.2 | 1248.09 | 1385.69 |
| Histone H4 | TVTAMDVVYALK | 534.2 | 732.92 | 1732.84 | 2371.89 |
| Histone H4 | TVTAMDVVYALK | 290.41 | 137.44 | 647.62 | 678.58 |
| Histone H4 | TVTAMDVVYALK | 3641.43 | 3958.3 | 11749.48 | 14488.25 |
| Histone H4 | TVTAMDVVYALK | 1020.63 | 1185.09 | 3007.79 | 4000.29 |
| Histone H4 | TVTAMDVVYALK | 155.07 | 104.91 | 252.7 | 252.57 |
| Histone H4 | TVTAMDVVYALK | 88.87 | 49.92 | 130.21 | 91.93 |
| Histone H4 | TVTAMDVVYALK | 229.7 | 284.9 | 383.73 | 329.87 |
| Histone H4 | TVTAMDVVYALK | 1133.77 | 1496.29 | 2304.82 | 3537.75 |
| Histone H4 | TVTAMDVVYALK | 512.03 | 476.63 | 1407.13 | 1357.88 |
| Histone H4 | TVTAMDVVYALK | 2482.4 | 2935.61 | 8342.7 | 11884.13 |
| Histone H4 | TVTAMDVVYALK | 371.36 | 437.82 | 916.89 | 867.23 |
| Histone H4 | TVTAMDVVYALK | 316 | 162.76 | 365.06 | 414.71 |
| Histone H4 | TVTAMDVVYALK | 1162.49 | 680.01 | 2526.41 | 2889.86 |
| Histone H4 | TVTAMDVVYALK | 2051.04 | 2042.78 | 6111.49 | 7679.43 |
| Histone H4 | TVTAMDVVYALK | 38.16 | 59.33 | 116.65 | 276.41 |
| Histone H4 | TVTAMDVVYALK | 688.37 | 1139.02 | 1078.94 | 1150.33 |
| Histone H4 | TVTAMDVVYALK | 741.67 | 660.33 | 1478.41 | 1543.95 |
| Histone H4 | TVTAMDVVYALK | 1191.43 | 1225.03 | 3384.46 | 3553.49 |
| Histone H4 | TVTAMDVVYALK | 1059.27 | 1410.08 | 3012.86 | 2933.13 |
| Histone H4 | TVTAMDVVYALK | 347.32 | 259.9 | 551.03 | 663.24 |
| Histone H4 | TVTAMDVVYALK | 204.37 | 233.73 | 454.55 | 618.54 |
| Histone H4 | TVTAMDVVYALK | 1004.11 | 1008.63 | 2382.26 | 2509.14 |
| Histone H4 | TVTAMDVVYALK | 615.21 | 495.3 | 1381.85 | 1436.99 |
| Histone H4 | TVTAMDVVYALK | 256.62 | 177.99 | 467.58 | 336.23 |
| Histone H4 | TVTAMDVVYALK | 108.37 | 143.86 | 145.98 | 188.52 |

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|---|---|---|---|---|---|
| Histone H4 | TVTAMDVVYALK | 373.65 | 424.74 | 1609.12 | 1617.69 |
| Histone H4 | TVTAMDVVYALK | 529.49 | 453.32 | 634.35 | 788.68 |
| Histone H4 | TVTAMDVVYALK | 93.68 | 106.25 | 251.67 | 218.18 |
| Histone H4 | TVTAMDVVYALK | 11.8 | 4.31 | 115.9 | 134.68 |
| Histone H4 | TVTAMDVVYALK | 690.93 | 779.74 | 2459.29 | 2703.68 |
| Histone H4 | TVTAMDVVYALK | 248.32 | 41.23 | 241.9 | 166.96 |
| Histone H4 | TVTAMDVVYALK | 2157.29 | 2183.77 | 6194.48 | 6833.86 |
| Histone H4 | TVTAMDVVYALK | 484.07 | 685.6 | 1438.4 | 2019.66 |
| Histone H4 | TVTAMDVVYALK | 1550.96 | 704.17 | 2247.77 | 2185.74 |
| Histone H4 | TVTAMDVVYALK | 204.39 | 232.12 | 481.17 | 345.86 |
| Histone H4 | TVTAMDVVYALK | 154.5 | 54.4 | 146.88 | 129.05 |
| Histone H4 | TVTAMDVVYALK | 204.39 | 232.53 | 513.85 | 400.49 |
| Histone H4 | TVTAMDVVYALK | 975.03 | 371.55 | 812.64 | 390.42 |
| Histone H4 | TVTAMDVVYALK | 1240.03 | 572.86 | 1372.4 | 1888.16 |
| Histone H4 | TVTAMDVVYALK | 400.12 | 256.09 | 280.14 | 250.3 |
| Histone H4 | TVTAMDVVYALK | 535.62 | 592.44 | 698.32 | 1045.56 |
| Histone H4 | TVTAMDVVYALK | 162.54 | 111.15 | 129.11 | 312.93 |
| Histone H4 | TVTAMDVVYALK | 486.95 | 401.07 | 981.72 | 920.38 |
| Histone H4 | TVTAMDVVYALK | 436.43 | 286.29 | 833.95 | 938.02 |
| Histone H4 | TVTAMDVVYALK | 1329.79 | 640.39 | 1639.13 | 2541.41 |
| Histone H4 | TVTAMDVVYALK | 1482.98 | 1569.89 | 4299.15 | 3773.46 |
| Histone H4 | TVTAMDVVYALK | 162.86 | 79.59 | 146.63 | 225.74 |
| Histone H4 | TVTAMDVVYALK | 1556.37 | 1127.42 | 2407.82 | 2892.47 |
| Histone H4 | TVTAMDVVYALK | 131.53 | 90.23 | 160.82 | 163.34 |
| Histone H4 | TVTAMDVVYALK | 153.68 | 136.18 | 359.96 | 580.58 |
| Histone H4 | TVTAMDVVYALK | 119.98 | 60.94 | 375.62 | 82.97 |
| Histone H4 | TVTAMDVVYALK | 38.29 | 46.8 | 97.85 | 72.16 |
| Histone H4 | TVTAMDVVYALK | 282.5 | 175.08 | 516.72 | 383.12 |
| Histone H4 | TVTAMDVVYALK | 204.22 | 249.11 | 971.35 | 683.6 |
| Histone H4 | TVTAMDVVYALK | 381.97 | 134.55 | 241.98 | 206.28 |
| Histone H4 | TVTAMDVVYALK | 551.54 | 508.94 | 2217.49 | 2578.92 |
| Histone H4 | TVTAMDVVYALK | 25.6 | 23.82 | 4.39 | 51.31 |
| Histone H4 | TVTAMDVVYALK | 296.22 | 202.65 | 1017.22 | 925.22 |
| Histone H4 | TVTAMDVVYALK | 1654.33 | 492.08 | 1350.35 | 622.38 |
| Histone H4 | TVTAMDVVYALK | 761.77 | 376.76 | 857.85 | 784.93 |
| Histone H4 | TVTAMDVVYALK | 157.88 | 146.23 | 591.87 | 490.89 |
| Histone H4 | TVTAMDVVYALK | 69.33 | 65.21 | 137.02 | 84.84 |
| Histone H4 | TVTAMDVVYALK | 383.1 | 448.43 | 668.26 | 578.86 |
| Histone H4 | TVTAMDVVYALK | 1715.21 | 1817.81 | 1716.06 | 2151.59 |
| Histone H4 | TVTAMDVVYALK | 235.28 | 158.78 | 219.38 | 134.03 |
| Histone H4 | TVTAMDVVYALK | 1715.21 | 1817.81 | 1716.06 | 2151.59 |
| Histone H4 | TVTAMDVVYALK | 410.26 | 318 | 638.1 | 604.29 |
| Histone H4 | TVTAMDVVYALK | 1961.32 | 2077.22 | 6917.62 | 533.09 |
| Histone H4 | TVTAMDVVYALK | 255.08 | 330.81 | 573.01 | 328.28 |
| Histone H4 | TVTAMDVVYALK | 178.99 | 188.48 | 233.22 | 400.1 |
| Histone H4 | TVTAMDVVYALK | 759.16 | 1166.61 | 1741.72 | 1931.11 |
| Histone H4 | TVTAMDVVYALK | 333.68 | 224.95 | 415.15 | 259.39 |
| Histone H4 | TVTAMDVVYALK | 128.4 | 80.71 | 377.51 | 226.39 |
| Histone H4 | TVTAMDVVYALK | 180.58 | 31.66 | 325.3 | 240.78 |
| Histone H4 | TVTAMDVVYALK | 133.23 | 135.16 | 165.96 | 182.89 |
| Histone H4 | TVTAMDVVYALK | 133.23 | 135.16 | 165.96 | 182.89 |
| Histone H4 | TVTAMDVVYALK | 164.02 | 71.6 | 165.42 | 154 |
| Histone H4 | TVTAMDVVYALK | 235.28 | 158.78 | 219.38 | 134.03 |
| Histone H4 | TVTAMDVVYALK | 1715.21 | 1817.81 | 1716.06 | 2151.59 |
| Histone H4 | TVTAMDVVYALK | 1715.21 | 1817.81 | 1716.06 | 2151.59 |
| Histone H4 | TVTAMDVVYALK | 547.98 | 116.07 | 122.54 | 202.69 |
| Histone H4 | TVTAMDVVYALKR | 89.83 | 60.68 | 179.48 | 356.94 |
| Histone H4 | TVTAMDVVYALKR | 624.52 | 745.35 | 2436.13 | 3688.29 |
| Histone H4 | TVTAMDVVYALKR | 404.19 | 279.23 | 876.04 | 1091.57 |
| Histone H4 | TVTAMDVVYALKR | 83.07 | 90.79 | 310.67 | 359.66 |
| Histone H4 | TVTAMDVVYALKR | 386.21 | 459.93 | 1151.91 | 1534.22 |
| Histone H4 | TVTAMDVVYALKR | 947.85 | 1779.54 | 3495.91 | 4304.26 |
| Histone H4 | TVTAMDVVYALKR | 218.7 | 201.43 | 723.4 | 636.55 |
| Histone H4 | TVTAMDVVYALKR | 863.13 | 682.36 | 1911.44 | 1941.31 |

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|---|---|---|---|---|---|
| Histone H4 | TVTAMDVVYALKR | 1474.87 | 1626.14 | 4205.74 | 4899.15 |
| Histone H4 | TVTAMDVVYALKR | 83.2 | 77.92 | 148.9 | 338.76 |
| Histone H4 | TVTAMDVVYALKR | 1475.03 | 1823.28 | 3602.31 | 4129.81 |
| Histone H4 | TVTAMDVVYALKR | 462.04 | 309.15 | 885.8 | 1340.32 |
| Histone H4 | TVTAMDVVYALKR | 673.97 | 1391.99 | 1915.61 | 2212.91 |
| Histone H4 | TVTAMDVVYALKR | 1185.34 | 869.45 | 2007.63 | 2670.06 |
| Histone H4 | TVTAMDVVYALKR | 614.8 | 322.74 | 930.42 | 1386.47 |
| Histone H4 | TVTAMDVVYALKR | 160.19 | 130.62 | 398.1 | 396.66 |
| Histone H4 | TVTAMDVVYALKR | 1242.01 | 1334.68 | 2083.46 | 2275.06 |
| Histone H4 | TVTAMDVVYALKR | 848.13 | 780.89 | 2092.26 | 1755.6 |
| Histone H4 | TVTAMDVVYALKR | 1283.31 | 1722 | 4155.07 | 4223.51 |
| Histone H4 | TVTAMDVVYALKR | 255.45 | 187.92 | 459.49 | 653.31 |
| Histone H4 | TVTAMDVVYALKR | 435.94 | 334.34 | 1012.32 | 693.12 |
| Histone H4 | TVTAMDVVYALKR | 130.99 | 143.77 | 173.97 | 361.92 |
| Histone H4 | TVTAMDVVYALKR | 133.23 | 135.16 | 165.96 | 182.89 |
| Histone H4 | TVTAMDVVYALKR | 306.84 | 323.37 | 751.24 | 835.93 |
| Histone H4 | TVTAMDVVYALKR | 427.17 | 669.14 | 1237.87 | 985.85 |
| Histone H4 | TVTAMDVVYALKR | 1241.55 | 954.7 | 1892.97 | 2017.17 |
| Histone H4 | TVTAMDVVYALKR | 179.93 | 95.47 | 362.7 | 432.14 |
| Histone H4 | TVTAMDVVYALKR | 752.47 | 550.92 | 627.77 | 1033.25 |
| Histone H4 | TYTEHAK | 101.32 | 202.2 | 583.81 | 502.57 |
| Histone H4 | VFLENVIR | 254.79 | 359.2 | 446.26 | 625.12 |
| Histone H4 | VFLENVIR | 492.22 | 305.69 | 946.69 | 965.31 |
| Histone H4 | VFLENVIR | 1055.58 | 710.89 | 2188.63 | 2463.99 |
| Histone H4 | VFLENVIR | 776.09 | 771.2 | 1505.72 | 2393.51 |
| Histone H4 | VFLENVIR | 226.01 | 223.53 | 1093.05 | 1008.2 |
| Histone H4 | VFLENVIR | 281.97 | 227.19 | 493.86 | 567.98 |
| Histone H4 | VFLENVIR | 203.36 | 334.05 | 602.32 | 636.18 |
| Histone H4 | VFLENVIR | 611.23 | 781.94 | 2483.28 | 1912.2 |
| Histone H4 | VFLENVIR | 1047.15 | 1331.48 | 3807.07 | 4817.28 |
| Histone H4 | VFLENVIR | 645.39 | 917.91 | 2759.52 | 3568.53 |
| Histone H4 | VFLENVIR | 460.68 | 443.44 | 630.93 | 680.76 |
| Histone H4 | VFLENVIR | 570.27 | 680.13 | 1712.08 | 1958.25 |
| Histone H4 | VFLENVIR | 1548.2 | 1722.32 | 4285.7 | 4569.04 |
| Histone H4 | VFLENVIR | 1183.1 | 878.43 | 4869.15 | 4932.29 |
| Histone H4 | VFLENVIR | 11620.7 | 10729.82 | 43276.81 | 49944.15 |
| Histone H4 | VFLENVIR | 2830.24 | 2612.6 | 8472.07 | 10848.16 |
| Histone H4 | VFLENVIR | 2516.57 | 1793.64 | 6783.11 | 6975.01 |
| Histone H4 | VFLENVIR | 3118.66 | 1883.43 | 7847.37 | 7551.8 |
| Histone H4 | VFLENVIR | 2830.29 | 1862.29 | 7715.92 | 9586.64 |
| Histone H4 | VFLENVIR | 1601.79 | 1746.58 | 4112.63 | 4982.11 |
| Histone H4 | VFLENVIR | 4863.89 | 4032.88 | 18207.48 | 20052.28 |
| Histone H4 | VFLENVIR | 1492 | 1316.74 | 3704.1 | 4272.59 |
| Histone H4 | VFLENVIR | 1212 | 789.2 | 1943.6 | 2186.64 |
| Histone H4 | VFLENVIR | 1025.76 | 784.42 | 1000.83 | 1321.66 |
| Histone H4 | VFLENVIR | 901.32 | 1057.98 | 2605.3 | 2139.58 |
| Histone H4 | VFLENVIR | 6849.22 | 7460.79 | 31253.03 | 33096.69 |
| Histone H4 | VFLENVIR | 6719.59 | 6118.54 | 25786.26 | 29564.57 |
| Histone H4 | VFLENVIR | 7936.19 | 8261.8 | 26421.38 | 28186.75 |
| Histone H4 | VFLENVIR | 5763.78 | 4167.41 | 17031.1 | 20175 |
| Histone H4 | VFLENVIR | 2421.85 | 1577.51 | 8194.38 | 9665.17 |
| Histone H4 | VFLENVIR | 257.29 | 112.41 | 517.76 | 411.09 |
| Histone H4 | VFLENVIR | 631.27 | 717.01 | 1047.27 | 1842.72 |
| Histone H4 | VFLENVIR | 1068.16 | 744.32 | 1658.96 | 1940.49 |
| Histone H4 | VFLENVIR | 702.01 | 323.7 | 1201.79 | 1064.83 |
| Histone H4 | VFLENVIR | 613.84 | 736.81 | 3323.19 | 3100.85 |
| Histone H4 | VFLENVIR | 633.04 | 329.68 | 1796.87 | 2190.83 |
| Histone H4 | VFLENVIR | 225.08 | 315.32 | 597.87 | 713.33 |
| Histone H4 | VFLENVIR | 229.26 | 328.54 | 779.72 | 1701.61 |
| Histone H4 | VFLENVIR | 2436.84 | 2436.8 | 7174.22 | 9390.71 |
| Histone H4 | VFLENVIR | 14133.58 | 11505.17 | 50339.68 | 51907.64 |
| Histone H4 | VFLENVIR | 10380.69 | 11005.62 | 34816.27 | 37295.36 |
| Histone H4 | VFLENVIR | 230.79 | 176.8 | 620.76 | 353.04 |
| Histone H4 | VFLENVIR | 1301.03 | 1141.87 | 4011.74 | 4566.24 |

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|---|---|---|---|---|---|
| Histone H4 | VFLENVIR | 257.14 | 127.42 | 414.12 | 504.66 |
| Histone H4 | VFLENVIR | 14459.43 | 12608.92 | 47630.13 | 52160 |
| Histone H4 | VFLENVIR | 13125.08 | 14015.14 | 49287.52 | 55141.61 |
| Histone H4 | VFLENVIR | 9074.04 | 10419.29 | 36268.84 | 40568.48 |
| Histone H4 | VFLENVIR | 13082.49 | 14499.23 | 46666.65 | 51912.41 |
| Histone H4 | VFLENVIR | 16571.04 | 17177.67 | 59256.57 | 65214.6 |
| Histone H4 | VFLENVIR | 333.2 | 272.16 | 634.8 | 532.69 |
| Histone H4 | VFLENVIR | 619.66 | 268.46 | 1044.53 | 1379.54 |
| Histone H4 | VFLENVIR | 128.12 | 107.78 | 581.66 | 591.5 |
| Histone H4 | VFLENVIR | 407.15 | 625.5 | 544.06 | 406.68 |
| Histone H4 | VFLENVIR | 307.04 | 303.21 | 471.12 | 767.86 |
| Histone H4 | VFLENVIR | 229.05 | 348.59 | 1065.46 | 557.04 |
| Histone H4 | VFLENVIR | 152.31 | 271.03 | 77.11 | 277.1 |
| Histone H4 | VFLENVIR | 375.77 | 1172.61 | 2477.67 | 556.57 |
| Histone H4 | VFLENVIR | 12870.23 | 11533.38 | 46021.14 | 45481.41 |
| Histone H4 | VFLENVIR | 308.07 | 201.83 | 376.38 | 740.71 |
| Histone H4 | VFLENVIR | 204.6 | 211.4 | 281.78 | 448.2 |
| Histone H4 | VFLENVIR | 411.02 | 242.76 | 527.12 | 560.83 |
| Histone H4 | VFLENVIR | 615.5 | 785.93 | 2057.17 | 1930.94 |
| Histone H4 | VFLENVIR | 307.02 | 305.55 | 355.37 | 364.53 |
| Histone H4 | VFLENVIR | 384.86 | 275.01 | 304.4 | 367.29 |
| Histone H4 | VFLENVIR | 230.21 | 234.25 | 334.27 | 365.76 |
| Histone H4 | VFLENVIR | 270.12 | 333.93 | 363.47 | 892.78 |
| Histone H4 | VFLENVIR | 192.05 | 174.73 | 226.92 | 209.2 |
| Histone H4 | VFLENVIR | 577.99 | 1087.57 | 2964.84 | 4482.25 |
| Histone H4 | VFLENVIR | 51.39 | 29.47 | 56.05 | 33.54 |
| Histone H4 | VFLENVIR | 307.76 | 232.21 | 151.14 | 453.82 |
| Histone H4 | VFLENVIR | 100.6 | 273.75 | 131.83 | 171.05 |
| Histone H4 | VFLENVIR | 308.06 | 202.72 | 332.13 | 497.17 |
| Histone H4 | VFLENVIR | 460.94 | 417.87 | 617.99 | 984.54 |
| Histone H4 | VFLENVIR | 821.14 | 574.84 | 2916.15 | 3104.27 |
| Histone H4 | VFLENVIR | 53.46 | 37.19 | 38.67 | 23.43 |
| Histone H4 | VFLENVIR | 434.93 | 433.62 | 1104.37 | 992.26 |
| Histone H4 | VFLENVIR | 588.5 | 474.87 | 1107.82 | 527.85 |
| Histone H4 | VFLENVIR | 139.8 | 230.92 | 191.92 | 401.76 |
| Histone H4 | VFLENVIR | 358.26 | 348.96 | 573.72 | 611.99 |
| Histone H4 | VFLENVIR | 77.2 | 31.97 | 50.25 | 40.29 |
| Histone H4 | VFLENVIR | 44.06 | 8.4 | 8.25 | 25.21 |
| Histone H4 | VFLENVIR | 126.74 | 244.55 | 203.99 | 401.52 |
| Histone H4 | VFLENVIR | 44716.94 | 47274.21 | 175637.5 | 189045.3 |
| Histone H4 | VFLENVIR | 178.77 | 210.25 | 433.62 | 545.35 |
| Histone H4 | VFLENVIR | 255.03 | 335.43 | 557.17 | 380.72 |
| Histone H4 | VFLENVIR | 178.74 | 213.13 | 291.14 | 136.98 |
| Histone H4 | VFLENVIR | 686.89 | 434.97 | 1603.97 | 1881.64 |
| Histone H4 | VFLENVIR | 546.43 | 587.94 | 508.94 | 782.58 |
| Histone H4 | VFLENVIR | 193.25 | 56.55 | 324.18 | 224.14 |
| Histone H4 | VFLENVIR | 748.43 | 524.45 | 1473.17 | 2036.71 |
| Histone H4 | VFLENVIR | 230.11 | 243.92 | 281.8 | 377.24 |
| Histone H4 | VFLENVIR | 204.66 | 205.68 | 564.74 | 620.14 |
| Histone H4 | VFLENVIR | 438.45 | 85.95 | 524.43 | 408.63 |
| Histone H4 | VFLENVIR | 231.26 | 130.29 | 366.63 | 367.36 |
| Three-prime repair exonuclease 1 | ACSPAASEITGLSTAVLAAHGR | 50.7 | 97.06 | 119.27 | 109.62 |
| Three-prime repair exonuclease 1 | VTELCLLAVHR | 564.13 | 435.35 | 651.76 | 425.04 |
| Three-prime repair exonuclease 1 | ACSPAASEITGLSTAVLAAHGR | 89.63 | 80.76 | 144.46 | 159.47 |
| Three-prime repair exonuclease 1 | ACSPAASEITGLSTAVLAAHGR | 229.72 | 282.44 | 505.29 | 680.26 |
| Three-prime repair exonuclease 1 | ACSPAASEITGLSTAVLAAHGR | 154.04 | 100.73 | 197.42 | 64.76 |
| Three-prime repair exonuclease 1 | ACSPAASEITGLSTAVLAAHGR | 268.2 | 310.9 | 233.05 | 567.03 |
| Three-prime repair exonuclease 1 | ACSPAASEITGLSTAVLAAHGR | 362.01 | 297.89 | 1756.22 | 2454.59 |
| Three-prime repair exonuclease 1 | ITALK | 1251.83 | 790.37 | 1367.36 | 1774.23 |
| Three-prime repair exonuclease 1 | ITALK | 5207.99 | 6738.58 | 7781.5 | 8787.21 |
| Three-prime repair exonuclease 1 | ITALK | 2346.25 | 3940.06 | 4738.81 | 5784.97 |
| Three-prime repair exonuclease 1 | ITALK | 855.8 | 661.48 | 896.53 | 1208.04 |
| Three-prime repair exonuclease 1 | LAFLR | 788 | 657.64 | 909.87 | 1063.43 |
| Three-prime repair exonuclease 1 | LGLL | 1296.99 | 1434.54 | 5346.49 | 5340.23 |

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|---|---|---|---|---|---|
| Three-prime repair exonuclease 1 | LGLL | 667.11 | 261.48 | 2492.45 | 2908.78 |
| Three-prime repair exonuclease 1 | LGLL | 3314.76 | 3998.01 | 22099.16 | 20825.3 |
| Three-prime repair exonuclease 1 | LGLL | 3659.85 | 3414.84 | 18140.3 | 21295.9 |
| Three-prime repair exonuclease 1 | LGLL | 332.65 | 326.7 | 492.06 | 841.9 |
| Three-prime repair exonuclease 1 | LLAI | 196.22 | 188.4 | 226.96 | 250.42 |
| Three-prime repair exonuclease 1 | LLAI | 75.78 | 172.69 | 115.6 | 69.95 |
| Three-prime repair exonuclease 1 | VTELCLLAVHR | 416.35 | 248.87 | 205.4 | 317.8 |
| Three-prime repair exonuclease 1 | VTELCLLAVHR | 486.76 | 419.96 | 420.36 | 518.87 |
| Three-prime repair exonuclease 1 | VTELCLLAVHR | 411.49 | 197.03 | 234.46 | 320.56 |
| Three-prime repair exonuclease 1 | VTELCLLAVHR | 614.31 | 477.22 | 1056.14 | 455.28 |
| Three-prime repair exonuclease 1 | VTELCLLAVHR | 589.13 | 625.16 | 745.43 | 905.53 |
| Three-prime repair exonuclease 1 | VTELCLLAVHR | 435.82 | 345.67 | 451.89 | 485.21 |
| TATA-binding protein-associated factor 2N | QSSYSQQPYNNQGQQQNMESSGSQGGR | 25.48 | 36.12 | 34.8 | 49.69 |
| TATA-binding protein-associated factor 2N | SGDWVCPNPSCGNMNFAR | 179.5 | 138.23 | 163.69 | 246.98 |
| TATA-binding protein-associated factor 2N | GGFQGRGGDPK | 2648.94 | 1907.22 | 3817.53 | 3799.47 |
| TATA-binding protein-associated factor 2N | NSCNQCNEPRPEDSRPSGGDFRGR | 153.84 | 120.11 | 302.94 | 476.11 |
| TATA-binding protein-associated factor 2N | AAIDWFDGK | 1690.87 | 2200.75 | 3872.62 | 4678.16 |
| TATA-binding protein-associated factor 2N | AAIDWFDGK | 1124.95 | 772.47 | 1547.74 | 1504.67 |
| TATA-binding protein-associated factor 2N | AAIDWFDGK | 973.1 | 774.48 | 1419.34 | 1356.64 |
| TATA-binding protein-associated factor 2N | AAIDWFDGK | 1137.38 | 927.55 | 1809.4 | 2608.44 |
| TATA-binding protein-associated factor 2N | AAIDWFDGK | 841.14 | 727.19 | 1636.12 | 1857.17 |
| TATA-binding protein-associated factor 2N | AAIDWFDGK | 1734.33 | 1099.03 | 2095.94 | 2309.46 |
| TATA-binding protein-associated factor 2N | EFFK | 2347.59 | 2318.67 | 2866.59 | 4261.27 |
| TATA-binding protein-associated factor 2N | GEATVSFDDPPSAK | 462.84 | 230.06 | 965.8 | 920.35 |
| TATA-binding protein-associated factor 2N | GEATVSFDDPPSAK | 844.55 | 709.19 | 1982.01 | 2143.95 |
| TATA-binding protein-associated factor 2N | GEATVSFDDPPSAK | 1302.43 | 1216.16 | 1714.64 | 1859.46 |
| TATA-binding protein-associated factor 2N | GEATVSFDDPPSAK | 533.26 | 506.89 | 1055.69 | 379.99 |
| TATA-binding protein-associated factor 2N | GGGYGGDRGGGYGGDRGGGYGGDR | 68.25 | 65.79 | 218.83 | 254.5 |
| TATA-binding protein-associated factor 2N | GGGYGGDRGGGYGGDRGGYGGDR | 68.25 | 65.79 | 218.83 | 254.5 |
| TATA-binding protein-associated factor 2N | GGGYGGDRGGGYGGDRGGYGGDR | 68.25 | 65.79 | 218.83 | 254.5 |
| TATA-binding protein-associated factor 2N | GGGYGGDRGGYGGDRGGGYGGDR | 68.25 | 65.79 | 218.83 | 254.5 |
| TATA-binding protein-associated factor 2N | GGGYGGDRGGYGGDRGGGYGGDR | 68.25 | 65.79 | 218.83 | 254.5 |
| TATA-binding protein-associated factor 2N | GGGYGGDRGGYGGK | 214.94 | 254.04 | 847.4 | 900.72 |
| TATA-binding protein-associated factor 2N | IGII | 1296.99 | 1434.54 | 5346.49 | 5340.23 |
| TATA-binding protein-associated factor 2N | IGII | 667.11 | 261.48 | 2492.45 | 2908.78 |
| TATA-binding protein-associated factor 2N | IGII | 3314.76 | 3998.01 | 22099.16 | 20825.3 |
| TATA-binding protein-associated factor 2N | IGII | 3659.85 | 3414.84 | 18140.3 | 21295.9 |
| TATA-binding protein-associated factor 2N | IGII | 332.65 | 326.7 | 492.06 | 841.9 |
| TATA-binding protein-associated factor 2N | NIIK | 540.63 | 204.34 | 676.13 | 887.3 |
| TATA-binding protein-associated factor 2N | NIIK | 359.27 | 249.9 | 363.8 | 1049.81 |
| TATA-binding protein-associated factor 2N | NIIK | 202.84 | 385.47 | 613.68 | 578.56 |
| TATA-binding protein-associated factor 2N | QIGIIK | 552.18 | 339.74 | 1595.82 | 1830.59 |
| TATA-binding protein-associated factor 2N | QIGIIK | 408.77 | 465.35 | 1013.97 | 1253.81 |
| TATA-binding protein-associated factor 2N | QIGIIK | 1245.03 | 1355.72 | 2361.43 | 2766.64 |
| TATA-binding protein-associated factor 2N | QIGIIK | 1695.09 | 1570.93 | 4108.48 | 5299.81 |
| TATA-binding protein-associated factor 2N | QIGIIK | 1965.56 | 1231.93 | 3610.65 | 3949.82 |
| TATA-binding protein-associated factor 2N | QIGIIK | 408.27 | 514.39 | 1036.59 | 1219.28 |
| TATA-binding protein-associated factor 2N | QIGIIK | 1484.27 | 1974.38 | 2636.06 | 3057.4 |
| TATA-binding protein-associated factor 2N | QIGIIK | 1188.09 | 1236.48 | 2617.86 | 3275.82 |
| TATA-binding protein-associated factor 2N | QIGIIK | 508.25 | 743.06 | 1805 | 2664.69 |
| TATA-binding protein-associated factor 2N | QIGIIK | 1162.86 | 1175.69 | 3164.38 | 3516.78 |
| TATA-binding protein-associated factor 2N | QIGIIK | 554.16 | 675.22 | 2067.25 | 2864.93 |
| TATA-binding protein-associated factor 2N | QIGIIK | 2166.04 | 2276.32 | 4084.24 | 4616.54 |
| TATA-binding protein-associated factor 2N | QIGIIK | 1521.86 | 920.27 | 3206.97 | 2824.07 |
| TATA-binding protein-associated factor 2N | QIGIIK | 961.18 | 1101.74 | 1338.3 | 2712.24 |
| TATA-binding protein-associated factor 2N | QIGIIK | 1012.87 | 781.27 | 3171.9 | 3076.45 |
| TATA-binding protein-associated factor 2N | QSSYSQQPYNNQGQQQNMESSGSQGGR | 25.62 | 22.18 | 85.75 | 98.62 |
| NEDD4 family-interacting protein 2 | AAAMAAAAAETSQR | 10142.08 | 9260.43 | 11862.39 | 16951.67 |
| NEDD4 family-interacting protein 2 | SQRVCASGPSMLNSAR | 21.59 | 0 | 178.63 | 67.99 |
| NEDD4 family-interacting protein 2 | LGLL | 1296.99 | 1434.54 | 5346.49 | 5340.23 |
| NEDD4 family-interacting protein 2 | LGLL | 667.11 | 261.48 | 2492.45 | 2908.78 |
| NEDD4 family-interacting protein 2 | LGLL | 3314.76 | 3998.01 | 22099.16 | 20825.3 |
| NEDD4 family-interacting protein 2 | LGLL | 3659.85 | 3414.84 | 18140.3 | 21295.9 |
| NEDD4 family-interacting protein 2 | LGLL | 332.65 | 326.7 | 492.06 | 841.9 |

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|---|---|---|---|---|---|
| NEDD4 family-interacting protein 2 | LLLF | 125.2 | 77.21 | 136.77 | 133.97 |
| NEDD4 family-interacting protein 2 | LSLIK | 460.8 | 430.99 | 342.12 | 528.29 |
| NEDD4 family-interacting protein 2 | LSLIK | 967.35 | 810.9 | 490.09 | 723.21 |
| NEDD4 family-interacting protein 2 | LSLIK | 939.79 | 1299.55 | 2110.11 | 2415.64 |
| NEDD4 family-interacting protein 2 | LSLIK | 993.34 | 1754.1 | 2140.52 | 2229.4 |
| NEDD4 family-interacting protein 2 | LSLIK | 886.34 | 1687.27 | 1636.55 | 3061.11 |
| NEDD4 family-interacting protein 2 | LSLIK | 1495.08 | 1863.91 | 2316.71 | 3550.47 |
| Platelet-activating factor acetylhydrolase IB subunit beta | IIVLGLLPR | 213.18 | 215 | 125.73 | 202.83 |
| Platelet-activating factor acetylhydrolase IB subunit beta | SQGDSNPAAIPHAAEDIQGDDRWMSQHNR | 412.32 | 114.31 | 493.66 | 409.19 |
| Platelet-activating factor acetylhydrolase IB subunit beta | VNQLLK | 610.52 | 746.25 | 1325.93 | 1587.32 |
| Platelet-activating factor acetylhydrolase IB subunit beta | GLLP | 206.92 | 0 | 95.22 | 278.73 |
| Platelet-activating factor acetylhydrolase IB subunit beta | IIVLGLLPR | 212.61 | 270.69 | 245.07 | 259.14 |
| Platelet-activating factor acetylhydrolase IB subunit beta | IIVLGLLPR | 231.62 | 201.69 | 184.73 | 195.67 |
| Platelet-activating factor acetylhydrolase IB subunit beta | IIVLGLLPR | 261.2 | 257.44 | 137.58 | 250.8 |
| Platelet-activating factor acetylhydrolase IB subunit beta | IIVLGLLPR | 288.67 | 309.87 | 209.05 | 260.66 |
| Platelet-activating factor acetylhydrolase IB subunit beta | IIVLGLLPR | 163.13 | 159.34 | 136.74 | 137.31 |
| Platelet-activating factor acetylhydrolase IB subunit beta | IIVLGLLPR | 287.64 | 305.41 | 220.62 | 242.73 |
| Platelet-activating factor acetylhydrolase IB subunit beta | LENIK | 1091.11 | 1455.77 | 1220.86 | 2041.96 |
| Platelet-activating factor acetylhydrolase IB subunit beta | LENIK | 678.07 | 667.87 | 700.09 | 817.51 |
| Platelet-activating factor acetylhydrolase IB subunit beta | LENIK | 424.89 | 574.85 | 644.34 | 1207.51 |
| Platelet-activating factor acetylhydrolase IB subunit beta | LENIK | 1392.58 | 1033.36 | 1969.34 | 1944.17 |
| Platelet-activating factor acetylhydrolase IB subunit beta | LGLL | 1296.99 | 1434.54 | 5346.49 | 5340.23 |
| Platelet-activating factor acetylhydrolase IB subunit beta | LGLL | 667.11 | 261.48 | 2492.45 | 2908.78 |
| Platelet-activating factor acetylhydrolase IB subunit beta | LGLL | 3314.76 | 3998.01 | 22099.16 | 20825.3 |
| Platelet-activating factor acetylhydrolase IB subunit beta | LGLL | 3659.85 | 3414.84 | 18140.3 | 21295.9 |
| Platelet-activating factor acetylhydrolase IB subunit beta | LGLL | 332.65 | 326.7 | 492.06 | 841.9 |
| Platelet-activating factor acetylhydrolase IB subunit beta | LLPR | 640.2 | 366.14 | 1243.74 | 910.95 |
| Platelet-activating factor acetylhydrolase IB subunit beta | NQLLK | 2432.28 | 4270.55 | 5946.87 | 8139.86 |
| Platelet-activating factor acetylhydrolase IB subunit beta | QLLK | 2159.8 | 3638.02 | 3341.89 | 4582.17 |
| Platelet-activating factor acetylhydrolase IB subunit beta | QLLK | 1331.14 | 1464.69 | 1921.29 | 2240.57 |
| Platelet-activating factor acetylhydrolase IB subunit beta | VNQLLK | 80.06 | 69.44 | 154.56 | 134.16 |
| Platelet-activating factor acetylhydrolase IB subunit beta | VSLPK | 1556.8 | 2468.41 | 1974.36 | 2483.26 |
| Platelet-activating factor acetylhydrolase IB subunit beta | VSLPK | 1437.17 | 1521 | 2098.27 | 3542.22 |
| Nuclease-sensitive element-binding protein 1 | EDGNEEDKENQGDETQGQQPPQR | 96.02 | 87.43 | 482.63 | 609.36 |
| Nuclease-sensitive element-binding protein 1 | EDVFVHQTAIK | 332.94 | 297.58 | 654.88 | 631.44 |
| Nuclease-sensitive element-binding protein 1 | GAEAANVTGPGGVPVQGSK | 2378.55 | 1919.19 | 4908.02 | 6298.8 |
| Nuclease-sensitive element-binding protein 1 | RPQYSNPPVQGEVMEGADNQGAGEQGRPVR | 25.39 | 44.33 | 267.03 | 449.09 |
| Nuclease-sensitive element-binding protein 1 | NGYGFINR | 2010.85 | 3140.89 | 7788.62 | 7482.09 |
| Nuclease-sensitive element-binding protein 1 | RPQYSNPPVQGEVMEGADNQGAGEQGR | 128.03 | 116.68 | 141.69 | 172.89 |
| Nuclease-sensitive element-binding protein 1 | VLGTVK | 2175.54 | 1870.04 | 8402.6 | 9538.78 |
| Nuclease-sensitive element-binding protein 1 | NDTKEDVFVHQTAIK | 788.95 | 670.31 | 1662.17 | 1267.71 |
| Nuclease-sensitive element-binding protein 1 | WFNVR | 2035.79 | 2485.23 | 4971.8 | 6900.76 |
| Nuclease-sensitive element-binding protein 1 | GAEAANVTGPGGVPVQGSKYA | 76.62 | 90.03 | 371.94 | 288.91 |
| Nuclease-sensitive element-binding protein 1 | EDGNEEDKENQGDETQGQQPPQR | 12.73 | 18.84 | 85.28 | 51.37 |
| Nuclease-sensitive element-binding protein 1 | EDGNEEDKENQGDETQGQQPPQR | 16.02 | 13.45 | 73.75 | 123.55 |
| Nuclease-sensitive element-binding protein 1 | EDGNEEDKENQGDETQGQQPPQR | 46.96 | 41.13 | 452.74 | 562.6 |
| Nuclease-sensitive element-binding protein 1 | EDGNEEDKENQGDETQGQQPPQR | 25.87 | 0 | 53.97 | 136.87 |
| Nuclease-sensitive element-binding protein 1 | EDGNEEDKENQGDETQGQQPPQR | 7.39 | 15.02 | 80.91 | 132.97 |
| Nuclease-sensitive element-binding protein 1 | EDVFVHQTAIK | 201.82 | 486.55 | 723.59 | 496.48 |
| Nuclease-sensitive element-binding protein 1 | EDVFVHQTAIK | 432.47 | 783.41 | 938.01 | 1002.68 |
| Nuclease-sensitive element-binding protein 1 | GAEAANVTGPGGVPVQGSK | 1529.65 | 1746.64 | 4639.9 | 5519.73 |
| Nuclease-sensitive element-binding protein 1 | GAEAANVTGPGGVPVQGSK | 3541.01 | 2708.69 | 4411.92 | 4267.34 |
| Nuclease-sensitive element-binding protein 1 | GAEAANVTGPGGVPVQGSK | 307.37 | 270.78 | 797.74 | 652.95 |
| Nuclease-sensitive element-binding protein 1 | GAEAANVTGPGGVPVQGSK | 1258.04 | 1452.65 | 1242.57 | 890.97 |
| Nuclease-sensitive element-binding protein 1 | GAEAANVTGPGGVPVQGSK | 2199.47 | 2165.54 | 3856.74 | 4167.58 |
| Nuclease-sensitive element-binding protein 1 | GAEAANVTGPGGVPVQGSK | 987.98 | 1113.08 | 2593.81 | 2608.67 |
| Nuclease-sensitive element-binding protein 1 | GAEAANVTGPGGVPVQGSK | 4916.71 | 4132.66 | 11322.39 | 14972.61 |
| Nuclease-sensitive element-binding protein 1 | NDTKEDVFVHQTAIK | 1199.14 | 996 | 3994.87 | 4159.1 |
| Nuclease-sensitive element-binding protein 1 | NGYGFINR | 4012.75 | 4612.61 | 18393.51 | 21172.73 |
| Nuclease-sensitive element-binding protein 1 | NGYGFINR | 3176.86 | 3260.67 | 7005.02 | 8186.4 |
| Nuclease-sensitive element-binding protein 1 | NGYGFINR | 2645.23 | 4294.92 | 7843.94 | 7870.42 |
| Nuclease-sensitive element-binding protein 1 | NGYGFINR | 3889.74 | 4531.72 | 9441.4 | 9869.68 |
| Nuclease-sensitive element-binding protein 1 | NGYGFINR | 4061.56 | 3513.59 | 8857.19 | 10039.02 |
| Nuclease-sensitive element-binding protein 1 | RPQYSNPPVQGEVMEGADNQGAGEQGR | 49.14 | 251.73 | 133.33 | 173.1 |

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|---|---|---|---|---|---|
| Nuclease-sensitive element-binding protein 1 | RPQYSNPPVQGEVMEGADNQGAGEQGR | 473.78 | 318.79 | 365.86 | 829.19 |
| Nuclease-sensitive element-binding protein 1 | RPQYSNPPVQGEVMEGADNQGAGEQGR | 20.53 | 99.33 | 117.25 | 174.2 |
| Nuclease-sensitive element-binding protein 1 | RPQYSNPPVQGEVMEGADNQGAGEQGR | 51.02 | 65.5 | 402.49 | 185.05 |
| Nuclease-sensitive element-binding protein 1 | RPQYSNPPVQGEVMEGADNQGAGEQGR | 76.58 | 93.61 | 194.92 | 169.26 |
| Nuclease-sensitive element-binding protein 1 | RPQYSNPPVQGEVMEGADNQGAGEQGRPVR | 89.74 | 70.47 | 653.19 | 438.92 |
| Nuclease-sensitive element-binding protein 1 | RPQYSNPPVQGEVMEGADNQGAGEQGRPVR | 282.55 | 169.97 | 769.15 | 1492.78 |
| Nuclease-sensitive element-binding protein 1 | RPQYSNPPVQGEVMEGADNQGAGEQGRPVR | 154.48 | 56.66 | 460.76 | 822.59 |
| Nuclease-sensitive element-binding protein 1 | RPQYSNPPVQGEVMEGADNQGAGEQGRPVR | 435.55 | 372.5 | 402.41 | 363 |
| Nuclease-sensitive element-binding protein 1 | RPQYSNPPVQGEVMEGADNQGAGEQGRPVR | 51.3 | 38.22 | 474.64 | 412.38 |
| Nuclease-sensitive element-binding protein 1 | RPQYSNPPVQGEVMEGADNQGAGEQGRPVR | 25.66 | 17.67 | 95.82 | 201.26 |
| Nuclease-sensitive element-binding protein 1 | RPQYSNPPVQGEVMEGADNQGAGEQGRPVR | 21.1 | 43.05 | 346.11 | 394.39 |
| Nuclease-sensitive element-binding protein 1 | RPQYSNPPVQGEVMEGADNQGAGEQGRPVR | 89.68 | 76.14 | 372.81 | 252.7 |
| Nuclease-sensitive element-binding protein 1 | RPQYSNPPVQGEVMEGADNQGAGEQGRPVR | 38.29 | 46.81 | 97.08 | 96.95 |
| Nuclease-sensitive element-binding protein 1 | RPQYSNPPVQGEVMEGADNQGAGEQGRPVR | 25.67 | 17.03 | 127.16 | 18.2 |
| Nuclease-sensitive element-binding protein 1 | RPQYSNPPVQGEVMEGADNQGAGEQGRPVR | 0 | 49.69 | 96.98 | 97.98 |
| Nuclease-sensitive element-binding protein 1 | RPQYSNPPVQGEVMEGADNQGAGEQGRPVR | 21.1 | 43.05 | 346.11 | 394.39 |
| Nuclease-sensitive element-binding protein 1 | VLGTVK | 1904.25 | 2183.47 | 8998.43 | 11036.44 |
| Nuclease-sensitive element-binding protein 1 | VLGTVK | 2813.16 | 2810.19 | 10409.63 | 12165.63 |
| Nuclease-sensitive element-binding protein 1 | VLGTVK | 2173.26 | 2094.91 | 7233.67 | 7950.31 |
| Nuclease-sensitive element-binding protein 1 | VLGTVK | 3072.44 | 3683.1 | 10746.22 | 12183.84 |
| Nuclease-sensitive element-binding protein 1 | VLGTVK | 1474.8 | 1739.5 | 3226.15 | 3037.44 |
| Nuclease-sensitive element-binding protein 1 | VLGTVK | 2893.78 | 2505.13 | 8130.23 | 9659.56 |
| Nuclease-sensitive element-binding protein 1 | VLGTVK | 1138.28 | 1050.68 | 2789.36 | 3717.21 |
| Nuclease-sensitive element-binding protein 1 | VLGTVK | 1456.23 | 1978.69 | 2259.74 | 2606.42 |
| Nuclease-sensitive element-binding protein 1 | VLGTVK | 720.88 | 586.78 | 1788.71 | 2517.57 |
| Presenilins-associated rhomboid-like protein, mitochondrial | IWHEIR | 937.5 | 568.53 | 567.94 | 932.22 |
| Presenilins-associated rhomboid-like protein, mitochondrial | YFTSNPASK | 2498.89 | 3327.91 | 5897.58 | 6690.17 |
| Presenilins-associated rhomboid-like protein, mitochondrial | FNFF | 212.65 | 161.31 | 336.92 | 469.41 |
| Presenilins-associated rhomboid-like protein, mitochondrial | IVNI | 1633.97 | 1864.79 | 2774.58 | 2886.85 |
| Presenilins-associated rhomboid-like protein, mitochondrial | IVNI | 920.29 | 673.13 | 1254.48 | 1664.15 |
| Presenilins-associated rhomboid-like protein, mitochondrial | IVNI | 687.79 | 771.45 | 2083.14 | 1738.66 |
| Presenilins-associated rhomboid-like protein, mitochondrial | IWHEIR | 977.81 | 415.99 | 519.31 | 585.71 |
| Presenilins-associated rhomboid-like protein, mitochondrial | IWHEIR | 587.16 | 606.78 | 331.77 | 491.01 |
| Presenilins-associated rhomboid-like protein, mitochondrial | LDSI | 357.3 | 444.42 | 376.14 | 235.28 |
| Presenilins-associated rhomboid-like protein, mitochondrial | LDSI | 382.05 | 658.05 | 515.6 | 643.4 |
| Presenilins-associated rhomboid-like protein, mitochondrial | LIWK | 2403.98 | 3023.9 | 3730.95 | 5019.55 |
| Presenilins-associated rhomboid-like protein, mitochondrial | LLGRR | 1293.45 | 1358.52 | 2364.85 | 2041.05 |
| Presenilins-associated rhomboid-like protein, mitochondrial | VLVF | 214.94 | 147.47 | 214.9 | 200.87 |
| Presenilins-associated rhomboid-like protein, mitochondrial | VLVF | 191.24 | 148.49 | 198.22 | 255.16 |
| Presenilins-associated rhomboid-like protein, mitochondrial | VLVF | 263.78 | 215.47 | 236.31 | 234.14 |
| Presenilins-associated rhomboid-like protein, mitochondrial | WWNNLSDGQR | 573.03 | 406.66 | 761.71 | 1004.9 |
| Presenilins-associated rhomboid-like protein, mitochondrial | YESLK | 1538.24 | 1535.58 | 5953.25 | 5531.07 |
| Presenilins-associated rhomboid-like protein, mitochondrial | YESLK | 969.39 | 1673.58 | 4669.1 | 6246.91 |
| Presenilins-associated rhomboid-like protein, mitochondrial | YESLK | 4095.43 | 4529.43 | 17577.63 | 21368.12 |
| Presenilins-associated rhomboid-like protein, mitochondrial | YESLK | 3082.65 | 4164.64 | 11409.07 | 13751.92 |
| Presenilins-associated rhomboid-like protein, mitochondrial | YESLK | 1453.92 | 1568.73 | 7707.87 | 7208.38 |
| Presenilins-associated rhomboid-like protein, mitochondrial | YESLK | 1297.12 | 1527.93 | 6311.22 | 6729.36 |
| Presenilins-associated rhomboid-like protein, mitochondrial | YESLK | 1182.42 | 1051.88 | 4642.53 | 3828.26 |
| Presenilins-associated rhomboid-like protein, mitochondrial | YESLK | 2927.21 | 2712.91 | 7250.63 | 7875.29 |
| Presenilins-associated rhomboid-like protein, mitochondrial | YESLK | 1050.57 | 567.91 | 1567.04 | 2012.29 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 114.46 | 287.36 | 205.61 | 188.23 |
| 60S ribosomal protein L36 | EVCGFAPYER | 1019.22 | 473.6 | 2144.93 | 2704.23 |
| 60S ribosomal protein L36 | KREELSNVLAAMR | 2315.28 | 2319.24 | 7371.62 | 7309.64 |
| 60S ribosomal protein L36 | YPMAVGLNK | 2738.18 | 2877.79 | 7127.4 | 10627.19 |
| 60S ribosomal protein L36 | RAMELLK | 2301.97 | 2144.31 | 5009.86 | 6124.33 |
| 60S ribosomal protein L36 | ALRYPMAVGLNK | 918.95 | 1018.53 | 1779.5 | 1047.27 |
| 60S ribosomal protein L36 | AMELLK | 6962.89 | 5698.45 | 21473.25 | 25668.64 |
| 60S ribosomal protein L36 | AMELLK | 1318.32 | 923.14 | 2215.35 | 2853.39 |
| 60S ribosomal protein L36 | AMELLK | 4575.27 | 3824.04 | 16617.53 | 18873.96 |
| 60S ribosomal protein L36 | AMELLK | 1538.52 | 444.75 | 1722.42 | 2308.58 |

