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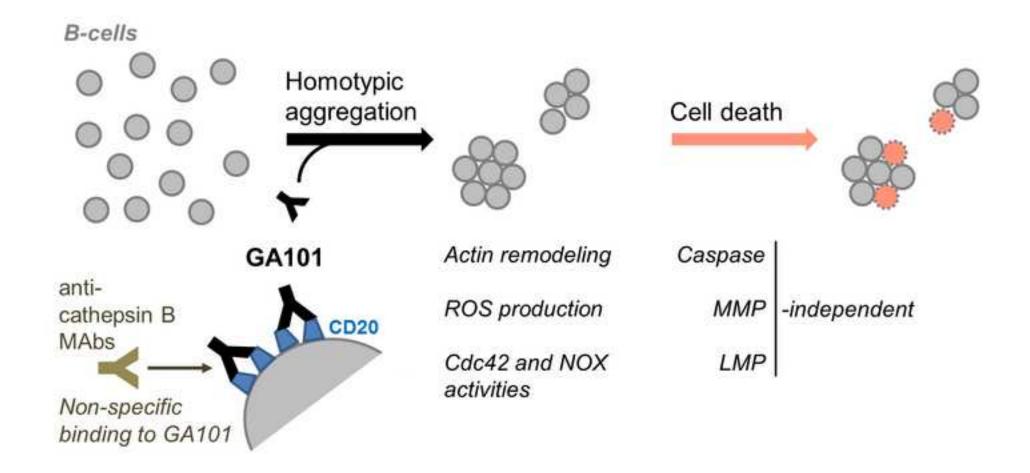
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*Highlights

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Lysosomal and mitochondrial permeabilization events do not occur in response to GA101

Several commercially available anti-cathepsin B antibodies recognize GA101

Cell killing by GA101 (obinutuzumab, Gazyva) may be cathepsin-independent

Cdc42 and NOX-dependent ROS production are possibly involved in GA101 cytotoxicity

Unexpected cross-reactivity of anti-cathepsin B antibodies leads to uncertainties regarding the mechanism of action of anti-CD20 monoclonal antibody GA101

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Abstract

GA101, also known as obinutuzumab or Gazyva (Gazyvaro), is a glycoengineered type II humanized antibody that targets the CD20 antigen expressed at the surface of B-cells. This novel anti-CD20 antibody is currently assessed in clinical trials with promising results as a single agent or as part of therapeutic combinations for the treatment of B-cell malignancies. Detailed understanding of the mechanisms of GA101-induced cell death is needed to get insight into possible resistance mechanisms occurring in patients. Although multiple in vitro and in vivo mechanisms have been suggested to describe the effects of GA101 on B-cells, currently available data are ambiguous. The aim of our study was to clarify the cellular mechanisms involved in GA101-induced cell death in vitro, and more particularly the respective roles played by lysosomal and mitochondrial membrane permeabilization. Our results confirm previous reports suggesting that GA101 triggers homotypic adhesion and caspase-independent cell death, two processes that are dependent on actin remodeling and involve the production of reactive oxygen species. With respect to lysosomal membrane permeabilization (LMP), our data suggest that lack of specificity of available antibodies directed against cathepsin B may have confounded previously published results, possibly challenging current LMP-driven model of GA101 action mode.

Key words:

Antibody-based immunotherapy, GA101, CD20, cathepsin B, lysosomal permeabilization, lymphomas, cell death

1. Introduction

The CD20 protein, which is selectively expressed on precursor and mature B cells, has been validated as a target antigen for immunotherapy in B-cell malignancies. Rituximab, a Type I chimeric (human/mouse) IgG1 anti-CD20 antibody, was approved for the treatment of patients with B-cell non-Hodgkin lymphoma (NHL) as far back as the late nineties. It has been shown that rituximab binding to CD20 may cause cell death through three distinct mechanisms: (1) activation of complement-dependent cytotoxicity (CDC) after CD20 relocalization into lipid rafts; (2) initiation of antibody-dependent cellular cytotoxicity (ADCC) and phagocytosis (ADCP) via Fc region binding to Fcγ receptors (FcγR) on innate immune effectors such as natural killer cells and macrophages; (3) direct induction of programmed cell death (PCD) [1-5]. Addition of rituximab to standard chemotherapy improves the clinical outcome of patients with NHL and chronic lymphocytic leukemia (CLL). However, a significant percentage (30-50%) of rituximab-treated patients fail to achieve complete or partial remission, and many experience disease relapse [3, 4, 6-14]. This has prompted research efforts to develop novel anti-CD20 antibodies with improved functional properties and greater clinical efficacy [5].