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|---|---|---|---|---|---|
| 60S ribosomal protein L36 | AMELLK | 1227.7 | 1471.35 | 1651.67 | 2169.75 |
| 60S ribosomal protein L36 | AMELLK | 1851.25 | 2845.47 | 5061.6 | 4615.99 |
| 60S ribosomal protein L36 | AMELLK | 2044.9 | 1585.36 | 3283.01 | 3666.71 |
| 60S ribosomal protein L36 | AMELLK | 1095.22 | 943.52 | 1599.4 | 1605.94 |
| 60S ribosomal protein L36 | AMELLK | 1861.68 | 1814.25 | 4227.74 | 5236.07 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 70.14 | 91.68 | 260.71 | 271.29 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 146.74 | 183.33 | 287.09 | 265.63 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 177.85 | 194.78 | 457.57 | 496.41 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 255.17 | 215.61 | 579.98 | 694.9 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 498.85 | 607.87 | 2090.74 | 2307.01 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 214.64 | 176.73 | 683.72 | 687.62 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 139.37 | 166.81 | 386.28 | 465.31 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 174.03 | 146.4 | 417.96 | 487.14 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 77.8 | 79.68 | 241.19 | 231.13 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 141.63 | 49.33 | 232.38 | 296.15 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 231.64 | 92.8 | 305.16 | 453.5 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 335.66 | 135.43 | 368.42 | 430.67 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 210.86 | 231.17 | 983.25 | 1215.69 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 222.38 | 156.79 | 311.74 | 351.65 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 255.05 | 226.67 | 671.33 | 740.41 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 238.23 | 80.71 | 240.93 | 365.51 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 244.05 | 143.83 | 288.66 | 359.19 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 271.01 | 139.33 | 199.57 | 258.31 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 128.45 | 75.56 | 472.54 | 610.17 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 127.93 | 127 | 376.14 | 245.99 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 189.05 | 152.37 | 599.29 | 798.27 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 272.4 | 108.7 | 326.54 | 314.05 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 141.86 | 133.51 | 163.05 | 175.47 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 488.18 | 279.78 | 753.46 | 628.37 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 2191.15 | 1498.13 | 4083.36 | 3896.81 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 2092.69 | 1970.44 | 4963.26 | 3542.27 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 593.32 | 317.19 | 1283.81 | 793.9 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 460.47 | 463.71 | 799.31 | 1567.17 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 3135.82 | 3804.41 | 5098.12 | 6833.38 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 307.52 | 255.52 | 275.61 | 551.43 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 49.41 | 224.86 | 185.09 | 222 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 568.75 | 511.19 | 660 | 1092.98 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 1647.19 | 2261.29 | 2526.93 | 3066.14 |
| 60S ribosomal protein L36 | EELSNVLAAMR | 126.53 | 264.72 | 483.64 | 451.25 |
| 60S ribosomal protein L36 | ELLK | 1331.14 | 1464.69 | 1921.29 | 2240.57 |
| 60S ribosomal protein L36 | ELLK | 569.43 | 869.56 | 642.15 | 1040.57 |
| 60S ribosomal protein L36 | ELLK | 631.39 | 918.11 | 938.93 | 1167.85 |
| 60S ribosomal protein L36 | ELLK | 485.14 | 579.53 | 777.31 | 880.2 |
| 60S ribosomal protein L36 | ELLK | 1331.98 | 1275.66 | 2386.22 | 2606.35 |
| 60S ribosomal protein L36 | ELLK | 1118.92 | 1368.09 | 1892.76 | 1206.11 |
| 60S ribosomal protein L36 | ELLK | 1114.11 | 1205 | 1892.83 | 2006.06 |
| 60S ribosomal protein L36 | ELLK | 2703.21 | 2609.44 | 4732.29 | 5170.87 |
| 60S ribosomal protein L36 | ELLK | 2218.14 | 2554.59 | 1989.37 | 2671.55 |
| 60S ribosomal protein L36 | EVCGFAPYER | 1787.75 | 2097.58 | 4791.26 | 7174.91 |
| 60S ribosomal protein L36 | EVCGFAPYER | 3088.36 | 2749.01 | 9448.33 | 8791.11 |
| 60S ribosomal protein L36 | EVCGFAPYER | 4636.12 | 4620.72 | 10654.49 | 12296.17 |
| 60S ribosomal protein L36 | EVCGFAPYER | 7120.9 | 7533.96 | 34775.89 | 39081.61 |
| 60S ribosomal protein L36 | EVCGFAPYER | 2758.01 | 2620.41 | 7818.74 | 8188.49 |
| 60S ribosomal protein L36 | EVCGFAPYER | 1754.44 | 2090.7 | 4615.29 | 5942.11 |
| 60S ribosomal protein L36 | EVCGFAPYER | 855.21 | 826.29 | 2267.21 | 2267.41 |
| 60S ribosomal protein L36 | EVCGFAPYER | 8279.18 | 8524.19 | 23726.99 | 23846.98 |
| 60S ribosomal protein L36 | EVCGFAPYER | 5637.5 | 6005.61 | 19912.65 | 24442.69 |
| 60S ribosomal protein L36 | EVCGFAPYER | 1508.04 | 2285.03 | 3298.62 | 3256.4 |
| 60S ribosomal protein L36 | EVCGFAPYER | 7713.18 | 8592.68 | 27306.78 | 32132.83 |
| 60S ribosomal protein L36 | EVCGFAPYER | 1556.58 | 2596.27 | 3309.79 | 3045.34 |
| 60S ribosomal protein L36 | EVCGFAPYER | 1728.11 | 2989.36 | 3661.04 | 2906.31 |
| 60S ribosomal protein L36 | EVCGFAPYER | 152.37 | 264.88 | 381 | 468.5 |
| 60S ribosomal protein L36 | EVCGFAPYER | 8384.15 | 8471.92 | 32151.29 | 31483.2 |
| 60S ribosomal protein L36 | EVCGFAPYER | 10696.41 | 8855.6 | 40441.77 | 39046.21 |

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|---|---|---|---|---|---|
| 60S ribosomal protein L36 | EVCGFAPYER | 4380.25 | 4474.2 | 10116.89 | 11647.72 |
| 60S ribosomal protein L36 | EVCGFAPYER | 1692.53 | 2143.55 | 2546.98 | 3143.68 |
| 60S ribosomal protein L36 | EVCGFAPYER | 751 | 1015.93 | 2576.65 | 2548.45 |
| 60S ribosomal protein L36 | EVCGFAPYER | 9655.37 | 8729.61 | 36819.42 | 36203.77 |
| 60S ribosomal protein L36 | EVCGFAPYER | 757.32 | 603.57 | 1037.13 | 840.97 |
| 60S ribosomal protein L36 | EVCGFAPYER | 2474.53 | 2011.26 | 4735.86 | 4120.77 |
| 60S ribosomal protein L36 | EVCGFAPYER | 1524.49 | 1085.41 | 1783.49 | 2179.61 |
| 60S ribosomal protein L36 | EVCGFAPYER | 1065.74 | 877.69 | 2250.94 | 2218.68 |
| 60S ribosomal protein L36 | EVCGFAPYER | 565 | 668.73 | 752.71 | 1356.43 |
| 60S ribosomal protein L36 | EVCGFAPYERR | 1787.75 | 2097.58 | 4791.26 | 7174.91 |
| 60S ribosomal protein L36 | KREELSNVLAAMR | 2433.82 | 2734.85 | 8452.01 | 10544.9 |
| 60S ribosomal protein L36 | KREELSNVLAAMR | 1787.93 | 3144.03 | 7865.32 | 9185.53 |
| 60S ribosomal protein L36 | KREELSNVLAAMR | 2672.78 | 3381.97 | 8437.06 | 9516.36 |
| 60S ribosomal protein L36 | KREELSNVLAAMR | 1123.87 | 1198.53 | 2602.86 | 3575.19 |
| 60S ribosomal protein L36 | KREELSNVLAAMR | 786.86 | 770.08 | 990.09 | 1512.58 |
| 60S ribosomal protein L36 | KREELSNVLAAMR | 1531.72 | 1116.45 | 2509.01 | 2837.76 |
| 60S ribosomal protein L36 | KREELSNVLAAMR | 2119.79 | 2696.5 | 4265.91 | 4654.86 |
| 60S ribosomal protein L36 | KREELSNVLAAMR | 354.19 | 751.06 | 1442.19 | 1911.02 |
| 60S ribosomal protein L36 | KREELSNVLAAMR | 1138.74 | 1005.34 | 1360.19 | 1571.13 |
| 60S ribosomal protein L36 | LAAMRK | 1507.23 | 1514.13 | 2181.49 | 2895.17 |
| 60S ribosomal protein L36 | MELLK | 645.9 | 228.68 | 363.23 | 238.44 |
| 60S ribosomal protein L36 | YPMAVGLNK | 203.09 | 360.73 | 559.79 | 918.98 |
| 60S ribosomal protein L36 | YPMAVGLNK | 2338.43 | 2585.36 | 7632.89 | 7984.36 |
| 60S ribosomal protein L36 | YPMAVGLNK | 1444.5 | 1754.94 | 3318.06 | 3338 |
| 60S ribosomal protein L36 | YPMAVGLNK | 4446.6 | 3664.16 | 12710.69 | 13966.16 |
| 60S ribosomal protein L36 | YPMAVGLNK | 1976.04 | 1686.68 | 5650.83 | 5096.96 |
| 60S ribosomal protein L36 | YPMAVGLNK | 3194.73 | 3729.65 | 5601.38 | 7134.7 |
| 60S ribosomal protein L36 | YPMAVGLNK | 1429.82 | 1609.62 | 3379.95 | 2984.53 |
| 60S ribosomal protein L36 | YPMAVGLNK | 713.2 | 601.17 | 1264.66 | 1741.33 |
| 60S ribosomal protein L36 | YPMAVGLNK | 332.85 | 306.65 | 1483.15 | 1170.26 |
| 60S ribosomal protein L36 | YPMAVGLNK | 773.67 | 584.06 | 1357.16 | 1167.77 |
| 60S ribosomal protein L36 | YPMAVGLNK | 205.95 | 77.91 | 497.66 | 372.41 |
| Estradiol 17-beta-dehydrogenase 11 | NPSTSLGPTLEPEEVVNR | 100.63 | 270.76 | 279.65 | 190.29 |
| Estradiol 17-beta-dehydrogenase 11 | LVLWDINK | 152.77 | 226 | 388.17 | 312.4 |
| Estradiol 17-beta-dehydrogenase 11 | ESFVK | 1599.27 | 2207.85 | 2846.15 | 3988.64 |
| Estradiol 17-beta-dehydrogenase 11 | FIPK | 3105.58 | 3175 | 3950.66 | 5222.85 |
| Estradiol 17-beta-dehydrogenase 11 | LAVL | 667.11 | 261.48 | 2492.45 | 2908.78 |
| Estradiol 17-beta-dehydrogenase 11 | LAVLK | 2035.83 | 1523.99 | 9543.57 | 10535.47 |
| Estradiol 17-beta-dehydrogenase 11 | LAVLK | 1665.34 | 1744.59 | 6637.53 | 7664.58 |
| Estradiol 17-beta-dehydrogenase 11 | LAVLK | 815.91 | 1091.67 | 2953.61 | 4086.81 |
| Estradiol 17-beta-dehydrogenase 11 | LAVLK | 561.34 | 604.43 | 1712.88 | 1985.18 |
| Estradiol 17-beta-dehydrogenase 11 | LAVLK | 1483 | 1461.14 | 5370.26 | 5191.79 |
| Estradiol 17-beta-dehydrogenase 11 | LAVLK | 540.21 | 670.58 | 1922.34 | 2521.13 |
| Estradiol 17-beta-dehydrogenase 11 | LAVLK | 648.3 | 1055.44 | 2647.25 | 4185.83 |
| Estradiol 17-beta-dehydrogenase 11 | LAVLK | 1782.02 | 1493.33 | 8054.43 | 9583.17 |
| Estradiol 17-beta-dehydrogenase 11 | LAVLK | 871.54 | 595.46 | 1179.4 | 1649.04 |
| Estradiol 17-beta-dehydrogenase 11 | LAVLK | 1192.9 | 654.58 | 2609.21 | 2263.56 |
| Estradiol 17-beta-dehydrogenase 11 | LAVLK | 1512.71 | 653.93 | 830.6 | 1005.18 |
| Estradiol 17-beta-dehydrogenase 11 | LAVLK | 1185.07 | 1321.63 | 1980.6 | 2865.3 |
| Estradiol 17-beta-dehydrogenase 11 | LAVLK | 3228.25 | 4566.36 | 4088.17 | 6488.61 |
| Estradiol 17-beta-dehydrogenase 11 | LAVLK | 875.25 | 973.71 | 2507.6 | 2814.37 |
| Estradiol 17-beta-dehydrogenase 11 | LAVLK | 1012.58 | 1129.67 | 1470.03 | 1562.85 |
| Estradiol 17-beta-dehydrogenase 11 | LFIPK | 1353.59 | 1055.15 | 4970.4 | 6172.1 |
| Estradiol 17-beta-dehydrogenase 11 | LFIPK | 1202.21 | 1330.66 | 3439.14 | 2901.53 |
| Estradiol 17-beta-dehydrogenase 11 | LFIPK | 690.28 | 737.49 | 3647.59 | 4405.51 |
| Estradiol 17-beta-dehydrogenase 11 | LTEQK | 584.78 | 948.71 | 1138.98 | 1630.23 |
| Estradiol 17-beta-dehydrogenase 11 | NPSTSLGPTLEPEEVVNR | 282.45 | 179.73 | 286.76 | 341.52 |
| Estradiol 17-beta-dehydrogenase 11 | NPSTSLGPTLEPEEVVNR | 153.1 | 193.44 | 82.78 | 253.23 |
| Zinc finger protein-like 1 | LCNIPLASR | 409.21 | 422.03 | 602.13 | 724.21 |
| Zinc finger protein-like 1 | LATVNWAR | 2320.76 | 1351.97 | 3072.66 | 2071.43 |
| Zinc finger protein-like 1 | VNVCEHCLVANHAK | 2968.29 | 3015.86 | 3868.94 | 3302.54 |
| Zinc finger protein-like 1 | VYDTR | 1357.7 | 1713.52 | 525.75 | 533.65 |
| Zinc finger protein-like 1 | ARLLR | 652.99 | 911.35 | 1673.27 | 1931.99 |
| Zinc finger protein-like 1 | ARLLR | 1080.13 | 732.01 | 1638.98 | 1877.24 |

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|---|---|---|---|---|---|
| Zinc finger protein-like 1 | LATVNWAR | 1728.52 | 1353.27 | 3317.12 | 2628.22 |
| Zinc finger protein-like 1 | LCNIPLASR | 1054.26 | 841.82 | 1726.87 | 2154.96 |
| Zinc finger protein-like 1 | LCNIPLASR | 622.91 | 904.7 | 1261.24 | 1012.43 |
| Zinc finger protein-like 1 | LCNIPLASR | 2011.24 | 1400 | 2629 | 2426.83 |
| Zinc finger protein-like 1 | LCNIPLASR | 460.86 | 425.88 | 647.68 | 979.77 |
| Zinc finger protein-like 1 | LCNIPLASR | 456.83 | 823.15 | 850.56 | 861.96 |
| Zinc finger protein-like 1 | LCNIPLASR | 498.79 | 508.14 | 694.8 | 808.48 |
| Zinc finger protein-like 1 | LGLL | 1296.99 | 1434.54 | 5346.49 | 5340.23 |
| Zinc finger protein-like 1 | LGLL | 667.11 | 261.48 | 2492.45 | 2908.78 |
| Zinc finger protein-like 1 | LGLL | 3314.76 | 3998.01 | 22099.16 | 20825.3 |
| Zinc finger protein-like 1 | LGLL | 3659.85 | 3414.84 | 18140.3 | 21295.9 |
| Zinc finger protein-like 1 | LGLL | 332.65 | 326.7 | 492.06 | 841.9 |
| Zinc finger protein-like 1 | LLAL | 196.22 | 188.4 | 226.96 | 250.42 |
| Zinc finger protein-like 1 | LLAL | 75.78 | 172.69 | 115.6 | 69.95 |
| Zinc finger protein-like 1 | LLGF | 658.89 | 647.68 | 705.21 | 939.96 |
| Zinc finger protein-like 1 | LTLL | 114.69 | 158.48 | 37.77 | 113.82 |
| Zinc finger protein-like 1 | LTLL | 201.09 | 132.94 | 186.59 | 209.92 |
| Zinc finger protein-like 1 | LTLL | 192.95 | 85.86 | 151.74 | 325.05 |
| Putative transferase CAF17, mitochondrial | LLTQDEGPALVPGGR | 793.24 | 1310.37 | 1845.59 | 2098.48 |
| Putative transferase CAF17, mitochondrial | GCYIGQELTAR | 315.48 | 320.15 | 879.01 | 418.59 |
| Putative transferase CAF17, mitochondrial | AGYAHFLNVQGR | 1181.92 | 1207.58 | 2155.28 | 1769.64 |
| Putative transferase CAF17, mitochondrial | AGAAAILIRDPR | 410.48 | 296.48 | 424.97 | 311.38 |
| Putative transferase CAF17, mitochondrial | AILIR | 2985.64 | 3641.8 | 8639.29 | 10643.07 |
| Putative transferase CAF17, mitochondrial | AILIR | 807.23 | 1311.26 | 2069.48 | 2004.08 |
| Putative transferase CAF17, mitochondrial | GCYIGQELTAR | 357.99 | 376.29 | 499.28 | 460.02 |
| Putative transferase CAF17, mitochondrial | ILIR | 386.99 | 489.76 | 684.01 | 680.12 |
| Putative transferase CAF17, mitochondrial | ILIR | 912.1 | 950.18 | 1143.27 | 1280.65 |
| Putative transferase CAF17, mitochondrial | ILIR | 556.67 | 959.36 | 927.48 | 1147.92 |
| Putative transferase CAF17, mitochondrial | ILIR | 1415.65 | 1626.01 | 1823.04 | 1846.6 |
| Putative transferase CAF17, mitochondrial | ILIR | 279.39 | 481.67 | 627.51 | 552.92 |
| Putative transferase CAF17, mitochondrial | ILIR | 487.03 | 393.55 | 449.11 | 438.94 |
| Putative transferase CAF17, mitochondrial | LALYR | 2078.86 | 1421.47 | 2542.53 | 3101.04 |
| Putative transferase CAF17, mitochondrial | LGLL | 1296.99 | 1434.54 | 5346.49 | 5340.23 |
| Putative transferase CAF17, mitochondrial | LGLL | 667.11 | 261.48 | 2492.45 | 2908.78 |
| Putative transferase CAF17, mitochondrial | LGLL | 3314.76 | 3998.01 | 22099.16 | 20825.3 |
| Putative transferase CAF17, mitochondrial | LGLL | 3659.85 | 3414.84 | 18140.3 | 21295.9 |
| Putative transferase CAF17, mitochondrial | LGLL | 332.65 | 326.7 | 492.06 | 841.9 |
| Putative transferase CAF17, mitochondrial | LLRVR | 5138.54 | 4769.86 | 11009.6 | 13833.13 |
| Putative transferase CAF17, mitochondrial | LLTQDEGPALVPGGR | 2129.58 | 2049.29 | 2948.53 | 3945.9 |
| Putative transferase CAF17, mitochondrial | LLTQDEGPALVPGGR | 1893.53 | 1966.14 | 2235.31 | 2760.61 |
| Putative transferase CAF17, mitochondrial | LLTQDEGPALVPGGR | 2035.5 | 1769.72 | 2389.16 | 2902.2 |
| Serine protease 56 | ELLAWDPPQELQADAAR | 153.64 | 139.66 | 187.9 | 298.33 |
| Serine protease 56 | LAPALALPAPALR | 150.89 | 92.13 | 208.83 | 203.35 |
| Serine protease 56 | VPLLSTDTCR | 731.55 | 809.16 | 802.13 | 1154.8 |
| Serine protease 56 | AGLGGR | 510.98 | 580.38 | 533.95 | 755.53 |
| Serine protease 56 | AAQR | 206.2 | 53.15 | 444.83 | 501 |
| Serine protease 56 | AGLGGR | 511.45 | 534.11 | 640.39 | 1026.37 |
| Serine protease 56 | AGLGGR | 680.96 | 382.53 | 761.99 | 753.45 |
| Serine protease 56 | ELLAWDPPQELQADAAR | 128.29 | 90.91 | 139.23 | 236.51 |
| Serine protease 56 | ELLAWDPPQELQADAAR | 68.29 | 61.97 | 88.47 | 63.72 |
| Serine protease 56 | LAVL | 667.11 | 261.48 | 2492.45 | 2908.78 |
| Serine protease 56 | LGLL | 1296.99 | 1434.54 | 5346.49 | 5340.23 |
| Serine protease 56 | LGLL | 667.11 | 261.48 | 2492.45 | 2908.78 |
| Serine protease 56 | LGLL | 3314.76 | 3998.01 | 22099.16 | 20825.3 |
| Serine protease 56 | LGLL | 3659.85 | 3414.84 | 18140.3 | 21295.9 |
| Serine protease 56 | LGLL | 332.65 | 326.7 | 492.06 | 841.9 |
| Serine protease 56 | LGLLR | 772.6 | 1009.43 | 1169.95 | 1102.84 |
| Serine protease 56 | LGLLR | 484.95 | 598.57 | 527.29 | 833.2 |
| Serine protease 56 | LGLLR | 889.11 | 1094.25 | 961.9 | 1189.95 |
| Serine protease 56 | LGLLR | 1108.53 | 1543.55 | 1229.93 | 1769.51 |
| Serine protease 56 | LGLLR | 980.63 | 1519.85 | 1222.12 | 845.75 |
| Serine protease 56 | LGLLR | 881.63 | 875.5 | 1172.56 | 719.34 |
| Serine protease 56 | LGLLR | 988.01 | 896.86 | 1055.42 | 1203.53 |
| Serine protease 56 | LGLLR | 252.97 | 539.23 | 483.12 | 768.99 |

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|---|---|---|---|---|---|
| Serine protease 56 | LGLLR | 610.41 | 650.31 | 1125.48 | 924.24 |
| Serine protease 56 | LGLLR | 584.6 | 647.49 | 986.93 | 1677.42 |
| Serine protease 56 | LGLLR | 1447.92 | 1203.54 | 1220.32 | 1386.83 |
| Serine protease 56 | LGLLR | 801.22 | 734.4 | 1425.97 | 1094.17 |
| Serine protease 56 | LLGLLR | 483.61 | 518.69 | 653.99 | 1107.19 |
| Serine protease 56 | LLGLLR | 256.04 | 236.08 | 148.95 | 522.7 |
| Serine protease 56 | LLGLLR | 615.77 | 227.28 | 542.91 | 587.06 |
| Serine protease 56 | LLGLLR | 653.77 | 834.29 | 1705.62 | 3119 |
| Serine protease 56 | LLGLLR | 382.83 | 475.12 | 625.77 | 933.52 |
| Serine protease 56 | LLGLLR | 1067.95 | 871.8 | 2002.55 | 1568.66 |
| Serine protease 56 | VPLLSTDTCR | 917.96 | 477.34 | 1214.3 | 455.52 |
| Serine protease 56 | VPLLSTDTCR | 328.07 | 247.41 | 601.49 | 796.62 |
| Serine protease 56 | VPLLSTDTCR | 581.86 | 705.01 | 864.41 | 1347.42 |
| 40S ribosomal protein S29 | GHQQLYWSHPR | 248.74 | 319.03 | 700.09 | 625.75 |
| 40S ribosomal protein S29 | YGLNMCR | 2285.36 | 2190.09 | 4454.89 | 4537.8 |
| 40S ribosomal protein S29 | DIGFIKLD | 11087.82 | 11355.44 | 32419.86 | 41222.38 |
| 40S ribosomal protein S29 | DIGFIK | 2220.52 | 3382.97 | 4193.79 | 3923.4 |
| 40S ribosomal protein S29 | QYAKDIGFIKLD | 1007.21 | 1128.21 | 2253.41 | 2398.64 |
| 40S ribosomal protein S29 | FRQYAK | 673.48 | 1014.93 | 1261.42 | 2580.31 |
| 40S ribosomal protein S29 | DIGFIK | 2284.69 | 1617.45 | 4912.44 | 6015.3 |
| 40S ribosomal protein S29 | DIGFIK | 3793.57 | 3607.42 | 8602.48 | 10475.49 |
| 40S ribosomal protein S29 | DIGFIK | 3787.58 | 3454.83 | 2183.08 | 2736.91 |
| 40S ribosomal protein S29 | DIGFIK | 1660.79 | 1980.87 | 2678.95 | 2073.93 |
| 40S ribosomal protein S29 | DIGFIK | 3867.68 | 4370.6 | 6535.15 | 7775.89 |
| 40S ribosomal protein S29 | DIGFIKLD | 13050.58 | 14885.72 | 46813.57 | 55837.01 |
| 40S ribosomal protein S29 | DIGFIKLD | 26102.08 | 28190.88 | 71172.73 | 90047.1 |
| 40S ribosomal protein S29 | DIGFIKLD | 3935.97 | 2304.71 | 7044.35 | 7977.99 |
| 40S ribosomal protein S29 | DIGFIKLD | 811.79 | 1179.41 | 3203.13 | 3393.27 |
| 40S ribosomal protein S29 | DIGFIKLD | 2141.39 | 2051.88 | 5755.72 | 6349.43 |
| 40S ribosomal protein S29 | DIGFIKLD | 8598.66 | 9512.96 | 17420.31 | 19058.96 |
| 40S ribosomal protein S29 | GHQQLYWSHPR | 229.75 | 279.81 | 369.51 | 384.23 |
| 40S ribosomal protein S29 | GHQQLYWSHPR | 1984.18 | 2265.45 | 2682.26 | 3230.04 |
| 40S ribosomal protein S29 | GHQQLYWSHPR | 1461.63 | 1339.09 | 2390.54 | 4011.44 |
| 40S ribosomal protein S29 | GHQQLYWSHPR | 1935.59 | 1427.12 | 2575.47 | 2827.64 |
| 40S ribosomal protein S29 | GHQQLYWSHPR | 341.71 | 388.57 | 589.52 | 719.92 |
| 40S ribosomal protein S29 | YGLNMCR | 1212.4 | 1600.36 | 4528.28 | 4927.27 |
| 40S ribosomal protein S29 | YGLNMCR | 969.85 | 883.34 | 2216.58 | 2073.24 |
| 40S ribosomal protein S29 | YGLNMCR | 1135.67 | 776.78 | 1295.1 | 2144.42 |
| 40S ribosomal protein S29 | YGLNMCR | 4962.66 | 4912.04 | 12865.5 | 14438.77 |
| 40S ribosomal protein S29 | YGLNMCR | 3999.81 | 3869.48 | 10414.79 | 12588.92 |
| 40S ribosomal protein S29 | YGLNMCR | 860.09 | 1301.74 | 1974.37 | 2183.16 |
| Prostaglandin E synthase 3 | KGESGQSWPR | 1003.92 | 1347.13 | 3191.3 | 3344.77 |
| Prostaglandin E synthase 3 | SILCCLR | 723.13 | 897.05 | 1644.88 | 1861.72 |
| Prostaglandin E synthase 3 | DVNVNFEK | 1039.94 | 1298.61 | 2055.59 | 1862.69 |
| Prostaglandin E synthase 3 | SKLTFSCLGGSDNFK | 153.11 | 192.47 | 130.58 | 378.63 |
| Prostaglandin E synthase 3 | KGESGQSWPR | 577.09 | 857.15 | 2717.48 | 2962.58 |
| Prostaglandin E synthase 3 | KGESGQSWPR | 429.05 | 589.56 | 965.06 | 1046.95 |
| Prostaglandin E synthase 3 | KGESGQSWPR | 576.01 | 857.7 | 2641.29 | 2709.29 |
| Prostaglandin E synthase 3 | KGESGQSWPR | 666.92 | 705.9 | 1199.99 | 1749.05 |
| Prostaglandin E synthase 3 | KGESGQSWPR | 924.09 | 616.96 | 2157.42 | 2673.3 |
| Prostaglandin E synthase 3 | SILCCLR | 1051.58 | 680.83 | 2520.15 | 1896.49 |
| Prostaglandin E synthase 3 | SILCCLR | 2176.64 | 3143.82 | 7674.32 | 7789.98 |
| Prostaglandin E synthase 3 | SILCCLR | 2906.25 | 3612.9 | 8338.28 | 10294.41 |
| Prostaglandin E synthase 3 | SILCCLR | 1944.39 | 1622.22 | 4008.95 | 4271.17 |
| Prostaglandin E synthase 3 | SILCCLR | 1332.41 | 1552.18 | 3014.5 | 4081.83 |
| Prostaglandin E synthase 3 | SILCCLR | 5750.32 | 4965.42 | 15795.9 | 18690.34 |
| Prostaglandin E synthase 3 | SILCCLR | 806.47 | 535.59 | 1453.99 | 1861.51 |
| Prostaglandin E synthase 3 | SILCCLR | 1518.18 | 1496.84 | 3475.36 | 3571.97 |
| Prostaglandin E synthase 3 | SILCCLR | 604.08 | 424.99 | 964.75 | 1101.78 |
| Prostaglandin E synthase 3 | SILCCLR | 1385.54 | 1515.99 | 3811.76 | 5485.4 |
| Prostaglandin E synthase 3 | SILCCLR | 1113.35 | 854.51 | 1468.08 | 2792.15 |
| Prostaglandin E synthase 3 | SILCCLR | 1090.4 | 1525.95 | 2592.38 | 4656.44 |
| Prostaglandin E synthase 3 | SILCCLR | 3898.41 | 3355.93 | 8531.04 | 7568.51 |
| Prostaglandin E synthase 3 | SILCCLR | 612.31 | 781.86 | 1100.27 | 1519.65 |

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|---|---|---|---|---|---|
| Prostaglandin E synthase 3 | SILCCLR | 1006.78 | 1277.31 | 2006.98 | 2742.34 |
| Prostaglandin E synthase 3 | SILCCLR | 670.69 | 1077.68 | 1677.91 | 2813.75 |
| Prostaglandin E synthase 3 | SILCCLR | 408.84 | 458.25 | 566.83 | 890.52 |
| Prostaglandin E synthase 3 | SILCCLR | 1316.78 | 1181.06 | 3557.83 | 4363.56 |
| Prostaglandin E synthase 3 | SILCCLR | 1128.29 | 867.82 | 1978.32 | 1838.67 |
| Phosphatidylserine decarboxylase proenzyme, mitochondrial | GSYNDFSFVTHTNR | 243.81 | 167.13 | 413.55 | 299.83 |
| Phosphatidylserine decarboxylase proenzyme, mitochondrial | NLSEFFR | 653.09 | 901.83 | 813.78 | 724.08 |
| Phosphatidylserine decarboxylase proenzyme, mitochondrial | GVTYSLESFLGPR | 413.7 | 297.53 | 1052.72 | 785.14 |
| Phosphatidylserine decarboxylase proenzyme, mitochondrial | ILNFGQVK | 984.73 | 902.6 | 1368.73 | 1163.47 |
| Phosphatidylserine decarboxylase proenzyme, mitochondrial | DFNFQLK | 804.64 | 503.27 | 1357.23 | 1470.14 |
| Phosphatidylserine decarboxylase proenzyme, mitochondrial | EITAL | 696.39 | 346.62 | 567.28 | 483.28 |
| Phosphatidylserine decarboxylase proenzyme, mitochondrial | EITAL | 846.76 | 809.64 | 1207.1 | 642.43 |
| Phosphatidylserine decarboxylase proenzyme, mitochondrial | EITAL | 840.21 | 712.18 | 1371.35 | 1274.4 |
| Phosphatidylserine decarboxylase proenzyme, mitochondrial | FLLR | 993.65 | 1617.09 | 1683.05 | 1522.96 |
| Phosphatidylserine decarboxylase proenzyme, mitochondrial | FLLR | 1306.18 | 1590.35 | 2020.16 | 2264.02 |
| Phosphatidylserine decarboxylase proenzyme, mitochondrial | FLLR | 2250.35 | 2670.49 | 3744.21 | 4025.15 |
| Phosphatidylserine decarboxylase proenzyme, mitochondrial | FLLR | 7295.87 | 8226.42 | 10784.35 | 13712.01 |
| Phosphatidylserine decarboxylase proenzyme, mitochondrial | FLLR | 1721.03 | 1135.92 | 2128.23 | 2658.95 |
| Phosphatidylserine decarboxylase proenzyme, mitochondrial | GSYNDFSFVTHTNR | 360.04 | 173.92 | 290.01 | 241.52 |
| Phosphatidylserine decarboxylase proenzyme, mitochondrial | GSYNDFSFVTHTNR | 360.04 | 173.92 | 290.01 | 241.52 |
| Phosphatidylserine decarboxylase proenzyme, mitochondrial | GSYNDFSFVTHTNR | 348.98 | 202.7 | 183.38 | 299.51 |
| Phosphatidylserine decarboxylase proenzyme, mitochondrial | GSYNDFSFVTHTNR | 436.11 | 317.98 | 544.13 | 619 |
| Phosphatidylserine decarboxylase proenzyme, mitochondrial | GSYNDFSFVTHTNR | 306.23 | 383.13 | 350.45 | 364.65 |
| Phosphatidylserine decarboxylase proenzyme, mitochondrial | ILNF | 423.9 | 353.62 | 687.59 | 880.8 |
| Phosphatidylserine decarboxylase proenzyme, mitochondrial | LGLL | 1296.99 | 1434.54 | 5346.49 | 5340.23 |
| Phosphatidylserine decarboxylase proenzyme, mitochondrial | LGLL | 667.11 | 261.48 | 2492.45 | 2908.78 |
| Phosphatidylserine decarboxylase proenzyme, mitochondrial | LGLL | 3314.76 | 3998.01 | 22099.16 | 20825.3 |
| Phosphatidylserine decarboxylase proenzyme, mitochondrial | LGLL | 3659.85 | 3414.84 | 18140.3 | 21295.9 |
| Phosphatidylserine decarboxylase proenzyme, mitochondrial | LGLL | 332.65 | 326.7 | 492.06 | 841.9 |
| Phosphatidylserine decarboxylase proenzyme, mitochondrial | LSEF | 256.82 | 158.75 | 141.81 | 69.66 |
| Phosphatidylserine decarboxylase proenzyme, mitochondrial | MFLLR | 1319.09 | 1379.31 | 2837.98 | 3218.58 |
| 40S ribosomal protein S26 | NIVEAAAVR | 1406.43 | 1686.12 | 3564.35 | 4573.86 |
| 40S ribosomal protein S26 | DISEASVFDAYVLPK | 282.25 | 198.94 | 613.84 | 529.54 |
| 40S ribosomal protein S26 | LHYCVSCAIHSK | 1316.59 | 2158.1 | 3098.78 | 3433.8 |
| 40S ribosomal protein S26 | DISEASVFDAYVLPK | 358.27 | 348.04 | 619.27 | 707.29 |
| 40S ribosomal protein S26 | DISEASVFDAYVLPK | 386.98 | 65.03 | 471.29 | 438.48 |
| 40S ribosomal protein S26 | DISEASVFDAYVLPK | 641.63 | 438.37 | 218.57 | 319.91 |
| 40S ribosomal protein S26 | DISEASVFDAYVLPK | 307.01 | 306.09 | 328.71 | 394.04 |
| 40S ribosomal protein S26 | FVIR | 976.09 | 1117.79 | 4000.14 | 3822.14 |
| 40S ribosomal protein S26 | FVIR | 1115.99 | 1019.13 | 2835.9 | 3064.67 |
| 40S ribosomal protein S26 | FVIR | 1107.62 | 888.16 | 2537 | 2709.99 |
| 40S ribosomal protein S26 | KFVIR | 2145.23 | 1673.2 | 2346.46 | 3611.83 |
| 40S ribosomal protein S26 | NIVEAAAVR | 2241.64 | 2253.7 | 6628.23 | 6751.44 |
| 40S ribosomal protein S26 | NIVEAAAVR | 12780.12 | 12031.88 | 44723.49 | 47193.19 |
| 40S ribosomal protein S26 | NIVEAAAVR | 1235.82 | 988.44 | 1574.6 | 2106.91 |
| 40S ribosomal protein S26 | NIVEAAAVR | 1449.35 | 1381.6 | 3311.11 | 3179.89 |
| 40S ribosomal protein S26 | NIVEAAAVR | 1691.46 | 972.73 | 2649.84 | 2798.51 |
| 40S ribosomal protein S26 | NIVEAAAVR | 937.18 | 1025.19 | 1489.23 | 1929.84 |
| 40S ribosomal protein S26 | NIVEAAAVR | 1292.48 | 1348.35 | 2977.96 | 2596.68 |
| 40S ribosomal protein S26 | NIVEAAAVR | 1132.59 | 1719.44 | 2600.12 | 2676.27 |
| 40S ribosomal protein S26 | NIVEAAAVR | 6736.26 | 6599.67 | 11711.49 | 14637.64 |
| Plasminogen activator inhibitor 1 RNA-binding protein | EMTLDEWK | 1452.26 | 1200.97 | 9150.69 | 11934.84 |
| Plasminogen activator inhibitor 1 RNA-binding protein | PGHLQEGFGCVVTNR | 1774.88 | 1241.05 | 2049.47 | 2129.75 |
| Plasminogen activator inhibitor 1 RNA-binding protein | RPDQQLQGEGK | 53 | 82.66 | 344.44 | 398.78 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 238.03 | 207.02 | 535.88 | 786.67 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SSASAPDVDDPEAFPALA | 25.87 | 0 | 50.18 | 48.97 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SSFSHYSGLK | 406.32 | 707.08 | 1777.59 | 1915.03 |
| Plasminogen activator inhibitor 1 RNA-binding protein | EETQPPVALK | 1452.65 | 1162.59 | 3335.52 | 4561.14 |
| Plasminogen activator inhibitor 1 RNA-binding protein | GFVLHK | 676.94 | 459.93 | 724.61 | 1186.35 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SEEAHAEDSVMDHHFR | 487.13 | 383.02 | 969.52 | 936.04 |

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|---|---|---|---|---|---|
| Plasminogen activator inhibitor 1 RNA-binding protein | AKVEFNIR | 383.65 | 393.93 | 809.11 | 1184.08 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SSASAPDVDDPEAFPAL | 0 | 25.35 | 23.43 | 24.52 |
| Plasminogen activator inhibitor 1 RNA-binding protein | VEFNIR | 3936.18 | 4517.93 | 9155.57 | 8664.04 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SKSEEAHAEDSVMDHHFR | 287.97 | 378.59 | 163.21 | 176.2 |
| Plasminogen activator inhibitor 1 RNA-binding protein | EAGGGGVGGPGAKSAAQAAAQTNSNAAGK | 595.87 | 172.05 | 794.64 | 725.26 |
| Plasminogen activator inhibitor 1 RNA-binding protein | AAGK | 63.27 | 132.37 | 188.19 | 240.83 |
| Plasminogen activator inhibitor 1 RNA-binding protein | AAGK | 301.5 | 425.68 | 922.42 | 964.99 |
| Plasminogen activator inhibitor 1 RNA-binding protein | AKVEFNIR | 1401.52 | 2065.14 | 6375.2 | 6247 |
| Plasminogen activator inhibitor 1 RNA-binding protein | AKVEFNIR | 1389.73 | 1527.41 | 3604.02 | 2995.45 |
| Plasminogen activator inhibitor 1 RNA-binding protein | AKVEFNIR | 2275.43 | 2426.25 | 3713.14 | 5345.04 |
| Plasminogen activator inhibitor 1 RNA-binding protein | AKVEFNIR | 3870.6 | 3231.14 | 6082.73 | 7437.14 |
| Plasminogen activator inhibitor 1 RNA-binding protein | EMTLDEWK | 1399.62 | 1294.96 | 9800.66 | 9921.68 |
| Plasminogen activator inhibitor 1 RNA-binding protein | EMTLDEWK | 853.45 | 1000.31 | 2335.35 | 2419.38 |
| Plasminogen activator inhibitor 1 RNA-binding protein | EMTLDEWK | 458.33 | 675.49 | 862.34 | 816.48 |
| Plasminogen activator inhibitor 1 RNA-binding protein | EMTLDEWK | 561.34 | 711.1 | 2606.29 | 3499.64 |
| Plasminogen activator inhibitor 1 RNA-binding protein | EMTLDEWK | 724.31 | 461.38 | 3032.34 | 2384.75 |
| Plasminogen activator inhibitor 1 RNA-binding protein | EMTLDEWK | 581.21 | 556.26 | 884.65 | 848.92 |
| Plasminogen activator inhibitor 1 RNA-binding protein | EMTLDEWK | 900.96 | 880.83 | 3390.82 | 5117.41 |
| Plasminogen activator inhibitor 1 RNA-binding protein | EMTLDEWK | 574.54 | 683.67 | 1468.05 | 1141.57 |
| Plasminogen activator inhibitor 1 RNA-binding protein | EMTLDEWK | 203.12 | 357.72 | 708.93 | 717.64 |
| Plasminogen activator inhibitor 1 RNA-binding protein | EMTLDEWK | 256.88 | 152.32 | 459.7 | 614.98 |
| Plasminogen activator inhibitor 1 RNA-binding protein | EVLK | 796.48 | 777.65 | 1165.19 | 1070.14 |
| Plasminogen activator inhibitor 1 RNA-binding protein | EVLK | 1332.13 | 1047.96 | 1681.8 | 2087.14 |
| Plasminogen activator inhibitor 1 RNA-binding protein | FEVLK | 3498.29 | 2355.17 | 2641.23 | 2554.76 |
| Plasminogen activator inhibitor 1 RNA-binding protein | FEVLK | 2048.16 | 2007.96 | 1514.82 | 2979.76 |
| Plasminogen activator inhibitor 1 RNA-binding protein | FEVLK | 2999 | 1790.05 | 2214.13 | 2602.7 |
| Plasminogen activator inhibitor 1 RNA-binding protein | FEVLK | 386.68 | 95.14 | 259.6 | 556.91 |
| Plasminogen activator inhibitor 1 RNA-binding protein | GFVLHK | 1198.35 | 967.54 | 5192.52 | 6979.42 |
| Plasminogen activator inhibitor 1 RNA-binding protein | GFVLHK | 2131.97 | 1493.67 | 3457.2 | 4836.67 |
| Plasminogen activator inhibitor 1 RNA-binding protein | GFVLHK | 1295.22 | 971.1 | 1895.77 | 3058.31 |
| Plasminogen activator inhibitor 1 RNA-binding protein | GFVLHK | 318.36 | 674.84 | 1833.4 | 1529.57 |
| Plasminogen activator inhibitor 1 RNA-binding protein | GGVGGPGAK | 2153.8 | 2315.32 | 3157.32 | 3761.39 |
| Plasminogen activator inhibitor 1 RNA-binding protein | PGHLQEGFGCVVTNR | 357.73 | 401.87 | 830.54 | 389.87 |
| Plasminogen activator inhibitor 1 RNA-binding protein | PGHLQEGFGCVVTNR | 1239.06 | 1094.5 | 1529.02 | 1827.69 |
| Plasminogen activator inhibitor 1 RNA-binding protein | PGHLQEGFGCVVTNR | 729.25 | 1142.84 | 1591.04 | 2279.86 |
| Plasminogen activator inhibitor 1 RNA-binding protein | PGHLQEGFGCVVTNR | 657.52 | 996.23 | 2085.26 | 2868.7 |
| Plasminogen activator inhibitor 1 RNA-binding protein | PGHLQEGFGCVVTNR | 1269.31 | 1297.4 | 2657.47 | 1799.99 |
| Plasminogen activator inhibitor 1 RNA-binding protein | PGHLQEGFGCVVTNR | 357.76 | 399.15 | 645.85 | 1066.09 |
| Plasminogen activator inhibitor 1 RNA-binding protein | PGHLQEGFGCVVTNR | 152.35 | 267.35 | 258.81 | 242.97 |
| Plasminogen activator inhibitor 1 RNA-binding protein | PGHLQEGFGCVVTNR | 813.49 | 1544.03 | 1915.16 | 1685 |
| Plasminogen activator inhibitor 1 RNA-binding protein | PGHLQEGFGCVVTNR | 385.65 | 196.84 | 338.57 | 289.29 |
| Plasminogen activator inhibitor 1 RNA-binding protein | PGHLQEGFGCVVTNR | 696.65 | 852.83 | 950.38 | 1736.96 |
| Plasminogen activator inhibitor 1 RNA-binding protein | PGHLQEGFGCVVTNR | 3438.74 | 2919.76 | 6526.53 | 5743.21 |
| Plasminogen activator inhibitor 1 RNA-binding protein | PGHLQEGFGCVVTNR | 939.71 | 562.79 | 1481.7 | 1658.9 |
| Plasminogen activator inhibitor 1 RNA-binding protein | RPDQQLQGEGK | 118.49 | 208.02 | 1137.12 | 1047.95 |
| Plasminogen activator inhibitor 1 RNA-binding protein | RPDQQLQGEGK | 126.16 | 194.84 | 803.38 | 783.68 |
| Plasminogen activator inhibitor 1 RNA-binding protein | RPDQQLQGEGK | 117.47 | 202.28 | 839.44 | 961.32 |
| Plasminogen activator inhibitor 1 RNA-binding protein | RPDQQLQGEGK | 197.34 | 183.94 | 1081.71 | 1006.19 |
| Plasminogen activator inhibitor 1 RNA-binding protein | RPDQQLQGEGK | 218.39 | 231.66 | 984.63 | 493.5 |
| Plasminogen activator inhibitor 1 RNA-binding protein | RPDQQLQGEGK | 901.42 | 729.02 | 4941.52 | 5506.33 |
| Plasminogen activator inhibitor 1 RNA-binding protein | RPDQQLQGEGK | 170.23 | 203.27 | 1182.61 | 1111.54 |
| Plasminogen activator inhibitor 1 RNA-binding protein | RPDQQLQGEGK | 277.53 | 346.28 | 842.44 | 724.26 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 209.16 | 292.74 | 656.41 | 566.57 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 68.48 | 43.07 | 171.44 | 200.47 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 182.36 | 175.14 | 1359.24 | 1578.44 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 380.78 | 358.14 | 1845.43 | 1895.96 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 185.32 | 201.24 | 908.3 | 1023.93 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 301.26 | 235.67 | 854.67 | 797.76 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 484.99 | 807.1 | 3988.2 | 4659.67 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 67.45 | 144.42 | 268.12 | 200.23 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 67.45 | 144.42 | 268.12 | 200.23 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 51.33 | 35.24 | 196.44 | 243.26 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 114.34 | 192.55 | 268.48 | 508.95 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 1246.29 | 911.41 | 6091.31 | 7696.12 |

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|---|---|---|---|---|---|
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 1013.8 | 1221.68 | 4786.37 | 5369.67 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 20.82 | 70.96 | 243.44 | 321.34 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 37.44 | 131.23 | 392.4 | 453.08 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 877.6 | 1167.49 | 3551.57 | 4496.62 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 42.14 | 91.74 | 148 | 200.97 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 42.14 | 91.74 | 148 | 200.97 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 252.09 | 307.05 | 1121.07 | 1252.77 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 67.9 | 100.36 | 318.42 | 652.62 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 127.84 | 135.46 | 489.88 | 515.62 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 127.84 | 135.46 | 489.88 | 515.62 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 101.72 | 162.79 | 510.65 | 730.58 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 327.34 | 851.08 | 1965.02 | 2312.21 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 230.49 | 206.41 | 433.79 | 827.96 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 826.75 | 552.61 | 1548.51 | 2214.78 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 101.39 | 195.64 | 163.34 | 145.82 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 1498.8 | 1389.97 | 4524.58 | 4648.62 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 1498.8 | 1389.97 | 4524.58 | 4648.62 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 252.09 | 307.05 | 1121.07 | 1252.77 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 230.49 | 206.41 | 433.79 | 827.96 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 205.12 | 160.26 | 256.61 | 570.36 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 205.12 | 160.26 | 256.61 | 570.36 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 230.49 | 206.41 | 433.79 | 827.96 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 67.9 | 100.36 | 318.42 | 652.62 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 205.12 | 160.26 | 256.61 | 570.36 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 205.12 | 160.26 | 256.61 | 570.36 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 205.12 | 160.26 | 256.61 | 570.36 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 205.12 | 160.26 | 256.61 | 570.36 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 20.82 | 70.96 | 243.44 | 321.34 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 205.12 | 160.26 | 256.61 | 570.36 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 205.12 | 160.26 | 256.61 | 570.36 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 1498.8 | 1389.97 | 4524.58 | 4648.62 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGK | 177.27 | 358.89 | 373.43 | 519.28 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SAAQAAAQTNSNAAGKQLR | 68.1 | 80.28 | 87.7 | 50.48 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SEEAHAEDSVMDHHFR | 565.16 | 227.03 | 740.69 | 905.3 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SEEAHAEDSVMDHHFR | 487.13 | 383.02 | 969.52 | 936.04 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SEEAHAEDSVMDHHFR | 2452.89 | 2872.51 | 4657.35 | 7613.77 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SEEAHAEDSVMDHHFR | 6892.5 | 6588.82 | 11569.3 | 12600.35 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SEEAHAEDSVMDHHFR | 565.16 | 227.03 | 740.69 | 905.3 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SEEAHAEDSVMDHHFR | 2062.64 | 1641.47 | 3261.41 | 3977.26 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SKSEEAHAEDSVMDHHFR | 450.42 | 393.23 | 492.75 | 633.3 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SSASAPDVDDPEAFPALA | 51.01 | 66.61 | 347.7 | 289.01 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SSASAPDVDDPEAFPALA | 229.87 | 268.24 | 1207.36 | 862.44 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SSASAPDVDDPEAFPALA | 178.58 | 229.1 | 778.15 | 831.5 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SSASAPDVDDPEAFPALA | 77.33 | 19.7 | 18.89 | 179.52 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SSASAPDVDDPEAFPALA | 76.85 | 67.18 | 224.74 | 91.23 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SSASAPDVDDPEAFPALA | 0 | 0 | 50.13 | 48.95 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SSASAPDVDDPEAFPALA | 25.34 | 49.82 | 0 | 25.92 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SSASAPDVDDPEAFPALA | 0 | 10.01 | 37.31 | 23.81 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SSASAPDVDDPEAFPALA | 0 | 10.01 | 36.91 | 36.73 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SSASAPDVDDPEAFPALA | 1231.26 | 801.13 | 2133.7 | 2231.31 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SSASAPDVDDPEAFPALA | 949.11 | 910.99 | 1456.66 | 1579.07 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SSASAPDVDDPEAFPALA | 763.18 | 875.82 | 1697.12 | 1528.9 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SSASAPDVDDPEAFPALA | 1443.83 | 1501.72 | 2123.37 | 2575.74 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SSASAPDVDDPEAFPALA | 21.55 | 0 | 0 | 0 |
| Plasminogen activator inhibitor 1 RNA-binding protein | SSFSHYSGLK | 518.11 | 513.61 | 1364 | 1570.66 |
| Plasminogen activator inhibitor 1 RNA-binding protein | VEFNIR | 10218.06 | 8243.4 | 25139.02 | 30840.79 |
| Plasminogen activator inhibitor 1 RNA-binding protein | YIQK | 1033.73 | 1380.04 | 1879.71 | 2790.94 |
| Methyl-CpG-binding domain protein 1 | SDTYYQSPTGDR | 461.14 | 398.15 | 475.9 | 930.99 |
| Methyl-CpG-binding domain protein 1 | FAMK | 3007.55 | 3711.17 | 9382.64 | 10454.26 |
| Methyl-CpG-binding domain protein 1 | FAMK | 1285.38 | 1836.7 | 3420.35 | 5620.44 |
| Methyl-CpG-binding domain protein 1 | FAMK | 3003.9 | 3327.02 | 8186.22 | 10407.54 |
| Methyl-CpG-binding domain protein 1 | FAMK | 2988.79 | 3969.03 | 5738.11 | 9092.73 |
| Methyl-CpG-binding domain protein 1 | FAMK | 1494.31 | 1833.07 | 3100.39 | 4688.25 |
| Methyl-CpG-binding domain protein 1 | FAMK | 3849.62 | 4453.29 | 8255.63 | 11007.05 |

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|---|---|---|---|---|---|
| Methyl-CpG-binding domain protein 1 | FAMK | 1137.72 | 1425.27 | 2824.93 | 3427.63 |
| Methyl-CpG-binding domain protein 1 | FAMK | 4737.05 | 3585.63 | 8722.35 | 13012.68 |
| Protein YIF1B | RIPVSQPGMADPHQLFDDTSSAQSR | 561.78 | 561.27 | 973.93 | 873.13 |
| Protein YIF1B | ILADAAAEGVPVR | 598.68 | 532.14 | 737.5 | 1327.31 |
| Protein YIF1B | MHPAGLAAAAAGTPR | 385.16 | 244.52 | 534.92 | 479.98 |
| Protein YIF1B | ADPHQLFDDTSSAQSR | 51.74 | 0 | 74.52 | 99.26 |
| Protein YIF1B | ADPHQLFDDTSSAQSR | 102.15 | 120.59 | 43.07 | 19.02 |
| Protein YIF1B | ILADAAAEGVPVR | 510.07 | 563.4 | 951.88 | 1280.58 |
| Protein YIF1B | ILADAAAEGVPVR | 1069.64 | 704.56 | 1067.04 | 1817.04 |
| Protein YIF1B | LFGK | 9062.24 | 8818.6 | 14750.69 | 20824.39 |
| Protein YIF1B | LFGK | 3401.04 | 3453.03 | 6827.18 | 7258.8 |
| Protein YIF1B | LFGK | 5285.29 | 7186.07 | 10414.68 | 15434.6 |
| Protein YIF1B | LFGK | 1512.12 | 2840.11 | 3378.09 | 4968.55 |
| Protein YIF1B | LFGK | 1118.23 | 1329.95 | 1654.16 | 2890.87 |
| Protein YIF1B | LFGK | 2473.12 | 2469.67 | 3872.74 | 3759.92 |
| Protein YIF1B | LFGK | 6430.53 | 8720.22 | 14102.57 | 17149.91 |
| Protein YIF1B | LGLL | 1296.99 | 1434.54 | 5346.49 | 5340.23 |
| Protein YIF1B | LGLL | 667.11 | 261.48 | 2492.45 | 2908.78 |
| Protein YIF1B | LGLL | 3314.76 | 3998.01 | 22099.16 | 20825.3 |
| Protein YIF1B | LGLL | 3659.85 | 3414.84 | 18140.3 | 21295.9 |
| Protein YIF1B | LGLL | 332.65 | 326.7 | 492.06 | 841.9 |
| Protein YIF1B | LRLK | 3814.3 | 3262.06 | 4759.66 | 4438.43 |
| Protein YIF1B | MHPAGLAAAAAGTPR | 77.09 | 43.48 | 119.89 | 197.87 |
| Cofilin-1 | ASGVAVSDGVIK | 409.96 | 348.25 | 419.01 | 719.95 |
| Cofilin-1 | HELQANCYEEVKDR | 1036.62 | 669.12 | 5015.88 | 3869.9 |
| Cofilin-1 | KSSTPEEVK | 143.75 | 159.6 | 461.01 | 636.08 |
| Cofilin-1 | YALYDATYETK | 76.35 | 116.54 | 338.1 | 499.02 |
| Cofilin-1 | MLPDKDCR | 2437.85 | 1805.34 | 9631.12 | 10574.73 |
| Cofilin-1 | AVLFCLSEDKK | 332.77 | 314.68 | 1086.15 | 1249.33 |
| Cofilin-1 | LGGSAVISLEGKPL | 1098.29 | 534.07 | 1364.21 | 975.19 |
| Cofilin-1 | NIILEEGK | 1215.19 | 898.92 | 2195.69 | 1715.47 |
| Cofilin-1 | SSTPEEVKK | 257.54 | 299.93 | 708.54 | 1096.01 |
| Cofilin-1 | MIYASSK | 489.91 | 746.97 | 1891.6 | 1463.07 |
| Cofilin-1 | CTLAEK | 1441.53 | 1516.06 | 2752.15 | 3945.22 |
| Cofilin-1 | VFNDMK | 1718.58 | 1803.63 | 2883.56 | 4230.03 |
| Cofilin-1 | HELQANCYEEVK | 253.33 | 503.76 | 747.22 | 738.06 |
| Cofilin-1 | LTGIKHELQANCYEEVKDR | 2366.39 | 1312.47 | 2998.04 | 3725.28 |
| Cofilin-1 | ASGVAVSDGVIK | 912.86 | 768.68 | 1608.18 | 2267.64 |
| Cofilin-1 | ASGVAVSDGVIK | 332.81 | 310.66 | 1285.05 | 1212.98 |
| Cofilin-1 | ASGVAVSDGVIK | 76.65 | 86.37 | 552.8 | 565.17 |
| Cofilin-1 | ASGVAVSDGVIK | 384.18 | 341.86 | 830.02 | 957.56 |
| Cofilin-1 | ASGVAVSDGVIK | 3239.26 | 2308.09 | 9271.03 | 10069.33 |
| Cofilin-1 | ASGVAVSDGVIK | 354.51 | 720.2 | 1158.86 | 1153.3 |
| Cofilin-1 | ASGVAVSDGVIK | 153.69 | 134.7 | 433.06 | 546.78 |
| Cofilin-1 | ASGVAVSDGVIK | 333.1 | 282.23 | 403.06 | 540.36 |
| Cofilin-1 | ASGVAVSDGVIK | 437.41 | 189.26 | 523.96 | 456.78 |
| Cofilin-1 | ASGVAVSDGVIK | 5337.72 | 4772.07 | 15968.2 | 18228.72 |
| Cofilin-1 | ASGVAVSDGVIK | 411.8 | 166.32 | 476.05 | 386.47 |
| Cofilin-1 | ASGVAVSDGVIK | 320.25 | 275 | 754.74 | 609 |
| Cofilin-1 | ASGVAVSDGVIK | 436.37 | 291.98 | 552.71 | 852.95 |
| Cofilin-1 | ASGVAVSDGVIK | 281.29 | 294.55 | 993.92 | 1326.09 |
| Cofilin-1 | ASGVAVSDGVIK | 152.4 | 262.78 | 484.64 | 559.87 |
| Cofilin-1 | ASGVAVSDGVIK | 656.09 | 818.26 | 1585.69 | 2286.15 |
| Cofilin-1 | ASGVAVSDGVIK | 229.97 | 258.61 | 406.58 | 692.96 |
| Cofilin-1 | ASGVAVSDGVIK | 281.95 | 228.89 | 409.92 | 429.4 |
| Cofilin-1 | ASGVAVSDGVIK | 522.32 | 735.85 | 993.04 | 1189.02 |
| Cofilin-1 | ASGVAVSDGVIK | 308.88 | 122.11 | 487.26 | 861.89 |
| Cofilin-1 | ASGVAVSDGVIK | 13061.64 | 9962.8 | 38226.1 | 43702.24 |
| Cofilin-1 | ASGVAVSDGVIK | 253.6 | 476.4 | 1036.1 | 830.35 |
| Cofilin-1 | ASGVAVSDGVIK | 799.01 | 633.54 | 944.48 | 1390.46 |
| Cofilin-1 | ASGVAVSDGVIK | 792.23 | 1091.27 | 2421.91 | 1965.34 |
| Cofilin-1 | ASGVAVSDGVIK | 204.91 | 181.16 | 500.36 | 102.34 |
| Cofilin-1 | ASGVAVSDGVIK | 986.88 | 1008.59 | 4096.44 | 4520.31 |
| Cofilin-1 | ASGVAVSDGVIK | 333.15 | 276.54 | 418.46 | 646.18 |

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|---|---|---|---|---|---|
| Cofilin-1 | ASGVAVSDGVIK | 462.78 | 235.83 | 680.7 | 321.74 |
| Cofilin-1 | ASGVAVSDGVIK | 125.58 | 358.48 | 370.5 | 622.54 |
| Cofilin-1 | ASGVAVSDGVIK | 868.72 | 980.94 | 1854.96 | 2364.06 |
| Cofilin-1 | ASGVAVSDGVIK | 505.84 | 237.2 | 454.8 | 612.97 |
| Cofilin-1 | ASGVAVSDGVIK | 153.72 | 132.39 | 546.99 | 868.34 |
| Cofilin-1 | ASGVAVSDGVIK | 308.07 | 202.07 | 364.24 | 289.12 |
| Cofilin-1 | ASGVAVSDGVIK | 279.45 | 476.08 | 903.98 | 935.16 |
| Cofilin-1 | ASGVAVSDGVIK | 152.93 | 209.97 | 542.2 | 331.33 |
| Cofilin-1 | ASGVAVSDGVIK | 178.49 | 237.94 | 341.16 | 136.42 |
| Cofilin-1 | AVLF | 438.29 | 421.77 | 774.37 | 921.2 |
| Cofilin-1 | AVLFCLSEDKK | 1063.84 | 1065.38 | 3558.4 | 4606.62 |
| Cofilin-1 | AVLFCLSEDKK | 357.85 | 389.52 | 1122.01 | 1749.1 |
| Cofilin-1 | CTLAEK | 900.14 | 642.42 | 2049.52 | 2566.23 |
| Cofilin-1 | CTLAEK | 2117.17 | 1998.61 | 3426.81 | 3367.17 |
| Cofilin-1 | CTLAEK | 2651.97 | 2353.09 | 4196.9 | 5130.43 |
| Cofilin-1 | CTLAEK | 615.9 | 852.71 | 1465.36 | 1369.25 |
| Cofilin-1 | DGVIK | 510.3 | 541.23 | 664.54 | 1100.17 |
| Cofilin-1 | DGVIK | 691.04 | 450.48 | 608.72 | 1129.16 |
| Cofilin-1 | HELQANCYEEVKDR | 191.16 | 156.59 | 436.17 | 465.79 |
| Cofilin-1 | HELQANCYEEVKDR | 1911.16 | 2245.05 | 3054.31 | 4037.46 |
| Cofilin-1 | HELQANCYEEVKDR | 1926.21 | 2141.42 | 7966.3 | 8401.51 |
| Cofilin-1 | HELQANCYEEVKDR | 574.85 | 333.52 | 1181.72 | 1720.24 |
| Cofilin-1 | HELQANCYEEVKDR | 140.76 | 135.59 | 330.04 | 401.29 |
| Cofilin-1 | HELQANCYEEVKDR | 217.46 | 217.27 | 582.6 | 501.59 |
| Cofilin-1 | HELQANCYEEVKDR | 283.54 | 72.45 | 483.49 | 845.12 |
| Cofilin-1 | HELQANCYEEVKDR | 1406.44 | 1472.69 | 3856.32 | 5023.27 |
| Cofilin-1 | HELQANCYEEVKDR | 2425.7 | 2261.21 | 7284.35 | 7893.59 |
| Cofilin-1 | HELQANCYEEVKDR | 611.35 | 1089.56 | 2371.45 | 2515.07 |
| Cofilin-1 | HELQANCYEEVKDR | 332.68 | 642.27 | 1051.3 | 861.5 |
| Cofilin-1 | HELQANCYEEVKDR | 824.64 | 760.92 | 1198.03 | 973.95 |
| Cofilin-1 | HELQANCYEEVKDR | 231.53 | 104.46 | 367.22 | 400.76 |
| Cofilin-1 | KSSTPEEVK | 287.88 | 388.31 | 1119.15 | 1427.08 |
| Cofilin-1 | KSSTPEEVK | 343.12 | 355.75 | 1197.34 | 1391.54 |
| Cofilin-1 | KSSTPEEVK | 80.63 | 118.8 | 317.11 | 443.45 |
| Cofilin-1 | LAEKL | 4468.26 | 3651.83 | 5688.17 | 8123.33 |
| Cofilin-1 | LEGK | 2875.13 | 2113.23 | 3383.03 | 3619.79 |
| Cofilin-1 | LGGSAVISLEGKPL | 375.74 | 324.96 | 419.96 | 313.75 |
| Cofilin-1 | LGGSAVISLEGKPL | 785 | 315.58 | 660.65 | 399.01 |
| Cofilin-1 | LTGIK | 1005.95 | 1146.6 | 1933.42 | 2676.77 |
| Cofilin-1 | LTGIK | 5316.1 | 4568.04 | 8427.77 | 8182.08 |
| Cofilin-1 | LTGIK | 5139.77 | 4223.03 | 8907.06 | 12769.64 |
| Cofilin-1 | LTGIK | 4238.08 | 4477.84 | 6415.28 | 8007.41 |
| Cofilin-1 | LTGIK | 2581.48 | 2401.89 | 5339.46 | 5211.2 |
| Cofilin-1 | LTGIK | 3339.67 | 3771.5 | 5021.52 | 7282.55 |
| Cofilin-1 | LTGIK | 10055.94 | 10004.87 | 19181.96 | 23484.29 |
| Cofilin-1 | LTGIK | 4297.9 | 5483.04 | 7534.69 | 10990.4 |
| Cofilin-1 | MIYASSK | 1083.65 | 809.94 | 1440.91 | 1554.28 |
| Cofilin-1 | MIYASSK | 1970.13 | 3121.74 | 4416.81 | 6706.2 |
| Cofilin-1 | MIYASSK | 12769.82 | 13475.62 | 31587.11 | 38304.7 |
| Cofilin-1 | MIYASSK | 1717.83 | 2835.37 | 3656.9 | 4686.6 |
| Cofilin-1 | MIYASSK | 1009.54 | 1536.56 | 2896.02 | 2947.78 |
| Cofilin-1 | MIYASSK | 2878.08 | 1821.94 | 5069.04 | 6039.82 |
| Cofilin-1 | MIYASSK | 2613.95 | 2066.32 | 2937.49 | 4909.18 |
| Cofilin-1 | MIYASSK | 988.23 | 875.45 | 1741.55 | 1746.75 |
| Cofilin-1 | MIYASSK | 505.09 | 416.85 | 719.44 | 1001.8 |
| Cofilin-1 | MIYASSK | 906.01 | 1019.65 | 1558.58 | 1854.05 |
| Cofilin-1 | MIYASSK | 1203.67 | 1186.18 | 1698.06 | 2369 |
| Cofilin-1 | MIYASSK | 2285.84 | 3099.96 | 5507.7 | 6484.2 |
| Cofilin-1 | MIYASSK | 1384.64 | 2349.36 | 3069.03 | 3550.08 |
| Cofilin-1 | MIYASSK | 624.08 | 469.55 | 1293.71 | 890.85 |
| Cofilin-1 | MIYASSK | 1989.09 | 1567.23 | 2469.66 | 3403.32 |
| Cofilin-1 | MIYASSK | 586.7 | 546.18 | 778.35 | 1365.06 |
| Cofilin-1 | MIYASSK | 2555.14 | 3089.9 | 6295.1 | 8316.57 |
| Cofilin-1 | MIYASSK | 114.4 | 187.37 | 311.82 | 365.42 |

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|---|---|---|---|---|---|
| Cofilin-1 | MLPDKDCR | 834.02 | 1430.02 | 5032.87 | 6096.36 |
| Cofilin-1 | MLPDKDCR | 2441.5 | 2189.62 | 8267.57 | 11494.94 |
| Cofilin-1 | MLPDKDCR | 284.18 | 434.53 | 1452.35 | 1710.5 |
| Cofilin-1 | MLPDKDCR | 1497.24 | 1330.84 | 2189.52 | 2835.99 |
| Cofilin-1 | MLPDKDCR | 978.28 | 1007.71 | 2416.34 | 3762.82 |
| Cofilin-1 | MLPDKDCR | 378.54 | 367.28 | 444.19 | 594.59 |
| Cofilin-1 | MLPDKDCR | 410.32 | 312.59 | 905.11 | 947.07 |
| Cofilin-1 | MLPDKDCR | 383.17 | 441.31 | 1020.44 | 702.2 |
| Cofilin-1 | MLPDKDCR | 526.76 | 829.97 | 3076.07 | 3418.64 |
| Cofilin-1 | MLPDKDCR | 682.07 | 591.9 | 2049.77 | 2717.81 |
| Cofilin-1 | NIILEEGK | 1192.39 | 1130.88 | 2932.25 | 1627.87 |
| Cofilin-1 | SKMIYASSK | 63.24 | 135.23 | 100 | 239.56 |
| Cofilin-1 | SKMIYASSK | 905.72 | 836.07 | 2077.02 | 2744.76 |
| Cofilin-1 | SSTPEEVKK | 567.54 | 736.77 | 1686.37 | 1873.03 |
| Cofilin-1 | VFNDMK | 2431.36 | 2871.56 | 7336.64 | 5704.85 |
| Cofilin-1 | VFNDMK | 2718.07 | 3800.53 | 8948.26 | 11505.85 |
| Cofilin-1 | VFNDMK | 6842.93 | 8613.82 | 18546.37 | 21670.38 |
| Cofilin-1 | VFNDMK | 1502.45 | 1773.85 | 1798.03 | 2212.04 |
| Cofilin-1 | YALYDATYETK | 75.88 | 162.85 | 602.05 | 1369.41 |
| Cofilin-1 | YALYDATYETK | 1380.67 | 1252.71 | 4938.68 | 4107.86 |
| Cofilin-1 | YALYDATYETK | 3219.85 | 2417.17 | 10169.27 | 11420.24 |
| Cofilin-1 | YALYDATYETK | 2456.74 | 2066.43 | 5475.96 | 3792.33 |
| Cofilin-1 | YALYDATYETK | 2075.91 | 1713.45 | 4811.79 | 5681.65 |
| Cofilin-1 | YALYDATYETK | 5287.08 | 4988.5 | 22256 | 29181.92 |
| Cofilin-1 | YALYDATYETK | 3372.64 | 4874.97 | 18452.42 | 21150.57 |
| Cofilin-1 | YALYDATYETK | 51.51 | 17.51 | 221.71 | 297.81 |
| Cofilin-1 | YALYDATYETK | 386.64 | 843.32 | 1067.68 | 675.5 |
| Cofilin-1 | YALYDATYETK | 280.29 | 392.8 | 1243.64 | 1063.58 |
| Cofilin-1 | YALYDATYETK | 901.3 | 528.03 | 1267.92 | 1700.39 |
| Cofilin-1 | YALYDATYETK | 1513.95 | 1807.94 | 2250.28 | 1779.79 |
| Cofilin-1 | YALYDATYETK | 609.44 | 958.98 | 1710.76 | 1663.35 |
| Cofilin-1 | YALYDATYETK | 280.29 | 392.8 | 1243.64 | 1063.58 |
| Cofilin-1 | YALYDATYETK | 280.29 | 392.8 | 1243.64 | 1063.58 |
| Cofilin-1 | YALYDATYETK | 1161.33 | 901.35 | 836.54 | 1063.67 |
| 60S ribosomal protein L23 | ECADLWPR | 1943.86 | 2099.55 | 4760.01 | 5813.83 |
| 60S ribosomal protein L23 | GSAITGPVAK | 4595.47 | 4275.66 | 10691.75 | 12786.79 |
| 60S ribosomal protein L23 | ISLGLPVGAVINCADNTGAK | 333.56 | 236.81 | 1105.74 | 800.71 |
| 60S ribosomal protein L23 | LPAAGVGDMVMATVK | 287.35 | 439.74 | 1076.86 | 1226.54 |
| 60S ribosomal protein L23 | NLYIISVK | 4310.44 | 4137.4 | 16288.94 | 17809.01 |
| 60S ribosomal protein L23 | VHPAVVIR | 768.41 | 891.4 | 2609.43 | 2326.69 |
| 60S ribosomal protein L23 | IASNAGSIA | 1604.1 | 1305.82 | 2237.71 | 3520.27 |
| 60S ribosomal protein L23 | GSAITGPVAKECADLWPR | 448.68 | 564.56 | 587.61 | 618.32 |
| 60S ribosomal protein L23 | GKPELR | 325.62 | 276.48 | 874.2 | 1058.51 |
| 60S ribosomal protein L23 | ISLGLPVGAVIN | 89.09 | 134.55 | 38.97 | 126.24 |
| 60S ribosomal protein L23 | ECADLWPR | 4837.89 | 4899.24 | 12839.32 | 16144.97 |
| 60S ribosomal protein L23 | ECADLWPR | 1724.14 | 1786.23 | 2926.42 | 3522.97 |
| 60S ribosomal protein L23 | ECADLWPR | 7160.48 | 8517.35 | 25399.5 | 26283.57 |
| 60S ribosomal protein L23 | ECADLWPR | 4136.71 | 3004.14 | 10751.87 | 13678.76 |
| 60S ribosomal protein L23 | ECADLWPR | 7114.68 | 7510.59 | 28188.83 | 30508.13 |
| 60S ribosomal protein L23 | ECADLWPR | 3092.55 | 3079.49 | 9414.84 | 9242 |
| 60S ribosomal protein L23 | ECADLWPR | 3462.35 | 3139.98 | 8312.05 | 10009.92 |
| 60S ribosomal protein L23 | ECADLWPR | 3223.95 | 4034.25 | 9522.02 | 10828.21 |
| 60S ribosomal protein L23 | ECADLWPR | 5087.1 | 4958.54 | 12715.69 | 14443.43 |
| 60S ribosomal protein L23 | ECADLWPR | 5895.88 | 5052.56 | 15685.96 | 14677.11 |
| 60S ribosomal protein L23 | ECADLWPR | 4579.14 | 3654.88 | 12471 | 12424.52 |
| 60S ribosomal protein L23 | ECADLWPR | 3988.82 | 4423.99 | 10418.22 | 14147.6 |
| 60S ribosomal protein L23 | ECADLWPR | 3236.2 | 4419.13 | 9746.62 | 11685.26 |
| 60S ribosomal protein L23 | ECADLWPR | 3566.8 | 3883.96 | 10061.94 | 11580.45 |
| 60S ribosomal protein L23 | ECADLWPR | 3834.59 | 3810.1 | 10553.46 | 11474.74 |
| 60S ribosomal protein L23 | ECADLWPR | 1090.66 | 2031.98 | 2878.27 | 2882.16 |
| 60S ribosomal protein L23 | ECADLWPR | 633.95 | 877.95 | 2331.47 | 2929.13 |
| 60S ribosomal protein L23 | ECADLWPR | 835.11 | 896.92 | 2942.69 | 2229.5 |
| 60S ribosomal protein L23 | ECADLWPR | 849.11 | 1003.35 | 1084.03 | 1745.93 |
| 60S ribosomal protein L23 | ECADLWPR | 3014.38 | 4207.24 | 7903.06 | 9296.91 |

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|---|---|---|---|---|---|
| 60S ribosomal protein L23 | ECADLWPR | 1699.01 | 1822.51 | 4468.55 | 4657.06 |
| 60S ribosomal protein L23 | ECADLWPR | 5831.78 | 8620.09 | 5079.98 | 6344.65 |
| 60S ribosomal protein L23 | ECADLWPR | 4238.94 | 3967.28 | 11827.9 | 12326.3 |
| 60S ribosomal protein L23 | ECADLWPR | 5203.32 | 5710.61 | 14713.85 | 14572.22 |
| 60S ribosomal protein L23 | ECADLWPR | 1001.07 | 1096.83 | 2126.32 | 2548.31 |
| 60S ribosomal protein L23 | ECADLWPR | 548.97 | 443.94 | 1506.14 | 1522.47 |
| 60S ribosomal protein L23 | ECADLWPR | 2265.73 | 3491.33 | 6114.65 | 7604.15 |
| 60S ribosomal protein L23 | ECADLWPR | 1670.25 | 1153.13 | 2314.37 | 2864.09 |
| 60S ribosomal protein L23 | ECADLWPR | 1170 | 1214.91 | 1463.87 | 2317.54 |
| 60S ribosomal protein L23 | ECADLWPR | 918.25 | 555.55 | 1067.59 | 1518.58 |
| 60S ribosomal protein L23 | ECADLWPR | 432.64 | 660.17 | 1395.58 | 1256.02 |
| 60S ribosomal protein L23 | ECADLWPR | 674.02 | 961.13 | 623.04 | 1294.96 |
| 60S ribosomal protein L23 | ECADLWPR | 1996.52 | 1790.66 | 3783.34 | 4625.66 |
| 60S ribosomal protein L23 | ECADLWPR | 2073.43 | 2276.83 | 3547.43 | 3734.41 |
| 60S ribosomal protein L23 | ECADLWPR | 1789.06 | 1117.33 | 1894.4 | 1833.01 |
| 60S ribosomal protein L23 | ECADLWPR | 436.99 | 230.24 | 1051.42 | 646.22 |
| 60S ribosomal protein L23 | GKPELR | 216.8 | 282.74 | 431.75 | 701.15 |
| 60S ribosomal protein L23 | GSAITGPVAK | 485.71 | 523.06 | 1015.18 | 1263.32 |
| 60S ribosomal protein L23 | GSAITGPVAK | 5504.86 | 5812.67 | 10528.35 | 12505.47 |
| 60S ribosomal protein L23 | GSAITGPVAK | 255.93 | 246.33 | 919.03 | 674.56 |
| 60S ribosomal protein L23 | GSAITGPVAK | 513.48 | 333.38 | 775.49 | 1274.14 |
| 60S ribosomal protein L23 | GSAITGPVAK | 5716.29 | 5668.45 | 13908.95 | 15881.44 |
| 60S ribosomal protein L23 | GSAITGPVAK | 7748.96 | 6971.97 | 16072.62 | 18294.97 |
| 60S ribosomal protein L23 | GSAITGPVAK | 253.73 | 463.77 | 702.95 | 1185.33 |
| 60S ribosomal protein L23 | GSAITGPVAK | 4216.23 | 5147.4 | 8533.15 | 10535.08 |
| 60S ribosomal protein L23 | GSAITGPVAK | 755.22 | 598.84 | 1385.32 | 835.87 |
| 60S ribosomal protein L23 | GSAITGPVAK | 308.08 | 200.19 | 457.2 | 592.68 |
| 60S ribosomal protein L23 | GSAITGPVAKECADLWPR | 75.6 | 190.02 | 163.26 | 162 |
| 60S ribosomal protein L23 | GSAITGPVAKECADLWPR | 562.75 | 359.41 | 584.01 | 554.4 |
| 60S ribosomal protein L23 | IASNAGSIA | 953.83 | 763.37 | 1667.19 | 2094.07 |
| 60S ribosomal protein L23 | IASNAGSIA | 1587.72 | 1540.88 | 3010.1 | 3233.28 |
| 60S ribosomal protein L23 | IASNAGSIA | 1955.89 | 1868.16 | 3821.79 | 3621.94 |
| 60S ribosomal protein L23 | IASNAGSIA | 1669.01 | 1594.98 | 3280.34 | 2984.66 |
| 60S ribosomal protein L23 | IASNAGSIA | 2023.65 | 1663.19 | 4032.14 | 4293.86 |
| 60S ribosomal protein L23 | IASNAGSIA | 1965.93 | 2153.6 | 4717.99 | 4672.55 |
| 60S ribosomal protein L23 | IASNAGSIA | 1412.76 | 1379.95 | 1665.5 | 2947.8 |
| 60S ribosomal protein L23 | IASNAGSIA | 679.81 | 921.64 | 1810.54 | 2303.24 |
| 60S ribosomal protein L23 | IASNAGSIA | 1148.38 | 1542.13 | 1845.51 | 2222.81 |
| 60S ribosomal protein L23 | IASNAGSIA | 2006.01 | 1171.83 | 2127.01 | 3061.98 |
| 60S ribosomal protein L23 | IASNAGSIA | 9556.42 | 8824.95 | 23742.57 | 25824.08 |
| 60S ribosomal protein L23 | IASNAGSIA | 1929.36 | 2149.4 | 3198.26 | 3374.27 |
| 60S ribosomal protein L23 | IASNAGSIA | 1476.51 | 1251.39 | 2205.93 | 1642.52 |
| 60S ribosomal protein L23 | IASNAGSIA | 1797.53 | 1131.44 | 2282.44 | 2146.73 |
| 60S ribosomal protein L23 | IISVK | 2044.28 | 1859.27 | 2501.39 | 4084.44 |
| 60S ribosomal protein L23 | ISLGLPVGAVINCADNTGAK | 189.2 | 243.88 | 646.63 | 461.62 |
| 60S ribosomal protein L23 | ISLGLPVGAVINCADNTGAK | 281.47 | 276.41 | 614.04 | 752.83 |
| 60S ribosomal protein L23 | ISLGLPVGAVINCADNTGAK | 230.11 | 244.68 | 456.94 | 443.6 |
| 60S ribosomal protein L23 | ISLGLPVGAVINCADNTGAK | 270.12 | 227.73 | 510.72 | 721.26 |
| 60S ribosomal protein L23 | ISLGLPVGAVINCADNTGAK | 987.74 | 1030.86 | 3736.51 | 3699.59 |
| 60S ribosomal protein L23 | ISLGLPVGAVINCADNTGAK | 76.61 | 90.99 | 324.46 | 188.06 |
| 60S ribosomal protein L23 | ISLGLPVGAVINCADNTGAK | 536.09 | 758.45 | 2218.21 | 3454.26 |
| 60S ribosomal protein L23 | ISLGLPVGAVINCADNTGAK | 218.87 | 78.23 | 434.14 | 375.72 |
| 60S ribosomal protein L23 | ISLGLPVGAVINCADNTGAK | 140.85 | 127.13 | 216.03 | 247.97 |
| 60S ribosomal protein L23 | ISLGLPVGAVINCADNTGAK | 218.47 | 117.91 | 175.28 | 187.63 |
| 60S ribosomal protein L23 | ISLGLPVGAVINCADNTGAK | 536.09 | 758.45 | 2218.21 | 3454.26 |
| 60S ribosomal protein L23 | ISLGLPVGAVINCADNTGAK | 12.86 | 6.23 | 176.37 | 119.23 |
| 60S ribosomal protein L23 | LPAAGVGDMVMATVK | 355.52 | 300.56 | 690.75 | 964.24 |
| 60S ribosomal protein L23 | LPAAGVGDMVMATVK | 958.81 | 590.99 | 1612.8 | 1949.67 |
| 60S ribosomal protein L23 | LPAAGVGDMVMATVK | 688.95 | 337.52 | 1044.8 | 1118.04 |
| 60S ribosomal protein L23 | LPAAGVGDMVMATVK | 746.37 | 90.06 | 469.15 | 425.52 |
| 60S ribosomal protein L23 | LPAAGVGDMVMATVK | 205.63 | 109.43 | 216.28 | 271.1 |
| 60S ribosomal protein L23 | LPAAGVGDMVMATVK | 281.42 | 281.71 | 352.26 | 520.49 |
| 60S ribosomal protein L23 | LPAAGVGDMVMATVK | 255.62 | 276.9 | 684.74 | 298.79 |
| 60S ribosomal protein L23 | LPAAGVGDMVMATVK | 438.2 | 110.92 | 566.64 | 627.82 |

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|---|---|---|---|---|---|
| 60S ribosomal protein L23 | LPAAGVGDMVMATVK | 453.41 | 310.1 | 498.32 | 445.61 |
| 60S ribosomal protein L23 | LPAAGVGDMVMATVK | 206.44 | 29.77 | 323.8 | 291.37 |
| 60S ribosomal protein L23 | LPAAGVGDMVMATVK | 308.04 | 204.21 | 258.5 | 371.88 |
| 60S ribosomal protein L23 | LPAAGVGDMVMATVK | 308.04 | 204.21 | 258.5 | 371.88 |
| 60S ribosomal protein L23 | LPAAGVGDMVMATVK | 1005.34 | 1099.61 | 1654 | 2215.03 |
| 60S ribosomal protein L23 | LPAAGVGDMVMATVK | 386.16 | 146.12 | 292.49 | 215.65 |
| 60S ribosomal protein L23 | NLYIISVK | 256.4 | 199.77 | 667.5 | 602.95 |
| 60S ribosomal protein L23 | NLYIISVK | 4974.55 | 5758.81 | 21572.13 | 24229.53 |
| 60S ribosomal protein L23 | NLYIISVK | 6386.3 | 7239.02 | 22430.64 | 26427.46 |
| 60S ribosomal protein L23 | NLYIISVK | 256.82 | 158.97 | 130.86 | 431.3 |
| 60S ribosomal protein L23 | NLYIISVK | 794.24 | 1637.37 | 1676.79 | 2090.87 |
| 60S ribosomal protein L23 | NLYIISVK | 734.25 | 649.6 | 1344.73 | 1372.56 |
| 60S ribosomal protein L23 | NLYIISVK | 588.31 | 387 | 1678.37 | 1518.87 |
| 60S ribosomal protein L23 | NLYIISVK | 634.1 | 1076.08 | 2582.85 | 2866.18 |
| 60S ribosomal protein L23 | NLYIISVK | 1806.77 | 1069.5 | 3344.62 | 3830.96 |
| 60S ribosomal protein L23 | NLYIISVK | 514.01 | 280.27 | 847.65 | 1237.09 |
| 60S ribosomal protein L23 | NLYIISVK | 535.13 | 746.88 | 1836.78 | 1958.06 |
| 60S ribosomal protein L23 | NLYIISVK | 451.79 | 364.21 | 752.91 | 933.46 |
| 60S ribosomal protein L23 | NLYIISVK | 614.47 | 355.52 | 1863.44 | 2031.49 |
| 60S ribosomal protein L23 | NLYIISVK | 1587.99 | 1301.11 | 4125.28 | 5283.21 |
| 60S ribosomal protein L23 | NLYIISVK | 2996.22 | 3128.92 | 8758.87 | 10743.05 |
| 60S ribosomal protein L23 | NLYIISVK | 2911.55 | 3834.37 | 10235.78 | 13411.16 |
| 60S ribosomal protein L23 | NLYIISVK | 1755.04 | 1925.2 | 1842.72 | 2988.45 |
| 60S ribosomal protein L23 | NLYIISVK | 1223.24 | 1380.62 | 3762.85 | 4135.12 |
| 60S ribosomal protein L23 | NLYIISVK | 1529.55 | 1649.81 | 4324.2 | 4369.58 |
| 60S ribosomal protein L23 | NLYIISVK | 329.83 | 605.18 | 1088.34 | 1314.13 |
| 60S ribosomal protein L23 | NLYIISVK | 332.99 | 292.31 | 915.29 | 516.77 |
| 60S ribosomal protein L23 | NLYIISVK | 687.74 | 776.38 | 722.63 | 908.56 |
| 60S ribosomal protein L23 | NLYIISVK | 231.67 | 90.69 | 409.44 | 170.73 |
| 60S ribosomal protein L23 | NLYIISVK | 231.56 | 100.78 | 549.04 | 433.13 |
| 60S ribosomal protein L23 | NLYIISVK | 308.31 | 177.84 | 285.21 | 396.32 |
| 60S ribosomal protein L23 | NLYIISVK | 192.06 | 173.69 | 278.25 | 254.33 |
| 60S ribosomal protein L23 | NLYIISVK | 318.8 | 98.85 | 324.6 | 288.51 |
| 60S ribosomal protein L23 | NLYIISVK | 255.55 | 283.71 | 347.9 | 662.58 |
| 60S ribosomal protein L23 | NLYIISVK | 918.91 | 1234.85 | 1504.01 | 1362.08 |
| 60S ribosomal protein L23 | NLYIISVK | 787.49 | 1027.54 | 1868.46 | 2077.32 |
| 60S ribosomal protein L23 | NLYIISVK | 701.57 | 473.63 | 1020.4 | 997.74 |
| 60S ribosomal protein L23 | VAKECADLWPR | 111.4 | 58.12 | 120.67 | 139.41 |
| 60S ribosomal protein L23 | VHPAVVIR | 858.99 | 772.34 | 1411.86 | 1229.08 |
| 60S ribosomal protein L23 | VHPAVVIR | 230.52 | 204.14 | 546.29 | 592.29 |
| 60S ribosomal protein L23 | VHPAVVIR | 230.22 | 233.76 | 358.52 | 418.35 |
| Protein JTB | TTPECGPTGYVEK | 510.83 | 594.52 | 952.01 | 1210.7 |
| Protein JTB | FTLK | 1809.78 | 1729.15 | 3574.53 | 4790.2 |
| Protein JTB | FTLK | 1767.73 | 2160.22 | 2989.2 | 3960.75 |
| Protein JTB | FTLK | 547.31 | 607.39 | 873.36 | 1048.26 |
| Protein JTB | FTLK | 1627.32 | 2734.63 | 3759.35 | 4574.7 |
| Protein JTB | FTLK | 1911.43 | 2218.46 | 4688.15 | 4534.27 |
| Protein JTB | FTLK | 4138.82 | 4284.51 | 6236.36 | 8080.89 |
| Protein JTB | FTLK | 4718.26 | 5654.16 | 7475.93 | 9239.33 |
| Protein JTB | FTLK | 8334.66 | 9744.92 | 15902.56 | 18922.15 |
| Protein JTB | LVIIR | 3653.4 | 2562.22 | 4702.84 | 4564.1 |
| Protein JTB | LVIIR | 2066.67 | 3158 | 6897.09 | 4862.41 |
| Protein JTB | TTPECGPTGYVEK | 789.29 | 955.81 | 942.23 | 1074.1 |
| Protein JTB | TTPECGPTGYVEK | 513.34 | 347.07 | 949.58 | 674.93 |
| Protein JTB | TTPECGPTGYVEK | 408.49 | 493.34 | 534.28 | 794.26 |
| Protein JTB | VALI | 1296.99 | 1434.54 | 5346.49 | 5340.23 |
| Protein JTB | VALI | 3314.76 | 3998.01 | 22099.16 | 20825.3 |
| Protein JTB | VALI | 3659.85 | 3414.84 | 18140.3 | 21295.9 |
| Myeloid-associated differentiation marker | ALTQPLGLLR | 611.23 | 250.51 | 367.43 | 695.44 |
| Myeloid-associated differentiation marker | TTITTTTTTSSSGLGSPMIVGSPR | 178.7 | 216.92 | 103.97 | 351.09 |
| Myeloid-associated differentiation marker | FPLSWR | 712.36 | 790.41 | 1427.67 | 857.56 |
| Myeloid-associated differentiation marker | MPVTVTR | 1292.85 | 1418.39 | 2596.94 | 3151.88 |
| Myeloid-associated differentiation marker | ALTQPLGLLR | 231.21 | 135.44 | 112.1 | 249.7 |
| Myeloid-associated differentiation marker | ALTQPLGLLR | 154.42 | 62.41 | 176.34 | 0 |

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|---|---|---|---|---|---|
| Myeloid-associated differentiation marker | FPLSWR | 1264.83 | 782.61 | 639.78 | 816.21 |
| Myeloid-associated differentiation marker | FPLSWR | 488.59 | 238.51 | 453.1 | 205.81 |
| Myeloid-associated differentiation marker | LGLL | 1296.99 | 1434.54 | 5346.49 | 5340.23 |
| Myeloid-associated differentiation marker | LGLL | 667.11 | 261.48 | 2492.45 | 2908.78 |
| Myeloid-associated differentiation marker | LGLL | 3314.76 | 3998.01 | 22099.16 | 20825.3 |
| Myeloid-associated differentiation marker | LGLL | 3659.85 | 3414.84 | 18140.3 | 21295.9 |
| Myeloid-associated differentiation marker | LGLL | 332.65 | 326.7 | 492.06 | 841.9 |
| Myeloid-associated differentiation marker | LGLLR | 772.6 | 1009.43 | 1169.95 | 1102.84 |
| Myeloid-associated differentiation marker | LGLLR | 484.95 | 598.57 | 527.29 | 833.2 |
| Myeloid-associated differentiation marker | LGLLR | 889.11 | 1094.25 | 961.9 | 1189.95 |
| Myeloid-associated differentiation marker | LGLLR | 1108.53 | 1543.55 | 1229.93 | 1769.51 |
| Myeloid-associated differentiation marker | LGLLR | 980.63 | 1519.85 | 1222.12 | 845.75 |
| Myeloid-associated differentiation marker | LGLLR | 881.63 | 875.5 | 1172.56 | 719.34 |
| Myeloid-associated differentiation marker | LGLLR | 988.01 | 896.86 | 1055.42 | 1203.53 |
| Myeloid-associated differentiation marker | LGLLR | 252.97 | 539.23 | 483.12 | 768.99 |
| Myeloid-associated differentiation marker | LGLLR | 610.41 | 650.31 | 1125.48 | 924.24 |
| Myeloid-associated differentiation marker | LGLLR | 584.6 | 647.49 | 986.93 | 1677.42 |
| Myeloid-associated differentiation marker | LGLLR | 1447.92 | 1203.54 | 1220.32 | 1386.83 |
| Myeloid-associated differentiation marker | LGLLR | 801.22 | 734.4 | 1425.97 | 1094.17 |
| Myeloid-associated differentiation marker | LLRL | 912.1 | 950.18 | 1143.27 | 1280.65 |
| Myeloid-associated differentiation marker | LLRL | 556.67 | 959.36 | 927.48 | 1147.92 |
| Myeloid-associated differentiation marker | TTITTTTTSSSGLGSPMIVGSPR | 808.24 | 573.42 | 1225.34 | 998.61 |
| Myeloid-associated differentiation marker | TTITTTTTSSSGLGSPMIVGSPR | 153.12 | 191.37 | 185.14 | 281.37 |
| Myeloid-associated differentiation marker | TTITTTTTSSSGLGSPMIVGSPR | 1363.87 | 1422.58 | 2022.93 | 3901.98 |
| Myeloid-associated differentiation marker | TTITTTTTSSSGLGSPMIVGSPR | 178.7 | 216.92 | 103.97 | 351.09 |
| Myeloid-associated differentiation marker | VFVK | 984.88 | 780.68 | 1814.1 | 1640.08 |
| Myeloid-associated differentiation marker | VFVK | 921.32 | 571.73 | 1745.12 | 992.7 |
| Myeloid-associated differentiation marker | VFVK | 905.51 | 1814.23 | 2307.38 | 1956.18 |
| RNA-binding protein FUS | APKPDGPGGGPGGSHMGGNYGDDR | 218.2 | 144.88 | 331.2 | 514.92 |
| RNA-binding protein FUS | GEATVSFDDPPSAK | 462.84 | 230.06 | 965.8 | 920.35 |
| RNA-binding protein FUS | TGQPMINLYTDR | 456.59 | 208.92 | 757.52 | 678.83 |
| RNA-binding protein FUS | AAIDWFDGK | 1690.87 | 2200.75 | 3872.62 | 4678.16 |
| RNA-binding protein FUS | CPNPTCENMNFSWR | 231.04 | 152.22 | 559.19 | 379.89 |
| RNA-binding protein FUS | QIGIIK | 552.18 | 339.74 | 1595.82 | 1830.59 |
| RNA-binding protein FUS | LKGEATVSFDDPPSAK | 404.58 | 453.58 | 601.01 | 765.47 |
| RNA-binding protein FUS | GGRGGGDRGGFGPGK | 742.53 | 575.85 | 813.88 | 861.27 |
| RNA-binding protein FUS | FGGPR | 1838.5 | 1870.35 | 526.74 | 380.73 |
| RNA-binding protein FUS | GGDRGGFR | 1217.24 | 1016.16 | 2665.32 | 2309.57 |
| RNA-binding protein FUS | AAIDWFDGK | 1124.95 | 772.47 | 1547.74 | 1504.67 |
| RNA-binding protein FUS | AAIDWFDGK | 973.1 | 774.48 | 1419.34 | 1356.64 |
| RNA-binding protein FUS | AAIDWFDGK | 1137.38 | 927.55 | 1809.4 | 2608.44 |
| RNA-binding protein FUS | AAIDWFDGK | 841.14 | 727.19 | 1636.12 | 1857.17 |
| RNA-binding protein FUS | AAIDWFDGK | 1734.33 | 1099.03 | 2095.94 | 2309.46 |
| RNA-binding protein FUS | APKPDGPGGGPGGSHMGGNYGDDR | 42.51 | 55.15 | 94.7 | 158.27 |
| RNA-binding protein FUS | APKPDGPGGGPGGSHMGGNYGDDR | 196.1 | 200.22 | 493.63 | 604.55 |
| RNA-binding protein FUS | CPNPTCENMNFSWR | 126.55 | 263.27 | 555.12 | 433.73 |
| RNA-binding protein FUS | CPNPTCENMNFSWR | 231.04 | 152.22 | 559.19 | 379.89 |
| RNA-binding protein FUS | FGGPR | 3785.59 | 3119.23 | 440.73 | 513.11 |
| RNA-binding protein FUS | GEATVSFDDPPSAK | 844.55 | 709.19 | 1982.01 | 2143.95 |
| RNA-binding protein FUS | GEATVSFDDPPSAK | 1302.43 | 1216.16 | 1714.64 | 1859.46 |
| RNA-binding protein FUS | GEATVSFDDPPSAK | 533.26 | 506.89 | 1055.69 | 379.99 |
| RNA-binding protein FUS | GGGNGR | 1039.82 | 778.62 | 1129.88 | 1362.16 |
| RNA-binding protein FUS | IGII | 1296.99 | 1434.54 | 5346.49 | 5340.23 |
| RNA-binding protein FUS | IGII | 667.11 | 261.48 | 2492.45 | 2908.78 |
| RNA-binding protein FUS | IGII | 3314.76 | 3998.01 | 22099.16 | 20825.3 |
| RNA-binding protein FUS | IGII | 3659.85 | 3414.84 | 18140.3 | 21295.9 |
| RNA-binding protein FUS | IGII | 332.65 | 326.7 | 492.06 | 841.9 |
| RNA-binding protein FUS | QIGIIK | 408.77 | 465.35 | 1013.97 | 1253.81 |
| RNA-binding protein FUS | QIGIIK | 1245.03 | 1355.72 | 2361.43 | 2766.64 |
| RNA-binding protein FUS | QIGIIK | 1695.09 | 1570.93 | 4108.48 | 5299.81 |
| RNA-binding protein FUS | QIGIIK | 1965.56 | 1231.93 | 3610.65 | 3949.82 |
| RNA-binding protein FUS | QIGIIK | 408.27 | 514.39 | 1036.59 | 1219.28 |
| RNA-binding protein FUS | QIGIIK | 1484.27 | 1974.38 | 2636.06 | 3057.4 |
| RNA-binding protein FUS | QIGIIK | 1188.09 | 1236.48 | 2617.86 | 3275.82 |