Obinutuzumab (GA101) is a Type II humanized mouse IgG1κ anti-CD20 antibody with a glycoengineered Fc fragment [15] to enhance Fc receptor binding affinity (in particular for FcγRIIIa). GA101 is currently under phase III clinical trials for the treatment of patients with NHL [16, 17] and has been approved for patients with previously untreated CLL [18-21]. In vivo studies have indicated superior anti-lymphoma activity for this third-generation anti-CD20 antibody over rituximab [15, 22, 23]. Positional mapping showed that the epitope of GA101 partially overlaps the epitope of rituximab and extends towards the C-terminus of CD20 which contributes to the high binding affinity of GA101 for CD20 [5, 15, 24]. Protein

tomography analysis indicated that, contrary to rituximab bivalent binding to CD20, GA101 preferentially binds to CD20 monovalently, which favors intra- rather than inter-CD20 tetramer binding [5, 24, 25]. Both structural features and CD20-binding characteristics of GA101 make it different from rituximab in terms of mode of action: GA101 does not provoke CD20 relocalization in lipid rafts and subsequent CDC, but induces stronger homotypic adhesion (HA) and direct PCD [5, 15]. In addition, the glycoengineered fragment of GA101 leads to enhanced ADCC and ADCP activity [1, 2, 15, 26, 27].

Although rituximab has been demonstrated to induce apoptosis of non-Hodgkin lymphoma cell lines in vitro [28, 29], evidence from numerous investigations does not appear to support this observation especially in the in vivo context [30-37]. For its part, GA101 is thought to trigger non-apoptotic (necrotic-like) cell death without the need of CD20 cross-linking. The current proposal on the sequence of events leading to GA101-induced "programmed necrosis" is as follows: (i) binding of GA101 to the extracellular domain of CD20 followed by HA, (ii) peripheral reorganization of the actin cytoskeleton, (iii) lysosomal membrane permeabilization (LMP), (iv) cathepsin B release to the cytosol, (v) NADPH oxidase (NOX)-mediated (i.e., non-mitochondrial) reactive oxygen species (ROS) production, and (iv) loss of plasma membrane integrity [38, 39].

However, not all cells die by caspase-independent cell death upon exposure to GA101 as both procaspase-3 overexpression and caspase-3 activation were reported in the human non-Hodgkin's lymphoma B cell line RL cells [40]. Moreover, cell surface exposure of phosphatidylserine (PS) was consistently observed upon GA101 treatment in a variety of cell lines, raising the possibility of a transition from apoptosis to secondary necrosis for a fraction of the B-cell population [15, 40]. In fact, there is evidence that GA101 can induce mitochondrial membrane permeabilization (MMP) [39, 41], but this event was considered as secondary to LMP and cathepsin B release [39]. The ability of GA101 to trigger necrosis,

apoptosis or both may reflect features of the same cell death pathway that converge on mitochondria and/or lysosomes in a cell type- and/or context-specific manner. Alternatively, the choice of GA101-induced cell death by necrosis or apoptosis may depend on which of the two events occurs first: LMP or MMP.

Motivated by these concerns, we sought to undertake an accurate kinetic analysis of LMP and MMP in GA101-treated B cells. The present study was also carried out with the premise that detailed understanding of the role of mitochondria and lysosomes in GA101-induced cell death can provide insights for GA101 use in therapy and help overcome possible resistance mechanisms.

2. Material and Methods

2.1. Cell culture and treatments

Raji or SUDHL-4 cells were cultured in RPMI 1640 medium (PAA) containing 10% fetal calf serum, 2mM L-glutamine, 100 units penicillin, and 100µg streptomycin. Cells were seeded at 0.5 x 10⁶ cells/mL and treated with 10µg/ml of GA101 (provided by Roche Pharma) or rituximab (MabThera Lot: H0623, Roche) for different periods of time.

2.2. HA assay

Cells were seeded in 8-well imaging chambers (Zell-Kontakt, Germany) and recorded every 5min for 24h using phase-contrast time-lapse videomicroscopy (inverted Axiovert 100M, Zeiss) in an environment at 37°C with 5% CO2. In other experiments, microphotographs of untreated cells and cells receiving pre-treatment with different inhibitors or treatment by GA101 were taken using an inverted Leica microscope. Images were processed using ImageJ software.

2.3. Cell death analysis by flow cytometry

In a first set of experiments, cells were treated with GA101 or Rituximab for 6, 12, 24 and 48h or left untreated. Treated cells were harvested by centrifugation at 1800rpm for 5 min and resuspended in 100µL of Annexin V/propidium iodide labeling solution (Annexin-V-FLUOS Staining kit, Roche). Cells were then analyzed by flow cytometry (Becton Dickinson, LSR II) after an incubation period of 15min in the dark at room temperature.

In a second set of experiments, cells were first pre-treated with different inhibitors for 1 or 2h: Latrunculin B (Enzo Life Science), Tiron (Sigma-Aldrich), Z-VAD-FMK, Z-DEVD-FMK, Z-IETD-FMK, Z-LEHD-FMK (BD biosciences), CA-074-Me (Calbiochem), GW4869 (Calbiochem), Nec-1s (Calbiochem), diphenyleneiodonium (Calbiochem), ML141 (Santa

Cruz). The cells were then left untreated or were treated with GA101 for 6h and analyzed by flow cytometry after AV/PI labeling.