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|---|---|---|---|---|---|
| RNA-binding protein FUS | QIGIIK | 508.25 | 743.06 | 1805 | 2664.69 |
| RNA-binding protein FUS | QIGIIK | 1162.86 | 1175.69 | 3164.38 | 3516.78 |
| RNA-binding protein FUS | QIGIIK | 554.16 | 675.22 | 2067.25 | 2864.93 |
| RNA-binding protein FUS | QIGIIK | 2166.04 | 2276.32 | 4084.24 | 4616.54 |
| RNA-binding protein FUS | QIGIIK | 1521.86 | 920.27 | 3206.97 | 2824.07 |
| RNA-binding protein FUS | QIGIIK | 961.18 | 1101.74 | 1338.3 | 2712.24 |
| RNA-binding protein FUS | QIGIIK | 1012.87 | 781.27 | 3171.9 | 3076.45 |
| RNA-binding protein FUS | TGQPMINLYTDR | 225.51 | 698.6 | 1104.52 | 694.34 |
| RNA-binding protein FUS | TGQPMINLYTDR | 1283.68 | 1047.76 | 1815.74 | 1956.74 |
| RNA-binding protein FUS | TGQPMINLYTDR | 251.9 | 644.89 | 1483.85 | 870.92 |
| RNA-binding protein FUS | TGQPMINLYTDR | 350.97 | 218.64 | 664.2 | 948.12 |
| Cellular nucleic acid-binding protein | CGETGHVAINCSK | 288.51 | 431.71 | 1203.73 | 1096.57 |
| Cellular nucleic acid-binding protein | EQCCYNCGKPGHLAR | 427.45 | 321.74 | 1028.19 | 975.52 |
| Cellular nucleic acid-binding protein | TSEVNCYR | 214.44 | 90.61 | 263.86 | 370 |
| Cellular nucleic acid-binding protein | CGETGHVAINCSK | 621.15 | 652.71 | 1977.91 | 1883.76 |
| Cellular nucleic acid-binding protein | EQCCYNCGKPGHLAR | 133.45 | 113.68 | 376.95 | 459.39 |
| Cellular nucleic acid-binding protein | EQCCYNCGKPGHLAR | 275.38 | 346.14 | 697.86 | 675.36 |
| Cellular nucleic acid-binding protein | EQCCYNCGKPGHLAR | 59.67 | 61.8 | 128.65 | 156.47 |
| Cellular nucleic acid-binding protein | TSEVNCYR | 114.59 | 168.43 | 184.08 | 367.79 |
| Cellular nucleic acid-binding protein | TSEVNCYR | 286.05 | 462.32 | 602.85 | 484.09 |
| 60S ribosomal protein L37 | GTSSFGK | 863.37 | 445.23 | 1725.98 | 2356.64 |
| 60S ribosomal protein L37 | AYHLQK | 781.61 | 437.73 | 2237.35 | 1767.75 |
| 60S ribosomal protein L37 | YNWSAK | 3172.16 | 4257.33 | 7506.21 | 8840.63 |
| 60S ribosomal protein L37 | AYHLQK | 634.77 | 584.37 | 2276.64 | 2583.5 |
| 60S ribosomal protein L37 | AYHLQK | 388.74 | 422.75 | 2237.2 | 2474.5 |
| 60S ribosomal protein L37 | GTSSFGK | 1184.79 | 1561.93 | 2860.02 | 3463.73 |
| 60S ribosomal protein L37 | GTSSFGK | 1016.71 | 827.7 | 2669.62 | 1941.09 |
| 60S ribosomal protein L37 | GTSSFGK | 956.45 | 930.76 | 2366.66 | 2086.95 |
| 60S ribosomal protein L37 | STCGKCGYPAK | 140.98 | 114.3 | 211.92 | 411 |
| 60S ribosomal protein L37 | YNWSAK | 458.9 | 618.66 | 1118.7 | 1194.26 |
| 60S ribosomal protein L37 | YNWSAK | 2360.84 | 2072.92 | 3910.81 | 5118.02 |
| 60S ribosomal protein L37 | YNWSAK | 3116.97 | 3326.67 | 6991.39 | 9748.11 |
| Sperm-associated antigen 7 | SIEEAMNEIR | 447.9 | 322.55 | 274.91 | 421.36 |
| Sperm-associated antigen 7 | AREQAARLK | 880.39 | 1317.05 | 1515.37 | 1420.48 |
| Sperm-associated antigen 7 | LIGK | 3497.2 | 4271.32 | 5463.79 | 5805.31 |
| Sperm-associated antigen 7 | LIGK | 6358.35 | 8191.63 | 19930.68 | 27872.12 |
| Sperm-associated antigen 7 | LIGK | 5627.84 | 5364.58 | 18307.75 | 21015.58 |
| Sperm-associated antigen 7 | LIGK | 4093.22 | 3045.08 | 7609.02 | 8332.05 |
| Sperm-associated antigen 7 | LIGK | 2955.88 | 3816.51 | 8510.03 | 11071 |
| Sperm-associated antigen 7 | LIGK | 1741.15 | 1701.46 | 2482.79 | 3844.17 |
| Sperm-associated antigen 7 | MIFK | 677.07 | 1085.37 | 1380.47 | 1550.73 |
| Sperm-associated antigen 7 | MIFK | 1096.1 | 1069.33 | 1436.07 | 1561.67 |
| Sperm-associated antigen 7 | SIEEAMNEIR | 229.69 | 285.48 | 355.26 | 417.19 |
| Sperm-associated antigen 7 | SIEEAMNEIR | 346.9 | 301.12 | 428.38 | 511.26 |
| Sperm-associated antigen 7 | SIEEAMNEIR | 409.67 | 376.09 | 319.63 | 539.21 |
| Sperm-associated antigen 7 | SIEEAMNEIR | 384.58 | 301.97 | 248.29 | 497 |
| Sperm-associated antigen 7 | SIEEAMNEIR | 280.9 | 333.25 | 357.59 | 235.46 |
| Sperm-associated antigen 7 | SIEEAMNEIR | 410.17 | 326.83 | 201.68 | 279.17 |
| Sperm-associated antigen 7 | SIEEAMNEIR | 383.66 | 393.13 | 476.31 | 437.47 |
| Zinc transporter 9 | LTELLENDPSVR | 192.83 | 98.22 | 179.46 | 235.41 |
| Zinc transporter 9 | TPEELETFMLK | 165.79 | 215.77 | 207.97 | 326.68 |
| Zinc transporter 9 | HVDLEIL | 360.39 | 139.16 | 731.44 | 348.21 |
| Zinc transporter 9 | SLEVWGSPEALAR | 334.71 | 123.12 | 342.58 | 316.19 |
| Zinc transporter 9 | SIQPEQVQR | 180.04 | 84.87 | 248.1 | 231.39 |
| Zinc transporter 9 | EALLGR | 3705.63 | 3359.52 | 6506.88 | 4776.22 |
| Zinc transporter 9 | EALLGR | 4614.58 | 5365.6 | 6119.38 | 7833.73 |
| Zinc transporter 9 | EALLGR | 4502.03 | 4145.08 | 6217.26 | 6139.92 |
| Zinc transporter 9 | EALLGR | 4435.04 | 5764.05 | 5843.65 | 7256.25 |
| Zinc transporter 9 | EALLGR | 2749.49 | 3250.34 | 3230.94 | 5672.09 |
| Zinc transporter 9 | EALLGR | 9819.95 | 9810.07 | 14204.4 | 16157.99 |
| Zinc transporter 9 | EALLGR | 1474.27 | 2004.88 | 2547.12 | 2951.51 |
| Zinc transporter 9 | EALLGR | 8154.17 | 6831.84 | 10721.44 | 11973.49 |
| Zinc transporter 9 | EALLGR | 2867.72 | 3377.92 | 4571.59 | 4349.36 |
| Zinc transporter 9 | GLGK | 314.32 | 435.35 | 609.97 | 798.82 |

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|---|---|---|---|---|---|
| Zinc transporter 9 | GLGK | 272.38 | 216.83 | 403.38 | 919.32 |
| Zinc transporter 9 | HVDLEIL | 230.2 | 235.92 | 252.04 | 525.85 |
| Zinc transporter 9 | LGISK | 6212.44 | 5798.33 | 2687.24 | 3461.96 |
| Zinc transporter 9 | LGISK | 6356.18 | 7980.2 | 3642.09 | 3873.59 |
| Zinc transporter 9 | LGISK | 4918.09 | 6230.62 | 3546.17 | 4981.69 |
| Zinc transporter 9 | LGISK | 6682.11 | 8544.92 | 2065.25 | 4492.65 |
| Zinc transporter 9 | LGISK | 2985.09 | 2632.98 | 3439.12 | 3614.87 |
| Zinc transporter 9 | LGLGK | 2356.27 | 2843.71 | 1808.85 | 1955.98 |
| Zinc transporter 9 | LGLGK | 626.52 | 548.15 | 1811.38 | 2284.23 |
| Zinc transporter 9 | LGLGK | 3374.36 | 2790.27 | 3114.67 | 3541.4 |
| Zinc transporter 9 | LGLGK | 2417.43 | 3184.19 | 1443.74 | 1517.98 |
| Zinc transporter 9 | LGLGK | 1274.08 | 1890.03 | 664.07 | 1384.76 |
| Zinc transporter 9 | LGLGK | 1116.54 | 1602.81 | 1088.33 | 1783.18 |
| Zinc transporter 9 | LGLGK | 2618.42 | 2689.07 | 1529.65 | 1972.05 |
| Zinc transporter 9 | LGLGK | 2948.83 | 3980.86 | 3490.53 | 3780.81 |
| Zinc transporter 9 | LLAL | 196.22 | 188.4 | 226.96 | 250.42 |
| Zinc transporter 9 | LLAL | 75.78 | 172.69 | 115.6 | 69.95 |
| Zinc transporter 9 | LQVR | 1159.51 | 1400.24 | 1323.59 | 1349.84 |
| Zinc transporter 9 | LQVR | 482.56 | 728.27 | 822.48 | 814.74 |
| Zinc transporter 9 | LTELLENDPSVR | 204.74 | 198.14 | 299.04 | 189.83 |
| Zinc transporter 9 | LTELLENDPSVR | 152.87 | 215.86 | 251.13 | 178.29 |
| Zinc transporter 9 | LTELLENDPSVR | 222.75 | 120.22 | 257.86 | 221.12 |
| Zinc transporter 9 | LTELLENDPSVR | 1008.35 | 696.39 | 951.03 | 775.41 |
| Zinc transporter 9 | LTELLENDPSVR | 335.25 | 69.8 | 424.95 | 261.26 |
| Zinc transporter 9 | SLEVWGSPEALAR | 356.98 | 476.2 | 613.65 | 835.38 |
| Zinc transporter 9 | SYLEK | 3331.68 | 2645.63 | 3511.26 | 3945.15 |
| Zinc transporter 9 | YLEK | 1033.73 | 1380.04 | 1879.71 | 2790.94 |
| Zinc transporter 9 | YLEK | 721.87 | 808.39 | 1247.96 | 1184.11 |
| Zinc transporter 9 | YLEK | 430.2 | 901.5 | 955.69 | 1126.27 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | HYQTIQEAGDWCVPSTEPK | 799.12 | 516.47 | 937.45 | 1085.92 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | DLSIK | 1090.73 | 1281.11 | 2415.67 | 2601.54 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | EFLDK | 29470.13 | 33626.17 | 1498.56 | 2512.54 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | EFLDK | 7395.71 | 9212.98 | 1561.97 | 1459.32 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | EFLDK | 1350.11 | 2569.58 | 812.22 | 1303.88 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | EFLDK | 7015.5 | 9010.84 | 1252.65 | 1811.17 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | ELFK | 2341.82 | 4378.22 | 2760.69 | 5011.31 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | ELFK | 812.14 | 826.51 | 925.19 | 1053.71 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | ELFK | 944.52 | 832.03 | 698.7 | 1348.21 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | ELFK | 613.05 | 814.67 | 804 | 1196.58 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | FLDK | 2467.9 | 2133.81 | 4495.56 | 5351.67 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | FLDK | 1675.88 | 1128.61 | 2070.47 | 2141.71 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | IYLK | 2324.6 | 1717.67 | 1510.6 | 2637.76 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | IYLK | 743.59 | 896.22 | 1185.32 | 1083.92 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | IYLK | 1557.06 | 1484.75 | 2494.9 | 3453.63 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | IYLK | 1927.03 | 2272.69 | 2160.85 | 2555.31 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | IYLK | 1294.53 | 2316.11 | 1214.3 | 1930.17 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | IYLK | 518.49 | 582.81 | 492.64 | 1086.48 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | IYLK | 2216.55 | 1647.85 | 2062.68 | 2686.04 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | IYLK | 2343.22 | 3069.36 | 2768.3 | 3350.47 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | IYLK | 2473.25 | 3626.5 | 3667.43 | 4183.62 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | IYLK | 2509.04 | 2856.39 | 3440.44 | 4955.48 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | IYLK | 1494.13 | 1319.79 | 2002.86 | 1611.01 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | IYLK | 1695.62 | 1412.87 | 1872.62 | 2723.39 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | IYLK | 1283.89 | 814.02 | 1090.45 | 971.03 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | LEYK | 809.45 | 1091.77 | 1855.35 | 1415.93 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | LEYK | 708.12 | 1102.77 | 1629.39 | 2302.64 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | LEYK | 1804.24 | 1319.01 | 3138.79 | 3512.38 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | LSIK | 4176.21 | 4527.06 | 6015.48 | 7909.73 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | LSIK | 4182.42 | 4658.64 | 5547.87 | 6978.64 |

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|---|---|---|---|---|---|
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | LSIK | 1606.57 | 2657.57 | 2434.23 | 3278.86 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | LSIK | 1409.61 | 1797.21 | 2312.38 | 3838.89 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | LSIK | 3456 | 3022.5 | 4359.44 | 4742.76 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | LSIK | 2878.2 | 3831.54 | 5604.06 | 6155.41 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | LSIK | 2937.04 | 4188.04 | 5253.42 | 5847.66 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | LSIK | 3252.42 | 4306.48 | 6749.05 | 8451.88 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | LSIK | 3070.36 | 2718.79 | 3562.78 | 5338.49 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | LSIK | 2693.93 | 4164.81 | 3942.42 | 5022.55 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | LSIK | 3177.26 | 3220.87 | 3812.72 | 3898.27 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | LSIK | 2575.5 | 4162.63 | 6452.12 | 7482.72 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | LSIK | 2873 | 3068.29 | 6039.6 | 6558.52 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | LSIK | 2476.65 | 2865.48 | 4811.9 | 4826.53 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | LSIK | 2667.5 | 1988.95 | 4121.63 | 4224.93 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | LSIK | 4234.88 | 3411.05 | 6964.9 | 7478.5 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | LSIK | 8445.18 | 8612.45 | 10773.67 | 13482.85 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | LSIK | 4313.71 | 6580.89 | 8061.56 | 9728.5 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | LSIK | 1762.81 | 1369.86 | 2370.95 | 3090.65 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | LSIK | 3641.4 | 3109.72 | 4843.86 | 6104.42 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | LSIK | 2637.23 | 2851.18 | 4505.17 | 4971.66 |
| [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial | LSIK | 2350.83 | 1572.36 | 3336.75 | 3843.43 |
| Thioredoxin-related transmembrane protein 4 | VDVIQEPGLSGR | 802.35 | 729.24 | 1198.37 | 1315.72 |
| Thioredoxin-related transmembrane protein 4 | ILEK | 2168.52 | 2775.92 | 4147.86 | 5694.36 |
| Thioredoxin-related transmembrane protein 4 | ILEK | 11589.07 | 11195.23 | 10157.11 | 11323.28 |
| Thioredoxin-related transmembrane protein 4 | ILEK | 9225.81 | 10849.63 | 8041.91 | 10038.98 |
| Thioredoxin-related transmembrane protein 4 | ILEK | 2738.47 | 3806.76 | 4044.26 | 5133.94 |
| Thioredoxin-related transmembrane protein 4 | ILEK | 7311.03 | 8430.18 | 5489.29 | 8351.38 |
| Thioredoxin-related transmembrane protein 4 | ILEK | 11190.85 | 11602.14 | 12444.6 | 16285.48 |
| Thioredoxin-related transmembrane protein 4 | VDVIQEPGLSGR | 154.2 | 84.43 | 364.67 | 533.14 |
| Thioredoxin-related transmembrane protein 4 | VDVIQEPGLSGR | 203.81 | 289.82 | 235.33 | 116.1 |
| Thioredoxin-related transmembrane protein 4 | VDVIQEPGLSGR | 253.23 | 513.37 | 963.5 | 917.83 |
| Thioredoxin-related transmembrane protein 4 | VDVIQEPGLSGR | 2019.36 | 2193.39 | 2606.89 | 2556.9 |
| Thioredoxin-related transmembrane protein 4 | VDVIQEPGLSGR | 783.11 | 1140.93 | 1062.68 | 1318.93 |
| Thioredoxin-related transmembrane protein 4 | VDVIQEPGLSGR | 1490.56 | 1991.4 | 2622.45 | 2512.22 |
| ER membrane protein complex subunit 9 | VPPVIVLENQGLR | 101.68 | 167.32 | 286.41 | 396.44 |
| ER membrane protein complex subunit 9 | QMVGALLEDR | 731.88 | 670.34 | 912.4 | 710.78 |
| ER membrane protein complex subunit 9 | ALAYVK | 20198.58 | 21870.54 | 1155.09 | 2786.22 |
| ER membrane protein complex subunit 9 | ALAYVK | 1749.86 | 2224.25 | 791.52 | 903.55 |
| ER membrane protein complex subunit 9 | ALAYVK | 18297.25 | 19397.98 | 1074.27 | 2632.4 |
| ER membrane protein complex subunit 9 | ALAYVK | 6984 | 8399.77 | 1703.03 | 2226.99 |
| ER membrane protein complex subunit 9 | ALAYVK | 11990.65 | 15349.26 | 1757.26 | 2523.08 |
| ER membrane protein complex subunit 9 | ALAYVK | 17732.8 | 18143.57 | 1313.2 | 2768.24 |
| ER membrane protein complex subunit 9 | ALAYVK | 8779.03 | 9778.43 | 1392.69 | 3092.05 |
| ER membrane protein complex subunit 9 | ALAYVK | 2791.5 | 3886.45 | 2088.83 | 2123.22 |
| ER membrane protein complex subunit 9 | ALAYVK | 14059.6 | 17537.3 | 2957.6 | 5475.9 |
| ER membrane protein complex subunit 9 | LALK | 4807.41 | 3973.87 | 7291.02 | 8675.79 |
| ER membrane protein complex subunit 9 | LALK | 6462.81 | 5104.97 | 9207 | 10203.54 |
| ER membrane protein complex subunit 9 | LALK | 4935.22 | 6984.92 | 7871.44 | 8905.76 |
| ER membrane protein complex subunit 9 | LALK | 2767.42 | 2648.94 | 5681.47 | 7251.8 |
| ER membrane protein complex subunit 9 | LALK | 5309.85 | 5717.08 | 7567.24 | 9480.53 |
| ER membrane protein complex subunit 9 | LALK | 4754.16 | 5298.9 | 8162.92 | 10410.83 |
| ER membrane protein complex subunit 9 | LALK | 2595.08 | 2972.84 | 5981.54 | 5760.8 |
| ER membrane protein complex subunit 9 | LALK | 4855.52 | 4859.74 | 9143.68 | 9749.7 |
| ER membrane protein complex subunit 9 | LALK | 3910.89 | 4463.17 | 9457.04 | 12051.94 |
| ER membrane protein complex subunit 9 | LALK | 3537.6 | 4003.62 | 5686.03 | 6397.93 |
| ER membrane protein complex subunit 9 | LALK | 3317.37 | 3314.27 | 5540.3 | 6042.49 |
| ER membrane protein complex subunit 9 | LALK | 7119.65 | 6806.23 | 12375.83 | 13831.81 |
| ER membrane protein complex subunit 9 | LALK | 6439.08 | 6598.25 | 14200.82 | 13875.28 |
| ER membrane protein complex subunit 9 | LALK | 2604.25 | 1961 | 3076.21 | 4309.8 |
| ER membrane protein complex subunit 9 | LALK | 1965.68 | 1964.77 | 3847.48 | 3742.81 |
| ER membrane protein complex subunit 9 | LALK | 6416.21 | 8858.25 | 12646.49 | 15126.99 |
| ER membrane protein complex subunit 9 | LALK | 2500.28 | 3296.77 | 4134.6 | 4446.36 |

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|---|---|---|---|---|---|
| ER membrane protein complex subunit 9 | LALK | 8357.22 | 9218.16 | 13686.1 | 18634.37 |
| ER membrane protein complex subunit 9 | LALK | 6876.88 | 8344.44 | 12332.76 | 20178.62 |
| ER membrane protein complex subunit 9 | LALK | 9922.49 | 10742.99 | 18210.58 | 20949.86 |
| ER membrane protein complex subunit 9 | LALK | 3382.8 | 4084.33 | 5771.32 | 7290.97 |
| ER membrane protein complex subunit 9 | LALK | 4034.46 | 4488.61 | 7107.29 | 7558.56 |
| ER membrane protein complex subunit 9 | LALK | 7226.89 | 11105.02 | 14595.61 | 18163.31 |
| ER membrane protein complex subunit 9 | LALK | 2073.81 | 2558.7 | 3804.49 | 3804.21 |
| ER membrane protein complex subunit 9 | LALK | 4276.08 | 4872.5 | 7603.66 | 9278.12 |
| ER membrane protein complex subunit 9 | LALK | 5269.75 | 6274.35 | 9402.47 | 9238.55 |
| ER membrane protein complex subunit 9 | LALK | 4830.63 | 4339.64 | 6665.33 | 9453.04 |
| ER membrane protein complex subunit 9 | LALK | 2033.88 | 1716.56 | 3641.52 | 4247.94 |
| ER membrane protein complex subunit 9 | LALK | 2069.95 | 3366.15 | 4620.13 | 6283.3 |
| ER membrane protein complex subunit 9 | LDDIR | 2720.26 | 2946.52 | 3686.77 | 4520.29 |
| Potassium channel subfamily K member 1 | QNEPFVATQSSACVDGPANH | 180.83 | 6.66 | 71.86 | 150.96 |
| Potassium channel subfamily K member 1 | MLQSLAGSSCVR | 127.54 | 165.74 | 269.99 | 88.68 |
| Potassium channel subfamily K member 1 | MFYVK | 1331.23 | 1243.61 | 1527.88 | 1830.59 |
| Potassium channel subfamily K member 1 | EDLLR | 6160.1 | 5225.04 | 4802.29 | 6456.38 |
| Potassium channel subfamily K member 1 | EDLLR | 2113.85 | 2113.69 | 2054.56 | 2233.39 |
| Potassium channel subfamily K member 1 | EDLLR | 6989.02 | 6521.22 | 4719.3 | 4355.54 |
| Potassium channel subfamily K member 1 | ELHELK | 1561.36 | 1166.18 | 1961.66 | 2367.84 |
| Potassium channel subfamily K member 1 | LHELK | 235.25 | 268.84 | 306.82 | 349.39 |
| Potassium channel subfamily K member 1 | LHELK | 1088.91 | 1140.98 | 1960.61 | 1714.44 |
| Potassium channel subfamily K member 1 | LLGF | 658.89 | 647.68 | 705.21 | 939.96 |
| Potassium channel subfamily K member 1 | LRQELR | 1553.76 | 1172.45 | 2317.46 | 2589.96 |
| Potassium channel subfamily K member 1 | MLQSLAGSSCVR | 814.87 | 662.55 | 1525.65 | 1464.16 |
| Syntaxin-binding protein 6 | EIFAPLDER | 382.43 | 514.12 | 187.05 | 374.07 |
| Syntaxin-binding protein 6 | NSAQQFAETAHK | 128.35 | 85.64 | 399.48 | 234.67 |
| Syntaxin-binding protein 6 | EIFAPLDER | 318.93 | 405.16 | 224.62 | 218.06 |
| Syntaxin-binding protein 6 | EIFAPLDER | 410.98 | 246.8 | 327.47 | 548.79 |
| Syntaxin-binding protein 6 | EIFAPLDER | 204.86 | 185.5 | 285.79 | 369.44 |
| dCTP pyrophosphatase 1 | TDGEPGPQGWSPR | 1518.47 | 2212.45 | 2489.38 | 3108.86 |
| dCTP pyrophosphatase 1 | FSFSPEPTLEDIRR | 865.15 | 588.8 | 1160.13 | 1731.74 |
| dCTP pyrophosphatase 1 | VDLPLAVLSK | 423.97 | 133.76 | 127.34 | 159.67 |
| dCTP pyrophosphatase 1 | AVLSK | 6212.44 | 5798.33 | 2687.24 | 3461.96 |
| dCTP pyrophosphatase 1 | AVLSK | 983.21 | 946.4 | 1601.52 | 1150.15 |
| dCTP pyrophosphatase 1 | AVLSK | 6356.18 | 7980.2 | 3642.09 | 3873.59 |
| dCTP pyrophosphatase 1 | LAVL | 667.11 | 261.48 | 2492.45 | 2908.78 |
| dCTP pyrophosphatase 1 | LAVLSK | 774.48 | 1142.47 | 911.53 | 597.21 |
| dCTP pyrophosphatase 1 | LAVLSK | 1770.01 | 2467.45 | 4485.07 | 3923.33 |
| dCTP pyrophosphatase 1 | LAVLSK | 2288.26 | 2967.11 | 4198.11 | 4220.49 |
| dCTP pyrophosphatase 1 | LEDIR | 1167.11 | 862.64 | 1826.34 | 1507.41 |
| dCTP pyrophosphatase 1 | LLAL | 196.22 | 188.4 | 226.96 | 250.42 |
| dCTP pyrophosphatase 1 | LLAL | 75.78 | 172.69 | 115.6 | 69.95 |
| dCTP pyrophosphatase 1 | TDGEPGPQGWSPR | 177.67 | 319.4 | 410.35 | 233.69 |
| dCTP pyrophosphatase 1 | TDGEPGPQGWSPR | 255.84 | 255.7 | 562.49 | 408.43 |
| DNA mismatch repair protein Mlh1 | RLDETVVNR | 715.81 | 662.51 | 826.79 | 966.8 |
| DNA mismatch repair protein Mlh1 | STTSLTSSSTSGSSDK | 204.39 | 231.92 | 171.67 | 175.79 |
| DNA mismatch repair protein Mlh1 | SIFGNAVSR | 1112.83 | 693.32 | 1145.65 | 1295.03 |
| DNA mismatch repair protein Mlh1 | TLPNASTVDNIR | 2571.57 | 1359.78 | 3309.85 | 3207.85 |
| DNA mismatch repair protein Mlh1 | EMIENCLDAK | 126.02 | 315.79 | 512.62 | 556.12 |
| DNA mismatch repair protein Mlh1 | SFVAGVIR | 385.62 | 198.98 | 232.81 | 374.31 |
| DNA mismatch repair protein Mlh1 | GPTSSNPR | 269.77 | 156.24 | 218.6 | 91.43 |
| DNA mismatch repair protein Mlh1 | LIQIQDNGTGIR | 101.66 | 168.92 | 207.32 | 450.97 |
| DNA mismatch repair protein Mlh1 | EFLK | 1494.32 | 1619.85 | 2211.89 | 2094.92 |
| DNA mismatch repair protein Mlh1 | EFLK | 2907.52 | 2317.5 | 3531.57 | 4064.15 |
| DNA mismatch repair protein Mlh1 | EFLK | 2062.34 | 1776.67 | 3117.12 | 3247.33 |
| DNA mismatch repair protein Mlh1 | EFLK | 1122.01 | 955.96 | 1896.21 | 2169.41 |
| DNA mismatch repair protein Mlh1 | EFLK | 1210.3 | 957.17 | 1938.28 | 1796.53 |
| DNA mismatch repair protein Mlh1 | EFLK | 1428.95 | 2014.48 | 3514.61 | 4106.41 |
| DNA mismatch repair protein Mlh1 | EFLK | 748.57 | 1149.49 | 2042.55 | 1821.84 |
| DNA mismatch repair protein Mlh1 | EFLK | 1505.78 | 1977.03 | 2054.07 | 2870.97 |
| DNA mismatch repair protein Mlh1 | EFLK | 1768.23 | 3281.77 | 4421.66 | 4871.36 |
| DNA mismatch repair protein Mlh1 | EFLK | 714.1 | 831.54 | 1513.97 | 1681.51 |
| DNA mismatch repair protein Mlh1 | EVIQR | 2308.53 | 2347.95 | 3741.81 | 5374.7 |

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|---|---|---|---|---|---|
| DNA mismatch repair protein Mlh1 | FILR | 993.65 | 1617.09 | 1683.05 | 1522.96 |
| DNA mismatch repair protein Mlh1 | FILR | 1306.18 | 1590.35 | 2020.16 | 2264.02 |
| DNA mismatch repair protein Mlh1 | FILR | 2250.35 | 2670.49 | 3744.21 | 4025.15 |
| DNA mismatch repair protein Mlh1 | FILR | 7295.87 | 8226.42 | 10784.35 | 13712.01 |
| DNA mismatch repair protein Mlh1 | FILR | 1721.03 | 1135.92 | 2128.23 | 2658.95 |
| DNA mismatch repair protein Mlh1 | FSVK | 534.5 | 703.32 | 802.58 | 916.36 |
| DNA mismatch repair protein Mlh1 | IFILR | 978.96 | 1046.62 | 2244.37 | 2762.61 |
| DNA mismatch repair protein Mlh1 | ILEV | 538.71 | 180.42 | 590.2 | 407.12 |
| DNA mismatch repair protein Mlh1 | ILEV | 581.57 | 945.93 | 1022.29 | 951.69 |
| DNA mismatch repair protein Mlh1 | IVEFLK | 1329.98 | 2005.4 | 71.25 | 146.71 |
| DNA mismatch repair protein Mlh1 | IVEFLK | 2702.73 | 2656.93 | 150.76 | 297.03 |
| DNA mismatch repair protein Mlh1 | IVEFLK | 2120.57 | 1981.25 | 17.53 | 202.03 |
| DNA mismatch repair protein Mlh1 | IVEFLK | 2269.44 | 1954.78 | 302.8 | 186.17 |
| DNA mismatch repair protein Mlh1 | IVEFLK | 5865.71 | 6757.3 | 0 | 602.32 |
| DNA mismatch repair protein Mlh1 | IVEFLK | 484.78 | 402.94 | 46.09 | 146.9 |
| DNA mismatch repair protein Mlh1 | IVEFLK | 5834.69 | 5565.98 | 246.3 | 610.54 |
| DNA mismatch repair protein Mlh1 | IVEFLK | 1757.64 | 1455.41 | 179.32 | 245.98 |
| DNA mismatch repair protein Mlh1 | IVEFLK | 868.11 | 1040.98 | 908.43 | 835.97 |
| DNA mismatch repair protein Mlh1 | IVEFLK | 3024.77 | 4031.55 | 279.43 | 411.61 |
| DNA mismatch repair protein Mlh1 | IVEFLK | 1868.48 | 2312.93 | 172.41 | 371.74 |
| DNA mismatch repair protein Mlh1 | IVEFLK | 5143.14 | 6549.99 | 114.29 | 381.52 |
| DNA mismatch repair protein Mlh1 | IVEFLK | 5091.47 | 5803.33 | 271.14 | 385.35 |
| DNA mismatch repair protein Mlh1 | IVEFLK | 1554.2 | 1128.85 | 164.18 | 169.44 |
| DNA mismatch repair protein Mlh1 | IVEFLK | 692.25 | 543.66 | 37.29 | 125.19 |
| DNA mismatch repair protein Mlh1 | IVEFLK | 417.44 | 353.62 | 125.93 | 172.27 |
| DNA mismatch repair protein Mlh1 | LAFK | 1793.47 | 1000.15 | 1876.92 | 2158.65 |
| DNA mismatch repair protein Mlh1 | LAFK | 1711.02 | 1593.23 | 1883.12 | 3627.6 |
| DNA mismatch repair protein Mlh1 | LIGL | 667.11 | 261.48 | 2492.45 | 2908.78 |
| DNA mismatch repair protein Mlh1 | STTSLTSSSTSGSSDK | 235.67 | 226.84 | 468.05 | 325.91 |
| DNA mismatch repair protein Mlh1 | STTSLTSSSTSGSSDK | 603.9 | 761.55 | 805.63 | 1185.49 |
| DNA mismatch repair protein Mlh1 | TLAFK | 2011.31 | 2456.94 | 3162.99 | 4707.72 |
| DNA mismatch repair protein Mlh1 | TLPNASTVDNIR | 2001.6 | 2458.73 | 3801.54 | 4188.27 |
| DNA mismatch repair protein Mlh1 | TLPNASTVDNIR | 1536.45 | 2031.81 | 2316.85 | 3297.57 |
| DNA mismatch repair protein Mlh1 | TLPNASTVDNIR | 1987.39 | 1734.93 | 4020.55 | 4891.46 |
| DNA mismatch repair protein Mlh1 | TLPNASTVDNIR | 2693.47 | 2188.41 | 4531.64 | 5086.66 |
| DNA mismatch repair protein Mlh1 | TLPNASTVDNIR | 1536.45 | 2031.81 | 2316.85 | 3297.57 |
| DNA mismatch repair protein Mlh1 | VEFLK | 2458.61 | 1881.36 | 688.33 | 925.75 |
| DNA mismatch repair protein Mlh1 | VEFLK | 3498.29 | 2355.17 | 2641.23 | 2554.76 |
| DNA mismatch repair protein Mlh1 | VEFLK | 2048.16 | 2007.96 | 1514.82 | 2979.76 |
| DNA mismatch repair protein Mlh1 | VIVK | 8409.48 | 7565.38 | 10626.73 | 12828.12 |
| DNA mismatch repair protein Mlh1 | VIVK | 7855.86 | 9176.85 | 13631.04 | 15549.12 |
| DNA mismatch repair protein Mlh1 | YLPK | 1983.48 | 2653.6 | 4494.01 | 4354.62 |
| Vacuolar protein sorting-associated protein 4B | LHLGTTQNSLTEADFR | 1315.03 | 1248.49 | 1824.63 | 2058.88 |
| Vacuolar protein sorting-associated protein 4B | WSDVAGLEGAK | 1066.87 | 1191.22 | 1630.65 | 2507.62 |
| Vacuolar protein sorting-associated protein 4B | IYIPLPEPHAR | 436.39 | 290.26 | 637.8 | 350.74 |
| Vacuolar protein sorting-associated protein 4B | FTEDFGQEG | 1242.34 | 664.1 | 1212.29 | 1202.26 |
| Vacuolar protein sorting-associated protein 4B | GILLFGPPGTGK | 49.65 | 201.01 | 87.27 | 97.36 |
| Vacuolar protein sorting-associated protein 4B | AIDLASK | 7987.47 | 8727.37 | 11234.52 | 14939.53 |
| Vacuolar protein sorting-associated protein 4B | DALMQPVR | 1757.36 | 1589.8 | 3585.42 | 3342.3 |
| Vacuolar protein sorting-associated protein 4B | AAMFK | 861.87 | 913.12 | 1351.77 | 1073.02 |
| Vacuolar protein sorting-associated protein 4B | LGESEK | 17899.53 | 24649.29 | 3557.38 | 5854.46 |
| Vacuolar protein sorting-associated protein 4B | ARENK | 693.54 | 1160.22 | 1659.89 | 1887.07 |
| Vacuolar protein sorting-associated protein 4B | DLLK | 483.65 | 620.77 | 657.51 | 919.8 |
| Vacuolar protein sorting-associated protein 4B | DLLK | 540.63 | 204.34 | 676.13 | 887.3 |
| Vacuolar protein sorting-associated protein 4B | DLLK | 521.31 | 729.63 | 932.37 | 1400.54 |
| Vacuolar protein sorting-associated protein 4B | DLLK | 1797.5 | 1985.09 | 1756.43 | 1876.51 |
| Vacuolar protein sorting-associated protein 4B | DLLK | 1306.03 | 1180 | 1309.5 | 1375.78 |
| Vacuolar protein sorting-associated protein 4B | DLLK | 359.27 | 249.9 | 363.8 | 1049.81 |
| Vacuolar protein sorting-associated protein 4B | DLLK | 2094.81 | 1972.93 | 2278.93 | 2601.34 |
| Vacuolar protein sorting-associated protein 4B | DLLK | 1492.76 | 1560.71 | 2483.4 | 2262.26 |
| Vacuolar protein sorting-associated protein 4B | DLLK | 619.46 | 926.01 | 1177.19 | 1371.24 |
| Vacuolar protein sorting-associated protein 4B | DLLK | 1375.58 | 904.24 | 1557.19 | 1713.44 |
| Vacuolar protein sorting-associated protein 4B | DLLK | 1112.05 | 1196.14 | 1062.07 | 1621.92 |
| Vacuolar protein sorting-associated protein 4B | DLLK | 202.84 | 385.47 | 613.68 | 578.56 |

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|---|---|---|---|---|---|
| Vacuolar protein sorting-associated protein 4B | DLLK | 255.67 | 272.64 | 895.21 | 413.55 |
| Vacuolar protein sorting-associated protein 4B | DLVSK | 483.17 | 774.52 | 872.62 | 1082.38 |
| Vacuolar protein sorting-associated protein 4B | DLVSK | 266.6 | 256.48 | 377.74 | 584.72 |
| Vacuolar protein sorting-associated protein 4B | EYLK | 430.2 | 901.5 | 955.69 | 1126.27 |
| Vacuolar protein sorting-associated protein 4B | FTEDFGQEG | 860.64 | 715.45 | 1453.96 | 2120.11 |
| Vacuolar protein sorting-associated protein 4B | GILLFGPPGTGK | 76.82 | 70.32 | 69.66 | 99.38 |
| Vacuolar protein sorting-associated protein 4B | GILLFGPPGTGK | 102.7 | 66.3 | 173.9 | 67.24 |
| Vacuolar protein sorting-associated protein 4B | GILLFGPPGTGK | 153.9 | 113.69 | 195 | 118.5 |
| Vacuolar protein sorting-associated protein 4B | IDSL | 357.3 | 444.42 | 376.14 | 235.28 |
| Vacuolar protein sorting-associated protein 4B | IDSL | 382.05 | 658.05 | 515.6 | 643.4 |
| Vacuolar protein sorting-associated protein 4B | ILLF | 125.2 | 77.21 | 136.77 | 133.97 |
| Vacuolar protein sorting-associated protein 4B | ILPIK | 934.54 | 754.68 | 1316.7 | 1138.52 |
| Vacuolar protein sorting-associated protein 4B | ILPIK | 975.58 | 529.77 | 1175.11 | 747.74 |
| Vacuolar protein sorting-associated protein 4B | ILPIK | 411.8 | 166.2 | 481.82 | 692.3 |
| Vacuolar protein sorting-associated protein 4B | ILPIK | 637.98 | 692.09 | 659.66 | 508.99 |
| Vacuolar protein sorting-associated protein 4B | ILPIK | 3774.52 | 3787.88 | 7564.15 | 8710.41 |
| Vacuolar protein sorting-associated protein 4B | ILPIK | 978.43 | 673.44 | 1877.09 | 1558.47 |
| Vacuolar protein sorting-associated protein 4B | ILPIK | 2794.73 | 1972.22 | 4961.82 | 5548.74 |
| Vacuolar protein sorting-associated protein 4B | ILPIK | 4116.57 | 3823.81 | 8416.42 | 11247.83 |
| Vacuolar protein sorting-associated protein 4B | ILPIK | 2468.36 | 2194.89 | 4663.89 | 4451.87 |
| Vacuolar protein sorting-associated protein 4B | ILPIK | 1118.31 | 1853.37 | 3421 | 4338.18 |
| Vacuolar protein sorting-associated protein 4B | ILPIK | 1142.35 | 968.15 | 2229.61 | 2232.48 |
| Vacuolar protein sorting-associated protein 4B | ILPIK | 606.41 | 619.66 | 847.61 | 875.39 |
| Vacuolar protein sorting-associated protein 4B | IYIPLPEPHAR | 1151.48 | 1023.06 | 1500.66 | 1256.32 |
| Vacuolar protein sorting-associated protein 4B | IYIPLPEPHAR | 384.35 | 324.77 | 398.23 | 285.91 |
| Vacuolar protein sorting-associated protein 4B | IYIPLPEPHAR | 487.56 | 340.31 | 527.35 | 483.36 |
| Vacuolar protein sorting-associated protein 4B | IYIPLPEPHAR | 281.92 | 232.48 | 232.59 | 317.44 |
| Vacuolar protein sorting-associated protein 4B | LGESEK | 8089.46 | 7055 | 1940.82 | 2306.14 |
| Vacuolar protein sorting-associated protein 4B | LGESEK | 10756.59 | 11739.75 | 3771.54 | 5510.9 |
| Vacuolar protein sorting-associated protein 4B | LPIK | 607.14 | 1185.62 | 1411.98 | 1268.22 |
| Vacuolar protein sorting-associated protein 4A | IYIPLPEEAAR | 934.43 | 978.11 | 1275.16 | 941.6 |
| Vacuolar protein sorting-associated protein 4A | LHLGSTPHNLTDANIHELAR | 484.72 | 621.47 | 1842.09 | 1375.56 |
| Vacuolar protein sorting-associated protein 4A | NLFELAR | 356.86 | 487.73 | 1320.61 | 1262.36 |
| Vacuolar protein sorting-associated protein 4A | DLLK | 483.65 | 620.77 | 657.51 | 919.8 |
| Vacuolar protein sorting-associated protein 4A | DLLK | 540.63 | 204.34 | 676.13 | 887.3 |
| Vacuolar protein sorting-associated protein 4A | DLLK | 521.31 | 729.63 | 932.37 | 1400.54 |
| Vacuolar protein sorting-associated protein 4A | DLLK | 1797.5 | 1985.09 | 1756.43 | 1876.51 |
| Vacuolar protein sorting-associated protein 4A | DLLK | 1306.03 | 1180 | 1309.5 | 1375.78 |
| Vacuolar protein sorting-associated protein 4A | DLLK | 359.27 | 249.9 | 363.8 | 1049.81 |
| Vacuolar protein sorting-associated protein 4A | DLLK | 2094.81 | 1972.93 | 2278.93 | 2601.34 |
| Vacuolar protein sorting-associated protein 4A | DLLK | 1492.76 | 1560.71 | 2483.4 | 2262.26 |
| Vacuolar protein sorting-associated protein 4A | DLLK | 619.46 | 926.01 | 1177.19 | 1371.24 |
| Vacuolar protein sorting-associated protein 4A | DLLK | 1375.58 | 904.24 | 1557.19 | 1713.44 |
| Vacuolar protein sorting-associated protein 4A | DLLK | 1112.05 | 1196.14 | 1062.07 | 1621.92 |
| Vacuolar protein sorting-associated protein 4A | DLLK | 202.84 | 385.47 | 613.68 | 578.56 |
| Vacuolar protein sorting-associated protein 4A | DLLK | 255.67 | 272.64 | 895.21 | 413.55 |
| Vacuolar protein sorting-associated protein 4A | DLMSK | 3795.24 | 4931.86 | 7812.64 | 8787.54 |
| Vacuolar protein sorting-associated protein 4A | DLMSK | 1288.35 | 2075.07 | 3798.72 | 5146.57 |
| Vacuolar protein sorting-associated protein 4A | GILLFGPPGTGK | 49.65 | 201.01 | 87.27 | 97.36 |
| Vacuolar protein sorting-associated protein 4A | GILLFGPPGTGK | 76.82 | 70.32 | 69.66 | 99.38 |
| Vacuolar protein sorting-associated protein 4A | GILLFGPPGTGK | 102.7 | 66.3 | 173.9 | 67.24 |
| Vacuolar protein sorting-associated protein 4A | GILLFGPPGTGK | 153.9 | 113.69 | 195 | 118.5 |
| Vacuolar protein sorting-associated protein 4A | ILLF | 125.2 | 77.21 | 136.77 | 133.97 |
| Vacuolar protein sorting-associated protein 4A | ILPIK | 934.54 | 754.68 | 1316.7 | 1138.52 |
| Vacuolar protein sorting-associated protein 4A | ILPIK | 975.58 | 529.77 | 1175.11 | 747.74 |
| Vacuolar protein sorting-associated protein 4A | ILPIK | 411.8 | 166.2 | 481.82 | 692.3 |
| Vacuolar protein sorting-associated protein 4A | ILPIK | 637.98 | 692.09 | 659.66 | 508.99 |
| Vacuolar protein sorting-associated protein 4A | ILPIK | 3774.52 | 3787.88 | 7564.15 | 8710.41 |
| Vacuolar protein sorting-associated protein 4A | ILPIK | 978.43 | 673.44 | 1877.09 | 1558.47 |
| Vacuolar protein sorting-associated protein 4A | ILPIK | 2794.73 | 1972.22 | 4961.82 | 5548.74 |
| Vacuolar protein sorting-associated protein 4A | ILPIK | 4116.57 | 3823.81 | 8416.42 | 11247.83 |
| Vacuolar protein sorting-associated protein 4A | ILPIK | 2468.36 | 2194.89 | 4663.89 | 4451.87 |
| Vacuolar protein sorting-associated protein 4A | ILPIK | 1118.31 | 1853.37 | 3421 | 4338.18 |
| Vacuolar protein sorting-associated protein 4A | ILPIK | 1142.35 | 968.15 | 2229.61 | 2232.48 |

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|---|---|---|---|---|---|
| Vacuolar protein sorting-associated protein 4A | ILPIK | 606.41 | 619.66 | 847.61 | 875.39 |
| Vacuolar protein sorting-associated protein 4A | IYIPLPEEAAR | 177.46 | 340.08 | 398.97 | 565.34 |
| Vacuolar protein sorting-associated protein 4A | IYIPLPEEAAR | 533.61 | 790.72 | 577.7 | 996.76 |
| Vacuolar protein sorting-associated protein 4A | IYIPLPEEAAR | 358.81 | 295.31 | 672.27 | 875.53 |
| Vacuolar protein sorting-associated protein 4A | IYIPLPEEAAR | 25.64 | 19.66 | 0 | 50.83 |
| Vacuolar protein sorting-associated protein 4A | IYIPLPEEAAR | 281.7 | 254.14 | 438.44 | 286 |
| Vacuolar protein sorting-associated protein 4A | LFELAR | 102.71 | 64.79 | 248.31 | 166.5 |
| Vacuolar protein sorting-associated protein 4A | LGESEK | 17899.53 | 24649.29 | 3557.38 | 5854.46 |
| Vacuolar protein sorting-associated protein 4A | LGESEK | 8089.46 | 7055 | 1940.82 | 2306.14 |
| Vacuolar protein sorting-associated protein 4A | LGESEK | 10756.59 | 11739.75 | 3771.54 | 5510.9 |
| Vacuolar protein sorting-associated protein 4A | LPIK | 607.14 | 1185.62 | 1411.98 | 1268.22 |
| Exocyst complex component 7 | AVEYFQDNSPDSPELNK | 494.01 | 448.29 | 640.99 | 300.82 |
| Exocyst complex component 7 | GFNDGLEELCK | 307.03 | 304.51 | 407.06 | 361.86 |
| Exocyst complex component 7 | LEEYLGSMAK | 128.46 | 74.29 | 109.45 | 190.82 |
| Exocyst complex component 7 | EHIEQQIQTYQR | 511.6 | 519.28 | 681.89 | 820.93 |
| Exocyst complex component 7 | YGVEQVGDMIDR | 154.2 | 84.8 | 346.25 | 291.14 |
| Exocyst complex component 7 | AWAIPDTEQR | 510.97 | 581.54 | 1061.64 | 987.78 |
| Exocyst complex component 7 | VTDYIAEK | 10012.46 | 11215.91 | 1188.7 | 1072.57 |
| Exocyst complex component 7 | LLFERGK | 461.42 | 370.03 | 323.47 | 418.78 |
| Exocyst complex component 7 | TRHSK | 461.54 | 358.59 | 995.08 | 676.82 |
| Exocyst complex component 7 | AVEYFQDNSPDSPELNK | 385.9 | 172.02 | 288.85 | 282.19 |
| Exocyst complex component 7 | DSLEK | 2289.17 | 2770.89 | 3050.25 | 4134.82 |
| Exocyst complex component 7 | DSLEK | 693.72 | 610.56 | 764.89 | 887.31 |
| Exocyst complex component 7 | DSLEK | 1632.91 | 1331.37 | 2250.92 | 2214.68 |
| Exocyst complex component 7 | DSLEK | 2723.3 | 2858.68 | 5520.85 | 8149.8 |
| Exocyst complex component 7 | DSLEK | 669.08 | 811.25 | 1246.73 | 1469.16 |
| Exocyst complex component 7 | FLQK | 3312.82 | 3551.44 | 3186.68 | 3370.69 |
| Exocyst complex component 7 | FLQK | 2051.3 | 3399.92 | 2911.57 | 3980.78 |
| Exocyst complex component 7 | FLQK | 6492.49 | 5363.91 | 7352.81 | 7479.64 |
| Exocyst complex component 7 | GFNDGLEELCK | 256.08 | 231.94 | 353.96 | 569 |
| Exocyst complex component 7 | GFNDGLEELCK | 334.24 | 169.5 | 602.93 | 558.07 |
| Exocyst complex component 7 | GLLP | 206.92 | 0 | 95.22 | 278.73 |
| Exocyst complex component 7 | GNLQLNLLSK | 582.77 | 721.84 | 453.84 | 471.62 |
| Exocyst complex component 7 | GNLQLNLLSK | 582.77 | 721.84 | 453.84 | 471.62 |
| Exocyst complex component 7 | ILDL | 538.71 | 180.42 | 590.2 | 407.12 |
| Exocyst complex component 7 | ILDL | 581.57 | 945.93 | 1022.29 | 951.69 |
| Exocyst complex component 7 | LLFER | 1951.11 | 1064.14 | 1644.48 | 1353.09 |
| Exocyst complex component 7 | LLFERGK | 409.53 | 390.51 | 883.34 | 652.58 |
| Exocyst complex component 7 | LLSK | 4234.88 | 3411.05 | 6964.9 | 7478.5 |
| Exocyst complex component 7 | LLSK | 3980.54 | 4816.7 | 5542.92 | 8038.88 |
| Exocyst complex component 7 | LLSK | 8445.18 | 8612.45 | 10773.67 | 13482.85 |
| Exocyst complex component 7 | LLSK | 1471.64 | 1945.58 | 3628.55 | 5240.62 |
| Exocyst complex component 7 | LLSK | 2693.93 | 4164.81 | 3942.42 | 5022.55 |
| Exocyst complex component 7 | LLSK | 2350.83 | 1572.36 | 3336.75 | 3843.43 |
| Exocyst complex component 7 | LLSK | 3177.26 | 3220.87 | 3812.72 | 3898.27 |
| Exocyst complex component 7 | LLSK | 1518.04 | 2042.29 | 3833.99 | 4348.4 |
| Exocyst complex component 7 | LLSK | 1351.59 | 1891.18 | 2291.31 | 2357.75 |
| Exocyst complex component 7 | LLSK | 3181.41 | 3130.42 | 4495.21 | 6836.12 |
| Exocyst complex component 7 | LLSK | 7071.17 | 9255.36 | 11240.11 | 15044.85 |
| Exocyst complex component 7 | LLSK | 8217.78 | 10548.13 | 12023.17 | 14109.44 |
| Exocyst complex component 7 | LLSK | 4182.42 | 4658.64 | 5547.87 | 6978.64 |
| Exocyst complex component 7 | LLSK | 4313.71 | 6580.89 | 8061.56 | 9728.5 |
| Exocyst complex component 7 | LLSK | 3641.4 | 3109.72 | 4843.86 | 6104.42 |
| Exocyst complex component 7 | LLSK | 2637.23 | 2851.18 | 4505.17 | 4971.66 |
| Exocyst complex component 7 | LLSK | 1994.71 | 2607.99 | 3198.42 | 3294.41 |
| Exocyst complex component 7 | LLSK | 12618.85 | 11156.78 | 16157.18 | 19470.8 |
| Exocyst complex component 7 | LLSK | 1409.61 | 1797.21 | 2312.38 | 3838.89 |
| Exocyst complex component 7 | LLSK | 3887.16 | 3190.46 | 4151.19 | 5313.17 |
| Exocyst complex component 7 | LLSK | 2878.2 | 3831.54 | 5604.06 | 6155.41 |
| Exocyst complex component 7 | LNKV | 984.03 | 651.82 | 851.56 | 1355.47 |
| Exocyst complex component 7 | LSFIR | 2258.1 | 2330.02 | 3802.96 | 3642.53 |
| Exocyst complex component 7 | LSFIR | 3557.89 | 4232.24 | 5844.4 | 6219.67 |
| Exocyst complex component 7 | LSFIR | 3643.36 | 3022.31 | 3469.21 | 5265.32 |
| Exocyst complex component 7 | LSFIR | 2946.79 | 3331.18 | 3615.59 | 5125.07 |