2.4. ROS detection

10⁶ cells were first pre-treated for 2h with different inhibitors: Latrunculin B, Tiron, DPI, or ML141, and then treated with GA101 and the ROS marker carboxy-H2DCFDA (25mM, Molecular Probes) for 30min, 1h, 3h, 6h or left untreated. Carboxy-H2DCFDA is oxidized in the presence of ROS to carboxy-DCF, which emits green fluorescence. ROS detection was analyzed by flow cytometry and data were processed using the FlowJo software.

2.5. Subcellular fractionation

Cells (4x10⁷) were harvested 4h after treatment with GA101 and rinsed in cold SET buffer (250mM sucrose, 1mM EDTA, 10mM Tris, pH 7.4) by centrifugation at 1200rpm for 5min. Cells were resuspended in 0.5mL of cold SET buffer containing ETDA-free anti-protease cocktail (APC, Roche) and then subjected to 30 strokes on ice using a Dounce homogenizer. A centrifugation at 1000g at 4°C for 10min was performed to separate supernatant from cell/nuclei pellet. The supernatant was collected and the pellet was resuspended in 0.5mL of cold SET buffer containing APC. The suspension was then subjected to another 30 strokes and to centrifugation as described above. The supernatants were pooled and centrifuged at 20000g, 4°C for 20 min. The pellet was washed with 1mL SET buffer containing APC and lysed with 50μL of lysis buffer (Thermo Scientific) to obtain a mitochondria/lysosome fraction. The supernatant was ultracentrifuged at 100000g at 4°C for 60 min. The supernatant (corresponding to the cytosol fraction) was collected and the pellet was resuspended in 50 μL of lysis buffer to obtain a vesicle-rich fraction. To obtain only the mitochondria/lysosome and cytosolic fractions, treated cells were subjected to the same protocol with SE buffer (250 mM

sucrose, 1mM EDTA, pH 7.4) instead of SET solution, skipping out the ultracentrifugation step.

2.6. Antibodies

Primary antibodies used were mouse anti-LAMP1 (Abcam), anti-bovine serum albumin (ab79872, Abcam), anti-PDK1 (ab110025, Abcam), anti-cytochrome C (MAB897, BD Pharmingen), anti-β-actin (A-5441, Sigma), anti-α-tubulin (sc-32293, Santa Cruz), and rabbit anti-cathepsin B (EML-SA361, Enzo), anti-cathepsin B (ab30443, Abcam), anti-cathepsin B (sc-13985, Santa Cruz), anti-cathepsin D (ab75852, Abcam), anti-AIF (551429, BD Pharmingen), anti-endonuclease G (3035, ProSci), anti-activated caspase-3 (9661, Cell Signaling), anti-caspase-3 (9662, Cell Signaling). Peroxidase-conjugated secondary antibodies were as follows: rabbit anti-mouse (P0161, Dako), and goat anti-rabbit (12-348, Millipore Corporation) antibodies.

Supplementary Materials and Methods are available.

3. Results

3.1. GA101 treatment induces rapid and sustained homotypic adhesion

To test the effect of GA101 on cell-cell adhesion, we selected Raji cells, a prototypical chemoresistant BL-derived cell line expressing high level of CD20 (data not shown). As shown in **Fig. 1**, under normal culture conditions, Raji cells displayed a natural tendency to form clusters. Within 1h of treatment by GA101, adjacent cells underwent marked HA, forming large cellular aggregates. Rituximab also induced HA of Raji cells, with virtually similar kinetics. We also observed that the addition of GA101 or rituximab to SUDHL-4 cells, a human diffuse large B-cell lymphoma cell line, also triggered HA, albeit with distinct kinetics (GA101: ~ 1h; rituximab: ~ 4h) (**Supplementary Fig. 1**). Thus, although HA seems to be of larger amplitude and higher velocity with GA101, induction of this phenomenon is not restricted to this mAb and appears to be a shared property with rituximab.

3.2. GA101-treated cells undergo cell death through a caspase-independent pathway

Apoptosis and necrosis are two types of cell death with distinct morphological and biochemical features. Apoptotic cells are often characterized by fragmented nuclei, PS surface exposure, separation of cell fragments into apoptotic bodies, whereas necrotic cells are mainly defined by loss of plasma membrane integrity and swelling of cellular organelles including mitochondria [42]. Although programmed necrosis has been suggested to represent the major route to cell death in GA101-treated cells [38, 39], GA101 has also been reported to trigger cell death showing a mixture of hallmarks typically found in apoptosis and necrosis [15, 40]. To gain further insight into this issue, we performed dual staining with fluorescent Annexin V (AV) and propidium iodide (PI) (on mechanically dissociated cells) followed by flow cytometry to distinguish between apoptotic and necrotic cell populations following treatment by GA101. In this test, AV+ (positive)/PI- (negative) cells are classically considered as

apoptotic cells and PI+cells as necrotic cells. However, it is the movement of cells from AV-/PI- status (viable) to AV+/PI- (early apoptotic cells with membrane integrity) and eventually to AV+/PI+ (end stage apoptosis or secondary necrosis, with plasma membrane rupture) which is truly indicative of apoptosis (AV-/PI+ cells corresponding to primary necrotic cells). As shown in Fig. 2A, GA101 treatment reduced the viable cell fraction by 60% 6h post-treatment. Approximately 20% of GA101-treated cells showed AV+/PI- staining at 6h, and the proportion of AV+/PI- cells gradually diminished to less than 2% at 48h post-treatment. The proportion of AV+/PI+ cells followed a similar pattern, whereas the percentage of AV-/PI+ cells, which was about 4% at 6h, roughly doubled during the assessed time points to reach 30% at 48h. Rituximab was less efficient than GA101 in inducing the death of Raji cells and AV+/PI+ dead cells were only marginally detected after treatment with this antibody (Fig. 2A). Our results indicate that GA101 addition did not result in the classical phenotypic pattern of cells transitioning from early apoptosis to late apoptosis and necrosis.

Pre-treatment with a pan-caspase chemical inhibitor or with caspase selective inhibitors had almost no effect on the proportion of cells stained with AV and/or PI (Fig. 2B), further suggesting that this cell death is not induced through a caspase-dependent apoptotic pathway. These observations suggest that either (i) GA101 promotes caspase-independent apoptosis in a subpopulation of Raji cells and necrosis in another subpopulation of the cell culture, (ii) or that the process by which cells undergo their demise exhibit both apoptotic-like and necrotic-like signatures. Note that induction of cell death by GA101 also appears to be independent of RIPK1 (a necrosis mediator) or sphingomyelinase (an apoptotic mediator) activity (Supplementary Fig. 2).

3.3. Inhibition of actin remodeling and oxidative damage but not of cathepsin B activity can protect cells against GA101-induced cell death

Reorganization of cortical actin cytoskeleton and production of ROS by NOX following cytosolic release of active cathepsin B from lysosomes have been suggested to play a key role in GA101-induced cell death of B-lymphoma cells [38, 39]. Here, we examined the effect of inhibiting actin polymerization (with Latrunculin B, Lat B), cathepsin B activity (with CA-074-Me, a membrane-permeable selective inhibitor of this enzyme) or ROS function (by using the ROS scavenger Tiron) on the death of Raji cells cultured in presence of GA101. As shown in **Fig. 2C**, the death of GA101-treated cells was fully prevented when the cells were pre-treated with LatB, confirming the upstream role of actin remodeling in the death cascade. Pre-treatment with Tiron partially reduced cell mortality after GA101 treatment, mainly by decreasing the percentage of AV+/PI+ (27%) and AV-/PI+ cells (11%). In contrast, pre-treatment with CA-074-Me could not rescue Raji cells from GA101-induced death (**Fig. 2C**). These results demonstrate that actin reorganization and ROS production are involved in the

induction of cell death by GA101, but challenge a role for cathepsin B in this process. We thus decided to undertake biochemical experiments to formally determine whether or not LMP and/or MMP occur in response to GA101 addition.

3.4. MMP and LMP do not occur in response to GA101

To determine whether MMP takes place during GA101-induced cell death, we analyzed the localization of a panel of mitochondrial proteins following GA101 treatment: PDK1, a mitochondrial matrix protein, and Cytochrome c (Cyt-c), Endonuclease G (EndoG) and AIF, three mitochondrial intermembrane proteins respectively involved in apoptosis (Cyt-c) or caspase-independent cell death (EndoG, AIF). Untreated cells and GA101-treated cells were subjected to subcellular fractionation to obtain a fraction enriched in mitochondria and lysosomes (Mito/Lyso) and a cytosolic fraction. As shown in **Fig. 3A**, at each time point, the abundance of PDK1, Cyt-c, EndoG and AIF in the Mito/Lyso fraction of GA101-treated cells

was nearly identical to that found in the Mito/Lyso fraction of untreated cells. Importantly, no significant release of these proteins into the cytosol or change in their amount in the Mito/Lyso fraction was detected with GA101-treated cells (except for EndoG, which was slightly more abundant in the Mito/Lyso fraction following GA101 treatment). Similarly, there was no observable increase in the quantity of active caspase-3 in the cytosolic fraction of GA101-treated cells, compared to controls (**Fig. 3A**). UVB-induced cleavage of caspase-3 and cytosolic release of Cyt-c were used as positive controls for MMP (**Supplementary Fig. 3**). Collectively, these data indicate that GA101 treatment did not trigger MMP and processing of the effector caspase-3.