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|---|---|---|---|---|---|
| Exocyst complex component 7 | LSFIR | 1558.08 | 1490.97 | 2023.86 | 1900.88 |
| Exocyst complex component 7 | NLLK | 540.63 | 204.34 | 676.13 | 887.3 |
| Exocyst complex component 7 | NLLK | 359.27 | 249.9 | 363.8 | 1049.81 |
| Exocyst complex component 7 | NLLK | 202.84 | 385.47 | 613.68 | 578.56 |
| Exocyst complex component 7 | NLLSK | 1332.71 | 1629.09 | 2612.92 | 3422.51 |
| Exocyst complex component 7 | QIIK | 2159.8 | 3638.02 | 3341.89 | 4582.17 |
| Exocyst complex component 7 | QIIK | 1331.14 | 1464.69 | 1921.29 | 2240.57 |
| Exocyst complex component 7 | QNLLK | 2432.28 | 4270.55 | 5946.87 | 8139.86 |
| Exocyst complex component 7 | QNLLK | 1200.97 | 1347.17 | 2360.93 | 3907 |
| Exocyst complex component 7 | VTDYIAEK | 7086.88 | 9618.79 | 970.21 | 1845.43 |
| Exocyst complex component 7 | VTDYIAEK | 5248.62 | 4958.24 | 5117.58 | 6610.07 |
| Exocyst complex component 7 | VTDYIAEK | 7498.43 | 7362.27 | 715.31 | 1011.62 |
| Exocyst complex component 7 | VTDYIAEK | 10794.14 | 10795.77 | 703.18 | 1500.68 |
| Exocyst complex component 7 | VTDYIAEK | 10238.38 | 11236.13 | 956.23 | 1419.97 |
| Exocyst complex component 7 | VTDYIAEK | 15878.62 | 17502.82 | 1666.98 | 1522.23 |
| Exocyst complex component 7 | VTDYIAEK | 2739.31 | 3724.16 | 1531.38 | 2042.22 |
| Exocyst complex component 7 | VTDYIAEK | 11357.74 | 11070.67 | 943.14 | 1394.14 |
| Exocyst complex component 7 | VTDYIAEK | 9261.23 | 8414.13 | 1742.44 | 1623.11 |
| Exocyst complex component 7 | VTDYIAEK | 1156.27 | 762.81 | 793.67 | 999.41 |
| Exocyst complex component 7 | VTDYIAEK | 853.9 | 742.45 | 355.94 | 237.1 |
| Exocyst complex component 7 | YGVEQVGDMIDR | 102.44 | 91.74 | 192.62 | 247.63 |
| Exocyst complex component 7 | YGVEQVGDMIDR | 255.02 | 336.31 | 301.19 | 390.04 |
| Exocyst complex component 7 | YIAEK | 20413.75 | 23803.27 | 25981.3 | 33100.46 |
| Exocyst complex component 7 | YIAEK | 7649.31 | 9371.31 | 9608.52 | 12986.74 |
| Exocyst complex component 7 | YIAEK | 1607.76 | 1050.49 | 2035.66 | 1826.77 |
| Exocyst complex component 7 | YIAEK | 5789.75 | 7452.73 | 8459.87 | 9026.57 |
| Exocyst complex component 7 | YIAEK | 2365.18 | 3559.61 | 3914.83 | 4209.53 |
| Exocyst complex component 7 | YILK | 1494.13 | 1319.79 | 2002.86 | 1611.01 |
| Exocyst complex component 7 | YILK | 1695.62 | 1412.87 | 1872.62 | 2723.39 |
| Exocyst complex component 7 | YILK | 1557.06 | 1484.75 | 2494.9 | 3453.63 |
| Exocyst complex component 7 | YILK | 1283.89 | 814.02 | 1090.45 | 971.03 |
| Probable palmitoyltransferase ZDHHC20 | LVGMDPEQASVTNQNEYAR | 333.7 | 222.6 | 531.31 | 614.37 |
| Probable palmitoyltransferase ZDHHC20 | EGIVK | 153.4 | 164.03 | 259.77 | 426.73 |
| Probable palmitoyltransferase ZDHHC20 | EGIVK | 728.04 | 730.32 | 1416.93 | 1299.98 |
| Probable palmitoyltransferase ZDHHC20 | EGIVK | 541.46 | 973.28 | 1092.56 | 951.76 |
| Probable palmitoyltransferase ZDHHC20 | EGIVK | 205.13 | 159.21 | 308.71 | 517.72 |
| Probable palmitoyltransferase ZDHHC20 | EGIVK | 281.16 | 307.2 | 368.8 | 771.11 |
| Probable palmitoyltransferase ZDHHC20 | EGIVK | 330.72 | 516.99 | 979.64 | 830.05 |
| Probable palmitoyltransferase ZDHHC20 | ITFV | 6247.1 | 4395.82 | 7418.04 | 8582.38 |
| Probable palmitoyltransferase ZDHHC20 | ITFV | 8484.71 | 6941.7 | 11735.1 | 12459.63 |
| Probable palmitoyltransferase ZDHHC20 | ITFV | 1720.85 | 1366.21 | 2386.29 | 2665.33 |
| Probable palmitoyltransferase ZDHHC20 | ITFV | 462.46 | 267.13 | 409.78 | 338.23 |
| Probable palmitoyltransferase ZDHHC20 | QLIK | 2159.8 | 3638.02 | 3341.89 | 4582.17 |
| Probable palmitoyltransferase ZDHHC20 | QLIK | 1331.14 | 1464.69 | 1921.29 | 2240.57 |
| Probable palmitoyltransferase ZDHHC20 | QVFGDEK | 19152.47 | 18840.85 | 7787.54 | 9315.26 |
| Aldo-keto reductase family 1 member C2 | YKPVCNQVECHPYFNQR | 356 | 572.87 | 515.94 | 279.31 |
| Aldo-keto reductase family 1 member C2 | SIGVSNFNHR | 832.48 | 624.86 | 1304.12 | 1337.2 |
| Aldo-keto reductase family 1 member C2 | AIDGLNR | 1840.27 | 1908.16 | 1468.77 | 2316.03 |
| Aldo-keto reductase family 1 member C2 | AIRSK | 1299.13 | 1116.91 | 2965.91 | 2381.52 |
| Aldo-keto reductase family 1 member C2 | ALIALR | 2130.13 | 1462.15 | 2629.49 | 3688.47 |
| Aldo-keto reductase family 1 member C2 | ALIALR | 1445.17 | 1901.1 | 2734.3 | 3054.56 |
| Aldo-keto reductase family 1 member C2 | ALIALR | 891.42 | 971.87 | 1954.45 | 1432.67 |
| Aldo-keto reductase family 1 member C2 | DAGLAK | 2440.6 | 3129.01 | 4354.65 | 6223.49 |
| Aldo-keto reductase family 1 member C2 | DIVLVAY | 204.85 | 186.51 | 235.66 | 320.49 |
| Aldo-keto reductase family 1 member C2 | EDIFYTSK | 487.59 | 337.43 | 670.15 | 1093.76 |
| Aldo-keto reductase family 1 member C2 | EDIFYTSK | 5896.95 | 6117.37 | 6944.08 | 8426.08 |
| Aldo-keto reductase family 1 member C2 | EDIFYTSK | 4211.43 | 4558.22 | 5515.5 | 6482.61 |
| Aldo-keto reductase family 1 member C2 | EDIFYTSK | 5308.44 | 4899.55 | 5567.29 | 5847.32 |
| Aldo-keto reductase family 1 member C2 | EDIFYTSK | 1530.18 | 1906.3 | 2803.82 | 2017.02 |
| Aldo-keto reductase family 1 member C2 | ELVR | 334.17 | 388.86 | 709.55 | 798.59 |
| Aldo-keto reductase family 1 member C2 | ELVR | 153.27 | 176.51 | 174.96 | 329.95 |
| Aldo-keto reductase family 1 member C2 | ELVR | 180.45 | 257.22 | 444.12 | 348.36 |
| Aldo-keto reductase family 1 member C2 | GVVVLAK | 899.73 | 1002.41 | 732.53 | 1190.29 |
| Aldo-keto reductase family 1 member C2 | GVVVLAK | 2292.22 | 2470.17 | 1851.35 | 2830.15 |

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|---|---|---|---|---|---|
| Aldo-keto reductase family 1 member C2 | GVVVLAK | 6137.6 | 5852.19 | 4924.8 | 5955.8 |
| Aldo-keto reductase family 1 member C2 | GVVVLAK | 2182.99 | 1559.03 | 3334.64 | 2677.53 |
| Aldo-keto reductase family 1 member C2 | GVVVLAK | 2191.13 | 2031.97 | 3420.12 | 4326.19 |
| Aldo-keto reductase family 1 member C2 | IADGSVK | 7063.25 | 8016.85 | 6099.47 | 7417.4 |
| Aldo-keto reductase family 1 member C2 | IADGSVK | 8993.66 | 8785.51 | 6319.86 | 8334.01 |
| Aldo-keto reductase family 1 member C2 | IADGSVK | 7400.73 | 6802 | 7086.63 | 6840.74 |
| Aldo-keto reductase family 1 member C2 | IADGSVK | 4734.21 | 5142.79 | 4735.17 | 6269.9 |
| Aldo-keto reductase family 1 member C2 | IADGSVK | 1865.02 | 2548.89 | 2395.49 | 2782.13 |
| Aldo-keto reductase family 1 member C2 | IADGSVK | 4990.08 | 6671.64 | 5189.46 | 7127.81 |
| Aldo-keto reductase family 1 member C2 | IADGSVK | 1332.42 | 1444.62 | 781.64 | 1763.02 |
| Aldo-keto reductase family 1 member C2 | IADGSVK | 2473.89 | 2393.91 | 4213.56 | 4508.53 |
| Aldo-keto reductase family 1 member C2 | ILNK | 3059.4 | 3270.14 | 3615.93 | 4312.52 |
| Aldo-keto reductase family 1 member C2 | ILNK | 1259.27 | 1224.83 | 1231.17 | 1605.55 |
| Aldo-keto reductase family 1 member C2 | ILNK | 1325.13 | 782.29 | 1817.38 | 2421.19 |
| Aldo-keto reductase family 1 member C2 | ILNK | 3077.34 | 3518.82 | 4227.04 | 4991.5 |
| Aldo-keto reductase family 1 member C2 | ILNK | 2975.59 | 3251.68 | 4836.32 | 5153.56 |
| Aldo-keto reductase family 1 member C2 | ILNK | 2814.58 | 2350.52 | 3781.49 | 3872.46 |
| Aldo-keto reductase family 1 member C2 | ILNK | 2417.43 | 3184.19 | 1443.74 | 1517.98 |
| Aldo-keto reductase family 1 member C2 | ILNK | 5458.27 | 8180.95 | 5991.74 | 5731.38 |
| Aldo-keto reductase family 1 member C2 | ILNK | 2618.42 | 2689.07 | 1529.65 | 1972.05 |
| Aldo-keto reductase family 1 member C2 | ILNK | 1264.79 | 1317.9 | 1128.14 | 873.49 |
| Aldo-keto reductase family 1 member C2 | ILNK | 12239 | 11238.33 | 15004.76 | 17913 |
| Aldo-keto reductase family 1 member C2 | ILNK | 2356.27 | 2843.71 | 1808.85 | 1955.98 |
| Aldo-keto reductase family 1 member C2 | ILNK | 4307.1 | 5106.36 | 6027.83 | 7668.98 |
| Aldo-keto reductase family 1 member C2 | ILNK | 3115.72 | 4088.26 | 4055.47 | 4179.6 |
| Aldo-keto reductase family 1 member C2 | ILNK | 1621.83 | 2851.96 | 1751.8 | 2219.03 |
| Aldo-keto reductase family 1 member C2 | LEAVK | 770.82 | 759.85 | 1767.79 | 820.31 |
| Aldo-keto reductase family 1 member C2 | LEAVKL | 2519.48 | 2463.71 | 1125.39 | 1156.47 |
| Aldo-keto reductase family 1 member C2 | LIAL | 196.22 | 188.4 | 226.96 | 250.42 |
| Aldo-keto reductase family 1 member C2 | LIAL | 75.78 | 172.69 | 115.6 | 69.95 |
| Aldo-keto reductase family 1 member C2 | LIALR | 1064.7 | 1086.65 | 1758.36 | 1345.73 |
| Aldo-keto reductase family 1 member C2 | LLDFCK | 2443.36 | 2430.64 | 1018.86 | 3437.38 |
| Aldo-keto reductase family 1 member C2 | LLDFCK | 3156.71 | 2166.28 | 950.11 | 1164.04 |
| Aldo-keto reductase family 1 member C2 | LLDFCK | 584.25 | 1213.06 | 297.88 | 341.24 |
| Aldo-keto reductase family 1 member C2 | LLDFCK | 1598.31 | 1451.62 | 1375.91 | 2029.51 |
| Aldo-keto reductase family 1 member C2 | REDIFYTSK | 3968.48 | 4412.33 | 7824.67 | 6872.69 |
| Aldo-keto reductase family 1 member C2 | REDIFYTSK | 2379.98 | 2948.08 | 6399.02 | 5902.75 |
| Aldo-keto reductase family 1 member C2 | REDIFYTSK | 2340.04 | 2851.25 | 3409.78 | 4893.78 |
| Aldo-keto reductase family 1 member C2 | REDIFYTSK | 4228.89 | 4641.33 | 6233.41 | 8846.47 |
| Aldo-keto reductase family 1 member C2 | SKIADGSVK | 1191.1 | 1577.59 | 1902.78 | 1815.65 |
| Aldo-keto reductase family 1 member C2 | TPALIALR | 3378.64 | 2686.5 | 1051.33 | 1289.96 |
| Aldo-keto reductase family 1 member C2 | TPALIALR | 2239.19 | 2602.1 | 1264.15 | 1806.51 |
| Aldo-keto reductase family 1 member C2 | TPALIALR | 2255.81 | 2343.77 | 524.96 | 1222.51 |
| Aldo-keto reductase family 1 member C2 | TPALIALR | 1179.07 | 1382.32 | 596.2 | 688.49 |
| Aldo-keto reductase family 1 member C2 | TPALIALR | 6453.89 | 6518.47 | 4954.79 | 5246.53 |
| Aldo-keto reductase family 1 member C2 | TPALIALR | 6915.88 | 6938.27 | 4888.33 | 5957.99 |
| Aldo-keto reductase family 1 member C2 | TPALIALR | 3156.15 | 2753.16 | 2718.22 | 2439.14 |
| Aldo-keto reductase family 1 member C2 | TPALIALR | 201.3 | 537.14 | 137.52 | 275.55 |
| Aldo-keto reductase family 1 member C2 | TPALIALR | 1254.39 | 537.03 | 805.25 | 1115.26 |
| Aldo-keto reductase family 1 member C2 | TPALIALR | 10811.29 | 10377.82 | 7326.01 | 7582.83 |
| Aldo-keto reductase family 1 member C2 | TPALIALR | 13336.11 | 14548.57 | 9094.25 | 8652.33 |
| Aldo-keto reductase family 1 member C2 | TPALIALR | 5367.82 | 4989.71 | 4134.26 | 4747.75 |
| Aldo-keto reductase family 1 member C2 | TPALIALR | 1507.94 | 1231.21 | 1067.8 | 1360.47 |
| Aldo-keto reductase family 1 member C2 | TPALIALR | 1140.76 | 1550.64 | 1399.39 | 1654.04 |
| Aldo-keto reductase family 1 member C2 | TPALIALR | 154.15 | 89.45 | 116.76 | 199.02 |
| Aldo-keto reductase family 1 member C2 | YKPVCNQVECHPYFNQR | 467.67 | 284.64 | 801.34 | 597.97 |
| Aldo-keto reductase family 1 member C2 | YKPVCNQVECHPYFNQR | 4088.88 | 5070.41 | 786.79 | 1395.52 |
| Aldo-keto reductase family 1 member C2 | YQCVK | 3918.4 | 3721.27 | 2193.51 | 2460.86 |
| Monoacylglycerol lipase ABHD6 | SSLDDLSIDGQVK | 381.03 | 652.73 | 729.25 | 372.14 |
| Monoacylglycerol lipase ABHD6 | NLHLVCVDMPGHEGTTR | 1967.3 | 1911.36 | 2813.41 | 2894.67 |
| Monoacylglycerol lipase ABHD6 | AAVEK | 166.31 | 164.88 | 276.95 | 282.6 |
| Monoacylglycerol lipase ABHD6 | FLPK | 3105.58 | 3175 | 3950.66 | 5222.85 |
| Monoacylglycerol lipase ABHD6 | LSVVK | 1792.18 | 2723.96 | 1448.89 | 2084.68 |
| Monoacylglycerol lipase ABHD6 | SIDGQVK | 3955.18 | 3917.87 | 2599.33 | 2547.64 |

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|---|---|---|---|---|---|
| NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3 | YSVMINK | 815.52 | 1130.84 | 1177.21 | 1810.58 |
| NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3 | VGAFLK | 1544.64 | 1541.76 | 1635.03 | 1374.1 |
| NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3 | VGAFLK | 558.23 | 592.68 | 922.43 | 1231.57 |
| NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3 | VGAFLK | 947.18 | 994.66 | 1633.22 | 1815.68 |
| NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3 | VGAFLK | 1025.43 | 923.82 | 1871.92 | 1235.89 |
| NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3 | VGAFLK | 957.55 | 714.86 | 755.37 | 926.43 |
| NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3 | VGAFLK | 822.08 | 695.16 | 524.43 | 484.92 |
| NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3 | VGAFLK | 3542.88 | 3375.58 | 564.06 | 463.31 |
| NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3 | VGAFLK | 807.52 | 1176.54 | 1711.74 | 2755.84 |
| 26S proteasome non-ATPase regulatory subunit 3 | AIQLEYSEAR | 961.69 | 1369.79 | 1373.96 | 1220.45 |
| 26S proteasome non-ATPase regulatory subunit 3 | AIQLEYSEARR | 2968.81 | 3390.4 | 4168.99 | 4526.28 |
| 26S proteasome non-ATPase regulatory subunit 3 | DGVIEASINHEK | 409.22 | 420.88 | 658.79 | 627.77 |
| 26S proteasome non-ATPase regulatory subunit 3 | ELDTVTLEDIK | 835.69 | 308.31 | 834.88 | 792.8 |
| 26S proteasome non-ATPase regulatory subunit 3 | ELDTVTLEDIKEHVK | 937.14 | 1136.01 | 1911.93 | 2067.39 |
| 26S proteasome non-ATPase regulatory subunit 3 | EMIDIYSTR | 788.21 | 850.09 | 1122.89 | 1321.66 |
| 26S proteasome non-ATPase regulatory subunit 3 | EPQLAFHQR | 1741.91 | 2052.27 | 2519.61 | 2920 |
| 26S proteasome non-ATPase regulatory subunit 3 | HDADGQATLLNLLLR | 312.22 | 323.44 | 515.53 | 500.02 |
| 26S proteasome non-ATPase regulatory subunit 3 | LQLDSPEDAEFIVAK | 203.77 | 293.01 | 77.9 | 201.73 |
| 26S proteasome non-ATPase regulatory subunit 3 | MISLSYSR | 1212.16 | 1624.32 | 1907.92 | 2033.92 |
| 26S proteasome non-ATPase regulatory subunit 3 | SVFPEQANNNEWAR | 612.63 | 430.67 | 705.68 | 708.04 |
| 26S proteasome non-ATPase regulatory subunit 3 | AVQGFFTSNNATR | 744.72 | 784.69 | 1006.57 | 1935.05 |
| 26S proteasome non-ATPase regulatory subunit 3 | EREQQDLEFAK | 1314.14 | 910.1 | 1332.95 | 1734.9 |
| 26S proteasome non-ATPase regulatory subunit 3 | LNHYVLYK | 2089.79 | 2256.98 | 3139.26 | 5374.37 |
| 26S proteasome non-ATPase regulatory subunit 3 | YLYYTGR | 1562.48 | 1374.81 | 3073.17 | 2247.67 |
| 26S proteasome non-ATPase regulatory subunit 3 | EQQDLEFAK | 4919.45 | 4820.08 | 6189.96 | 7822.54 |
| 26S proteasome non-ATPase regulatory subunit 3 | ISDDLMQK | 3053.39 | 3118.51 | 4596.2 | 5304.04 |
| 26S proteasome non-ATPase regulatory subunit 3 | FNQVLDQFGEK | 115.35 | 92.77 | 94.35 | 84.63 |
| 26S proteasome non-ATPase regulatory subunit 3 | ALDLVAAK | 10562.66 | 12602.16 | 3522.41 | 5318.37 |
| 26S proteasome non-ATPase regulatory subunit 3 | VYEFLDK | 870.41 | 920.18 | 1290.71 | 626.98 |
| 26S proteasome non-ATPase regulatory subunit 3 | GYVQSK | 354.01 | 556.26 | 600.47 | 573.62 |
| 26S proteasome non-ATPase regulatory subunit 3 | SFLHARLR | 408.19 | 522.38 | 641.55 | 1198.07 |
| 26S proteasome non-ATPase regulatory subunit 3 | AIQLEYSEAR | 867.59 | 1092.95 | 1264.91 | 1368.42 |
| 26S proteasome non-ATPase regulatory subunit 3 | AIQLEYSEAR | 696.72 | 420.71 | 836.88 | 1141.74 |
| 26S proteasome non-ATPase regulatory subunit 3 | AIQLEYSEAR | 2968.81 | 3390.4 | 4168.99 | 4526.28 |
| 26S proteasome non-ATPase regulatory subunit 3 | AIQLEYSEAR | 2137.58 | 2003.14 | 4138.51 | 3898.15 |
| 26S proteasome non-ATPase regulatory subunit 3 | ALDLVAAK | 3965.27 | 4303.67 | 3371.44 | 4437.55 |
| 26S proteasome non-ATPase regulatory subunit 3 | ALDLVAAK | 2355.55 | 2383.23 | 2675.49 | 2562.48 |
| 26S proteasome non-ATPase regulatory subunit 3 | ALDLVAAK | 2845.83 | 1816.91 | 4106.39 | 3335.07 |
| 26S proteasome non-ATPase regulatory subunit 3 | ALDLVAAK | 23795.87 | 26252.41 | 1634.26 | 3374.62 |
| 26S proteasome non-ATPase regulatory subunit 3 | AVGFK | 1779.23 | 1130.29 | 2193.44 | 2355.82 |
| 26S proteasome non-ATPase regulatory subunit 3 | AVQGFFTSNNATR | 1803.14 | 2172.78 | 2450.98 | 2198.18 |
| 26S proteasome non-ATPase regulatory subunit 3 | AVQGFFTSNNATR | 1521.67 | 939.08 | 1692.17 | 1814.91 |
| 26S proteasome non-ATPase regulatory subunit 3 | AVQGFFTSNNATR | 1560.47 | 1466.7 | 2311.27 | 1822.42 |
| 26S proteasome non-ATPase regulatory subunit 3 | AVQGFFTSNNATR | 1521.67 | 939.08 | 1692.17 | 1814.91 |
| 26S proteasome non-ATPase regulatory subunit 3 | AVQGFFTSNNATR | 559.02 | 514.74 | 573.13 | 872.75 |
| 26S proteasome non-ATPase regulatory subunit 3 | AVQGFFTSNNATR | 559.02 | 514.74 | 573.13 | 872.75 |
| 26S proteasome non-ATPase regulatory subunit 3 | DGVIEASINHEK | 926.66 | 1426.19 | 2063.42 | 1885.91 |
| 26S proteasome non-ATPase regulatory subunit 3 | DGVIEASINHEK | 2119.99 | 2251.65 | 2760.43 | 2428.24 |
| 26S proteasome non-ATPase regulatory subunit 3 | DGVIEASINHEK | 1670.52 | 1764.63 | 3074.01 | 4090.1 |
| 26S proteasome non-ATPase regulatory subunit 3 | EFLDK | 29470.13 | 33626.17 | 1498.56 | 2512.54 |
| 26S proteasome non-ATPase regulatory subunit 3 | EFLDK | 7395.71 | 9212.98 | 1561.97 | 1459.32 |
| 26S proteasome non-ATPase regulatory subunit 3 | EFLDK | 1350.11 | 2569.58 | 812.22 | 1303.88 |
| 26S proteasome non-ATPase regulatory subunit 3 | EFLDK | 7015.5 | 9010.84 | 1252.65 | 1811.17 |
| 26S proteasome non-ATPase regulatory subunit 3 | ELDTVTLEDIK | 617.49 | 482.71 | 613.78 | 762.21 |
| 26S proteasome non-ATPase regulatory subunit 3 | ELDTVTLEDIK | 358.22 | 353.58 | 345.22 | 596.22 |
| 26S proteasome non-ATPase regulatory subunit 3 | ELDTVTLEDIKEHVK | 985.53 | 1674.28 | 3352 | 3349.13 |
| 26S proteasome non-ATPase regulatory subunit 3 | ELDTVTLEDIKEHVK | 915.45 | 1044.75 | 1718.55 | 1908.99 |
| 26S proteasome non-ATPase regulatory subunit 3 | ELDTVTLEDIKEHVK | 154.45 | 59.94 | 298.57 | 214.25 |
| 26S proteasome non-ATPase regulatory subunit 3 | ELDTVTLEDIKEHVK | 2631.15 | 2601.53 | 3579.26 | 4261.96 |
| 26S proteasome non-ATPase regulatory subunit 3 | EMIDIYSTR | 2764.34 | 3484.7 | 3870.45 | 4809.27 |
| 26S proteasome non-ATPase regulatory subunit 3 | EMIDIYSTR | 2557.65 | 3373.83 | 4420.87 | 5073.94 |
| 26S proteasome non-ATPase regulatory subunit 3 | EMIDIYSTR | 981.17 | 721.61 | 1132.84 | 1210.61 |

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|---|---|---|---|---|---|
| 26S proteasome non-ATPase regulatory subunit 3 | EMIDIYSTR | 1972.93 | 1568.4 | 2843.51 | 3007.54 |
| 26S proteasome non-ATPase regulatory subunit 3 | EMIDIYSTR | 1844.02 | 1431.31 | 2703.77 | 3417.08 |
| 26S proteasome non-ATPase regulatory subunit 3 | EMIDIYSTR | 2106.74 | 2390.58 | 2851.64 | 2565.21 |
| 26S proteasome non-ATPase regulatory subunit 3 | EMIDIYSTR | 461.22 | 390.22 | 761.77 | 1010.42 |
| 26S proteasome non-ATPase regulatory subunit 3 | EMIDIYSTR | 1399.6 | 1722.7 | 1566.65 | 2379.12 |
| 26S proteasome non-ATPase regulatory subunit 3 | EMIDIYSTR | 405.52 | 787.02 | 964.64 | 896.94 |
| 26S proteasome non-ATPase regulatory subunit 3 | EPQLAFHQR | 609.08 | 569.23 | 832.28 | 917.36 |
| 26S proteasome non-ATPase regulatory subunit 3 | EQQDLEFAK | 1523.89 | 1889.93 | 2519.74 | 1857.95 |
| 26S proteasome non-ATPase regulatory subunit 3 | EQQDLEFAK | 589.73 | 1204.21 | 874.92 | 1552.34 |
| 26S proteasome non-ATPase regulatory subunit 3 | EQQDLEFAK | 2016.94 | 1475.39 | 2495.92 | 1945.86 |
| 26S proteasome non-ATPase regulatory subunit 3 | EQQDLEFAK | 4022.25 | 3674.12 | 5634.86 | 4152.76 |
| 26S proteasome non-ATPase regulatory subunit 3 | EQQDLEFAK | 1205.39 | 1654.72 | 1386.02 | 1656.93 |
| 26S proteasome non-ATPase regulatory subunit 3 | EREQQDLEFAK | 1572.98 | 1613.93 | 2695.2 | 4156.64 |
| 26S proteasome non-ATPase regulatory subunit 3 | EREQQDLEFAK | 1596.01 | 2104.39 | 2976.33 | 3099.55 |
| 26S proteasome non-ATPase regulatory subunit 3 | FLDK | 2467.9 | 2133.81 | 4495.56 | 5351.67 |
| 26S proteasome non-ATPase regulatory subunit 3 | FLDK | 1675.88 | 1128.61 | 2070.47 | 2141.71 |
| 26S proteasome non-ATPase regulatory subunit 3 | FVLR | 976.09 | 1117.79 | 4000.14 | 3822.14 |
| 26S proteasome non-ATPase regulatory subunit 3 | FVLR | 1115.99 | 1019.13 | 2835.9 | 3064.67 |
| 26S proteasome non-ATPase regulatory subunit 3 | FVLR | 1107.62 | 888.16 | 2537 | 2709.99 |
| 26S proteasome non-ATPase regulatory subunit 3 | ISDDLMQK | 2983.43 | 3435.25 | 1417.82 | 2509.81 |
| 26S proteasome non-ATPase regulatory subunit 3 | ISDDLMQK | 3746.53 | 3573.79 | 5651.18 | 7329.46 |
| 26S proteasome non-ATPase regulatory subunit 3 | ISDDLMQK | 3351.89 | 5116.76 | 3588.86 | 3831.77 |
| 26S proteasome non-ATPase regulatory subunit 3 | LDKL | 2055.16 | 1635.69 | 2617.23 | 3027.78 |
| 26S proteasome non-ATPase regulatory subunit 3 | LEDIK | 1127.43 | 1165.45 | 1779.47 | 1825.99 |
| 26S proteasome non-ATPase regulatory subunit 3 | LEDIK | 1091.11 | 1455.77 | 1220.86 | 2041.96 |
| 26S proteasome non-ATPase regulatory subunit 3 | LEDIK | 2805.77 | 3966.34 | 4999.15 | 6632.05 |
| 26S proteasome non-ATPase regulatory subunit 3 | LEDIK | 1160.78 | 955.7 | 2033.29 | 2250.35 |
| 26S proteasome non-ATPase regulatory subunit 3 | LEDIK | 1141.76 | 1451.42 | 1942.23 | 2126.54 |
| 26S proteasome non-ATPase regulatory subunit 3 | LEDIK | 1292.9 | 881.59 | 1917.22 | 1970.76 |
| 26S proteasome non-ATPase regulatory subunit 3 | LEFAK | 1205.33 | 1128.44 | 2580.21 | 2581.45 |
| 26S proteasome non-ATPase regulatory subunit 3 | LIIR | 386.99 | 489.76 | 684.01 | 680.12 |
| 26S proteasome non-ATPase regulatory subunit 3 | LIIR | 912.1 | 950.18 | 1143.27 | 1280.65 |
| 26S proteasome non-ATPase regulatory subunit 3 | LIIR | 556.67 | 959.36 | 927.48 | 1147.92 |
| 26S proteasome non-ATPase regulatory subunit 3 | LIIR | 1415.65 | 1626.01 | 1823.04 | 1846.6 |
| 26S proteasome non-ATPase regulatory subunit 3 | LIIR | 279.39 | 481.67 | 627.51 | 552.92 |
| 26S proteasome non-ATPase regulatory subunit 3 | LIIR | 487.03 | 393.55 | 449.11 | 438.94 |
| 26S proteasome non-ATPase regulatory subunit 3 | LIIRL | 229.51 | 303.98 | 717.46 | 474.46 |
| 26S proteasome non-ATPase regulatory subunit 3 | LLLR | 386.99 | 489.76 | 684.01 | 680.12 |
| 26S proteasome non-ATPase regulatory subunit 3 | LLLR | 769.62 | 771.66 | 1081.49 | 1259.46 |
| 26S proteasome non-ATPase regulatory subunit 3 | LLLR | 864.03 | 699.71 | 1475.57 | 835.82 |
| 26S proteasome non-ATPase regulatory subunit 3 | LLLR | 912.1 | 950.18 | 1143.27 | 1280.65 |
| 26S proteasome non-ATPase regulatory subunit 3 | LLLR | 556.67 | 959.36 | 927.48 | 1147.92 |
| 26S proteasome non-ATPase regulatory subunit 3 | LLLR | 1415.65 | 1626.01 | 1823.04 | 1846.6 |
| 26S proteasome non-ATPase regulatory subunit 3 | LLLR | 279.39 | 481.67 | 627.51 | 552.92 |
| 26S proteasome non-ATPase regulatory subunit 3 | LLLR | 487.03 | 393.55 | 449.11 | 438.94 |
| 26S proteasome non-ATPase regulatory subunit 3 | LNHYVLYK | 1991.45 | 3036.33 | 4734.22 | 4417.53 |
| 26S proteasome non-ATPase regulatory subunit 3 | LNHYVLYK | 491.74 | 672.08 | 748.99 | 767.94 |
| 26S proteasome non-ATPase regulatory subunit 3 | LNHYVLYK | 1122.8 | 1516.55 | 2034.41 | 1962.55 |
| 26S proteasome non-ATPase regulatory subunit 3 | LQLDSPEDAEFIVAK | 358.5 | 325.38 | 462.56 | 716.68 |
| 26S proteasome non-ATPase regulatory subunit 3 | MISLSYSR | 612.88 | 724.89 | 831.12 | 985.8 |
| 26S proteasome non-ATPase regulatory subunit 3 | MISLSYSR | 1067.11 | 848.45 | 1086.09 | 1945.01 |
| 26S proteasome non-ATPase regulatory subunit 3 | SLYDQAEK | 205.91 | 82.49 | 271.17 | 216.85 |
| 26S proteasome non-ATPase regulatory subunit 3 | SVFPEQANNNEWAR | 1334.05 | 1177.78 | 1635.38 | 1967.76 |
| 26S proteasome non-ATPase regulatory subunit 3 | SVFPEQANNNEWAR | 333.43 | 249.19 | 493.37 | 179.95 |
| 26S proteasome non-ATPase regulatory subunit 3 | SVFPEQANNNEWAR | 729.82 | 767.74 | 995.75 | 1584.23 |
| 26S proteasome non-ATPase regulatory subunit 3 | SVFPEQANNNEWAR | 757.97 | 964.91 | 1670.91 | 1887.02 |
| 26S proteasome non-ATPase regulatory subunit 3 | SVFPEQANNNEWAR | 757.97 | 964.91 | 1670.91 | 1887.02 |
| 26S proteasome non-ATPase regulatory subunit 3 | SVFPEQANNNEWAR | 757.97 | 964.91 | 1670.91 | 1887.02 |
| 26S proteasome non-ATPase regulatory subunit 3 | SVFPEQANNNEWAR | 774.5 | 927.46 | 1867.02 | 1798.41 |
| 26S proteasome non-ATPase regulatory subunit 3 | SVFPEQANNNEWAR | 774.5 | 927.46 | 1867.02 | 1798.41 |
| 26S proteasome non-ATPase regulatory subunit 3 | SVFPEQANNNEWAR | 459.25 | 584.63 | 566.64 | 912.8 |
| 26S proteasome non-ATPase regulatory subunit 3 | SVFPEQANNNEWAR | 799.43 | 911.81 | 1166.78 | 1871.64 |
| 26S proteasome non-ATPase regulatory subunit 3 | SVFPEQANNNEWAR | 1045.43 | 1075.05 | 1285.68 | 1585.83 |
| 26S proteasome non-ATPase regulatory subunit 3 | SVFPEQANNNEWAR | 774.5 | 927.46 | 1867.02 | 1798.41 |

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| 26S proteasome non-ATPase regulatory subunit 3 | SVFPEQANNNEWAR | 777.54 | 627.71 | 832.87 | 1115.95 |
| 26S proteasome non-ATPase regulatory subunit 3 | SVFPEQANNNEWAR | 610.5 | 640.86 | 1007.18 | 772.48 |
| 26S proteasome non-ATPase regulatory subunit 3 | VYEFLDK | 681.65 | 845.79 | 662.19 | 737.56 |
| 26S proteasome non-ATPase regulatory subunit 3 | YLYYTGR | 2091.53 | 1765.2 | 3258.21 | 3611.67 |
| ER membrane protein complex subunit 2 | ILQEDPTNTAAR | 359.04 | 271.96 | 550.19 | 486.52 |
| ER membrane protein complex subunit 2 | YDDAIQLYDR | 411 | 245.15 | 408.95 | 416.52 |
| ER membrane protein complex subunit 2 | AVEDMLETLQITQS | 38.41 | 34.64 | 60.68 | 48.34 |
| ER membrane protein complex subunit 2 | FEAMER | 541.24 | 888.68 | 1023.08 | 1366.69 |
| ER membrane protein complex subunit 2 | AQALK | 510.45 | 632.33 | 838.51 | 1051.07 |
| ER membrane protein complex subunit 2 | AQALK | 735 | 1000.94 | 1249.24 | 1590.88 |
| ER membrane protein complex subunit 2 | AVEDMLETLQITQS | 51.74 | 0 | 102.72 | 20.4 |
| ER membrane protein complex subunit 2 | ELSRK | 839 | 1470.76 | 1722.88 | 1731.87 |
| ER membrane protein complex subunit 2 | IAIRK | 3277.22 | 3558.51 | 945.89 | 791.13 |
| ER membrane protein complex subunit 2 | IAIRK | 1433.28 | 1054.93 | 1125.54 | 466.81 |
| ER membrane protein complex subunit 2 | IAIRK | 1352.52 | 1267.71 | 1002.16 | 1089.73 |
| ER membrane protein complex subunit 2 | IAIRK | 2126.67 | 2336.79 | 599.04 | 502.96 |
| ER membrane protein complex subunit 2 | ILQEDPTNTAAR | 333.42 | 250.79 | 414.76 | 467.79 |
| ER membrane protein complex subunit 2 | ILQEDPTNTAAR | 205.89 | 84.12 | 190.53 | 322 |
| ER membrane protein complex subunit 2 | ILQEDPTNTAAR | 612.04 | 1020.84 | 1566.53 | 1438.68 |
| ER membrane protein complex subunit 2 | YDDAIQLYDR | 643.53 | 676.23 | 838.89 | 899.42 |
| ER membrane protein complex subunit 2 | YDDAIQLYDR | 368.49 | 508.38 | 681.81 | 858.51 |
| ER membrane protein complex subunit 2 | YDDAIQLYDR | 152.35 | 266.85 | 283.86 | 268.34 |
| ER membrane protein complex subunit 2 | YDDAIQLYDR | 254.27 | 410.09 | 324.22 | 329.35 |
| ER membrane protein complex subunit 2 | YDDAIQLYDR | 659.91 | 759.33 | 1455.28 | 1719.03 |
| Cystathionine gamma-lyase | QGAPGQHSGFEYSR | 228.15 | 225.33 | 464.15 | 387.57 |
| Cystathionine gamma-lyase | NDRDVLGISDTLIR | 1045.38 | 1186.4 | 2267.25 | 1812.36 |
| Cystathionine gamma-lyase | EIFLK | 1147.73 | 1181.67 | 1541 | 2287.84 |
| Cystathionine gamma-lyase | EIFLK | 255.87 | 252.53 | 612.43 | 432.7 |
| Cystathionine gamma-lyase | EIFLK | 6520.37 | 6439.62 | 685.95 | 1228.61 |
| Cystathionine gamma-lyase | EIFLK | 868.14 | 718.71 | 1265.36 | 1637.86 |
| Cystathionine gamma-lyase | EIFLK | 3981.09 | 3378.83 | 392.91 | 538.85 |
| Cystathionine gamma-lyase | EIFLK | 5703.03 | 5382.34 | 451.18 | 623.75 |
| Cystathionine gamma-lyase | ELVK | 309.61 | 49.15 | 263.79 | 522.29 |
| Cystathionine gamma-lyase | ELVK | 152.9 | 212.58 | 413.29 | 361.64 |
| Cystathionine gamma-lyase | ELVK | 332.91 | 301.03 | 484.35 | 333 |
| Cystathionine gamma-lyase | FGLK | 838.74 | 964.25 | 1992.45 | 1300.43 |
| Cystathionine gamma-lyase | FYIK | 1069.88 | 1425.98 | 2772.48 | 2325.73 |
| Cystathionine gamma-lyase | FYIK | 1397.9 | 1784.48 | 2240.2 | 2349.9 |
| Cystathionine gamma-lyase | IFLK | 2800.73 | 2655.93 | 2713.72 | 2747.15 |
| Cystathionine gamma-lyase | IFLK | 848.14 | 885.96 | 2426.69 | 2268.47 |
| Cystathionine gamma-lyase | IFLK | 1293.11 | 2456.52 | 2411.93 | 2123.8 |
| Cystathionine gamma-lyase | IFLK | 2470.97 | 2256.62 | 2983.58 | 3778.41 |
| Cystathionine gamma-lyase | IFLK | 1295.7 | 1136.43 | 2013.16 | 2203.91 |
| Cystathionine gamma-lyase | IFLK | 1376.94 | 1088.83 | 1995.35 | 2068.54 |
| Cystathionine gamma-lyase | IFLK | 3125.37 | 3879.87 | 3903.38 | 4277.33 |
| Cystathionine gamma-lyase | IFLK | 562.75 | 571.7 | 1039.53 | 1023.44 |
| Cystathionine gamma-lyase | IFLK | 1216.57 | 1507.36 | 1879.53 | 2265.18 |
| Cystathionine gamma-lyase | NDRDVLGISDTLIR | 1363.15 | 1281.23 | 1996.51 | 1524.21 |
| Cystathionine gamma-lyase | QGAPGQHSGFEYSR | 0 | 102.93 | 18.65 | 19.47 |
| Cystathionine gamma-lyase | QGAPGQHSGFEYSR | 38.28 | 47.57 | 59.86 | 48.35 |
| Synaptogyrin-2 | QMYCVFNR | 1488.53 | 1446.63 | 1652.8 | 1699.04 |
| Synaptogyrin-2 | MESGAYGAAK | 714.27 | 1346.66 | 925.06 | 1148.46 |
| Synaptogyrin-2 | AGGSFDLR | 1375.59 | 2285.72 | 3005.32 | 2870.36 |
| Synaptogyrin-2 | AAITF | 1906.79 | 1506.97 | 326.64 | 367.1 |
| Synaptogyrin-2 | AAITF | 1609.38 | 1422.49 | 436.23 | 283.24 |
| Synaptogyrin-2 | MESGAYGAAK | 2606.58 | 2369.02 | 2511.71 | 3086.91 |
| Synaptogyrin-2 | MESGAYGAAK | 202.54 | 414.75 | 708.91 | 244.83 |
| Synaptogyrin-2 | MESGAYGAAK | 333.63 | 229.77 | 177.01 | 454.55 |
| Synaptogyrin-2 | QMYCVFNR | 805.03 | 783.99 | 979.91 | 968.12 |
| Synaptogyrin-2 | QMYCVFNR | 1061.34 | 992.55 | 1266.13 | 951.71 |
| N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase | QVSTVVCVHEPR | 436.9 | 239 | 618.51 | 1060.13 |
| N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase | VAQNGGFFR | 2220.52 | 3382.97 | 4193.79 | 3923.4 |
| N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase | EQPGGAHNPFK | 656.7 | 651.37 | 1860.76 | 1249.86 |

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| N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase | EFLLK | 308.85 | 124.53 | 367.58 | 341.56 |
| N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase | EFLLK | 3981.09 | 3378.83 | 392.91 | 538.85 |
| N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase | EFLLK | 2209.46 | 2454.97 | 1843.05 | 2609.3 |
| N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase | EFLLK | 3394.01 | 3614.75 | 4810.19 | 6039.68 |
| N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase | EFLLK | 5703.03 | 5382.34 | 451.18 | 623.75 |
| N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase | EFLLK | 6520.37 | 6439.62 | 685.95 | 1228.61 |
| N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase | EFLLK | 3244.52 | 4341.7 | 2323.16 | 2256.4 |
| N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase | EFLLK | 502.26 | 271.51 | 1324.03 | 136.2 |
| N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase | EFLLK | 3992.84 | 5622 | 2629.55 | 3009.99 |
| N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase | FLLK | 1512.27 | 2612.26 | 3319.52 | 3799.41 |
| N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase | FLLK | 848.14 | 885.96 | 2426.69 | 2268.47 |
| N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase | FLLK | 690.7 | 802.52 | 1226.74 | 1724.59 |
| N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase | FLLK | 1293.11 | 2456.52 | 2411.93 | 2123.8 |
| N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase | FLLK | 1075.62 | 1284.45 | 1614.56 | 3127.26 |
| N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase | FLLK | 1216.57 | 1507.36 | 1879.53 | 2265.18 |
| N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase | LLLR | 386.99 | 489.76 | 684.01 | 680.12 |
| N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase | LLLR | 769.62 | 771.66 | 1081.49 | 1259.46 |
| N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase | LLLR | 864.03 | 699.71 | 1475.57 | 835.82 |
| N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase | LLLR | 912.1 | 950.18 | 1143.27 | 1280.65 |
| N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase | LLLR | 556.67 | 959.36 | 927.48 | 1147.92 |
| N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase | LLLR | 1415.65 | 1626.01 | 1823.04 | 1846.6 |
| N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase | LLLR | 279.39 | 481.67 | 627.51 | 552.92 |
| N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase | LLLR | 487.03 | 393.55 | 449.11 | 438.94 |
| N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase | LLLRL | 229.51 | 303.98 | 717.46 | 474.46 |
| N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase | LLRL | 912.1 | 950.18 | 1143.27 | 1280.65 |
| N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase | LLRL | 556.67 | 959.36 | 927.48 | 1147.92 |
| N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase | VAQNGGFFR | 2220.52 | 3382.97 | 4193.79 | 3923.4 |
| Transcription factor A, mitochondrial | SAYNVYVAER | 1685.1 | 1707.04 | 3316.25 | 2272.13 |
| Transcription factor A, mitochondrial | SWEEQMIEVGR | 204.84 | 187.57 | 183.15 | 351.18 |
| Transcription factor A, mitochondrial | SSVLASCPK | 359.02 | 273.97 | 450.43 | 727.14 |
| Transcription factor A, mitochondrial | EQLPIFK | 1123.71 | 682 | 1505.95 | 1905.66 |
| Transcription factor A, mitochondrial | FVYL | 187.44 | 98.1 | 151.65 | 161.09 |
| Transcription factor A, mitochondrial | LLGK | 3497.2 | 4271.32 | 5463.79 | 5805.31 |
| Transcription factor A, mitochondrial | LLGK | 6358.35 | 8191.63 | 19930.68 | 27872.12 |
| Transcription factor A, mitochondrial | LLGK | 5627.84 | 5364.58 | 18307.75 | 21015.58 |
| Transcription factor A, mitochondrial | LLGK | 4093.22 | 3045.08 | 7609.02 | 8332.05 |
| Transcription factor A, mitochondrial | LLGK | 2955.88 | 3816.51 | 8510.03 | 11071 |
| Transcription factor A, mitochondrial | LLGK | 1741.15 | 1701.46 | 2482.79 | 3844.17 |
| Transcription factor A, mitochondrial | LRFSK | 1996.71 | 1346.75 | 2869.9 | 3484.67 |
| Transcription factor A, mitochondrial | LRFSK | 2869.99 | 1664.06 | 4982.92 | 4850.74 |
| Transcription factor A, mitochondrial | LRFSK | 3955.2 | 4234.57 | 5975.25 | 8638.17 |
| Transcription factor A, mitochondrial | LRFSK | 1515.26 | 1358.97 | 1369.93 | 2181.45 |
| Transcription factor A, mitochondrial | LRFSK | 774.5 | 821.67 | 1302.27 | 1311.11 |
| Transcription factor A, mitochondrial | LRFSK | 1300.41 | 884.15 | 1124.43 | 1583.67 |
| Transcription factor A, mitochondrial | LTLL | 114.69 | 158.48 | 37.77 | 113.82 |
| Transcription factor A, mitochondrial | LTLL | 201.09 | 132.94 | 186.59 | 209.92 |
| Transcription factor A, mitochondrial | LTLL | 192.95 | 85.86 | 151.74 | 325.05 |
| Transcription factor A, mitochondrial | SAYNVYVAER | 659 | 424.26 | 799.75 | 625.72 |
| Transcription factor A, mitochondrial | SAYNVYVAER | 498.2 | 353.68 | 1103.82 | 1244.04 |
| Transcription factor A, mitochondrial | SAYNVYVAER | 2509.42 | 2393.34 | 4058.25 | 5095.87 |
| Transcription factor A, mitochondrial | SAYNVYVAER | 1719.76 | 1687.56 | 3833.99 | 3227.23 |
| Transcription factor A, mitochondrial | SAYNVYVAER | 2149.01 | 2256.48 | 3426.11 | 3768.81 |
| Transcription factor A, mitochondrial | SWEEQMIEVGR | 101.8 | 155.1 | 252.21 | 274.52 |
| Transcription factor A, mitochondrial | SWEEQMIEVGR | 153.11 | 191.87 | 160.32 | 249.15 |
| Transcription factor A, mitochondrial | SWEEQMIEVGR | 357.86 | 389.21 | 445.78 | 603.66 |
| Transcription factor A, mitochondrial | VYLPR | 13648.57 | 13252.75 | 1997.47 | 2740.61 |
| Transcription factor A, mitochondrial | VYLPR | 3904.22 | 3313.83 | 1443.65 | 1622.89 |
| Transcription factor A, mitochondrial | VYLPR | 995.72 | 879.99 | 745.14 | 843.82 |
| Transcription factor A, mitochondrial | VYLPR | 5197.78 | 4768.5 | 2509.15 | 3073.21 |