In parallel, we analyzed if LMP, assessed by the release of active cathepsin B from lysosomes into the cytosol, occurred following GA101 treatment. Because cathepsin B can be detected in non-lysosomal compartments such as secretory granules [43-45], subcellular fractionation was conducted using lysates from untreated cells or GA101-treated cells to generate a cytosolic fraction, a Mito/Lyso fraction and a fraction containing vesicles (including Golgi- or microtubule-associated vesicles, endosomal and secretory vesicles). Cathepsin B usually exists as three forms: two pro-enzyme forms (38 kDa and 44 kDa, respectively) and an active form (31 kDa) [46, 47]. As shown in Fig. 3B, in untreated cells, active cathepsin B was detected in the Mito/Lyso and vesicle fractions but not in the cytosolic fraction. However, contrary to expectations, active cathepsin B was not found in the cytosolic fraction following GA101 treatment. This observation was extended to another lysosomal protein, cathepsin D, which like cathepsin B was not released from lysosomes to the cytosol upon exposure to GA101 (Fig. 3B) (note that cytosolic release of cathepsin D was observed after H₂O₂ treatment, see Supplementary Fig. 4). In addition, in contrast to a previous report [38], active cathepsin B was not released into the extracellular medium after GA101 treatment. Like

cathepsin B, the active form of cathepsin D was also undetectable in the extracellular medium derived from GA101-treated samples (**Fig. 4A**, upper panel, lanes 1-6).

Taken together, these results demonstrate that based on biochemical experiments, MMP and LMP do not occur in cells in response to GA101 treatment.

3.5. Polyclonal antibody ab30443 non-specifically binds to GA101

Our findings showing that GA101 does not trigger neither MMP nor LMP were in conflict with previously published data [38]. One possible explanation for this discrepancy was the use of different antibodies against cathepsin B. The authors of the above-cited publication used a rabbit serum polyclonal anti-cathepsin B antibody (ab30443) purchased from the Abcam company (Dr. Honeychurch, personal communication), while we used a commercial rabbit polyclonal antibody from Santa Cruz (sc-13985). As shown in Fig. 5A, antibody ab30443 revealed a clear signal at around 30 kDa when tested by western blot on the Mito/Lyso fractions derived from GA101-treated cells. This antibody also gave a positive signal with the extracellular medium (Fig. 5B) but not the cytosolic fraction of cells treated with GA101 (Fig. 5A), a result seemingly consistent with previously published observations [38]. However, quite surprisingly, a signal of identical molecular mass was also detected in samples of pure culture medium conditioned with GA101 in the complete absence of cells (**Fig. 4A**, lower panel, lanes 7-9). Furthermore, when we treated CD20-negative Jurkat cells with GA101 (i.e., human T lymphocytes which are not expected to react to GA101), we still observed a strong signal in the extracellular medium sample when probing the membrane with antibody ab30443 but not with antibody sc-13985 (Fig. 4B). A reasonable explanation for this unexpected finding is that ab30443 antibodies actually recognize GA101 chains (presumably the light chain which has an estimated MW of 24 kDa, CHEMBL1743048) instead of (or in addition to) cathepsin B.

In support to this hypothesis, we showed by immunofluorescence that ab30443 stained the surface and the pericortical region of GA101-treated Raji cells, and that this staining did not colocalize with the lysosomal compartment (**Supplementary Fig. 5**, upper panels). In contrast, by using the antibody sc-13985 specific to cathepsin B, we obtained a cytoplasmic labeling of cathepsin B in both non-treated and GA101-treated cells. In both cell populations, this antibody yielded a staining pattern consistent with partial colocalization with the lysosomal marker LAMP-1 (**Supplementary Fig. 5**, bottom panels).

During the course of this study, we also found that, in addition to ab30443, another commercially available rabbit serum polyclonal anti-cathepsin B antibody, EML-SA361, has an irrelevant specificity towards GA101 antibody chains (**Supplementary Table 1, Fig. 4A**, lower panel, lanes 7-9 and **Supplementary Fig. 6**). Altogether, our data point to major issues in the specificity of several commercial antibodies directed against cathepsin B when they are used in experiments in which GA101 or other related antibodies are present.

3.6. The activation status of major signaling and apoptotic molecules is only minimally modified by GA101 exposure

Since GA101-induced cell death did not seem to require MMP or LMP, we were interested in dissecting upstream signaling events that link GA101-CD20 ligation and commitment to cell death. We used a protein array strategy to examine the activation status of key signaling molecules at baseline or after treatment with GA101. Changes in the phosphorylation of various well-known actors of survival- and apoptosis-regulatory pathways were analyzed at different time after antibody addition. The phosphorylation levels of most of the analyzed proteins did not vary in response to GA101, compared to untreated samples (**Supplementary Fig. 7**).