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|---|---|---|---|---|---|
| Transcription factor A, mitochondrial | VYLPR | 19493.74 | 20975.31 | 3448.98 | 3610.95 |
| Transcription factor A, mitochondrial | VYLPR | 4456.27 | 5368.31 | 2310.28 | 3587.92 |
| Transcription factor A, mitochondrial | VYLPR | 35819.26 | 35069.48 | 4118.84 | 4872.14 |
| Aldose reductase | DYPFHEEF | 2189.29 | 2319.33 | 1020.16 | 1556.64 |
| Aldose reductase | EELFIVSK | 1528.95 | 2134.48 | 2105.95 | 2419.95 |
| Aldose reductase | LIQYCQSK | 456.58 | 848.12 | 574.05 | 435.94 |
| Aldose reductase | LLLNNGAK | 3085.24 | 3163.42 | 1991.82 | 2911.01 |
| Aldose reductase | MPILGLGTWK | 520.29 | 617.65 | 305.37 | 387.79 |
| Aldose reductase | NLVVIPK | 3258.74 | 3149.65 | 2356.32 | 2840.21 |
| Aldose reductase | SPPGQVTEAVK | 2723.21 | 3399.65 | 1792.49 | 2119.11 |
| Aldose reductase | TTAQVLIR | 4738.96 | 3396.84 | 4330.96 | 4365.33 |
| Aldose reductase | VCALLSCTSHK | 1867.31 | 2322.14 | 1795.43 | 1830.63 |
| Aldose reductase | VAIDVGYR | 6427.71 | 5169.16 | 5202.99 | 6013.11 |
| Aldose reductase | FPMQR | 1265.27 | 1270.27 | 982.41 | 1458.42 |
| Aldose reductase | AIAAKHNK | 513.4 | 235.09 | 531.68 | 595.02 |
| Aldose reductase | LWCTYHEK | 2237.56 | 848.86 | 1191.33 | 1457.91 |
| Aldose reductase | REELFIVSK | 2938.3 | 3000.57 | 3618.01 | 3854.42 |
| Aldose reductase | HIDCAHVYQNENEVGVAIQEK | 598.23 | 683.18 | 979.94 | 1018.85 |
| Aldose reductase | HNKTTAQVLIR | 312.68 | 278.13 | 361.59 | 571.11 |
| Aldose reductase | VCALLSC | 281.44 | 279.16 | 478.14 | 127.05 |
| Aldose reductase | AQVLIR | 645.23 | 614.29 | 652 | 1173.64 |
| Aldose reductase | DYPFHEEF | 3196.08 | 4340.44 | 1498.93 | 1185.09 |
| Aldose reductase | DYPFHEEF | 3184.72 | 3335.16 | 1801.58 | 1276.14 |
| Aldose reductase | DYPFHEEF | 2051.14 | 2138.56 | 841.25 | 1083.68 |
| Aldose reductase | DYPFHEEF | 1252.56 | 1462.57 | 399.44 | 665.35 |
| Aldose reductase | DYPFHEEF | 1758.91 | 1649 | 491.32 | 672.06 |
| Aldose reductase | DYPFHEEF | 1029.76 | 921.63 | 1219.96 | 1068.06 |
| Aldose reductase | DYPFHEEF | 485.7 | 524.42 | 841.52 | 683.68 |
| Aldose reductase | DYPFHEEF | 1302.65 | 769.2 | 898.5 | 773.55 |
| Aldose reductase | DYPFHEEF | 1158.1 | 1220.76 | 739.16 | 812.29 |
| Aldose reductase | DYPFHEEF | 540.04 | 369.01 | 191.98 | 502.08 |
| Aldose reductase | DYPFHEEF | 800.02 | 427.7 | 165.61 | 377.45 |
| Aldose reductase | DYPFHEEF | 460.67 | 444.19 | 540.49 | 544.76 |
| Aldose reductase | DYPFHEEF | 786.19 | 942.7 | 644.9 | 1027.55 |
| Aldose reductase | EELFIVSK | 2923.42 | 2448.75 | 2938.13 | 4449.7 |
| Aldose reductase | EGLVK | 153.4 | 164.03 | 259.77 | 426.73 |
| Aldose reductase | EGLVK | 728.04 | 730.32 | 1416.93 | 1299.98 |
| Aldose reductase | EGLVK | 541.46 | 973.28 | 1092.56 | 951.76 |
| Aldose reductase | EGLVK | 205.13 | 159.21 | 308.71 | 517.72 |
| Aldose reductase | EGLVK | 281.16 | 307.2 | 368.8 | 771.11 |
| Aldose reductase | EGLVK | 330.72 | 516.99 | 979.64 | 830.05 |
| Aldose reductase | FIVSK | 905.86 | 1460.48 | 1507.68 | 1406.73 |
| Aldose reductase | ILNK | 3059.4 | 3270.14 | 3615.93 | 4312.52 |
| Aldose reductase | ILNK | 1259.27 | 1224.83 | 1231.17 | 1605.55 |
| Aldose reductase | ILNK | 1325.13 | 782.29 | 1817.38 | 2421.19 |
| Aldose reductase | ILNK | 3077.34 | 3518.82 | 4227.04 | 4991.5 |
| Aldose reductase | ILNK | 2975.59 | 3251.68 | 4836.32 | 5153.56 |
| Aldose reductase | ILNK | 2814.58 | 2350.52 | 3781.49 | 3872.46 |
| Aldose reductase | ILNK | 2417.43 | 3184.19 | 1443.74 | 1517.98 |
| Aldose reductase | ILNK | 5458.27 | 8180.95 | 5991.74 | 5731.38 |
| Aldose reductase | ILNK | 2618.42 | 2689.07 | 1529.65 | 1972.05 |
| Aldose reductase | ILNK | 1264.79 | 1317.9 | 1128.14 | 873.49 |
| Aldose reductase | ILNK | 12239 | 11238.33 | 15004.76 | 17913 |
| Aldose reductase | ILNK | 2356.27 | 2843.71 | 1808.85 | 1955.98 |
| Aldose reductase | ILNK | 4307.1 | 5106.36 | 6027.83 | 7668.98 |
| Aldose reductase | ILNK | 3115.72 | 4088.26 | 4055.47 | 4179.6 |
| Aldose reductase | ILNK | 1621.83 | 2851.96 | 1751.8 | 2219.03 |
| Aldose reductase | LIQYCQSK | 4127.02 | 4280.17 | 2557.79 | 3110.58 |
| Aldose reductase | LIQYCQSK | 7096.8 | 6617.34 | 5313.98 | 6274.65 |
| Aldose reductase | LIQYCQSK | 2111.52 | 2449.75 | 2034.25 | 1844.95 |
| Aldose reductase | LIQYCQSK | 2166.32 | 2674.31 | 3012.11 | 3190.32 |
| Aldose reductase | LIRF | 611.59 | 533.85 | 711.67 | 1287.87 |
| Aldose reductase | LLLNNGAK | 4885.17 | 4696.27 | 2014.92 | 3011.21 |
| Aldose reductase | LLLNNGAK | 1925.06 | 2573.87 | 1737.24 | 2081.75 |

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|---|---|---|---|---|---|
| Aldose reductase | LLLNNGAK | 10831.74 | 9847.43 | 8701.19 | 6678.52 |
| Aldose reductase | LLLNNGAK | 13577.88 | 15130.07 | 6463.88 | 9096.93 |
| Aldose reductase | LLLNNGAK | 10855.14 | 11790.64 | 7275.73 | 8830.18 |
| Aldose reductase | LLLNNGAK | 10831.74 | 9847.43 | 8701.19 | 6678.52 |
| Aldose reductase | LLLNNGAK | 10855.14 | 11790.64 | 7275.73 | 8830.18 |
| Aldose reductase | LLLNNGAK | 4424.17 | 4071.53 | 5726.02 | 5180.4 |
| Aldose reductase | LLLNNGAK | 6011.16 | 7173.67 | 8421.37 | 9444.99 |
| Aldose reductase | LLLNNGAK | 6011.16 | 7173.67 | 8421.37 | 9444.99 |
| Aldose reductase | LLLNNGAK | 13577.88 | 15130.07 | 6463.88 | 9096.93 |
| Aldose reductase | LLLNNGAK | 4885.17 | 4696.27 | 2014.92 | 3011.21 |
| Aldose reductase | LLLNNGAK | 4424.17 | 4071.53 | 5726.02 | 5180.4 |
| Aldose reductase | LLLNNGAK | 3085.24 | 3163.42 | 1991.82 | 2911.01 |
| Aldose reductase | LSDLK | 1103.46 | 1300.11 | 1588.59 | 863.17 |
| Aldose reductase | LSDLK | 1090.73 | 1281.11 | 2415.67 | 2601.54 |
| Aldose reductase | LSDLK | 1116.61 | 1064.15 | 1511.15 | 2352 |
| Aldose reductase | LSDLK | 16862.64 | 17198.44 | 38064.49 | 49856.14 |
| Aldose reductase | LTQEK | 1360.56 | 1537.25 | 1468.89 | 1957.78 |
| Aldose reductase | LWCTYHEK | 1200.12 | 1324.56 | 1089.11 | 1907.21 |
| Aldose reductase | LWCTYHEK | 207.13 | 174.64 | 176.14 | 183.87 |
| Aldose reductase | MPILGLGTWK | 1269.72 | 1256.54 | 741.35 | 1045.9 |
| Aldose reductase | MPILGLGTWK | 205.58 | 114.81 | 109.61 | 271.94 |
| Aldose reductase | MPILGLGTWK | 356.82 | 172.95 | 136.85 | 194.84 |
| Aldose reductase | MPILGLGTWK | 538.01 | 462.96 | 339.34 | 545.61 |
| Aldose reductase | MPILGLGTWK | 330.92 | 497.76 | 334.23 | 482.38 |
| Aldose reductase | NLVVIPK | 2583.38 | 2426.91 | 2126.69 | 2172.01 |
| Aldose reductase | NLVVIPK | 2992.48 | 3817.36 | 2376.19 | 2548.81 |
| Aldose reductase | NLVVIPK | 15453.47 | 17804.41 | 9370.04 | 12770.19 |
| Aldose reductase | NLVVIPK | 958.61 | 1036.46 | 1279.04 | 974.54 |
| Aldose reductase | NLVVIPK | 2452.83 | 3090.94 | 2628.91 | 2329.32 |
| Aldose reductase | NLVVIPK | 1357.04 | 1246.16 | 1466.47 | 1474.88 |
| Aldose reductase | NLVVIPK | 2124.11 | 1844.26 | 1195.89 | 2037.21 |
| Aldose reductase | NLVVIPK | 877.5 | 1070.71 | 1105.33 | 936.45 |
| Aldose reductase | NLVVIPK | 2122.53 | 1788.1 | 2118.33 | 2542.44 |
| Aldose reductase | NLVVIPK | 1400.21 | 1129.87 | 1422.59 | 859.33 |
| Aldose reductase | NLVVIPK | 1061.06 | 808.25 | 969.2 | 1035.39 |
| Aldose reductase | NLVVIPK | 1773.88 | 2191.01 | 1922.53 | 2454.01 |
| Aldose reductase | NLVVIPK | 2257.54 | 1746.9 | 1693.53 | 2002.6 |
| Aldose reductase | NLVVIPK | 509.94 | 470.25 | 347.53 | 261.49 |
| Aldose reductase | NLVVIPK | 764.33 | 974.75 | 1426.44 | 685.33 |
| Aldose reductase | NLVVIPK | 561.04 | 527.59 | 408.81 | 632.12 |
| Aldose reductase | NLVVIPK | 482.34 | 643.48 | 336.6 | 262.81 |
| Aldose reductase | NLVVIPK | 797.01 | 938.33 | 502.19 | 356.76 |
| Aldose reductase | NLVVIPK | 535.33 | 515 | 647.02 | 455.15 |
| Aldose reductase | NLVVIPK | 414.56 | 319.32 | 556.69 | 381.79 |
| Aldose reductase | NLVVIPK | 624.96 | 382.61 | 484.58 | 307.05 |
| Aldose reductase | NLVVIPK | 2858.35 | 3452.52 | 2085.95 | 2551.96 |
| Aldose reductase | SPPGQVTEAVK | 6384.36 | 7111.46 | 3215.75 | 4026.22 |
| Aldose reductase | SPPGQVTEAVK | 6253.69 | 7467.74 | 4527.93 | 4750.72 |
| Aldose reductase | SPPGQVTEAVK | 2940.58 | 3200.32 | 2452.15 | 2787.83 |
| Aldose reductase | SPPGQVTEAVK | 6777.65 | 6977.98 | 6090.11 | 5667.92 |
| Aldose reductase | SPPGQVTEAVK | 8406.69 | 8266.97 | 4707.12 | 5845.68 |
| Aldose reductase | SPPGQVTEAVK | 5152.64 | 5504.63 | 5940.16 | 6750.85 |
| Aldose reductase | SPPGQVTEAVK | 5871.04 | 6442.85 | 5353.13 | 6667.23 |
| Aldose reductase | SPPGQVTEAVK | 1318.27 | 1247.58 | 2176.69 | 1782.42 |
| Aldose reductase | SPPGQVTEAVK | 1707.7 | 1921.22 | 1734.26 | 2893.26 |
| Aldose reductase | SPPGQVTEAVK | 1438.88 | 1459.09 | 2069.76 | 2200.44 |
| Aldose reductase | TLSDLK | 986.02 | 881.18 | 1040.6 | 1190.56 |
| Aldose reductase | TLSDLK | 1928.35 | 2036.58 | 2718.97 | 2882.09 |
| Aldose reductase | TTAQVLIR | 2177.85 | 2599.23 | 3067.19 | 3236.72 |
| Aldose reductase | TTAQVLIR | 12169.03 | 12193.54 | 7902.12 | 10352.37 |
| Aldose reductase | TTAQVLIR | 2127.92 | 2106.74 | 2452.97 | 2388.72 |
| Aldose reductase | TTAQVLIR | 3432.03 | 3050.3 | 1901.98 | 2612.74 |
| Aldose reductase | TTAQVLIR | 2576.36 | 2162.79 | 2664.58 | 3117.97 |
| Aldose reductase | TTAQVLIR | 1819.79 | 1379.08 | 2078.23 | 2729.94 |

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|---|---|---|---|---|---|
| Aldose reductase | TTAQVLIR | 1037.16 | 1360.65 | 2081.81 | 2115.97 |
| Aldose reductase | VAIDVGYR | 14168.46 | 14653.9 | 14769.45 | 14927.15 |
| Aldose reductase | VAIDVGYR | 2977.44 | 2005.82 | 3215.16 | 4275.66 |
| Aldose reductase | VAIDVGYR | 43109.25 | 43025.74 | 23501.78 | 27315.28 |
| Aldose reductase | VAIDVGYR | 11054.42 | 9442.27 | 12289.48 | 14939.11 |
| Aldose reductase | VCALLSC | 383.9 | 369.37 | 746.71 | 139.75 |
| Aldose reductase | VCALLSCTSHK | 1057.13 | 877.19 | 1296.7 | 645.04 |
| Aldose reductase | VCALLSCTSHK | 1612.32 | 1344.06 | 2283.98 | 2517.05 |
| Aldose reductase | VVIPK | 4659.01 | 6083.08 | 4294.28 | 5569.28 |
| Aldose reductase | VVIPK | 6031.82 | 7047.29 | 6991.05 | 8216.71 |
| Aldose reductase | VVIPK | 3661.58 | 3137.71 | 4396.13 | 4941.47 |
| Aldose reductase | VVIPK | 10341.22 | 8947.54 | 10174.57 | 11018.72 |
| Aldose reductase | VVIPK | 9190.29 | 9678.51 | 8977.17 | 11470.38 |
| Aldose reductase | VVIPK | 3186.44 | 2739.64 | 3382.57 | 4214.1 |
| Surfeit locus protein 2 | QGVEYVPACLVHR | 512.89 | 497.89 | 831.14 | 1076.54 |
| Surfeit locus protein 2 | LPELQVYTR | 435.35 | 392.81 | 674.96 | 647.33 |
| Surfeit locus protein 2 | LGSLK | 6356.18 | 7980.2 | 3642.09 | 3873.59 |
| Surfeit locus protein 2 | LGSLK | 1023.54 | 1004.19 | 2424.74 | 2389.86 |
| Surfeit locus protein 2 | LGSLK | 6682.11 | 8544.92 | 2065.25 | 4492.65 |
| Surfeit locus protein 2 | LGSLK | 6212.44 | 5798.33 | 2687.24 | 3461.96 |
| Surfeit locus protein 2 | LGSLK | 3330.6 | 3497.26 | 5748.44 | 6514.95 |
| Surfeit locus protein 2 | LGSLK | 1080.35 | 1136.45 | 2269.27 | 1460.74 |
| Surfeit locus protein 2 | LPGDVRAFLR | 1222.7 | 689.24 | 1317.26 | 1974.84 |
| Surfeit locus protein 2 | QGVEYVPACLVHR | 644.26 | 178.26 | 310.14 | 393.96 |
| Surfeit locus protein 2 | QGVEYVPACLVHR | 676.74 | 266.94 | 910.72 | 515.89 |
| Surfeit locus protein 2 | QLGSLK | 5145.29 | 2614.06 | 8745.64 | 4022.5 |
| Surfeit locus protein 2 | RAFLR | 2273.81 | 1735.66 | 1870.69 | 2133.95 |
| Serine/threonine-protein kinase MARK2 | NSATSADEQPHIGNYR | 89 | 143.54 | 233.01 | 225.01 |
| Serine/threonine-protein kinase MARK2 | TTPTPSTNSVLSTSTNR | 357.19 | 454.87 | 444.58 | 506.77 |
| Serine/threonine-protein kinase MARK2 | VPVASPSAHNISSSGGAPDR | 100.62 | 271.33 | 251.65 | 475.47 |
| Serine/threonine-protein kinase MARK2 | EEIQDSLVGQR | 127.28 | 190.71 | 312.22 | 344.35 |
| Serine/threonine-protein kinase MARK2 | VPASPLPGLER | 381.95 | 562.25 | 680.54 | 573.75 |
| Serine/threonine-protein kinase MARK2 | IANELKL | 1763.96 | 1043.96 | 1201.19 | 1227.92 |
| Serine/threonine-protein kinase MARK2 | IPFYMSTDCENLLK | 332.38 | 353.31 | 453.35 | 361.57 |
| Serine/threonine-protein kinase MARK2 | FLILNPSK | 180.02 | 87.01 | 142.65 | 198.7 |
| Serine/threonine-protein kinase MARK2 | EEIQDSLVGQR | 204.85 | 186.92 | 215.27 | 142.23 |
| Serine/threonine-protein kinase MARK2 | ENLLK | 999.94 | 888.79 | 1889.7 | 2038.79 |
| Serine/threonine-protein kinase MARK2 | ENLLK | 1203 | 720.98 | 1415.15 | 2014.67 |
| Serine/threonine-protein kinase MARK2 | ENLLK | 380.23 | 731.62 | 446.44 | 716.79 |
| Serine/threonine-protein kinase MARK2 | EVAVK | 541.46 | 973.28 | 1092.56 | 951.76 |
| Serine/threonine-protein kinase MARK2 | IANELKL | 1981.46 | 1469.88 | 2047.41 | 2623.95 |
| Serine/threonine-protein kinase MARK2 | IANELKL | 1774.55 | 1805.83 | 2516.73 | 2219.34 |
| Serine/threonine-protein kinase MARK2 | IANELKL | 30848.87 | 35282.73 | 2264.81 | 3591.41 |
| Serine/threonine-protein kinase MARK2 | IANELKL | 21733.49 | 23202.9 | 1428.84 | 2562.22 |
| Serine/threonine-protein kinase MARK2 | IANELKL | 47661.21 | 49897.16 | 786.09 | 2683.3 |
| Serine/threonine-protein kinase MARK2 | IANELKL | 2665.49 | 2718.95 | 3176.73 | 2726.96 |
| Serine/threonine-protein kinase MARK2 | IANELKL | 3322.55 | 3228.11 | 953.92 | 719.21 |
| Serine/threonine-protein kinase MARK2 | IANELKL | 14520.77 | 17400.01 | 1835.78 | 2128.39 |
| Serine/threonine-protein kinase MARK2 | IANELKL | 2582.63 | 2075.33 | 1276.81 | 1927.3 |
| Serine/threonine-protein kinase MARK2 | IANELKL | 19547.32 | 19298.13 | 634.25 | 2656.79 |
| Serine/threonine-protein kinase MARK2 | IANELKL | 31566.22 | 33132.98 | 1671 | 3414.74 |
| Serine/threonine-protein kinase MARK2 | IANELKL | 10562.66 | 12602.16 | 3522.41 | 5318.37 |
| Serine/threonine-protein kinase MARK2 | IANELKL | 1124 | 972.62 | 745.74 | 797.41 |
| Serine/threonine-protein kinase MARK2 | IANELKL | 23795.87 | 26252.41 | 1634.26 | 3374.62 |
| Serine/threonine-protein kinase MARK2 | IANELKL | 2331.47 | 1783.78 | 1087.49 | 1328.42 |
| Serine/threonine-protein kinase MARK2 | IANELKL | 2463.29 | 1951.25 | 671.24 | 987.84 |
| Serine/threonine-protein kinase MARK2 | IANELKL | 1438.56 | 1384.45 | 1454.58 | 758.28 |
| Serine/threonine-protein kinase MARK2 | IFSK | 3056.35 | 3570.66 | 4399.12 | 4841.04 |
| Serine/threonine-protein kinase MARK2 | IFSK | 1389.34 | 1672.03 | 2302.68 | 2188.84 |
| Serine/threonine-protein kinase MARK2 | IIDK | 1325.13 | 782.29 | 1817.38 | 2421.19 |
| Serine/threonine-protein kinase MARK2 | IIDK | 1259.27 | 1224.83 | 1231.17 | 1605.55 |
| Serine/threonine-protein kinase MARK2 | IIDK | 11494.35 | 11829.41 | 19877.02 | 24045.93 |
| Serine/threonine-protein kinase MARK2 | IIDK | 8107.16 | 8072.27 | 13308.71 | 15925.9 |
| Serine/threonine-protein kinase MARK2 | IIDK | 1686.04 | 2252.31 | 2137.37 | 2898.31 |

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|---|---|---|---|---|---|
| Serine/threonine-protein kinase MARK2 | IIDK | 1799.72 | 1871.91 | 3038.68 | 3494.33 |
| Serine/threonine-protein kinase MARK2 | IIDK | 2542.42 | 2325.42 | 3467.44 | 4284.44 |
| Serine/threonine-protein kinase MARK2 | IIDK | 2044.79 | 2765.98 | 3071.91 | 3593.15 |
| Serine/threonine-protein kinase MARK2 | IIDK | 11419.16 | 12769 | 18247.56 | 23009.46 |
| Serine/threonine-protein kinase MARK2 | IIDK | 4581.13 | 5798.65 | 7107.07 | 10954.17 |
| Serine/threonine-protein kinase MARK2 | IIDK | 1817.73 | 1794.65 | 2751.75 | 3695.78 |
| Serine/threonine-protein kinase MARK2 | IIDK | 6734.04 | 6925.33 | 10184.37 | 13283.95 |
| Serine/threonine-protein kinase MARK2 | IIDK | 2816.96 | 2116 | 3299.59 | 5206.11 |
| Serine/threonine-protein kinase MARK2 | IIDK | 6381.53 | 5263.29 | 12843.03 | 15057.89 |
| Serine/threonine-protein kinase MARK2 | IIDK | 1634.62 | 1694.21 | 1902.07 | 2653.86 |
| Serine/threonine-protein kinase MARK2 | IIDK | 2610.13 | 3614.15 | 4202.4 | 5576.11 |
| Serine/threonine-protein kinase MARK2 | IIDK | 1520.78 | 1558.44 | 3184.54 | 2618.89 |
| Serine/threonine-protein kinase MARK2 | IIDK | 8800.84 | 9644.57 | 14104.83 | 17354.68 |
| Serine/threonine-protein kinase MARK2 | IIDK | 994.06 | 1469.88 | 1517.2 | 2486.21 |
| Serine/threonine-protein kinase MARK2 | ILTGK | 1237.32 | 946.94 | 1760.25 | 1809.14 |
| Serine/threonine-protein kinase MARK2 | ITLK | 1465.44 | 1175.18 | 2133.76 | 2134.03 |
| Serine/threonine-protein kinase MARK2 | ITLK | 2032.65 | 1625.52 | 2511.72 | 3093.68 |
| Serine/threonine-protein kinase MARK2 | ITLK | 6851.05 | 8875.36 | 12546.63 | 18495.69 |
| Serine/threonine-protein kinase MARK2 | ITLK | 9475.64 | 11060.57 | 17223.33 | 22883.07 |
| Serine/threonine-protein kinase MARK2 | ITLK | 11098.45 | 12432.88 | 20943.33 | 25785.42 |
| Serine/threonine-protein kinase MARK2 | ITLK | 2987.22 | 3060.11 | 4110.36 | 4527.78 |
| Serine/threonine-protein kinase MARK2 | ITLK | 8161.22 | 8475.75 | 11768.29 | 12932.92 |
| Serine/threonine-protein kinase MARK2 | ITLK | 3087.61 | 3461.58 | 4680.58 | 6551.89 |
| Serine/threonine-protein kinase MARK2 | ITLK | 5883.14 | 6843.59 | 12399.68 | 15763.23 |
| Serine/threonine-protein kinase MARK2 | ITLK | 6196.24 | 6974.04 | 13256.44 | 14651.59 |
| Serine/threonine-protein kinase MARK2 | ITLK | 8833.79 | 6920.92 | 9303.18 | 12602.44 |
| Serine/threonine-protein kinase MARK2 | ITLK | 10036.18 | 11531.95 | 17595.63 | 21037.98 |
| Serine/threonine-protein kinase MARK2 | ITLK | 1293.32 | 2009.6 | 2763.76 | 4385.45 |
| Serine/threonine-protein kinase MARK2 | ITLK | 5768.95 | 4827.06 | 8848.78 | 10292.34 |
| Serine/threonine-protein kinase MARK2 | ITLK | 5226.47 | 6720.84 | 6463.66 | 9144.31 |
| Serine/threonine-protein kinase MARK2 | ITLK | 5559.77 | 6026.14 | 8012.02 | 9833.91 |
| Serine/threonine-protein kinase MARK2 | ITLK | 11357.95 | 13390.3 | 20715.65 | 25330.2 |
| Serine/threonine-protein kinase MARK2 | ITLK | 3511.51 | 3389.71 | 4235.7 | 6499.2 |
| Serine/threonine-protein kinase MARK2 | ITLK | 2408.07 | 2513.67 | 2679.12 | 3761.43 |
| Serine/threonine-protein kinase MARK2 | ITLK | 1554.97 | 1584.93 | 1376.55 | 1981.94 |
| Serine/threonine-protein kinase MARK2 | ITLK | 6275.11 | 6415.87 | 6323.86 | 7462.86 |
| Serine/threonine-protein kinase MARK2 | ITLK | 2869 | 2293.12 | 3549.31 | 5310.84 |
| Serine/threonine-protein kinase MARK2 | ITLK | 1402.72 | 2052.61 | 2469.56 | 3793.38 |
| Serine/threonine-protein kinase MARK2 | ITLK | 3464.79 | 3962.55 | 5377.96 | 6842.07 |
| Serine/threonine-protein kinase MARK2 | ITLK | 9629.82 | 11573.31 | 16506.83 | 20170.67 |
| Serine/threonine-protein kinase MARK2 | ITLK | 2220.2 | 2883.35 | 2155.12 | 3678.62 |
| Serine/threonine-protein kinase MARK2 | IVKL | 1071.45 | 1590.3 | 2510.33 | 3331.23 |
| Serine/threonine-protein kinase MARK2 | IVKL | 2944.6 | 2377.74 | 4777.68 | 5411.7 |
| Serine/threonine-protein kinase MARK2 | IVKL | 2298.42 | 2602.15 | 3385.07 | 5172.57 |
| Serine/threonine-protein kinase MARK2 | IVKL | 3592.95 | 2897 | 5810.44 | 6800.76 |
| Serine/threonine-protein kinase MARK2 | LEQIMK | 999.93 | 1315.06 | 1228.43 | 1775.26 |
| Serine/threonine-protein kinase MARK2 | LEQIMK | 662.14 | 752.56 | 398.88 | 515.18 |
| Serine/threonine-protein kinase MARK2 | NIVK | 127.27 | 191.64 | 266.02 | 165.17 |
| Serine/threonine-protein kinase MARK2 | NLLK | 540.63 | 204.34 | 676.13 | 887.3 |
| Serine/threonine-protein kinase MARK2 | NLLK | 359.27 | 249.9 | 363.8 | 1049.81 |
| Serine/threonine-protein kinase MARK2 | NLLK | 202.84 | 385.47 | 613.68 | 578.56 |
| Serine/threonine-protein kinase MARK2 | NSATSADEQPHIGNYR | 192.18 | 162.34 | 201.21 | 233.73 |
| Serine/threonine-protein kinase MARK2 | NSATSADEQPHIGNYR | 167.4 | 57.18 | 387.47 | 191.88 |
| Serine/threonine-protein kinase MARK2 | QNLK | 1331.98 | 1275.66 | 2386.22 | 2606.35 |
| Serine/threonine-protein kinase MARK2 | QNLK | 1114.11 | 1205 | 1892.83 | 2006.06 |
| Serine/threonine-protein kinase MARK2 | TTPTPSTNSVLSTSTNR | 4253.4 | 4879.22 | 6556.69 | 7601.61 |
| Serine/threonine-protein kinase MARK2 | TTPTPSTNSVLSTSTNR | 301.64 | 837.07 | 677.56 | 635.74 |
| Serine/threonine-protein kinase MARK2 | VPASPLPGLER | 409.18 | 425.28 | 388.06 | 940.8 |
| Serine/threonine-protein kinase MARK2 | VPASPLPGLER | 544.04 | 612.16 | 809.13 | 925.81 |
| Transmembrane and ubiquitin-like domain-containing protein 1 | FLNDSEQVAR | 763.65 | 723.53 | 983.93 | 1106.67 |
| Transmembrane and ubiquitin-like domain-containing protein 1 | FLNDSEQVAR | 823.35 | 1207.6 | 1180.97 | 1882.15 |
| Transmembrane and ubiquitin-like domain-containing protein 1 | FLNDSEQVAR | 462.44 | 268.87 | 323.92 | 616.75 |
| Transmembrane and ubiquitin-like domain-containing protein 1 | IGSLK | 6356.18 | 7980.2 | 3642.09 | 3873.59 |

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|---|---|---|---|---|---|
| Transmembrane and ubiquitin-like domain-containing protein 1 | IGSLK | 6682.11 | 8544.92 | 2065.25 | 4492.65 |
| Transmembrane and ubiquitin-like domain-containing protein 1 | IGSLK | 1023.54 | 1004.19 | 2424.74 | 2389.86 |
| Transmembrane and ubiquitin-like domain-containing protein 1 | IGSLK | 7326.05 | 8542.57 | 9555.7 | 11849.41 |
| Transmembrane and ubiquitin-like domain-containing protein 1 | IGSLK | 6212.44 | 5798.33 | 2687.24 | 3461.96 |
| Transmembrane and ubiquitin-like domain-containing protein 1 | IGSLK | 4918.09 | 6230.62 | 3546.17 | 4981.69 |
| Transmembrane and ubiquitin-like domain-containing protein 1 | IGSLK | 3330.6 | 3497.26 | 5748.44 | 6514.95 |
| Transmembrane and ubiquitin-like domain-containing protein 1 | IGSLK | 1080.35 | 1136.45 | 2269.27 | 1460.74 |
| Transmembrane and ubiquitin-like domain-containing protein 1 | LRLK | 3814.3 | 3262.06 | 4759.66 | 4438.43 |
| Transmembrane and ubiquitin-like domain-containing protein 1 | VTVLF | 152.87 | 109.27 | 98.32 | 128.99 |
| Hypoxia-inducible factor 1-alpha inhibitor | EEAGALGPAWDESQLR | 335.22 | 72.92 | 270.65 | 243.55 |
| Hypoxia-inducible factor 1-alpha inhibitor | AATAAEAVASGSGEPR | 279.14 | 506.66 | 722.06 | 640.53 |
| Hypoxia-inducible factor 1-alpha inhibitor | AATAAEAVASGSGEPR | 818.62 | 504.9 | 693.37 | 1581.21 |
| Hypoxia-inducible factor 1-alpha inhibitor | AATAAEAVASGSGEPR | 759.12 | 958 | 1369.96 | 1024.76 |
| Hypoxia-inducible factor 1-alpha inhibitor | DFSV | 1502.4 | 1459.39 | 2566.55 | 3024.36 |
| Hypoxia-inducible factor 1-alpha inhibitor | EEAGALGPAWDESQLR | 413.34 | 546.27 | 770.65 | 855.92 |
| Hypoxia-inducible factor 1-alpha inhibitor | EFVEK | 1350.11 | 2569.58 | 812.22 | 1303.88 |
| Hypoxia-inducible factor 1-alpha inhibitor | EFVEK | 7972.18 | 8110.09 | 5336.64 | 7017.85 |
| Hypoxia-inducible factor 1-alpha inhibitor | EFVEK | 6530.19 | 7277.48 | 4787.9 | 5370.37 |
| Hypoxia-inducible factor 1-alpha inhibitor | FAQIK | 1904.53 | 1623.93 | 2315.05 | 1269.4 |
| Hypoxia-inducible factor 1-alpha inhibitor | FAQIK | 2591.63 | 2463.16 | 2750.06 | 2395.08 |
| Hypoxia-inducible factor 1-alpha inhibitor | FAQIK | 4575.5 | 3269.45 | 2721.44 | 3363.76 |
| Hypoxia-inducible factor 1-alpha inhibitor | FAQIK | 1894.75 | 1951.68 | 1244.07 | 1874.41 |
| Hypoxia-inducible factor 1-alpha inhibitor | NTMIK | 463.15 | 198.91 | 1228.71 | 141.37 |
| Vitronectin | GQYCYELDEK | 717.84 | 674.84 | 528.68 | 1101.98 |
| Vitronectin | AVRPGYPK | 596.89 | 390.26 | 900.61 | 952.03 |
| Vitronectin | ILAL | 196.22 | 188.4 | 226.96 | 250.42 |
| Vitronectin | ILAL | 75.78 | 172.69 | 115.6 | 69.95 |
| Vitronectin | VYFFK | 1130.71 | 1160.74 | 883.52 | 1099.53 |
| Vitronectin | VYFFK | 1462.06 | 870.29 | 898.42 | 940.1 |
| Vitronectin | VYFFK | 990.64 | 743.71 | 589.99 | 1003.86 |
| Vitronectin | VYFFK | 1010.29 | 717.9 | 624.52 | 554.94 |
| Vitronectin | VYFFK | 945.97 | 902.08 | 632.42 | 730.42 |
| Vitronectin | VYFFK | 332.92 | 299.67 | 551.33 | 251.11 |
| Vitronectin | VYFFK | 777.35 | 646 | 832.95 | 544.13 |
| Vitronectin | VYFFK | 848.72 | 616.21 | 662.19 | 636 |
| Vitronectin | VYFFK | 1109.94 | 1191.79 | 593.73 | 713.78 |
| All-trans retinoic acid-induced differentiation factor | VAFYCK | 1087.21 | 1096.96 | 1644.73 | 1245.52 |
| All-trans retinoic acid-induced differentiation factor | GDLANTFR | 2439.54 | 2596.04 | 3648.87 | 3974.72 |
| All-trans retinoic acid-induced differentiation factor | LGLDL | 460.61 | 449.76 | 1116.4 | 1020.61 |
| All-trans retinoic acid-induced differentiation factor | LLAL | 196.22 | 188.4 | 226.96 | 250.42 |
| All-trans retinoic acid-induced differentiation factor | LLAL | 75.78 | 172.69 | 115.6 | 69.95 |
| All-trans retinoic acid-induced differentiation factor | QNLSK | 1618.69 | 2523.3 | 1266.18 | 2347.16 |
| All-trans retinoic acid-induced differentiation factor | QNLSK | 7313.04 | 7380.36 | 3957.27 | 3509.56 |
| All-trans retinoic acid-induced differentiation factor | QNLSK | 231.49 | 107.54 | 214.75 | 323.87 |
| All-trans retinoic acid-induced differentiation factor | QNLSK | 1028.13 | 1720.45 | 1284.23 | 1423.38 |
| F-box only protein 9 | TDAILLGHYR | 1550.41 | 2035.56 | 2079.88 | 2600.87 |
| F-box only protein 9 | VFAVITK | 736.82 | 501.23 | 483.27 | 695.98 |
| F-box only protein 9 | AIKF | 2230.81 | 2047.23 | 2573.04 | 2653.27 |
| F-box only protein 9 | AVITK | 3009.15 | 4191.8 | 5547.77 | 5900.88 |
| F-box only protein 9 | AVITK | 4610.26 | 4941.44 | 6745.51 | 6877.07 |
| F-box only protein 9 | ELFLK | 1147.73 | 1181.67 | 1541 | 2287.84 |
| F-box only protein 9 | ELFLK | 255.87 | 252.53 | 612.43 | 432.7 |
| F-box only protein 9 | ELFLK | 6520.37 | 6439.62 | 685.95 | 1228.61 |
| F-box only protein 9 | ELFLK | 868.14 | 718.71 | 1265.36 | 1637.86 |
| F-box only protein 9 | ELFLK | 3981.09 | 3378.83 | 392.91 | 538.85 |
| F-box only protein 9 | ELFLK | 5703.03 | 5382.34 | 451.18 | 623.75 |
| F-box only protein 9 | ESVLK | 384.25 | 547.34 | 877.47 | 803.1 |
| F-box only protein 9 | ESVLK | 260.95 | 282.07 | 409.37 | 337.03 |
| F-box only protein 9 | FEIDK | 2432.72 | 3375.8 | 1696.48 | 2205.95 |
| F-box only protein 9 | IEFK | 5980.65 | 6890.07 | 700.28 | 851.97 |
| F-box only protein 9 | IEFK | 2365.31 | 3014.86 | 702.85 | 1203.49 |
| F-box only protein 9 | LFLK | 2800.73 | 2655.93 | 2713.72 | 2747.15 |

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|---|---|---|---|---|---|
| F-box only protein 9 | LFLK | 848.14 | 885.96 | 2426.69 | 2268.47 |
| F-box only protein 9 | LFLK | 1293.11 | 2456.52 | 2411.93 | 2123.8 |
| F-box only protein 9 | LFLK | 2470.97 | 2256.62 | 2983.58 | 3778.41 |
| F-box only protein 9 | LFLK | 1295.7 | 1136.43 | 2013.16 | 2203.91 |
| F-box only protein 9 | LFLK | 1376.94 | 1088.83 | 1995.35 | 2068.54 |
| F-box only protein 9 | LFLK | 3125.37 | 3879.87 | 3903.38 | 4277.33 |
| F-box only protein 9 | LFLK | 562.75 | 571.7 | 1039.53 | 1023.44 |
| F-box only protein 9 | LFLK | 1216.57 | 1507.36 | 1879.53 | 2265.18 |
| F-box only protein 9 | YEAIK | 1208.75 | 1429.12 | 2001.89 | 2221.1 |
| F-box only protein 9 | YIFR | 1666.34 | 2177.73 | 2122.15 | 2490.05 |
| Squalene synthase | ANSMGLFLQK | 696.56 | 542.7 | 1558.17 | 1430.33 |
| Squalene synthase | CLGHPEEFYNLVR | 359.08 | 268.47 | 722.4 | 553.67 |
| Squalene synthase | MDQDSLSSSLK | 1612.55 | 1747.28 | 3772.43 | 4898.22 |
| Squalene synthase | TQNLPNCQLISR | 458.16 | 691.82 | 1012.57 | 1460.86 |
| Squalene synthase | YQTVIADICR | 563.75 | 366.79 | 215.26 | 586.72 |
| Squalene synthase | FMESK | 1473.05 | 1806.05 | 2440.55 | 3131.28 |
| Squalene synthase | MEFVK | 1243.36 | 1094.87 | 2079.76 | 2187.62 |
| Squalene synthase | ANSMGLFLQK | 891.23 | 459.25 | 1994.34 | 2327.44 |
| Squalene synthase | ANSMGLFLQK | 824.32 | 793.28 | 1726.17 | 1763.98 |
| Squalene synthase | ANSMGLFLQK | 179.27 | 160.97 | 316.32 | 266.79 |
| Squalene synthase | ANSMGLFLQK | 623.36 | 222.23 | 764.68 | 968.58 |
| Squalene synthase | CLGHPEEFYNLVR | 385.41 | 220.28 | 456.74 | 310.91 |
| Squalene synthase | CLGHPEEFYNLVR | 446.28 | 270.02 | 325.96 | 548.73 |
| Squalene synthase | CLGHPEEFYNLVR | 571.43 | 459.16 | 617.39 | 942.65 |
| Squalene synthase | EFLDK | 29470.13 | 33626.17 | 1498.56 | 2512.54 |
| Squalene synthase | EFLDK | 7395.71 | 9212.98 | 1561.97 | 1459.32 |
| Squalene synthase | EFLDK | 1350.11 | 2569.58 | 812.22 | 1303.88 |
| Squalene synthase | EFLDK | 7015.5 | 9010.84 | 1252.65 | 1811.17 |
| Squalene synthase | EFVK | 708.78 | 612.34 | 781.34 | 623.17 |
| Squalene synthase | EFVK | 1101.33 | 977.95 | 1150.01 | 1409.18 |
| Squalene synthase | FLDK | 2467.9 | 2133.81 | 4495.56 | 5351.67 |
| Squalene synthase | FLDK | 1675.88 | 1128.61 | 2070.47 | 2141.71 |
| Squalene synthase | FLQK | 3312.82 | 3551.44 | 3186.68 | 3370.69 |
| Squalene synthase | FLQK | 2051.3 | 3399.92 | 2911.57 | 3980.78 |
| Squalene synthase | FLQK | 6492.49 | 5363.91 | 7352.81 | 7479.64 |
| Squalene synthase | FMESK | 1676.86 | 2414.6 | 2972.57 | 3210.72 |
| Squalene synthase | IGGK | 272.38 | 216.83 | 403.38 | 919.32 |
| Squalene synthase | IPDSDPSSSK | 961.3 | 1514.91 | 1005.22 | 1426.65 |
| Squalene synthase | ISVEK | 1540.16 | 1558.88 | 1655.49 | 2261.64 |
| Squalene synthase | LSSSLK | 6305.55 | 6918.32 | 9229.28 | 9757.53 |
| Squalene synthase | LSSSLK | 842.46 | 916.03 | 215.13 | 268.73 |
| Squalene synthase | LSSSLK | 2600.52 | 3180.77 | 3548.45 | 4035.74 |
| Squalene synthase | LSSSLK | 822.08 | 695.16 | 524.43 | 484.92 |
| Squalene synthase | LSSSLK | 3542.88 | 3375.58 | 564.06 | 463.31 |
| Squalene synthase | LSSSLK | 1303.2 | 927.49 | 1736.49 | 1706.18 |
| Squalene synthase | LSSSLK | 5904.56 | 5578.24 | 7309 | 9026.91 |
| Squalene synthase | MDQDSLSSSLK | 2132.65 | 1958.31 | 4459.03 | 3652.79 |
| Squalene synthase | TQNLPNCQLISR | 460.39 | 472.25 | 589.85 | 701.19 |
| Squalene synthase | TQNLPNCQLISR | 203.81 | 289.52 | 250.22 | 476.38 |
| Squalene synthase | TQNLPNCQLISR | 773.46 | 924.08 | 1080.76 | 1529.11 |
| Squalene synthase | TQNLPNCQLISR | 332.16 | 374.98 | 658.78 | 410.77 |
| Squalene synthase | VMPK | 1180.91 | 1413.31 | 1556.35 | 2003.9 |
| Squalene synthase | YLVLR | 2851.67 | 2196.8 | 2845.35 | 4536.69 |
| Squalene synthase | YQTVIADICR | 884.4 | 388.83 | 502.63 | 844.63 |
| Integrator complex subunit 10 | SLFETLPGR | 435.75 | 352.65 | 745.29 | 712.6 |
| Integrator complex subunit 10 | YIIEGLTEK | 2296.8 | 2017.11 | 3927.7 | 3760.85 |
| Integrator complex subunit 10 | SAQGDCEFLVQR | 410.23 | 321.33 | 473.39 | 682.83 |
| Integrator complex subunit 10 | EFLDK | 29470.13 | 33626.17 | 1498.56 | 2512.54 |
| Integrator complex subunit 10 | EFLDK | 7395.71 | 9212.98 | 1561.97 | 1459.32 |
| Integrator complex subunit 10 | EFLDK | 1350.11 | 2569.58 | 812.22 | 1303.88 |
| Integrator complex subunit 10 | EFLDK | 7015.5 | 9010.84 | 1252.65 | 1811.17 |
| Integrator complex subunit 10 | EIDR | 103.21 | 15.61 | 126.25 | 44.94 |
| Integrator complex subunit 10 | EMLLK | 693.2 | 768.54 | 983.92 | 629.55 |
| Integrator complex subunit 10 | EMLLK | 621.52 | 403.4 | 745.44 | 552.25 |