3.7. Possible involvement of the Rho GTPase Cdc42 and NOX-dependent ROS production in GA101-induced cytotoxicity

We next devoted efforts to investigate the link between the early response (actin remodeling and HA) of B-lymphoma cells to GA101 and subsequent cell death events (i.e. increased oxidative stress). It has been reported that Cdc42, a member of the Rho family of GTPases, regulates actin reorganization and NOX-mediated ROS production [48], and can be activated in response to several cytotoxic chemicals (e.g. arsenic, ethanol and mycophenolic acid) [49-51]. Therefore, we investigated a potential role of Cdc42 in GA101-induced HA and cell death. Pre-treatment with the Cdc42 GTPase inhibitor ML141 or with the NOX inhibitor DPI prevented HA of Raji cells treated by GA101 (Supplementary Fig. 8A) and partially rescued these cells from GA101-induced cell death (Supplementary Fig. 8B). Pre-incubation with Lat B or DPI significantly reduced ROS production at 3h and 6h post-treatment, compared to cells pre-incubated with DMSO. In contrast, pre-treatment with ML141 could not prevent ROS production and even exacerbated it (Supplementary Fig. 8C). These results based on the use of chemical inhibitors suggest that in response to GA101 (i) the activities of Cdc42 and NOX may be involved in the induction of cell death; (ii) both actin remodeling and NOX activity may be implicated in HA and ROS production; (iii) Cdc42 activity may control HA but not ROS production.

4. Discussion

Previous studies on human cellular models have produced ambiguous results about the modality by which B-cells die in vitro upon GA101 treatment [15, 38-41], leaving the process of GA101-induced cell killing unclear. The aim of our study was to clarify the mode of cell death induced by GA101 in vitro, and in particular the potential involvement of lysosomal (LMP) and mitochondrial permeabilization (MMP) events. We provided definitive evidence that GA101 triggers HA and death of B-cells in culture, two processes absolutely dependent on actin remodeling and involving ROS production, as previously published [38, 39]. Our results showed that GA101 triggers a form of caspase-independent cell death exhibiting both apoptotic and necrotic features, also consistent with previous reports [38, 40].

Unexpectedly, by using biochemical techniques, we failed to detect clear evidence of MMP and LMP in GA101-treated cells, contrary to the literature [38, 39, 41]. In previous reports, LMP was inferred partly based on increased Lysotracker red or acridin orange stainings [38, 39]. However, general decrease in intracellular pH (as detected by lysotracker or acridine orange and incorrectly defined as LMP) might or might not be accompanied by LMP. The second argument in support of LMP relates to the fact that cathepsin B was seemingly detected in the extracellular medium of GA101-treated cells, contrary to Rituximab-treated cells or control cells (see Figure 6C in [38]; but note that signal saturation is obvious for BSA in the GA101 lane compared to Rituximab, resulting in a wrong quantitation of Cathepsin B signals). Increased cathepsin D expression was also previously reported in GA101-treated multicellular aggregates of lymphoma cells [41], but experiments were made using total cell lysates (prior to western blot analysis) (Dr. Bezombes, personal communication) and therefore do not provide any information as to whether cathepsin D was genuinely released from lysosomes. In our hands, lysosomal release of cathepsins B and D, assessed using specific

antibodies after cell fractionation, was not observed in GA101-treated Raji or SUDHL-4 cells. We therefore argue that lack of specificity of the commercial ab30443 antibody against cathepsin B probably resulted in misleading interpretations of cathepsin B release from lysosomes or secretion into the extracellular medium in response to GA101 treatment. This unexpected finding challenges current assumptions about the action mode of GA101 [38, 39, 41].

5. Conclusions

Although GA101 represents a promising new option for patients with B-cell malignancies, its mechanism of action remains enigmatic, at least in vitro. GA101-CD20 ligation is followed by an asynchronous process of cell mortality that do not strictly conform the criteria of apoptosis or programmed necrosis, two genetically-determined programs of cell death. The fact that HA represents a linchpin in GA101 action mode suggests that direct plasmamembrane-associated events (e.g. Cdc42 and NOX activities), physical stress due to HA or aggregation-induced aberrant genetic expression might play a role in the death sentence.

Author contributions

WWC organized the investigation, performed the experiments, analyzed data, interpreted results, prepared all figures/tables, and wrote the manuscript text. CN performed the experiments and analyzed data. LL and ACT performed the experiments. RJ performed protein array quantification. JK, AS and GS assisted to the research design and contributed to critical analysis of the results. AA directed, oversaw the research design, assisted in the experiment design, interpreted results and wrote the manuscript text. All co-authors critically reviewed the manuscript and all approved its final version.

Disclosures/conflict of interest

AS is employee of Institut Roche. The remaining authors declare no competing financial interests.

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Figure legends

Figure 1: GA101 or rituximab induce homotypic adhesion of Raji cells.

Microphotographs of control cells and cells treated with GA101 or rituximab (10 μ g/ml) were taken at 1, 4, 8, 12 and 20 h post-treatment using phase contrast videomicroscopy (Objective: 10x, scale bar: 100 μ m). Identical experiments were carried out using SUDHL-4 cells leading to similar results (not shown).