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|---|---|---|---|---|---|
| Integrator complex subunit 10 | FLDK | 2467.9 | 2133.81 | 4495.56 | 5351.67 |
| Integrator complex subunit 10 | FLDK | 1675.88 | 1128.61 | 2070.47 | 2141.71 |
| Integrator complex subunit 10 | LFLK | 2800.73 | 2655.93 | 2713.72 | 2747.15 |
| Integrator complex subunit 10 | LFLK | 848.14 | 885.96 | 2426.69 | 2268.47 |
| Integrator complex subunit 10 | LFLK | 1293.11 | 2456.52 | 2411.93 | 2123.8 |
| Integrator complex subunit 10 | LFLK | 2470.97 | 2256.62 | 2983.58 | 3778.41 |
| Integrator complex subunit 10 | LFLK | 1295.7 | 1136.43 | 2013.16 | 2203.91 |
| Integrator complex subunit 10 | LFLK | 1376.94 | 1088.83 | 1995.35 | 2068.54 |
| Integrator complex subunit 10 | LFLK | 3125.37 | 3879.87 | 3903.38 | 4277.33 |
| Integrator complex subunit 10 | LFLK | 562.75 | 571.7 | 1039.53 | 1023.44 |
| Integrator complex subunit 10 | LFLK | 1216.57 | 1507.36 | 1879.53 | 2265.18 |
| Integrator complex subunit 10 | LLLLLR | 451.94 | 349.07 | 384.46 | 330.16 |
| Integrator complex subunit 10 | LLLLLR | 229.82 | 273.13 | 273.95 | 291.83 |
| Integrator complex subunit 10 | LLLLLR | 278.69 | 338.3 | 328.78 | 362.21 |
| Integrator complex subunit 10 | LLLLLR | 200.42 | 199.21 | 155.7 | 240.44 |
| Integrator complex subunit 10 | LLLLR | 1750.41 | 1105.72 | 1972.26 | 1170.05 |
| Integrator complex subunit 10 | LLLLR | 229.51 | 303.98 | 717.46 | 474.46 |
| Integrator complex subunit 10 | LLLLR | 1332.93 | 2564.35 | 5070.19 | 1069.01 |
| Integrator complex subunit 10 | LLLLR | 639 | 592 | 926.35 | 1025 |
| Integrator complex subunit 10 | LLLLR | 469.82 | 390.94 | 641.42 | 692.34 |
| Integrator complex subunit 10 | LLLLR | 562.7 | 682.61 | 659.6 | 1176.4 |
| Integrator complex subunit 10 | LLLR | 386.99 | 489.76 | 684.01 | 680.12 |
| Integrator complex subunit 10 | LLLR | 769.62 | 771.66 | 1081.49 | 1259.46 |
| Integrator complex subunit 10 | LLLR | 864.03 | 699.71 | 1475.57 | 835.82 |
| Integrator complex subunit 10 | LLLR | 912.1 | 950.18 | 1143.27 | 1280.65 |
| Integrator complex subunit 10 | LLLR | 556.67 | 959.36 | 927.48 | 1147.92 |
| Integrator complex subunit 10 | LLLR | 1415.65 | 1626.01 | 1823.04 | 1846.6 |
| Integrator complex subunit 10 | LLLR | 279.39 | 481.67 | 627.51 | 552.92 |
| Integrator complex subunit 10 | LLLR | 487.03 | 393.55 | 449.11 | 438.94 |
| Integrator complex subunit 10 | LLYK | 2343.22 | 3069.36 | 2768.3 | 3350.47 |
| Integrator complex subunit 10 | LLYK | 1494.13 | 1319.79 | 2002.86 | 1611.01 |
| Integrator complex subunit 10 | LLYK | 1695.62 | 1412.87 | 1872.62 | 2723.39 |
| Integrator complex subunit 10 | LWLR | 1901.95 | 2198.09 | 3549.51 | 5049.93 |
| Integrator complex subunit 10 | MLIK | 3797.99 | 4660.04 | 5610.85 | 7416.45 |
| Integrator complex subunit 10 | MLIK | 1569.66 | 1197.98 | 2060.11 | 1919.83 |
| Integrator complex subunit 10 | MLLK | 3797.99 | 4660.04 | 5610.85 | 7416.45 |
| Integrator complex subunit 10 | MLLK | 1569.66 | 1197.98 | 2060.11 | 1919.83 |
| Integrator complex subunit 10 | MLLLL | 105.71 | 87.7 | 114.57 | 102.15 |
| Integrator complex subunit 10 | MLLLL | 138.51 | 144.93 | 195.45 | 216.9 |
| Integrator complex subunit 10 | MLLLL | 73.75 | 53.94 | 93.46 | 92.57 |
| Integrator complex subunit 10 | NLFLK | 587.9 | 533.46 | 764.83 | 386.79 |
| Integrator complex subunit 10 | NLFLK | 947.18 | 994.66 | 1633.22 | 1815.68 |
| Integrator complex subunit 10 | SLFETLPGR | 206.4 | 33.96 | 117.01 | 303.29 |
| Integrator complex subunit 10 | SLFETLPGR | 435.81 | 346.85 | 393.53 | 674.16 |
| Integrator complex subunit 10 | YGDILHR | 358.42 | 333.41 | 916.52 | 1241.93 |
| Formin-like protein 2 | AQGPAIDLSSSK | 1202.46 | 986.4 | 1531.9 | 1183.92 |
| Formin-like protein 2 | QQQELIAELR | 435.6 | 368.35 | 607.75 | 505.88 |
| Formin-like protein 2 | GSNLPSPVGNSVSR | 1154.75 | 1444.79 | 1424.71 | 1994.72 |
| Formin-like protein 2 | IHELEK | 13613.97 | 13479.75 | 1746.26 | 2478.26 |
| Formin-like protein 2 | VTLLEANR | 1680.33 | 1539.99 | 2714.43 | 2957.36 |
| Formin-like protein 2 | IAQDAFDDVVK | 204.34 | 237.14 | 286.41 | 241.4 |
| Formin-like protein 2 | KWELICDQER | 789.28 | 1382.68 | 1049.18 | 1717.09 |
| Formin-like protein 2 | EFILNNEGK | 2178.01 | 2689.34 | 3875.14 | 4591.54 |
| Formin-like protein 2 | NLAITLR | 760.89 | 1740.5 | 2016.5 | 1406.46 |
| Formin-like protein 2 | AIHVFDLK | 587.81 | 542.27 | 1126.88 | 967.18 |
| Formin-like protein 2 | NPPHTYIQK | 749.71 | 717.6 | 1009.26 | 1170.93 |
| Formin-like protein 2 | FLPTENEVK | 1273.54 | 1091.62 | 1757.7 | 2256.4 |
| Formin-like protein 2 | QSTLEK | 1175.78 | 643.47 | 1519.32 | 579.02 |
| Formin-like protein 2 | TLKNSR | 359.28 | 248.78 | 419.13 | 750.29 |
| Formin-like protein 2 | VLLDVK | 2497.29 | 2422.19 | 3899.09 | 6358.26 |
| Formin-like protein 2 | ARLLR | 652.99 | 911.35 | 1673.27 | 1931.99 |
| Formin-like protein 2 | ARLLR | 1080.13 | 732.01 | 1638.98 | 1877.24 |
| Formin-like protein 2 | EIFK | 2341.82 | 4378.22 | 2760.69 | 5011.31 |
| Formin-like protein 2 | EIFK | 812.14 | 826.51 | 925.19 | 1053.71 |

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|---|---|---|---|---|---|
| Formin-like protein 2 | EIFK | 944.52 | 832.03 | 698.7 | 1348.21 |
| Formin-like protein 2 | EIFK | 613.05 | 814.67 | 804 | 1196.58 |
| Formin-like protein 2 | ELLAA | 180.45 | 257.22 | 444.12 | 348.36 |
| Formin-like protein 2 | FDLK | 1243.81 | 1369.26 | 1430.49 | 1988.22 |
| Formin-like protein 2 | GENPK | 921.58 | 652.16 | 1063.56 | 1202.54 |
| Formin-like protein 2 | GENPK | 1129.65 | 840.08 | 1217.73 | 1481.08 |
| Formin-like protein 2 | GLAAVK | 1596.32 | 1755.28 | 1095.8 | 1390.3 |
| Formin-like protein 2 | GSNLPSPVGNSVSR | 1004.97 | 1668.4 | 2241.9 | 2070.87 |
| Formin-like protein 2 | GSNLPSPVGNSVSR | 803.96 | 1846.91 | 1541.6 | 1717.31 |
| Formin-like protein 2 | IAELR | 3086.24 | 5085.77 | 6680.64 | 9480.31 |
| Formin-like protein 2 | IAELR | 4316.75 | 2982.25 | 7344.61 | 7849.54 |
| Formin-like protein 2 | IAELR | 2604.82 | 2223.75 | 4012.92 | 4068.83 |
| Formin-like protein 2 | IAELR | 912.31 | 1035.72 | 1378.93 | 1830.16 |
| Formin-like protein 2 | IHELEK | 16461.74 | 16593.67 | 1365.73 | 2398.48 |
| Formin-like protein 2 | IHELEK | 9411.09 | 10736.22 | 1536.96 | 1621.45 |
| Formin-like protein 2 | IHELEK | 16814.38 | 19732.11 | 1735.49 | 2350.08 |
| Formin-like protein 2 | IHELEK | 717.53 | 599.08 | 234.75 | 295.28 |
| Formin-like protein 2 | IHELEK | 16742.99 | 16253.36 | 2435.27 | 1810.95 |
| Formin-like protein 2 | IHELEK | 18432.73 | 17608.64 | 2497.19 | 2959.35 |
| Formin-like protein 2 | IHELEK | 1910.76 | 2497.88 | 2516.81 | 1712.13 |
| Formin-like protein 2 | IHELEK | 1728.3 | 2226.3 | 1513.86 | 984.89 |
| Formin-like protein 2 | ILAL | 196.22 | 188.4 | 226.96 | 250.42 |
| Formin-like protein 2 | ILAL | 75.78 | 172.69 | 115.6 | 69.95 |
| Formin-like protein 2 | IPQK | 730.39 | 1562.49 | 1678.65 | 3257.86 |
| Formin-like protein 2 | ITVLK | 967.35 | 810.9 | 490.09 | 723.21 |
| Formin-like protein 2 | IVELEK | 1002.8 | 1245.06 | 1755.47 | 2852.44 |
| Formin-like protein 2 | LDKL | 2055.16 | 1635.69 | 2617.23 | 3027.78 |
| Formin-like protein 2 | LDVK | 809.25 | 1005.58 | 960.41 | 1254.65 |
| Formin-like protein 2 | LDVK | 984.03 | 651.82 | 851.56 | 1355.47 |
| Formin-like protein 2 | LDVK | 1530.77 | 891.31 | 2692.25 | 3075.59 |
| Formin-like protein 2 | LLDTK | 2426.96 | 3200 | 4828.71 | 4852 |
| Formin-like protein 2 | LLDTK | 1161.53 | 1201.1 | 2124.68 | 2616.16 |
| Formin-like protein 2 | LLDVK | 1102.04 | 1121.04 | 877.82 | 1658.6 |
| Formin-like protein 2 | LNNEGK | 995.91 | 755.13 | 1335.55 | 1679.24 |
| Formin-like protein 2 | NTLLK | 502.26 | 271.51 | 1324.03 | 136.2 |
| Formin-like protein 2 | NTLLK | 785.69 | 460.72 | 1563.83 | 378.08 |
| Formin-like protein 2 | NTLLK | 899.48 | 388.99 | 1982.44 | 100.49 |
| Formin-like protein 2 | NTLLK | 2246.5 | 816.78 | 5723.81 | 368.79 |
| Formin-like protein 2 | NTLLK | 281 | 322.53 | 887.34 | 105.42 |
| Formin-like protein 2 | QQQELIAELR | 178.02 | 283.96 | 619.68 | 275.42 |
| Formin-like protein 2 | QQQELIAELR | 1622 | 1132.45 | 4205.73 | 2406.75 |
| Formin-like protein 2 | QQQELIAELR | 634.38 | 622.91 | 1116.39 | 498.22 |
| Formin-like protein 2 | QSTLEK | 847.84 | 596.6 | 1901.48 | 745.95 |
| Formin-like protein 2 | TLLK | 6196.24 | 6974.04 | 13256.44 | 14651.59 |
| Formin-like protein 2 | VELEK | 6326.73 | 6847.57 | 9406.85 | 9969.75 |
| Formin-like protein 2 | VELEK | 1301.43 | 889.66 | 2124.72 | 2193.09 |
| Formin-like protein 2 | VELEK | 1614.61 | 1863.07 | 2877.67 | 3387.75 |
| Formin-like protein 2 | VELEK | 537.08 | 874.14 | 1225.58 | 1270.01 |
| Formin-like protein 2 | VFDLK | 2338.99 | 1571.98 | 3080.12 | 2709.11 |
| Formin-like protein 2 | YIQK | 1033.73 | 1380.04 | 1879.71 | 2790.94 |
| Ras-related protein Rab-9A | DATNVAAAFEEAVR | 177.95 | 290.9 | 276.86 | 447.06 |
| Ras-related protein Rab-9A | QVSTEEAQAWCR | 1488.44 | 1243.26 | 1660.14 | 2486.7 |
| Ras-related protein Rab-9A | VILLGDGGVGK | 482.7 | 608.32 | 531.95 | 837.2 |
| Ras-related protein Rab-9A | SDHLIQTDTVNLHR | 1361.19 | 1262.12 | 1832.11 | 2133.78 |
| Ras-related protein Rab-9A | DNGDYPYFETSAK | 335.69 | 345.64 | 820.49 | 627.07 |
| Ras-related protein Rab-9A | VLATEDR | 740.87 | 420.36 | 2181.68 | 454.15 |
| Ras-related protein Rab-9A | DATNVAAAFEEAVRR | 230.23 | 232.67 | 412.55 | 374.46 |
| Ras-related protein Rab-9A | DATNVAAAFEEAVR | 914.37 | 726.35 | 1249.91 | 1136.12 |
| Ras-related protein Rab-9A | DATNVAAAFEEAVR | 193.12 | 68.86 | 354.14 | 344.05 |
| Ras-related protein Rab-9A | DATNVAAAFEEAVR | 257.14 | 126.7 | 449.71 | 182.46 |
| Ras-related protein Rab-9A | DATNVAAAFEEAVR | 230.23 | 232.67 | 412.55 | 374.46 |
| Ras-related protein Rab-9A | DATNVAAAFEEAVRR | 483.47 | 744.95 | 791.88 | 796.46 |
| Ras-related protein Rab-9A | DATNVAAAFEEAVRR | 280.4 | 381.99 | 501.72 | 694.11 |
| Ras-related protein Rab-9A | DNGDYPYFETSAK | 701.73 | 671.04 | 669.27 | 1046.92 |

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|---|---|---|---|---|---|
| Ras-related protein Rab-9A | DNGDYPYFETSAK | 385.73 | 188.56 | 747.78 | 1051.12 |
| Ras-related protein Rab-9A | DNGDYPYFETSAK | 152.87 | 215.65 | 261.29 | 269.59 |
| Ras-related protein Rab-9A | DNGDYPYFETSAK | 49.93 | 173.06 | 192.29 | 92.75 |
| Ras-related protein Rab-9A | DNGDYPYFETSAK | 49.93 | 173.06 | 192.29 | 92.75 |
| Ras-related protein Rab-9A | EFLNK | 29470.13 | 33626.17 | 1498.56 | 2512.54 |
| Ras-related protein Rab-9A | EFLNK | 8418.44 | 9978.23 | 3628.36 | 5543.91 |
| Ras-related protein Rab-9A | EFLNK | 3317.01 | 3562.82 | 1863.66 | 2212.89 |
| Ras-related protein Rab-9A | EFLNK | 7015.5 | 9010.84 | 1252.65 | 1811.17 |
| Ras-related protein Rab-9A | FLNK | 1734 | 1981.99 | 3684.87 | 4026.39 |
| Ras-related protein Rab-9A | ILLGD | 1243.43 | 1194.05 | 2279.76 | 3355.83 |
| Ras-related protein Rab-9A | QVSTEEAQAWCR | 1648.49 | 1601.11 | 2573.66 | 3755.69 |
| Ras-related protein Rab-9A | QVSTEEAQAWCR | 750.53 | 530.03 | 1295.6 | 1150.84 |
| Ras-related protein Rab-9A | QVSTEEAQAWCR | 737.56 | 641.56 | 1145.26 | 810.37 |
| Ras-related protein Rab-9A | QVSTEEAQAWCR | 176.63 | 421.67 | 195.8 | 295.37 |
| Ras-related protein Rab-9A | QVSTEEAQAWCR | 408.96 | 447.02 | 589.98 | 752.81 |
| Ras-related protein Rab-9A | QVSTEEAQAWCR | 231.3 | 126.41 | 558.43 | 460.45 |
| Ras-related protein Rab-9A | SDHLIQTDTVNLHR | 1051.07 | 1581.88 | 2044.26 | 2356.5 |
| Ras-related protein Rab-9A | SDHLIQTDTVNLHR | 1393.86 | 1012.62 | 2299.21 | 1835.75 |
| Ras-related protein Rab-9A | SDHLIQTDTVNLHR | 708.45 | 1176.42 | 2080.44 | 1790.98 |
| Ras-related protein Rab-9A | SDHLIQTDTVNLHR | 896.44 | 1540.11 | 2283.53 | 2430.9 |
| Ras-related protein Rab-9A | SLFK | 2176.43 | 1888 | 4372.49 | 4064.77 |
| Ras-related protein Rab-9A | SLFK | 1602.55 | 2203.52 | 2250.56 | 3383.6 |
| Ras-related protein Rab-9A | SLFK | 876.9 | 1342.5 | 1332.59 | 2049.06 |
| Ras-related protein Rab-9A | SLFK | 379.51 | 803.01 | 1066.55 | 1188.16 |
| Ras-related protein Rab-9A | SLFK | 1564.59 | 1379.73 | 2130.2 | 3378.26 |
| Ras-related protein Rab-9A | SLFK | 582.6 | 951.15 | 1398.38 | 1676.65 |
| Ras-related protein Rab-9A | SSLFK | 1141.35 | 1279.85 | 1866.96 | 1780.44 |
| Ras-related protein Rab-9A | VILLGDGGVGK | 714.67 | 668.98 | 936.6 | 1442.33 |
| Ras-related protein Rab-9A | VILLGDGGVGK | 480.55 | 395.11 | 555.28 | 831.03 |
| Ras-related protein Rab-9A | VILLGDGGVGK | 664.72 | 603.73 | 1102.85 | 1268.3 |
| Ras-related protein Rab-9A | VILLGDGGVGK | 757.96 | 647.45 | 1257.89 | 1548.21 |
| Ras-related protein Rab-9A | VILLGDGGVGK | 998.47 | 1140.47 | 1998.26 | 2248.94 |
| Acyl-protein thioesterase 1 | ASFPQGPIGGANR | 1170.14 | 1200.86 | 1413.49 | 2448.29 |
| Acyl-protein thioesterase 1 | TLVNPANVTFK | 1179.69 | 1533.87 | 1394.91 | 1016.16 |
| Acyl-protein thioesterase 1 | STPLPAIVPAAR | 491.89 | 444.41 | 468.71 | 570.1 |
| Acyl-protein thioesterase 1 | ALIDQEVKNGIPSNR | 1937.56 | 1871.33 | 3572.86 | 4250.75 |
| Acyl-protein thioesterase 1 | ASFPQGPIGGANR | 1149.07 | 836.15 | 968.8 | 1728.46 |
| Acyl-protein thioesterase 1 | ASFPQGPIGGANR | 1911.43 | 2218.65 | 3242.49 | 2732.96 |
| Acyl-protein thioesterase 1 | ASFPQGPIGGANR | 2527.39 | 2533.53 | 4291.53 | 4083.01 |
| Acyl-protein thioesterase 1 | AVIF | 438.29 | 421.77 | 774.37 | 921.2 |
| Acyl-protein thioesterase 1 | FIDK | 2467.9 | 2133.81 | 4495.56 | 5351.67 |
| Acyl-protein thioesterase 1 | FIDK | 1675.88 | 1128.61 | 2070.47 | 2141.71 |
| Acyl-protein thioesterase 1 | IDKL | 2055.16 | 1635.69 | 2617.23 | 3027.78 |
| Acyl-protein thioesterase 1 | LPLR | 640.2 | 366.14 | 1243.74 | 910.95 |
| Acyl-protein thioesterase 1 | LTVEK | 3245.52 | 4988.12 | 3905.94 | 6233.01 |
| Acyl-protein thioesterase 1 | LTVEK | 1566.15 | 1225.5 | 3317.83 | 2637.04 |
| Acyl-protein thioesterase 1 | LTVEK | 4152.7 | 4189.91 | 5386.15 | 7810.68 |
| Acyl-protein thioesterase 1 | LTVEK | 1494.4 | 1611.53 | 2729.44 | 3567.07 |
| Acyl-protein thioesterase 1 | LTVEK | 1278 | 1715.42 | 2266.08 | 2856.94 |
| Acyl-protein thioesterase 1 | NVTFK | 3043.9 | 3205.78 | 3877.43 | 4922.46 |
| Acyl-protein thioesterase 1 | QFIDK | 29470.13 | 33626.17 | 1498.56 | 2512.54 |
| Acyl-protein thioesterase 1 | QFIDK | 7015.5 | 9010.84 | 1252.65 | 1811.17 |
| Acyl-protein thioesterase 1 | STPLPAIVPAAR | 463.25 | 189.55 | 414.99 | 363.67 |
| Acyl-protein thioesterase 1 | STPLPAIVPAAR | 853.39 | 793.24 | 1727.87 | 1140.48 |
| Acyl-protein thioesterase 1 | STPLPAIVPAAR | 488.09 | 394.56 | 395.19 | 551.53 |
| WW domain-binding protein 11 | AQLSQYFDAVK | 569.35 | 451.79 | 617.55 | 670.84 |
| WW domain-binding protein 11 | ELTPLQAMMLR | 278.53 | 566.54 | 315.41 | 289.87 |
| WW domain-binding protein 11 | FMNPTDQAR | 899.46 | 922.74 | 1642.46 | 2124.94 |
| WW domain-binding protein 11 | RRDEDMLYSPELAQR | 512.96 | 384.17 | 1137.38 | 812.34 |
| WW domain-binding protein 11 | FVPTALR | 3407.89 | 3413.78 | 605.29 | 628.7 |
| WW domain-binding protein 11 | AVSILPLLGHGVPR | 231.22 | 134.83 | 142.52 | 133.69 |
| WW domain-binding protein 11 | SEDDSAVPLAK | 965.42 | 1320.22 | 1844.34 | 1604.32 |
| WW domain-binding protein 11 | EMEGLL | 128.29 | 91.33 | 118.26 | 148.43 |
| WW domain-binding protein 11 | ELTPLQAM | 250.18 | 176.83 | 335.69 | 332.07 |

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|---|---|---|---|---|---|
| WW domain-binding protein 11 | AFMK | 4525.53 | 4695.89 | 4415.49 | 6751.71 |
| WW domain-binding protein 11 | AFMK | 3007.55 | 3711.17 | 9382.64 | 10454.26 |
| WW domain-binding protein 11 | AQLSQYFDAVK | 634.91 | 676.88 | 678.77 | 193.16 |
| WW domain-binding protein 11 | AVSILPLLGHGVPR | 137.42 | 146.99 | 97.51 | 148.68 |
| WW domain-binding protein 11 | DAVK | 1441.21 | 2292.24 | 3984.99 | 3276.45 |
| WW domain-binding protein 11 | ELTPLQAMMLR | 193.77 | 110.8 | 192 | 220.09 |
| WW domain-binding protein 11 | ELTPLQAMMLR | 229.94 | 260.69 | 304.13 | 455.39 |
| WW domain-binding protein 11 | EMEGLL | 229.93 | 261.68 | 255.06 | 371.99 |
| WW domain-binding protein 11 | EMEGLL | 360.04 | 173.46 | 312.72 | 344.34 |
| WW domain-binding protein 11 | EMEGLL | 257.1 | 131.42 | 216.31 | 219.65 |
| WW domain-binding protein 11 | EMEGLL | 204.05 | 265.63 | 154.73 | 275.11 |
| WW domain-binding protein 11 | FMNPTDQAR | 229.44 | 310.29 | 405.24 | 381.74 |
| WW domain-binding protein 11 | FVPTALR | 2415.33 | 2327.54 | 211.1 | 683.57 |
| WW domain-binding protein 11 | FVPTALR | 2035.75 | 1957.82 | 370.45 | 410.41 |
| WW domain-binding protein 11 | FVPTALR | 2247.21 | 2660.94 | 3058.38 | 3106.15 |
| WW domain-binding protein 11 | FVPTALR | 2510.02 | 2440.5 | 286.83 | 490.34 |
| WW domain-binding protein 11 | FVPTALR | 13233.75 | 12852.85 | 2076.87 | 3223.95 |
| WW domain-binding protein 11 | FVPTALR | 3796.69 | 3086.41 | 534.56 | 495.4 |
| WW domain-binding protein 11 | FVPTALR | 1550.46 | 1818.06 | 2573.22 | 2475.31 |
| WW domain-binding protein 11 | FVPTALR | 3887.79 | 3980.04 | 1526.15 | 1975.23 |
| WW domain-binding protein 11 | FVPTALR | 4576.35 | 4248.86 | 1130.24 | 1445.56 |
| WW domain-binding protein 11 | FVPTALR | 4131.9 | 3797.86 | 1984.09 | 1821.54 |
| WW domain-binding protein 11 | LYEK | 708.12 | 1102.77 | 1629.39 | 2302.64 |
| WW domain-binding protein 11 | RRDEDMLYSPELAQR | 714.84 | 652 | 977.97 | 1138.3 |
| WW domain-binding protein 11 | VLKD | 1985.44 | 2459.42 | 2975.86 | 4539.97 |
| ADP-ribosylation factor-like protein 1 | AILVVFANK | 460.54 | 244.13 | 278.3 | 473.04 |
| ADP-ribosylation factor-like protein 1 | ILILGLDGAGK | 165.11 | 283.6 | 152.93 | 299.93 |
| ADP-ribosylation factor-like protein 1 | WQIFK | 900.25 | 844.23 | 1108.55 | 877.42 |
| ADP-ribosylation factor-like protein 1 | AILVVFANK | 384.61 | 299.03 | 393.59 | 280.27 |
| ADP-ribosylation factor-like protein 1 | AILVVFANK | 1010.18 | 90.34 | 126.61 | 225.34 |
| ADP-ribosylation factor-like protein 1 | GAGK | 216.55 | 307.68 | 954 | 707.01 |
| ADP-ribosylation factor-like protein 1 | IGISK | 6212.44 | 5798.33 | 2687.24 | 3461.96 |
| ADP-ribosylation factor-like protein 1 | IGISK | 6356.18 | 7980.2 | 3642.09 | 3873.59 |
| ADP-ribosylation factor-like protein 1 | IGISK | 4918.09 | 6230.62 | 3546.17 | 4981.69 |
| ADP-ribosylation factor-like protein 1 | IGISK | 6682.11 | 8544.92 | 2065.25 | 4492.65 |
| ADP-ribosylation factor-like protein 1 | IGISK | 7142.75 | 6971.16 | 3334.23 | 3816.36 |
| ADP-ribosylation factor-like protein 1 | IGISK | 983.21 | 946.4 | 1601.52 | 1150.15 |
| ADP-ribosylation factor-like protein 1 | IGISK | 2985.09 | 2632.98 | 3439.12 | 3614.87 |
| ADP-ribosylation factor-like protein 1 | ILILGLDGAGK | 307.52 | 256.34 | 234.87 | 191.48 |
| ADP-ribosylation factor-like protein 1 | ILILGLDGAGK | 799.18 | 511.19 | 666.54 | 683 |
| ADP-ribosylation factor-like protein 1 | ILYR | 526.12 | 680.13 | 650.51 | 1023.27 |
| ADP-ribosylation factor-like protein 1 | ILYR | 589.71 | 354.57 | 724.47 | 922.15 |
| ADP-ribosylation factor-like protein 1 | LVAML | 103.95 | 48.77 | 132.24 | 132.23 |
| ADP-ribosylation factor-like protein 1 | LVAML | 173.67 | 75.61 | 144.31 | 168.13 |
| ADP-ribosylation factor-like protein 1 | QIFK | 944.52 | 832.03 | 698.7 | 1348.21 |
| ADP-ribosylation factor-like protein 1 | QIFK | 812.14 | 826.51 | 925.19 | 1053.71 |
| ADP-ribosylation factor-like protein 1 | QIFK | 2341.82 | 4378.22 | 2760.69 | 5011.31 |
| ADP-ribosylation factor-like protein 1 | WQIFK | 637.14 | 669.41 | 720.59 | 1487.08 |
| ADP-ribosylation factor-like protein 1 | WQIFK | 1182.53 | 1360.38 | 1509.25 | 1966.72 |
| ADP-ribosylation factor-like protein 1 | WQIFK | 595.96 | 1013.96 | 1699.53 | 1388.7 |
| MAP/microtubule affinity-regulating kinase 3 | SSTVPSSNTASGGMTR | 157.95 | 139.29 | 190.05 | 228.04 |
| MAP/microtubule affinity-regulating kinase 3 | TPVASTHSISSAATPDR | 89.92 | 51.93 | 293.05 | 242.41 |
| MAP/microtubule affinity-regulating kinase 3 | NSIASCADEQPHIGNYR | 487.18 | 378.44 | 1196.12 | 1230.34 |
| MAP/microtubule affinity-regulating kinase 3 | ENLLK | 999.94 | 888.79 | 1889.7 | 2038.79 |
| MAP/microtubule affinity-regulating kinase 3 | ENLLK | 1203 | 720.98 | 1415.15 | 2014.67 |
| MAP/microtubule affinity-regulating kinase 3 | ENLLK | 380.23 | 731.62 | 446.44 | 716.79 |
| MAP/microtubule affinity-regulating kinase 3 | EVAIK | 610.73 | 724.77 | 951.1 | 1138.43 |
| MAP/microtubule affinity-regulating kinase 3 | EVAIK | 810.28 | 797.48 | 1570.16 | 2299.78 |
| MAP/microtubule affinity-regulating kinase 3 | EVAIK | 1872.73 | 1467.66 | 2874.52 | 2381.52 |
| MAP/microtubule affinity-regulating kinase 3 | EVAIK | 1190.96 | 1697 | 3549.49 | 2900.05 |
| MAP/microtubule affinity-regulating kinase 3 | EVAIK | 2273.7 | 3448.11 | 2957.4 | 2913.3 |
| MAP/microtubule affinity-regulating kinase 3 | EVAIK | 2026.61 | 2753.66 | 3109.49 | 3904.91 |
| MAP/microtubule affinity-regulating kinase 3 | IAFK | 1793.47 | 1000.15 | 1876.92 | 2158.65 |
| MAP/microtubule affinity-regulating kinase 3 | IAFK | 1711.02 | 1593.23 | 1883.12 | 3627.6 |

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|---|---|---|---|---|---|
| MAP/microtubule affinity-regulating kinase 3 | IANELKL | 1981.46 | 1469.88 | 2047.41 | 2623.95 |
| MAP/microtubule affinity-regulating kinase 3 | IANELKL | 1763.96 | 1043.96 | 1201.19 | 1227.92 |
| MAP/microtubule affinity-regulating kinase 3 | IANELKL | 1774.55 | 1805.83 | 2516.73 | 2219.34 |
| MAP/microtubule affinity-regulating kinase 3 | IANELKL | 30848.87 | 35282.73 | 2264.81 | 3591.41 |
| MAP/microtubule affinity-regulating kinase 3 | IANELKL | 21733.49 | 23202.9 | 1428.84 | 2562.22 |
| MAP/microtubule affinity-regulating kinase 3 | IANELKL | 47661.21 | 49897.16 | 786.09 | 2683.3 |
| MAP/microtubule affinity-regulating kinase 3 | IANELKL | 2665.49 | 2718.95 | 3176.73 | 2726.96 |
| MAP/microtubule affinity-regulating kinase 3 | IANELKL | 3322.55 | 3228.11 | 953.92 | 719.21 |
| MAP/microtubule affinity-regulating kinase 3 | IANELKL | 14520.77 | 17400.01 | 1835.78 | 2128.39 |
| MAP/microtubule affinity-regulating kinase 3 | IANELKL | 2582.63 | 2075.33 | 1276.81 | 1927.3 |
| MAP/microtubule affinity-regulating kinase 3 | IANELKL | 19547.32 | 19298.13 | 634.25 | 2656.79 |
| MAP/microtubule affinity-regulating kinase 3 | IANELKL | 31566.22 | 33132.98 | 1671 | 3414.74 |
| MAP/microtubule affinity-regulating kinase 3 | IANELKL | 10562.66 | 12602.16 | 3522.41 | 5318.37 |
| MAP/microtubule affinity-regulating kinase 3 | IANELKL | 1124 | 972.62 | 745.74 | 797.41 |
| MAP/microtubule affinity-regulating kinase 3 | IANELKL | 23795.87 | 26252.41 | 1634.26 | 3374.62 |
| MAP/microtubule affinity-regulating kinase 3 | IANELKL | 2331.47 | 1783.78 | 1087.49 | 1328.42 |
| MAP/microtubule affinity-regulating kinase 3 | IANELKL | 2463.29 | 1951.25 | 671.24 | 987.84 |
| MAP/microtubule affinity-regulating kinase 3 | IANELKL | 1438.56 | 1384.45 | 1454.58 | 758.28 |
| MAP/microtubule affinity-regulating kinase 3 | IIDK | 1325.13 | 782.29 | 1817.38 | 2421.19 |
| MAP/microtubule affinity-regulating kinase 3 | IIDK | 1259.27 | 1224.83 | 1231.17 | 1605.55 |
| MAP/microtubule affinity-regulating kinase 3 | IIDK | 11494.35 | 11829.41 | 19877.02 | 24045.93 |
| MAP/microtubule affinity-regulating kinase 3 | IIDK | 8107.16 | 8072.27 | 13308.71 | 15925.9 |
| MAP/microtubule affinity-regulating kinase 3 | IIDK | 1686.04 | 2252.31 | 2137.37 | 2898.31 |
| MAP/microtubule affinity-regulating kinase 3 | IIDK | 1799.72 | 1871.91 | 3038.68 | 3494.33 |
| MAP/microtubule affinity-regulating kinase 3 | IIDK | 2542.42 | 2325.42 | 3467.44 | 4284.44 |
| MAP/microtubule affinity-regulating kinase 3 | IIDK | 2044.79 | 2765.98 | 3071.91 | 3593.15 |
| MAP/microtubule affinity-regulating kinase 3 | IIDK | 11419.16 | 12769 | 18247.56 | 23009.46 |
| MAP/microtubule affinity-regulating kinase 3 | IIDK | 4581.13 | 5798.65 | 7107.07 | 10954.17 |
| MAP/microtubule affinity-regulating kinase 3 | IIDK | 1817.73 | 1794.65 | 2751.75 | 3695.78 |
| MAP/microtubule affinity-regulating kinase 3 | IIDK | 6734.04 | 6925.33 | 10184.37 | 13283.95 |
| MAP/microtubule affinity-regulating kinase 3 | IIDK | 2816.96 | 2116 | 3299.59 | 5206.11 |
| MAP/microtubule affinity-regulating kinase 3 | IIDK | 6381.53 | 5263.29 | 12843.03 | 15057.89 |
| MAP/microtubule affinity-regulating kinase 3 | IIDK | 1634.62 | 1694.21 | 1902.07 | 2653.86 |
| MAP/microtubule affinity-regulating kinase 3 | IIDK | 2610.13 | 3614.15 | 4202.4 | 5576.11 |
| MAP/microtubule affinity-regulating kinase 3 | IIDK | 1520.78 | 1558.44 | 3184.54 | 2618.89 |
| MAP/microtubule affinity-regulating kinase 3 | IIDK | 8800.84 | 9644.57 | 14104.83 | 17354.68 |
| MAP/microtubule affinity-regulating kinase 3 | IIDK | 994.06 | 1469.88 | 1517.2 | 2486.21 |
| MAP/microtubule affinity-regulating kinase 3 | IPFYMSTDCENLLK | 332.38 | 353.31 | 453.35 | 361.57 |
| MAP/microtubule affinity-regulating kinase 3 | ISDQK | 2987.47 | 3036.22 | 4600.17 | 3368.25 |
| MAP/microtubule affinity-regulating kinase 3 | IVKL | 1071.45 | 1590.3 | 2510.33 | 3331.23 |
| MAP/microtubule affinity-regulating kinase 3 | IVKL | 2944.6 | 2377.74 | 4777.68 | 5411.7 |
| MAP/microtubule affinity-regulating kinase 3 | IVKL | 2298.42 | 2602.15 | 3385.07 | 5172.57 |
| MAP/microtubule affinity-regulating kinase 3 | IVKL | 3592.95 | 2897 | 5810.44 | 6800.76 |
| MAP/microtubule affinity-regulating kinase 3 | LEQIMK | 999.93 | 1315.06 | 1228.43 | 1775.26 |
| MAP/microtubule affinity-regulating kinase 3 | LEQIMK | 662.14 | 752.56 | 398.88 | 515.18 |
| MAP/microtubule affinity-regulating kinase 3 | LFSK | 3056.35 | 3570.66 | 4399.12 | 4841.04 |
| MAP/microtubule affinity-regulating kinase 3 | LFSK | 1389.34 | 1672.03 | 2302.68 | 2188.84 |
| MAP/microtubule affinity-regulating kinase 3 | LSLAK | 3807.56 | 4246.84 | 7664.89 | 7968.16 |
| MAP/microtubule affinity-regulating kinase 3 | NIVK | 127.27 | 191.64 | 266.02 | 165.17 |
| MAP/microtubule affinity-regulating kinase 3 | NLLK | 540.63 | 204.34 | 676.13 | 887.3 |
| MAP/microtubule affinity-regulating kinase 3 | NLLK | 359.27 | 249.9 | 363.8 | 1049.81 |
| MAP/microtubule affinity-regulating kinase 3 | NLLK | 202.84 | 385.47 | 613.68 | 578.56 |
| MAP/microtubule affinity-regulating kinase 3 | QNLK | 1331.98 | 1275.66 | 2386.22 | 2606.35 |
| MAP/microtubule affinity-regulating kinase 3 | QNLK | 1114.11 | 1205 | 1892.83 | 2006.06 |
| Uncharacterized protein CSNK1G2-AS1 | AGPRSTADTRPR | 2061.37 | 1553.88 | 1588.67 | 1488.34 |
| Uncharacterized protein CSNK1G2-AS1 | VAISK | 6212.44 | 5798.33 | 2687.24 | 3461.96 |
| Kelch-like ECH-associated protein 1 | IGVGVAVLNR | 1896.68 | 1548.08 | 1202.49 | 2139.46 |
| Kelch-like ECH-associated protein 1 | QAFGIMNELR | 359.53 | 224.13 | 361.15 | 340.66 |
| Kelch-like ECH-associated protein 1 | LADLQVPR | 426.08 | 350.89 | 229.32 | 167.9 |
| Kelch-like ECH-associated protein 1 | SALGITVHQGR | 822.43 | 553.93 | 1179.92 | 1367.5 |
| Kelch-like ECH-associated protein 1 | YEPER | 360.58 | 120.17 | 393.55 | 339.13 |
| Kelch-like ECH-associated protein 1 | DLNVR | 435.32 | 395.24 | 554.73 | 533.41 |
| Kelch-like ECH-associated protein 1 | IGVGVAVLNR | 1305.81 | 1733.83 | 1147.03 | 971.75 |
| Kelch-like ECH-associated protein 1 | IGVGVAVLNR | 3484.76 | 3798.34 | 1087.63 | 1690.32 |

| | | | | | |
|---|---|---|---|---|---|
| Kelch-like ECH-associated protein 1 | IGVGVAVLNR | 3727.72 | 3943.53 | 1419.15 | 1765.11 |
| Kelch-like ECH-associated protein 1 | IGVGVAVLNR | 2154.69 | 1908.76 | 925.15 | 1089.45 |
| Kelch-like ECH-associated protein 1 | IGVGVAVLNR | 3761.94 | 3115.93 | 1914.45 | 1892.97 |
| Kelch-like ECH-associated protein 1 | IGVGVAVLNR | 8734.21 | 10057.52 | 2325.42 | 3302.84 |
| Kelch-like ECH-associated protein 1 | IGVGVAVLNR | 2869.23 | 2696.41 | 991.83 | 1823.94 |
| Kelch-like ECH-associated protein 1 | IGVGVAVLNR | 2274.97 | 2046.4 | 1175.7 | 1524.17 |
| Kelch-like ECH-associated protein 1 | IGVGVAVLNR | 3131.11 | 1930.06 | 708.15 | 1210.49 |
| Kelch-like ECH-associated protein 1 | IGVGVAVLNR | 1797.49 | 2412.2 | 894.22 | 980.58 |
| Kelch-like ECH-associated protein 1 | IGVGVAVLNR | 2188.48 | 3037.78 | 2078.73 | 3109.77 |
| Kelch-like ECH-associated protein 1 | IGVGVAVLNR | 2556.5 | 2742.27 | 2210.08 | 3260.3 |
| Kelch-like ECH-associated protein 1 | IGVGVAVLNR | 2017.17 | 1026.66 | 863.07 | 1415.5 |
| Kelch-like ECH-associated protein 1 | IGVGVAVLNR | 3346.84 | 2637.06 | 2496.55 | 3635.45 |
| Kelch-like ECH-associated protein 1 | IGVGVAVLNR | 6512.01 | 6626.98 | 1980.13 | 2961.28 |
| Kelch-like ECH-associated protein 1 | IGVGVAVLNR | 4467.3 | 4810.42 | 1037.75 | 2201.62 |
| Kelch-like ECH-associated protein 1 | LIEF | 730.93 | 338.56 | 307.57 | 135.93 |
| Kelch-like ECH-associated protein 1 | LQVK | 858.84 | 680.67 | 1053.15 | 1421.2 |
| Kelch-like ECH-associated protein 1 | QAFGIMNELR | 1374.62 | 573 | 766.04 | 1791.26 |
| Retinoic acid receptor responder protein 2 | LVHCPIETQVLR | 730.99 | 546.16 | 835.68 | 1127.76 |
| Retinoic acid receptor responder protein 2 | LEFK | 5980.65 | 6890.07 | 700.28 | 851.97 |
| Retinoic acid receptor responder protein 2 | LEFK | 2365.31 | 3014.86 | 702.85 | 1203.49 |
| Retinoic acid receptor responder protein 2 | LGSEDK | 4758.08 | 4592.46 | 4583.98 | 6452.94 |
| Retinoic acid receptor responder protein 2 | LVHCPIETQVLR | 307.02 | 305.1 | 377.92 | 471.94 |
| Lymphocyte transmembrane adapter 1 | DGVTPTLSTIRGR | 661.9 | 776.23 | 399.07 | 424.82 |
| Lymphocyte transmembrane adapter 1 | RQVPYLR | 2918.01 | 1493.74 | 519.58 | 354.91 |
| Lymphocyte transmembrane adapter 1 | LLAI | 196.22 | 188.4 | 226.96 | 250.42 |
| Lymphocyte transmembrane adapter 1 | LLAI | 75.78 | 172.69 | 115.6 | 69.95 |

**Table S3.** Clinicopathological Characteristics of Clinical Samples and Expression of RNF219 and LGALS3 in HCC

| **Characteristics** | **No. patients** | **(%)** |
|---|---|---|
| **Age (years)** | | |
| ≤ 60 | 249 | 0.52 |
| > 60 | 226 | 0.48 |
| **Gender** | | |
| Male | 410 | 0.86 |
| Female | 65 | 0.14 |
| **HBsAg** | | |
| positive | 367 | 0.77 |
| negative | 108 | 0.23 |
| **HCV-Ab** | | |
| positive | 12 | 0.03 |
| negative | 463 | 0.97 |
| **AFP(ng/ml)** | | |
| > 20 | 319 | 0.67 |
| ≤ 20 | 156 | 0.33 |
| **Clinical stage** | | |
| I-II | 192 | 0.40 |
| III-IV | 283 | 0.60 |
| **Tumor size** | | |
| > 5 cm | 211 | 0.44 |
| ≤ 5 cm | 264 | 0.56 |
| **Intrahepatic control** | | |
| Yes | 342 | 0.72 |
| No | 133 | 0.28 |
| **Bone metastasis** | | |
| Yes | 38 | 0.08 |
| No | 437 | 0.92 |

Continued

**Table S3 (**Continued**)**

| **Characteristics** | **No. patients** | **(%)** |
|---|---|---|
| **Other extrahepatic metastasis** | | |
| Yes | 158 | 0.33 |
| No | 317 | 0.67 |
| **Vital status (at follow-up)** | | |
| Alive | 314 | 0.66 |
| Death due to liver cancer cause | 161 | 0.34 |
| **Expression of RNF219** | | |
| Low expression | 292 | 0.61 |
| High expression | 183 | 0.39 |
| **Expression of LGALS3** | | |
| Low expression | 283 | 0.60 |
| High expression | 192 | 0.40 |

HBsAg: hepatitis B surface antigen, HCV-Ab: hepatitis C virus antibody, AFP: α-fetoprotein, RNF219: ring finger protein 219

**Table S4.** Correlation between RNF219 and LGALS3 Expression and Clinicopathologic Charateristics of HCC Patient

| **Characteristics** | **RNF219 Protein level** | | **Chi-square test** | **LGALS3 Protein level** | | **Chi-square test** |
|---|---|---|---|---|---|---|
| | **Low** | **High** | ***P* value** | **Low** | **High** | ***P* value** |
| **Age (years)** | | | | | | |
| ≤ 60 | 158 | 91 | 0.201 | 149 | 100 | 0.903 |
| > 60 | 134 | 92 | | 134 | 92 | |
| **Gender** | | | | | | |
| Male | 253 | 157 | 0.447 | 241 | 169 | 0.373 |
| Female | 39 | 26 | | 42 | 23 | |
| **HBsAg** | | | | | | |
| positive | 221 | 146 | 0.178 | 216 | 151 | 0.554 |
| negative | 71 | 37 | | 67 | 41 | |
| **HCV-Ab** | | | | | | |
| positive | 7 | 5 | 0.520 | 9 | 3 | 0.270 |
| negative | 285 | 178 | | 274 | 189 | |
| **AFP (ng/ml)** | | | | | | |
| > 20 | 202 | 117 | 0.139 | 191 | 128 | 0.851 |
| ≤ 20 | 90 | 66 | | 92 | 64 | |
| **Clinical stage** | | | | | | |
| I-II | 78 | 114 | < 0.001 | 76 | 116 | < 0.001 |
| III-IV | 214 | 69 | | 207 | 76 | |
| **Tumor size** | | | | | | |
| > 5 cm | 128 | 83 | 0.409 | 133 | 78 | 0.170 |
| ≤ 5 cm | 164 | 100 | | 150 | 114 | |
| **Intrahepatic control** | | | | | | |
| Yes | 215 | 127 | 0.185 | 201 | 141 | 0.565 |
| No | 77 | 56 | | 82 | 51 | |
| **Bone metastasis** | | | | | | |
| Yes | 5 | 33 | < 0.001 | 8 | 30 | < 0.001 |
| No | 287 | 150 | | 275 | 162 | |

Continued

**Table S4 (**Continued**)**

| **Characteristics** | **RNF219 Protein level** | | **Chi-square test** | **LGALS3 Protein level** | | **Chi-square test** |
|---|---|---|---|---|---|---|
| | **Low** | **High** | ***P* value** | **Low** | **High** | ***P* value** |
| **Other extrahepatic metastasis** | | | | | | |
| Yes | 96 | 62 | 0.449 | 103 | 55 | 0.079 |
| No | 196 | 121 | | 180 | 137 | |
| **Vital status (at follow-up)** | | | | | | |
| Alive | 244 | 70 | < 0.001 | 261 | 53 | < 0.001 |
| Death | 48 | 113 | | 22 | 139 | |
| **Expression of LGALS3** | | | | **Expression of RNF219** | | |
| Low expression | 248 | 35 | < 0.001 | 248 | 44 | < 0.001 |
| High expression | 44 | 148 | | 35 | 148 | |

HBsAg: hepatitis B surface antigen, HCV-Ab: hepatitis C virus antibody, AFP: α-fetoprotein, RNF219: ring finger protein 219

**Table S5.** Univariate and Multivariate Analyses of Various Prognostic Parameters in HCC Patients by Cox-regression Analysis

| | **Univariate analysis** | | | **Multivariate analysis** | | |
|---|---|---|---|---|---|---|
| | C. OR | 95% CI | P-value | A. OR | 95% CI | P-value |
| Clinical stage | 1.542 | 1.105-2.152 | 0.011 | 2.246 | 1.526-3.306 | < 0.001 |
| Bone metastasis | 22.440 | 14.470-34.800 | < 0.001 | 4.235 | 2.108-7.449 | < 0.001 |
| Exp. of RNF219 | 1.414 | 1.334-1.498 | < 0.001 | 1.261 | 1.181-1.348 | < 0.001 |
| Exp. of LGALS3 | 1.379 | 1.279-1.485 | < 0.001 | 1.125 | 1.042-1.215 | 0.002 |

Exp.: Expression; Abbreviations: C. OR, crude odds ratio; CI, confidence interval; A. OR, adjusted odds ratio;

**Table S6.** Bone metastases related events

| Cell line | Mouse | Metastasis sites | | | | | | | | Fracture |
|---|---|---|---|---|---|---|---|---|---|---|
| | | Skull | Spine | Fore limb | Femur | Knee /tibia | Pelvis | Ribs/ sternum | Scapula | |
| HCCLM3-Parental (n=8) | 1 | - | - | + | + | + | - | - | + | - |
| | 2 | - | + | - | + | + | - | - | + | - |
| | 3 | - | - | - | + | + | - | - | - | - |
| | 4 | - | + | + | + | + | - | - | + | - |
| | 5 | + | + | + | + | + | - | - | - | + |
| | 6 | + | + | + | + | + | - | - | + | + |
| | 7 | - | + | - | + | + | + | - | - | - |
| | 8 | - | - | - | + | + | - | - | - | - |
| HCCLM3/RNF219 (n=8) | 1 | + | + | + | + | + | - | - | + | - |
| | 2 | + | + | + | + | + | + | - | + | + |
| | 3 | + | + | + | + | + | + | + | + | + |
| | 4 | + | + | + | + | + | + | + | + | + |
| | 5 | + | + | + | + | + | + | + | + | + |
| | 6 | - | + | + | + | + | - | + | + | - |
| | 7 | + | + | + | + | + | + | + | + | + |
| | 8 | - | - | - | + | - | - | - | - | + |
| Huh7 (n=8) | 1 | - | - | - | + | - | - | - | - | - |
| | 2 | - | - | + | + | + | - | - | - | - |
| | 3 | - | - | + | + | + | - | - | - | - |
| | 4 | - | - | - | + | + | - | - | - | - |
| | 5 | - | + | + | + | + | - | - | - | - |
| | 6 | - | + | + | + | + | - | + | - | - |
| | 7 | - | + | - | + | + | + | - | - | - |
| | 8 | + | + | + | + | + | - | - | - | - |
| Huh7/RNF219 (n=8) | 1 | + | + | + | + | + | - | - | - | + |
| | 2 | + | + | + | + | + | + | + | + | + |
| | 3 | + | + | + | + | + | + | + | + | + |
| | 4 | + | + | + | + | + | + | + | + | + |
| | 5 | - | + | + | + | + | + | + | - | + |
| | 6 | + | - | + | + | + | + | - | - | - |
| | 7 | - | + | + | + | + | - | + | + | + |
| | 8 | + | + | + | + | + | + | + | + | + |
| HCCLM3-BM4 (n=8) | 1 | - | + | + | + | + | - | - | + | + |
| | 2 | - | - | + | + | + | - | - | + | + |
| | 3 | - | - | + | + | + | - | - | + | + |
| | 4 | - | - | + | + | + | - | - | + | - |
| | 5 | - | - | + | + | + | - | - | - | - |
| | 6 | - | + | + | + | + | - | - | + | - |
| | 7 | - | + | + | + | + | - | - | - | + |
| | 8 | - | - | + | + | + | - | - | - | - |
| HCCLM3-BM4-RNF219 sh#1 (n=8) | 1 | - | - | - | - | - | - | - | - | - |
| | 2 | - | - | - | - | - | - | - | - | - |
| | 3 | - | - | - | - | - | - | - | - | - |
| | 4 | - | - | - | - | + | - | - | - | - |
| | 5 | - | - | - | - | - | - | - | - | - |
| | 6 | - | - | - | - | + | - | - | - | - |
| | 7 | - | - | - | - | - | - | - | - | - |
| | 8 | - | - | - | - | + | - | - | - | - |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| **HCCLM3-BM4-RNF219 sh#2 (n=8)** | **1** | - | - | - | - | - | - | - | - | - |
| | **2** | - | - | - | - | - | - | - | - | - |
| | **3** | - | - | - | - | - | - | - | - | - |
| | **4** | - | - | - | - | + | - | - | - | - |
| | **5** | - | - | - | - | + | - | - | - | - |
| | **6** | - | - | - | - | + | - | - | - | - |
| | **7** | - | - | - | - | + | - | - | - | - |
| | **8** | - | - | - | - | + | - | - | - | - |
| **MHCC97H (n=8)** | **1** | + | - | + | + | + | - | + | + | + |
| | **2** | + | - | + | + | + | - | + | + | + |
| | **3** | - | - | - | + | + | - | + | + | - |
| | **4** | - | - | + | + | + | - | + | + | + |
| | **5** | + | + | - | + | + | - | + | + | - |
| | **6** | - | - | - | + | + | - | + | + | - |
| | **7** | - | - | - | + | + | - | - | + | - |
| | **8** | + | - | + | + | + | - | + | + | + |
| **MHCC97H-RNF219 sh#1 (n=8)** | **1** | - | - | - | - | - | - | - | - | - |
| | **2** | - | - | - | - | - | - | - | - | - |
| | **3** | - | - | - | - | + | - | - | - | - |
| | **4** | - | - | - | - | - | - | - | - | - |
| | **5** | - | - | - | - | - | - | - | - | - |
| | **6** | - | - | - | - | + | - | - | - | - |
| | **7** | - | - | - | - | + | - | - | - | - |
| | **8** | - | - | - | - | - | - | - | - | - |
| **MHCC97H-RNF219 sh#2 (n=8)** | **1** | - | - | - | - | - | - | - | - | - |
| | **2** | - | - | - | - | - | - | - | - | - |
| | **3** | - | - | - | - | - | - | - | - | - |
| | **4** | - | - | - | - | + | - | - | - | - |
| | **5** | - | - | - | - | + | - | - | - | - |
| | **6** | - | - | - | - | - | - | - | - | - |
| | **7** | - | - | - | - | + | - | - | - | - |
| | **8** | - | - | - | - | - | - | - | - | - |