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Figure 3: MMP and LMP do not occur following GA101 treatment. (A) Cells were left untreated or treated with $10 \mu g/ml$ of GA101 for 6, 12 or 24 h, and subcellular fractionation followed by western blot analysis was performed. Abundance of the assayed mitochondrial

proteins in the mitochondria/lysosome (Mito/Lyso) fraction and in the cytosolic fraction was analyzed by western blotting. The MW (kDa) of each protein is indicated. At each time point, the abundance of PDK1, cytochrome C, Endonuclease G, and AIF in the Mito/Lyso fraction of GA101-treated Raji cells was similar to that found in the Mito/Lyso fraction of untreated cells. The presence of these proteins only in the Mito/Lyso fraction but not in the cytosolic fraction shows that subcellular fractionation was successful. No significant increase was observed in the quantity of the assayed proteins or in that of active caspase-3 in the cytosolic fraction of GA101-treated Raji cells, compared to controls. Note that actin, which was used as control for equal loading, was less abundant in the Mito/Lyso fraction after GA101 addition.

(B) Cells were left untreated or treated with 10 µg/ml of GA101 for 6 h, followed by subcellular fractionation. Abundance of lysosomal-associated membrane protein 1 (LAMP1), cathepsin B (labeled using antibody sc-13985) and cathepsin D in the mitochondria/lysosome (Mito/Lyso) fraction, in the cytosolic fraction and in the vesicle-rich fraction was analyzed by western blot. The MW (kDa) of each protein is indicated. NT: non-treated, GA: GA101. Similar results were obtained using SUDHL-4 cells (not shown).

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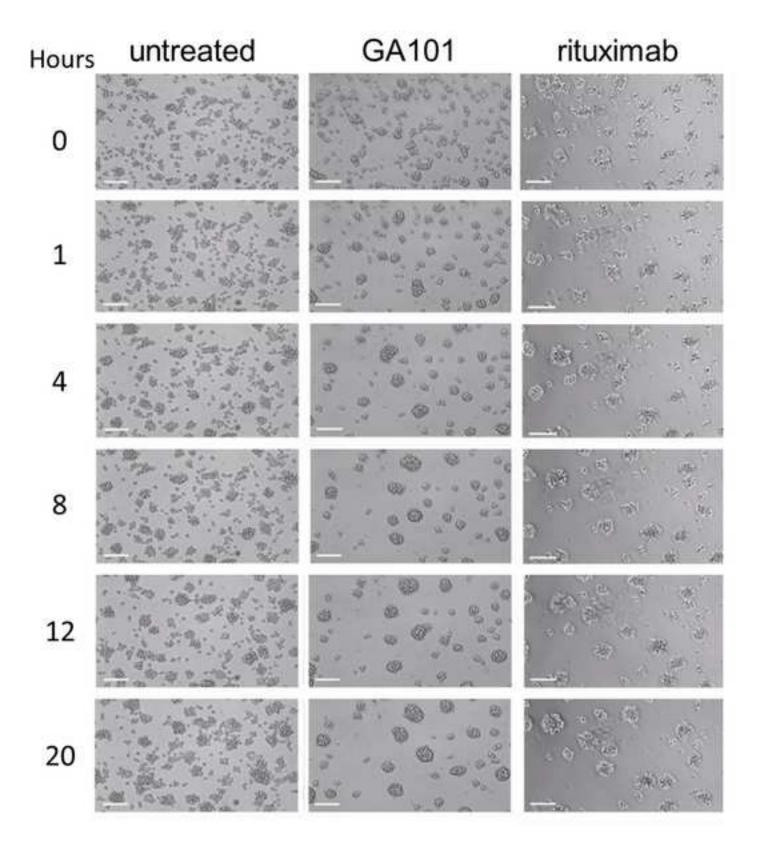


Figure2
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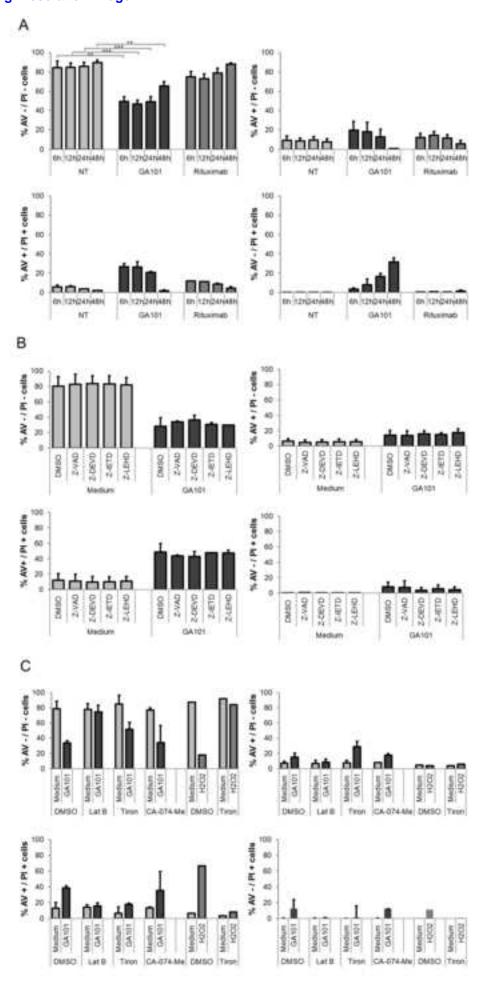
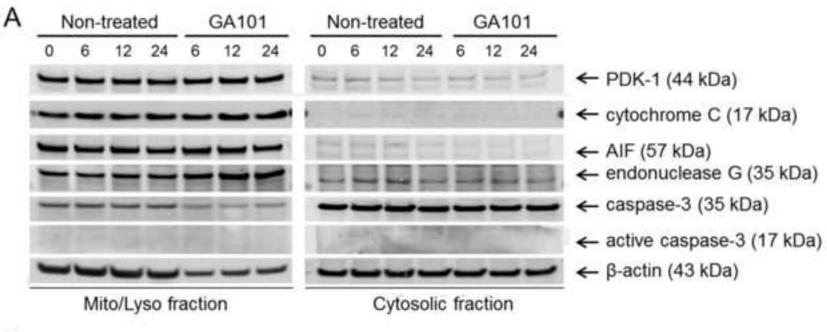