**Table S7.** List of quantified protein in HCC/RNF219-CM compared with HCC/vector-CM, and in mature

| Protein ID (Uniprot) | Gene name | Protein Name | Log2Foldchange | | **Pvalue** |
|---|---|---|---|---|---|
| | | | Proteins in osteodast OC/ pre-osteodast OP | Secreted proteins in RNF219/Vector cells culture medium | |
| P00558 | PGK1 | Phosphoglycerate kinase 1 | 0.98 | 2.756 | 1.90E-08 |
| P62249 | RS16 | 40S ribosomal protein S16 | 0.58 | 2.472 | 4.68E-02 |
| P53602 | MVD1 | Diphosphomevalonate decarboxylase | 1.03 | 2.011 | 4.67E-02 |
| P17931 | LEG3 | Galectin-3 | 1.79 | 1.997 | 6.01E-07 |
| P62888 | RL30 | 60S ribosomal protein L30 | 0.85 | 1.956 | 2.43E-02 |
| P46776 | RL27A | Ubiquitin-40S ribosomal protein S27a | 0.1 | 1.924 | 7.67E-03 |
| P43243 | MATR3 | Matrin-3 | 0.17 | 1.836 | 2.77E-03 |
| Q12874 | SF3A3 | Splicing factor 3A subunit 3 | 0.8 | 1.791 | 1.74E-04 |
| Q92688 | AN32B | Acidic leucine-rich nuclear phosphoprotein 32 family member B | 0.83 | 1.777 | 1.39E-03 |
| P61353 | RL27 | 60S ribosomal protein L27 | 0.88 | 1.691 | 1.04E-03 |
| P18124 | RL7 | 60S ribosomal protein L7 | 0.43 | 1.672 | 1.52E-02 |
| Q99613 | EIF3C | Eukaryotic translation initiation factor 3 subunit C | 0.78 | 1.613 | 1.00E-02 |
| P04792 | HSPB1 | Hsp70-binding protein 1 | 0.86 | 1.582 | 5.77E-04 |
| O14737 | PDCD5 | Programmed cell death protein 5 | 0.52 | 1.472 | 4.68E-02 |
| P19338 | NUCL | Nucleolin | 0.32 | 1.378 | 1.48E-05 |
| Q07955 | SRSF1 | Serine/arginine-rich splicing factor 1 | 1.69 | 1.346 | 2.18E-04 |
| P62913 | RL11 | 60S ribosomal protein L11 | 0.24 | 1.161 | 6.59E-04 |
| Q9P258 | RCC2 | Protein RCC2 | 0.36 | 1.141 | 3.98E-02 |
| P62906 | RL10A | 60S ribosomal protein L10a | 1.1 | 1.118 | 6.96E-04 |
| P30050 | RL12 | 60S ribosomal protein L12 | 1.03 | 1.035 | 5.18E-05 |
| Q99733 | NP1L4 | Nucleosome assembly protein 1-like 4 | 1.19 | 0.998 | 4.80E-02 |
| P84098 | RL19 | 60S ribosomal protein L19 | 0.25 | 0.913 | 9.45E-04 |
| P39019 | RS19 | 40S ribosomal protein S19 | 0.18 | 0.877 | 2.89E-02 |
| P47914 | RL29 | 60S ribosomal protein L29 -around 25k | 0.06 | 0.875 | 1.26E-04 |
| Q13765 | NACA | Nascent polypeptide-associated complex subunit alpha | 0.81 | 0.866 | 1.84E-04 |
| O60218 | AK1BA | Aldose reductase | 1.22 | 0.846 | 4.93E-03 |
| P62277 | RS13 | 40S ribosomal protein S13 | 0.89 | 0.826 | 1.01E-02 |
| P62244 | RS15A | 40S ribosomal protein S15a | 1.18 | 0.818 | 5.73E-04 |
| P05455 | LA | Lupus La protein homolog - around 50k | 0.35 | 0.817 | 1.34E-04 |
| P39687 | AN32A | Acidic leucine-rich nuclear phosphoprotein 32 family member A | 1.19 | 0.797 | 1.48E-04 |
| Q13263 | TIF1B | Transcription intermediary factor 1-beta | 0.65 | 0.79 | 8.50E-03 |
| Q6IBS0 | TWF2 | Twinfilin-2 | 1.62 | 0.786 | 6.09E-03 |
| Q99497 | PARK7 | Protein DJ-1 | 1.29 | 0.761 | 1.24E-02 |
| P40121 | CAPG | Macrophage-capping protein | 1.39 | 0.721 | 2.23E-02 |
| P26373 | RL13 | 60S ribosomal protein L13 | 0.17 | 0.696 | 3.50E-02 |
| Q01105 | SET | Protein SET | 0.89 | 0.694 | 2.29E-03 |
| Q86VP6 | CAND1 | Cullin-associated NEDD8-dissociated protein 1 | 0.79 | 0.691 | 2.70E-04 |
| P61626 | LYSC | Lysozyme C-1 | 0.12 | 0.689 | 3.73E-04 |
| P05388 | RLA0 | 60S acidic ribosomal protein P0 | 0.89 | 0.675 | 3.05E-03 |
| P05067 | A4 | Amyloid beta A4 precursor protein-binding family B member 1-interacting protein | 0.85 | 0.667 | 3.44E-06 |
| P04406 | G3P | Glyceraldehyde-3-phosphate dehydrogenase | 0.92 | 0.634 | 3.19E-04 |
| P07900 | HS90A | Heat shock protein HSP 90-alpha | 0.8 | 0.609 | 3.54E-04 |

| | | | | | |
|---|---|---|---|---|---|
| Q61937 | Npm1 | Nucleophosmin | 0.83 | 1.279 | 1.47E-03 |

**Table S8.** Potential trans-regulatory factors were enriched on the LGALS3 promoter in HCCLM3 cells

| Accession | Description | -10lgP | #Peptides | #Unique |
|---|---|---|---|---|
| P46937\|YAP1_HUMAN | Transcriptional coactivator YAP1 OS=Homo sapiens GN=YAP1 PE=1 SV=2 | 343.01 | 57 | 57 |
| P35222\|CTNB1_HUMAN | Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1 | 395.8 | 46 | 45 |
| P26358\|DNMT1_HUMAN | DNA (cytosine-5)-methyltransferase 1 OS=Homo sapiens GN=DNMT1 PE=1 SV=2 | 98.66 | 10 | 8 |
| Q8NFU7\|TET1_HUMAN | Tet methylcytosine dioxygenase 1 OS=Homo sapiens GN=TET PE=1 SV=1 | 124.14 | 9 | 9 |
| Q9Y3Y2\|CHTOP_HUMAN | Chromatin target of PRMT1 protein OS=Homo sapiens GN=CHTOP PE=1 SV=2 | 120.69 | 8 | 8 |
| Q99873\|ANM1_HUMAN | Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=2 | 49.46 | 9 | 7 |
| Q9UMN6\|KMT2B_HUMAN | Histone-lysine N-methyltransferase 2B OS=Homo sapiens GN=KMT2B PE=1 SV=1 | 136.52 | 10 | 10 |
| P35221\|CTNA1_HUMAN | Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=1 SV=1 | 16.37 | 5 | 4 |
| P25054\|APC_HUMAN | Adenomatous polyposis coli protein OS=Homo sapiens GN=APC PE=1 SV=2 | 13.1 | 3 | 3 |
| O60341\|KDM1A_HUMAN | Lysine-specific histone demethylase 1A OS=Homo sapiens GN=KDM1A PE=1 SV=1 | 19.72 | 5 | 5 |

| Protein Accession | Peptide | Unique | -10lgP | Mass | Length | Start | End |
|---|---|---|---|---|---|---|---|
| P46937\|YAP1_HUMAN | R.DESTDSGLSMSSYSVPR.T | Y | 97.51 | 1816.7784 | 17 | 395 | 411 |
| P46937\|YAP1_HUMAN | K.QPPPLAPQSPQGGVMGGSNSNQQQQMR.L | Y | 95.59 | 2818.324 | 27 | 281 | 307 |
| P46937\|YAP1_HUMAN | R.SQLPTLEQDGGTQNPVSSPGMSQELR.T | Y | 95.06 | 2755.3083 | 26 | 350 | 375 |
| P46937\|YAP1_HUMAN | R.DESTDSGLSM(+15.99)SSYSVPR.T | Y | 95.01 | 1832.7734 | 17 | 395 | 411 |
| P46937\|YAP1_HUMAN | R.QASTDAGTAGALTPQHVR.A | Y | 93.27 | 1779.8864 | 18 | 107 | 124 |
| P46937\|YAP1_HUMAN | R.GDSETDLEALFN(+.98)AVMNPK.T | Y | 89.86 | 1950.8881 | 18 | 59 | 76 |
| P46937\|YAP1_HUMAN | R.YFLN(+.98)HIDQTTTWQDPR.K | Y | 89.82 | 2034.9435 | 16 | 188 | 203 |
| P46937\|YAP1_HUMAN | R.GDSETDLEALFNAVMNPK.T | Y | 87.99 | 1949.9041 | 18 | 59 | 76 |
| P46937\|YAP1_HUMAN | R.TPDDFLNSVDEMDTGDTINQSTLPSQQNR.F | Y | 87.4 | 3237.4368 | 29 | 412 | 440 |
| P46937\|YAP1_HUMAN | R.Q(-17.03)ASTDAGTAGALTPQHVR.A | Y | 86.94 | 1762.8597 | 18 | 107 | 124 |
| P46937\|YAP1_HUMAN | R.QSSFEIPDDVPLPAGWEMAK.T | Y | 86.35 | 2216.0459 | 20 | 162 | 181 |
| P46937\|YAP1_HUMAN | R.AHSSPASLQLGAVSPGTLTPTGVVSGPAATPTAQHLR.Q | Y | 84.45 | 3533.8589 | 37 | 125 | 161 |
| P46937\|YAP1_HUMAN | R.TMTTN(+.98)SSDPFLNSGTYHSR.D | Y | 80.52 | 2115.9167 | 19 | 376 | 394 |
| P46937\|YAP1_HUMAN | H.SSPASLQLGAVSPGTLTPTGVVSGPAATPTAQHLR.Q | Y | 80.2 | 3325.7629 | 35 | 127 | 161 |
| P46937\|YAP1_HUMAN | K.QPPPLAPQSPQGGVM(+15.99)GGSNSNQQQQMR.L | Y | 80.18 | 2834.3188 | 27 | 281 | 307 |
| P46937\|YAP1_HUMAN | R.YFLNHIDQTTTWQDPR.K | Y | 79.86 | 2033.9595 | 16 | 188 | 203 |
| P46937\|YAP1_HUMAN | R.TPDDFLNSVDEM(+15.99)DTGDTINQSTLPSQQNR.F | Y | 79.85 | 3253.4316 | 29 | 412 | 440 |
| P46937\|YAP1_HUMAN | R.TMTTNSSDPFLNSGTYHSR.D | Y | 79.63 | 2114.9326 | 19 | 376 | 394 |
| P46937\|YAP1_HUMAN | R.KLPDSFFKPPEPK.S | Y | 79.07 | 1528.8289 | 13 | 90 | 102 |
| P46937\|YAP1_HUMAN | R.GDSETDLEALFNAVM(+15.99)NPK.T | Y | 78.56 | 1965.8989 | 18 | 59 | 76 |
| P46937\|YAP1_HUMAN | A.SLQLGAVSPGTLTPTGVVSGPAATPTAQHLR.Q | Y | 75.34 | 2983.6091 | 31 | 131 | 161 |
| P46937\|YAP1_HUMAN | K.QPPPLAPQSPQGGVMGGSNSNQQQQM(+15.99)R.L | Y | 73.73 | 2834.3188 | 27 | 281 | 307 |
| P46937\|YAP1_HUMAN | K.LPDSFFKPPEPK.S | Y | 72.39 | 1400.7339 | 12 | 91 | 102 |
| P46937\|YAP1_HUMAN | L.RSQLPTLEQDGGTQNPVSSPGMSQELR.T | Y | 69.8 | 2911.4094 | 27 | 349 | 375 |
| P46937\|YAP1_HUMAN | R.Q(-17.03)SSFEIPDDVPLPAGWEMAK.T | Y | 67.57 | 2199.0193 | 20 | 162 | 181 |
| P46937\|YAP1_HUMAN | R.SQLPTLEQDGGTQNPVSSPGM(+15.99)SQELR.T | Y | 66.83 | 2771.3032 | 26 | 350 | 375 |
| P46937\|YAP1_HUMAN | R.TMTTNSSDPFLN(+.98)SGTYHSR.D | Y | 64.49 | 2115.9167 | 19 | 376 | 394 |
| P46937\|YAP1_HUMAN | S.SFEIPDDVPLPAGWEMAK.T | Y | 63.67 | 2000.9553 | 18 | 164 | 181 |
| P46937\|YAP1_HUMAN | K.QPPPLAPQSPQGGVMGGSN(+.98)SNQQQQMR.L | Y | 62.7 | 2819.3079 | 27 | 281 | 307 |
| P46937\|YAP1_HUMAN | R.TPDDFLNSVDEMD.T | Y | 61.27 | 1496.5977 | 13 | 412 | 424 |
| P46937\|YAP1_HUMAN | R.QSSFEIPDDVPLPAGWEM(+15.99)AK.T | Y | 60.93 | 2232.0408 | 20 | 162 | 181 |
| P46937\|YAP1_HUMAN | L.SSDILNDMESVLAATK.L | Y | 60.81 | 1692.824 | 16 | 479 | 494 |
| P46937\|YAP1_HUMAN | R.TPDDFLN(+.98)SVDEMDTGDTINQSTLPSQQNR.F | Y | 58.76 | 3238.4209 | 29 | 412 | 440 |
| P46937\|YAP1_HUMAN | H.VRGDSETDLEALFNAVMNPK.T | Y | 58.63 | 2205.0735 | 20 | 57 | 76 |
| P46937\|YAP1_HUMAN | K.AMLSQMNVTAPTSPPVQQN.M | Y | 58.54 | 2012.9659 | 19 | 205 | 223 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| P46937\|YAP1_HUMAN | K.TANVPQTVPMR.L | Y | 55.47 | 1212.6285 | 11 | 77 | 87 |
| P46937\|YAP1_HUMAN | R.TPDDFLNSVDEM(+15.99)DTGDTINQSTLPSQQNR.F | Y | 54.16 | 3254.4158 | 29 | 412 | 440 |
| P46937\|YAP1_HUMAN | K.LDKESFLTWL | Y | 53.4 | 1250.6547 | 10 | 495 | 504 |
| P46937\|YAP1_HUMAN | V.RGDSETDLEALFNAVMNPK.T | Y | 53.24 | 2106.0051 | 19 | 58 | 76 |
| P46937\|YAP1_HUMAN | N.SSDPFLNSGTYHSR.D | Y | 47.23 | 1566.7063 | 14 | 381 | 394 |
| P46937\|YAP1_HUMAN | R.LQQLQMEK.E | Y | 47.15 | 1016.5325 | 8 | 308 | 315 |
| P46937\|YAP1_HUMAN | D.SETDLEALFNAVMNPK.T | Y | 47.05 | 1777.8556 | 16 | 61 | 76 |
| P46937\|YAP1_HUMAN | R.TPDDFLNSVDEM(+15.99)D.T | Y | 43.44 | 1512.5927 | 13 | 412 | 424 |
| P46937\|YAP1_HUMAN | R.GDSETDLEALFNAVMN(+.98)PK.T | Y | 41.45 | 1950.8881 | 18 | 59 | 76 |
| P46937\|YAP1_HUMAN | R.LKQQELLR.Q | Y | 39.64 | 1026.6185 | 8 | 320 | 327 |
| P46937\|YAP1_HUMAN | R.SQLPTLEQDGGTQN(+.98)PVSSPGM(+15.99)SQELR.T | Y | 37.47 | 2772.2871 | 26 | 350 | 375 |
| P46937\|YAP1_HUMAN | K.ESFLTWL | Y | 35.1 | 894.4487 | 7 | 498 | 504 |
| P46937\|YAP1_HUMAN | Q.SSFEIPDDVPLPAGWEMAK.T | Y | 34.21 | 2087.9873 | 19 | 163 | 181 |
| P46937\|YAP1_HUMAN | R.ISQSAPVK.Q | Y | 32.99 | 828.4705 | 8 | 273 | 280 |
| P46937\|YAP1_HUMAN | G.DSETDLEALFNAVMNPK.T | Y | 28.98 | 1892.8826 | 17 | 60 | 76 |
| P46937\|YAP1_HUMAN | R.GDSETDLEALFN.A | Y | 26.45 | 1309.5674 | 12 | 59 | 70 |
| P46937\|YAP1_HUMAN | R.TPDDFLNSVDEMDTGDTIN(+.98)QSTLPSQQNR.F | Y | 25.4 | 3238.4209 | 29 | 412 | 440 |
| P46937\|YAP1_HUMAN | K.QQELLR.Q | Y | 23.13 | 785.4395 | 6 | 322 | 327 |
| P46937\|YAP1_HUMAN | Q.QELLR.Q | Y | 21.01 | 657.381 | 5 | 323 | 327 |
| P46937\|YAP1_HUMAN | R.YFLNHIDQTTT.W | Y | 18.27 | 1351.6409 | 11 | 188 | 198 |
| P46937\|YAP1_HUMAN | R.GDSETDLEALFNAVMN.P | Y | 17.64 | 1724.7563 | 16 | 59 | 74 |
| P46937\|YAP1_HUMAN | L.Q(+.98)EALSSDILN(+.98)DM(+15.99)ESVLAATK.L | Y | 15.21 | 2152.0093 | 20 | 475 | 494 |
| P35222\|CTNB1_HUMAN | K.AAVSHWQQQSYLDSGIHSGATTTAPSLSGK.G | Y | 98.27 | 3084.49 | 30 | 20 | 49 |
| P35222\|CTNB1_HUMAN | K.HAVVNLINYQDDAELATR.A | Y | 85.2 | 2041.0228 | 18 | 134 | 151 |
| P35222\|CTNB1_HUMAN | Q.SYLDSGIHSGATTTAPSLSGK.G | Y | 84.84 | 2049.0015 | 21 | 29 | 49 |
| P35222\|CTNB1_HUMAN | R.TEPMAWNETADLGLDIGAQGEPLGYR.Q | Y | 79.72 | 2803.3123 | 26 | 685 | 710 |
| P35222\|CTNB1_HUMAN | R.TSM(+15.99)GGTQQQFVEGVR.M | Y | 79.7 | 1639.7625 | 15 | 551 | 565 |
| P35222\|CTNB1_HUMAN | R.TSMGGTQQQFVEGVR.M | Y | 77.84 | 1623.7675 | 15 | 551 | 565 |
| P35222\|CTNB1_HUMAN | R.NEGVATYAAAVLFR.M | Y | 77.35 | 1480.7673 | 14 | 648 | 661 |
| P35222\|CTNB1_HUMAN | Y.AITTLHNLLLHQEGAK.M | Y | 74.22 | 1757.9788 | 16 | 255 | 270 |
| P35222\|CTNB1_HUMAN | Y.LDSGIHSGATTTAPSLSGK.G | Y | 73.79 | 1798.9061 | 19 | 31 | 49 |
| P35222\|CTNB1_HUMAN | W.NETADLGLDIGAQGEPLGYR.Q | Y | 73.14 | 2088.0122 | 20 | 691 | 710 |
| P35222\|CTNB1_HUMAN | M.ATQADLM(+15.99)ELDMAMEPDR.K | Y | 70.15 | 1951.8325 | 17 | 2 | 18 |
| P35222\|CTNB1_HUMAN | S.YLDSGIHSGATTTAPSLSGK.G | Y | 69.03 | 1961.9694 | 20 | 30 | 49 |
| P35222\|CTNB1_HUMAN | R.HQEAEM(+15.99)AQNAVR.L | Y | 69.01 | 1398.631 | 12 | 475 | 486 |
| P35222\|CTNB1_HUMAN | K.HAVVNLIN(+.98)YQDDAELATR.A | Y | 68.71 | 2042.0068 | 18 | 134 | 151 |
| P35222\|CTNB1_HUMAN | R.MEEIVEGC(+57.02)TGALHILAR.D | Y | 68.41 | 1897.939 | 17 | 566 | 582 |
| P35222\|CTNB1_HUMAN | H.AVVNLINYQDDAELATR.A | Y | 67.59 | 1903.9639 | 17 | 135 | 151 |
| P35222\|CTNB1_HUMAN | M.ATQADLMELDMAMEPDR.K | Y | 67.25 | 1935.8376 | 17 | 2 | 18 |
| P35222\|CTNB1_HUMAN | M.ATQADLM(+15.99)ELDM(+15.99)AMEPDR.K | Y | 66.69 | 1967.8274 | 17 | 2 | 18 |
| P35222\|CTNB1_HUMAN | R.AAM(+15.99)FPETLDEGMQIPSTQFDAAHPTNVQR.L | Y | 66.62 | 3217.4807 | 29 | 96 | 124 |
| P35222\|CTNB1_HUMAN | R.TMQNTNDVETAR.C | Y | 66.38 | 1378.6147 | 12 | 201 | 212 |
| P35222\|CTNB1_HUMAN | R.HQEAEMAQNAVR.L | Y | 66.17 | 1382.6361 | 12 | 475 | 486 |
| P35222\|CTNB1_HUMAN | R.MSEDKPQDYK.K | Y | 65.62 | 1239.5441 | 10 | 662 | 671 |
| P35222\|CTNB1_HUMAN | K.LIILASGGPQALVNIMR.T | Y | 65.4 | 1765.0283 | 17 | 313 | 329 |
| P35222\|CTNB1_HUMAN | K.LIILASGGPQALVNIM(+15.99)R.T | Y | 64.96 | 1781.0233 | 17 | 313 | 329 |
| P35222\|CTNB1_HUMAN | R.HQEAEMAQN(+.98)AVR.L | Y | 64.86 | 1383.6201 | 12 | 475 | 486 |
| P35222\|CTNB1_HUMAN | T.TLHNLLLHQEGAK.M | Y | 64.77 | 1472.8099 | 13 | 258 | 270 |
| P35222\|CTNB1_HUMAN | K.MMVC(+57.02)QVGGIEALVR.T | Y | 64.11 | 1561.7778 | 14 | 436 | 449 |
| P35222\|CTNB1_HUMAN | K.EAAEAIEAEGATAPLTELLH.S | Y | 63.94 | 2035.0109 | 20 | 626 | 645 |
| P35222\|CTNB1_HUMAN | V.VNLINYQDDAELATR.A | Y | 62.14 | 1733.8584 | 15 | 137 | 151 |
| P35222\|CTNB1_HUMAN | L.ASGGPQALVNIMR.T | Y | 61.8 | 1312.6921 | 13 | 317 | 329 |
| P35222\|CTNB1_HUMAN | T.LHNLLLHQEGAK.M | Y | 61.26 | 1371.7622 | 12 | 259 | 270 |
| P35222\|CTNB1_HUMAN | M.ATQADLM(+15.99)ELDMAM(+15.99)EPDR.K | Y | 61.11 | 1967.8274 | 17 | 2 | 18 |
| P35222\|CTNB1_HUMAN | R.C(+57.02)TAGTLHNLSHHR.E | Y | 60.31 | 1502.7161 | 13 | 213 | 225 |
| P35222\|CTNB1_HUMAN | R.N(+.98)EGVATYAAAVLFR.M | Y | 60.19 | 1481.7513 | 14 | 648 | 661 |
| P35222\|CTNB1_HUMAN | K.LLHPPSHWPLIK.A | Y | 59.56 | 1436.8292 | 12 | 497 | 508 |
| P35222\|CTNB1_HUMAN | R.SPQMVSAIVR.T | Y | 59.34 | 1086.5856 | 10 | 191 | 200 |
| P35222\|CTNB1_HUMAN | K.AAVMVHQLSK.K | Y | 58.8 | 1082.5906 | 10 | 171 | 180 |

|  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|
| P35222\|CTNB1_HUMAN | K.EAAEAIEAEGATAPLTEL.L | Y | 58.64 | 1784.8679 | 18 | 626 | 643 |
| P35222\|CTNB1_HUMAN | R.LHYGLPVVVK.L | Y | 58.37 | 1123.6753 | 10 | 487 | 496 |
| P35222\|CTNB1_HUMAN | S.NKPAIVEAGGMQALGLHLTDPSQR.L | Y | 57.9 | 2502.3013 | 24 | 353 | 376 |
| P35222\|CTNB1_HUMAN | N.LINYQDDAELATR.A | Y | 56.97 | 1520.7471 | 13 | 139 | 151 |
| P35222\|CTNB1_HUMAN | K.LLNDEDQVVVNK.A | Y | 56.71 | 1384.7197 | 12 | 159 | 170 |
| P35222\|CTNB1_HUMAN | M.QALGLHLTDPSQR.L | Y | 56.41 | 1434.7579 | 13 | 364 | 376 |
| P35222\|CTNB1_HUMAN | F.YAITTLHNLLLHQEGAK.M | Y | 56.27 | 1921.0421 | 17 | 254 | 270 |
| P35222\|CTNB1_HUMAN | R.TMQNTN(+.98)DVETAR.C | Y | 56.25 | 1379.5988 | 12 | 201 | 212 |
| P26358\|DNMT1_HUMAN | R.VPTLAVPAISLPDDVR.R | Y | 53.26 | 1661.9352 | 16 | 10 | 25 |
| P26358\|DNMT1_HUMAN | R.VLEQLEDLDSR.V | Y | 44.2 | 1315.6619 | 11 | 910 | 920 |
| P26358\|DNMT1_HUMAN | R.Q(+.98)TIRHSTR.E | Y | 24.4 | 998.5258 | 8 | 602 | 609 |
| P26358\|DNMT1_HUMAN | F.TFNIK.L | Y | 21.99 | 621.3486 | 5 | 947 | 951 |
| P26358\|DNMT1_HUMAN | P.EIEIK.L | Y | 20.02 | 630.3588 | 5 | 1131 | 1135 |
| P26358\|DNMT1_HUMAN | R.FESPPK.T | Y | 19.05 | 703.3541 | 6 | 876 | 881 |
| P26358\|DNMT1_HUMAN | R.HIPLAPGSDWR.D | Y | 17.38 | 1247.6411 | 11 | 1427 | 1437 |
| P26358\|DNMT1_HUMAN | N.GILYR.V | Y | 14.53 | 620.3646 | 5 | 930 | 934 |
| Q8NFU7\|TET1_HUMAN | R.CGHGEEQK.L | Y | 56.04 | 854.7264 | 8 | 725 | 732 |
| Q8NFU7\|TET1_HUMAN | K.TLENNSYK.F | Y | 55.77 | 834.0024 | 8 | 835 | 842 |
| Q8NFU7\|TET1_HUMAN | K.DGSPVQPSLLSLMK.D | Y | 55.69 | 1459.4944 | 14 | 919 | 932 |
| Q8NFU7\|TET1_HUMAN | K.GDFSANVPEAEK.S | Y | 54.81 | 1329.2352 | 12 | 774 | 785 |
| Q8NFU7\|TET1_HUMAN | K.PTVVSYQENDR.Q | Y | 53.73 | 1195.4932 | 11 | 1213 | 1223 |
| Q8NFU7\|TET1_HUMAN | K.DSELPTCSCLDR.V | Y | 53.52 | 1226.4948 | 12 | 1466 | 1477 |
| Q8NFU7\|TET1_HUMAN | K.QYAPVAYQNQVEYENVAR.E | Y | 53.31 | 1817.8812 | 18 | 1679 | 1696 |
| Q8NFU7\|TET1_HUMAN | R.DIHNMNNGSTVVCTLTR.E | Y | 53.29 | 1738.9895 | 17 | 1724 | 1740 |
| Q8NFU7\|TET1_HUMAN | K.LSDTDEFGSK.E | Y | 53.18 | 1110.194 | 10 | 1763 | 1772 |
| Q9Y3Y2\|CHTOP_HUMAN | R.ASMQQQQQLASAR.N | Y | 77.5 | 1445.7045 | 13 | 39 | 51 |
| Q9Y3Y2\|CHTOP_HUMAN | R.LAQQMENRPSVQAALK.L | Y | 58.7 | 1782.941 | 16 | 55 | 70 |
| Q9Y3Y2\|CHTOP_HUMAN | K.QPTPVNIR.A | Y | 51.84 | 923.5189 | 8 | 31 | 38 |
| Q9Y3Y2\|CHTOP_HUMAN | R.ASMQQQQQLASAR.N | Y | 61.37 | 1445.7045 | 13 | 39 | 51 |
| Q9Y3Y2\|CHTOP_HUMAN | R.LAQQMENRPSVQAALK.L | Y | 55.43 | 1782.941 | 16 | 55 | 70 |
| Q9Y3Y2\|CHTOP_HUMAN | R.LAQQMENR.P | Y | 38.77 | 988.476 | 8 | 55 | 62 |
| Q9Y3Y2\|CHTOP_HUMAN | R.FTNMLK.N | Y | 36.61 | 752.3891 | 6 | 23 | 28 |
| Q9Y3Y2\|CHTOP_HUMAN | K.QPTPVNIR.A | Y | 35.07 | 923.5189 | 8 | 31 | 38 |
| Q99873\|ANM1_HUMAN | K.WLAPDGLIFPDR.A | Y | 49.46 | 1398.7295 | 12 | 174 | 185 |
| Q99873\|ANM1_HUMAN | K.EVDIYTVK.V | Y | 32.29 | 965.507 | 8 | 244 | 251 |
| Q99873\|ANM1_HUMAN | K.EPLVDVVDPK.Q | Y | 20.95 | 1109.5968 | 10 | 224 | 233 |
| Q99873\|ANM1_HUMAN | K.EPLVDVVDPK.Q | Y | 40.62 | 1109.5968 | 10 | 224 | 233 |
| Q99873\|ANM1_HUMAN | K.LDHVVTIIK.G | Y | 35.64 | 936.828 | 9 | 135 | 143 |
| Q99873\|ANM1_HUMAN | K.WLAPDGLIFPDR.A | Y | 43.19 | 1307.328 | 12 | 184 | 195 |
| Q99873\|ANM1_HUMAN | R.NDYVHALVAYFNIEFTR.C | Y | 17.64 | 1867.2324 | 17 | 277 | 293 |
| Q9UMN6\|KMT2B_HUMAN | R.GRPPLTPSQR.A | Y | 16.37 | 1107.6149 | 10 | 470 | 479 |
| Q9UMN6\|KMT2B_HUMAN | R.GAGGGGGR.G | Y | 68.09 | 879.7152 | 8 | 76 | 83 |
| Q9UMN6\|KMT2B_HUMAN | R.LADVAPTPPK.T | Y | 66.22 | 1061.076 | 10 | 216 | 225 |
| Q9UMN6\|KMT2B_HUMAN | R.GEEGTER.M | Y | 65.62 | 766.4209 | 7 | 232 | 238 |
| Q9UMN6\|KMT2B_HUMAN | K.VEVSPVLR.P | Y | 67.82 | 842.74 | 8 | 607 | 614 |
| Q9UMN6\|KMT2B_HUMAN | R.APTPPSTPVPLPEK.R | Y | 57.82 | 1436.5932 | 14 | 636 | 649 |
| Q9UMN6\|KMT2B_HUMAN | R.PSGPESPVQGPR.I | Y | 55.25 | 1236.7488 | 12 | 906 | 917 |
| Q9UMN6\|KMT2B_HUMAN | R.VQDCGSCVNCLDK.P | Y | 58.51 | 1450.5127 | 13 | 1025 | 1037 |
| Q9UMN6\|KMT2B_HUMAN | K.PTLQPVLQLK.A | Y | 58.61 | 1066.569 | 10 | 1176 | 1185 |
| Q9UMN6\|KMT2B_HUMAN | K.GNYCPICTR.C | Y | 62.22 | 945.3321 | 9 | 1385 | 1393 |
| P35221\|CTNA1_HUMAN | R.VIHVVTSEMDNYEPGVYTEK.V | Y | 107.87 | 2309.0886 | 20 | 552 | 571 |
| P35221\|CTNA1_HUMAN | K.NVPILYTASQAC(+57.02)LQHPDVAAYK.A | Y | 98.65 | 2458.2314 | 22 | 217 | 238 |
| P35221\|CTNA1_HUMAN | R.FTEQVEAAVEALSSDPAQPMDENEFIDASR.L | Y | 96.9 | 3295.4827 | 30 | 587 | 616 |
| P35221\|CTNA1_HUMAN | K.AHVLAASVEQATEN(+.98)FLEK.G | Y | 90.4 | 1956.9792 | 18 | 58 | 75 |
| P25054\|APC_HUMAN | K.SPSEGQTATTSPR.G | Y | 21.32 | 1317.6161 | 13 | 2260 | 2272 |
| P25054\|APC_HUMAN | K.REVPK.N | Y | 17.9 | 627.3704 | 5 | 1450 | 1454 |
| P25054\|APC_HUMAN | M.KEVLK.Q | Y | 16.29 | 615.3955 | 5 | 45 | 49 |
| O60341\|KDM1A_HUMAN | K.DEMVEQEFNR.L | Y | 33.28 | 1047.564 | 10 | 375 | 384 |
| O60341\|KDM1A_HUMAN | R.STSQTFIYK.C | Y | 26.69 | 988.0776 | 9 | 659 | 667 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| O60341\|KDM1A_HUMAN | R.VHSYLER.H | Y | 14.71 | 772.1651 | 7 | 252 | 258 |
| O60341\|KDM1A_HUMAN | R.GELFLFWNLYK.A | Y | 14.84 | 1198.0232 | 11 | 749 | 759 |
| O60341\|KDM1A_HUMAN | R.NGYSCVPVALAEGLDIK.L | Y | 21.61 | 1836.1717 | 17 | 856 | 872 |

**Table S9.** Primers and Oligonucleotides used in this study

| **Primer used for subcloning and plasmid construction:** | |
|---|---|
| RNF219-up | 5’-gccGCTAGCgccATGGAGCAGAAACTCATCTCTGAAGAGGATCTGGCTCAGACCGTGCAGAATGT-3’ |
| RNF219-dn | 5’-gccACTAGTTCAACTTTTAGTTGCTTTTG-3’ |
| RNF219- mutated primer up | 5’-GACGTACCTTCCCCAAGCTAATGTGGCTCGTGATGGGCAGAGTGAGCGAC-3’ |
| RNF219- mutated primer dn | 5’-GTCGCTCACTCTGCCCATCACGAGCCACATTAGCTTGGGGAAGGTACGTC-3’ |
| LGALS3-up | 5’-ATGGCAGACAATTTTTCGC-3’ |
| LGALS3-dn | 5’-TTATATCATGGTATATGAAGCACTG-3’ |
| CTNNA1-up | 5’-gccGCTAGCgccATGGACTACAAGGACGACGATGACAAGACTGCTGTCCATGCAGGC-3’ |
| CTNNA1-dn | 5’-gccACTAGTTTAGATGCTGTCCATAGCTTT-3’ |
| CTNNA1 1aa-290aa-up | 5’-gccGCTAGCgccATGGACTACAAGGACGACGATGACAAGACTGCTGTCCATGCAGGC-3’ |
| CTNNA1 1aa-290aa-dn | 5’-gccACTAGTTTAAATGATTTGTTTGTCAAA-3’ |
| CTNNA1 291aa-650aa-up | 5’-gccGCTAGCgccATGGACTACAAGGACGACGATGACAAGGTGGACCCCTTGAGCTTC-3’ |
| CTNNA1 291aa-650aa-dn | 5’-gccACTAGTTTAGACATCAAAATCTTCTGT-3’ |
| CTNNA1 651aa-906aa-up | 5’-gccGCTAGCgccATGGACTACAAGGACGACGATGACAAGAGAAGCAGGACGAGCGTC-3’ |
| CTNNA1 651aa-906aa-dn | 5’-gccACTAGTTTAGATGCTGTCCATAGCTTT-3’ |
| CTNNB1-up | 5’-ATGGCTACTCAAGCTGATTT-3’ |
| CTNNB1-dn | 5’-TTACAGGTCAGTATCAAACC-3’ |
| TCF4-up | 5’-ATGGACTACAAGGACGACGATGACAAGCCGCAGCTGAACGGCGG-3’ |
| TCF4-dn | 5’-CTATTCTAAAGACTTGGTGA-3’ |
| YAP1-up | 5’-ATGGATCCCGGGCAGCAG-3’ |
| YAP1-dn | 5’-CTATAACCATGTAAGAAAGCTTTCTTTAT-3’ |
| TEAD4-up | 5’-ATGTTGGAGGGCACGGC-3’ |
| TEAD4-dn | 5’-CATTCTTTCACCAGCCTGTAGATG-3’ |
| **Primer used for CAPTURE system** | |
| LGALS3-sgRNA-1 | 5’-ggagaaCCACCTTGTTGGTGTGACTTTGGATTGGGTAATAAAGAGCCGTTTATTGCATGTGTA-3’ |
| LGALS3-sgRNA-2 | 5’-ggagaaCCACCTTGTTGGCCCAGCCACACTGTGACTTCTATGTGCAAGCCTAGAGGGGACGA-3’ |
| LGALS3-sgRNA-3 | 5’-ggagaaCCACCTTGTTGGGCTTCTGTAACAAAATATCATAAACTGGGTAGCTTATAGGCAATA-3’ |
| LGALS3-sgRNA-4 | 5’-ggagaaCCACCTTGTTGGGTCAGTTCCCTAGGGAATAGACATTGAAAAGATTTTTGGTTTTGTA-3’ |
| LGALS3-sgRNA-5 | 5’-ggagaaCCACCTTGTTGGCTGGCGTTCGGGGAAGGTTGGCAGCACCTTACGAGACCCACACA-3’ |
| **Primer used for qPCR** | |
| c-Myc-up | 5’-GGCTCCTGGCAAAAGGTCA-3’ |
| c-Myc-dn | 5’-CTGCGTAGTTGTGCTGATGT-3’ |
| Axin2-up | 5’-CAACACCAGGCGGAACGAA-3’ |
| Axin2-dn | 5’-GCCCAATAAGGAGTGTAAGGACT-3’ |

| | |
|---|---|
| DKK1-up | 5’-CCTTGAACTCGGTTCTCAATTCC-3’ |
| DKK1-dn | 5’-CAATGGTCTGGTACTTATTCCCG-3’ |
| TWIST1-up | 5’-GTCCGCAGTCTTACGAGGAG-3’ |
| TWIST1-dn | 5’-GCTTGAGGGTCTGAATCTTGCT-3’ |
| SOX4-up | 5’-AGCGACAAGATCCCTTTCATTC-3’ |
| SOX4-dn | 5’-CGTTGCCGGACTTCACCTT-3’ |
| GBX2-up | 5’-CCGCCTTCAGCATAGACTCG-3’ |
| GBX2-dn | 5’-GGTAGCCGGTGTAGACGAAAT-3’ |
| CCND1-up | 5’-GGTGGGGTCATGTGTGTGG-3’ |
| CCND1-dn | 5’-CGGTTCAGGTACTCAGTCATCC-3’ |
| BIRC5-up | 5’-AGGACCACCGCATCTCTACAT-3’ |
| BIRC5-dn | 5’-AAGTCTGGCTCGTTCTCAGTG-3’ |
| CYR61-up | 5’-CTCGCCTTAGTCGTCACCC-3’ |
| CYR61-dn | 5’-CGCCGAAGTTGCATTCCAG-3’ |
| SOX2-up | 5’-GCCGAGTGGAAACTTTTGTCG-3’ |
| SOX2-dn | 5’-GGCAGCGTGTACTTATCCTTCT-3’ |
| LGALS3-up | 5’-ATGGCAGACAATTTTTCGCTCC-3’ |
| LGALS3-dn | 5’-GCCTGTCCAGGATAAGCCC-3’ |
| LGR5-up | 5’-CTCCCAGGTCTGGTGTGTTG-3’ |
| LGR5-dn | 5’-GAGGTCTAGGTAGGAGGTGAAG-3’ |
| Cyclin D1-up | 5’-GCTGCGAAGTGGAAACCATC-3’ |
| Cyclin D1-dn | 5’-CCTCCTTCTGCACACATTTGAA-3’ |
| SNAI2-up | 5’-CGAACTGGACACACATACAGTG-3’ |
| SNAI2-dn | 5’-CTGAGGATCTCTGGTTGTGGT-3’ |
| JAG1-up | 5’-GTCCATGCAGAACGTGAACG-3’ |
| JAG1-dn | 5’-GCGGGACTGATACTCCTTGA-3’ |
| CTGF-up | 5’-CAGCATGGACGTTCGTCTG-3’ |
| CTGF-dn | 5’-AACCACGGTTTGGTCCTTGG-3’ |
| AMOTL2-up | 5’-GCTCGTTGAGTGAACGGCT-3’ |
| AMOTL2-dn | 5’-CATGAGCTAGTACAACATGAGGG-3’ |
| IGFBP3-up | 5’-AGAGCACAGATACCCAGAACT-3’ |
| IGFBP3-dn | 5’-GGTGATTCAGTGTGTCTTCCATT-3’ |
| ITGB2-up | 5’-TGCGTCCTCTCTCAGGAGTG-3’ |
| ITGB2-dn | 5’-GGTCCATGATGTCGTCAGCC-3’ |
| GLI2-up | 5’-CTGCCTCCGAGAAGCAAGAAG-3’ |
| GLI2-dn | 5’-GCATGGAATGGTGGCAAGAG-3’ |
| AXL-up | 5’-GTGGGCAACCCAGGGAATATC-3’ |
| AXL-dn | 5’-GTACTGTCCCGTGTCGGAAAG-3’ |

| | |
|---|---|
| RNF219-up | 5’-GCCACATTTGCTTGGGGAAG-3’ |
| RNF219-dn | 5’-GCAAGCTGGACACTGGCTAT-3’ |
| **Primer used for ChIP-qPCR** | |
| LGALS3 P1 RT primer up | 5’-GATGTGACTTTGGATTGGGTAA-3’ |
| LGALS3 P1 RT primer dn | 5’-CTGTGGAGGCAAGGGATG-3’ |
| LGALS3 P2 RT primer up | 5’-CGTGCCAACCACTAAGAC-3’ |
| LGALS3 P2 RT primer dn | 5’-CTGGCTTATGTAAACTATGGAG-3’ |
| LGALS3 P3 RT primer up | 5’-GTCGGGAAATCCAAGATC-3’ |
| LGALS3 P3 RT primer dn | 5’-CACGGTGATGTATTAGGAAG-3’ |
| LGALS3 P4 RT primer up | 5’-AAGATTTTTGGTTTTGTATTCTACA-3’ |
| LGALS3 P4 RT primer dn | 5’-GCCACCGTTAGGTTCCGT-3’ |
| LGALS3 P5 RT primer up | 5’-CAGCCAACGAGCGGTGAG-3’ |
| LGALS3 P5 RT primer dn | 5’-CCTGGAGGGCAGAGCACA-3’ |
| RNF219 RT primer up | 5’-AGCGCACCGTGATTAATGGA-3’ |
| RNF219 RT primer dn | 5’-TATCCCTGCGATGCGTTTCT-3’ |
| **Primer used for 5-hmC / 5-mC Analysis** | |
| Control primer 1: | 5’-CTGTCATGGTGACAAAGGCATC-3’ |
| Control primer 2: | 5’-CAGGATTTCTCTATTATGAAGACCTTG-3’ |
| **SiRNA** | |
| Si RNF219#1 | 5’-CACTGGATTTGGATGGGTTAT-3’ |
| Si RNF219#2 | 5’-ATAACCCATCCAAATCCAGTG-3’ |
| Si LGALS3#1 | 5’-TGCTGATAACAATTCTGGGCAC-3’ |
| Si LGALS3#2 | 5’-TGAAGCGTGGGTTAAAGTGGA-3’ |
| Si CTNNB1#1 | 5’-CGCATGGAAGAAATAGTTGAA-3’ |
| Si CTNNB1#2 | 5’-GCTTGGAATGAGACTGCTGAT-3’ |
| Si YAP1#1 | 5’-CAGGTGATACTATCAACCAAA-3’ |
| Si YAP1#2 | 5’-TTTGGTTGATAGTATCACCTG-3’ |
| Si TET1#1 | 5’-CCTCCAGTCTTAATAAGGTTA-3’ |
| Si TET1#2 | 5’-TAACCTTATTAAGACTGGAGG-3’ |
| Si MLL4#1 | 5’-CGAATGGAAGAACAACGTGTA-3’ |
| Si MLL4#2 | 5’-TACACGTTGTTCTTCCATTCG-3’ |
| Si PRMT1#1 | 5’-TGAGCGTTCCTAGGCGGTTTC-3’ |
| Si PRMT1#2 | 5’-GAAACCGCCTAGGAACGCTCA-3’ |
| Si CHTOP#1 | 5’-TTTACAGATGTGTTGACTAAC-3’ |
| Si CHTOP#2 | 5’-ATCCAATTGGTTGTCCAGCTG-3’ |

## Abbreviations list

**LGALS3**, galectin 3; **ELISA**, enzyme-linked immunosorbent; **IF**, immunofluorescence; **µCT**, micro-CT; **RNF219**, ring finger protein 219; **IB**, immunoblotting; **IHC**, immunohistochemistry; **YAP1**, Yes1 associated transcriptional regulator; **CAPTURE**, CRISPR affinity purification in situ of regulatory elements; **co-IP**, co-immunoprecipitation; **ChIP**, chromatin immunoprecipitation; **BM**, bone metastasis; **HCC-BM**, HCC with bone metastasis; **SREs**, skeletal-related events; **TRAP**, tartrate-resistant acid phosphatase; **MMPs**, matrix metalloproteinases; -mu, mutated; **ShRNAs**, short hairpin RNAs; **TCF/LEF1**, T cell factor / lymphoid enhancer factor 1; **TEAD**, TEA domain; **siRNAs**, short interfering RNAs; **FB-dCas9**, N-terminal Flag and biotin-acceptor-site (FB)-tagged dCas9; **dCas9**, dead Cas9 **sgRNAs**, small guide RNAs; **DNMT1**, DNA methyltransferase 1; **CHTOP**, chromatin target of PRMT1; **PRMT1**, protein arginine methyltransferase 1; **TET1**, tet methylcytosine dioxygenase 1; **MLL4**, lysine methyltransferase 2D; **APC**, APC regulator of WNT signaling pathway; **LSD1**, lysine demethylase 1; **H3K4me3**, Histone H3 (tri methyl K4); **H4R3me1**, Histone H4 (mono methyl R3); **H4R3me2a**, Histone H4R3 Dimethyl Asymmetric; **H3R2me1**, Histone H3 (mono methyl R2); **H3R2me2s**, Histone H3 (symmetric di methyl R2); **H3R8me2s**, Histone H3 (symmetric di methyl R8); **c-SRC**, SRC proto-oncogene, non-receptor tyrosine kinase; **p-SYK**, phosphorylation-spleen associated tyrosine kinase; **p-VAV-3**, phosphorylation-vav guanine nucleotide exchange factor 3; **RAC1**, Rac family small GTPase 1; **CD98**, solute carrier family 7 member 5; **H3**, Histone 3; **CM**, conditioned media; w/v, weight/volume; **αvβ3**, integrin αVβ3; **BSA**, albumin from bovine serum; **DAPI**, 4',6-diamidino-2-phenylindole; **SI**, staining index; **TGF-β**, transforming growth factor beta 1;

**RANKL**, TNF superfamily member 11; **OPG**, TNF receptor superfamily member 11b; **MTT**, 3-(4, 5-Dimethylthiazol-2-yl)-2, 5- diphenyltetrazolium bromide; **DMSO**, dimethyl sulfoxide; **SEM**, scanning electron microscopy; **H&E stained**, hematoxylin-eosin staining; **ALP**, Alkaline phosphatase; **BLI**, bioluminescence imaging; **BMD**, bone mineral density; **OC**, osteoclast; **OP**, osteoclast precursor; **M-CSF**, macrophage-colony stimulating factor; **C-fos**, fos proto-oncogene; **AP-1**, transcription factor subunit; **Acp5**, acid phosphatase 5, tartrate resistant (TRAP); **Ctsk**, cathepsin K; **Nfat-c1**, nuclear factor of activated T cells, cytoplasmic, calcineurin dependent 1; **Dc-stamp**, dendrocyte expressed seven transmembrane protein; **qPCR**, quantitative Real-time PCR; **VH domain**, vinculin homology domain; **5mC/5hmC**, 5-methylcytosine/5-hydroxymethylcytosine; **WDR5**, WD repeat domain 5; **FDA**, Food and Drug Administration;