Figure3
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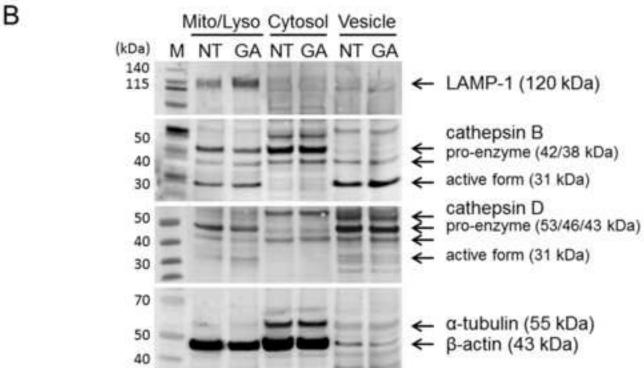
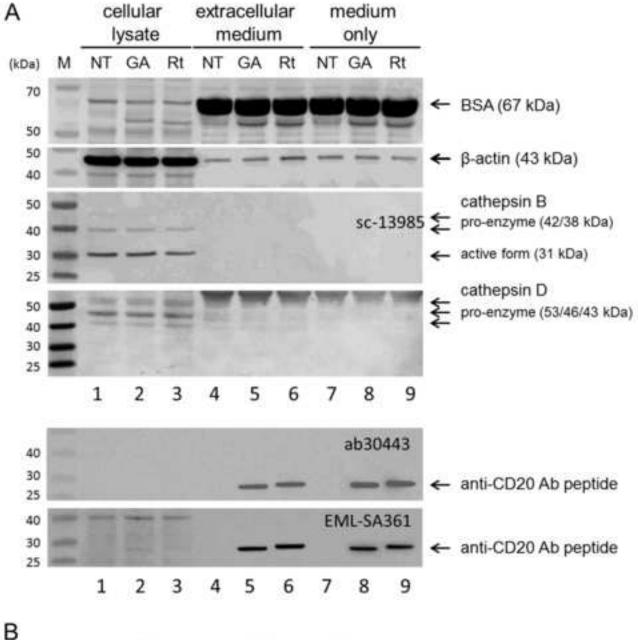


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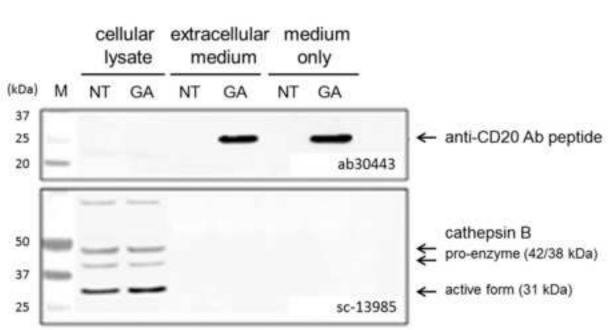
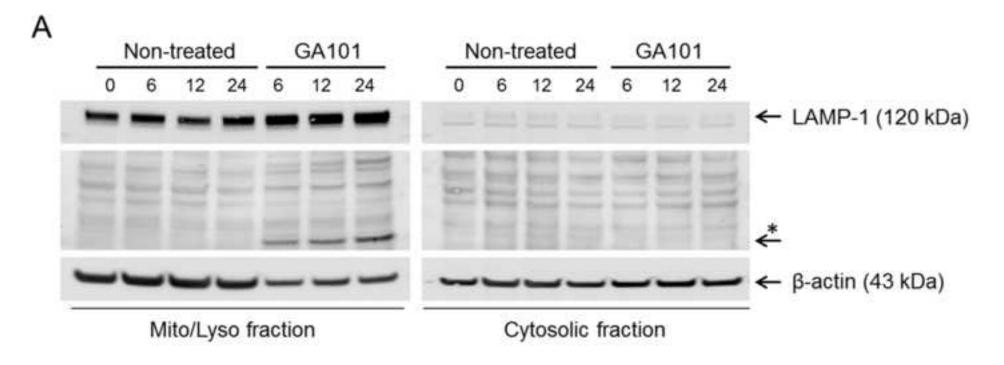


Figure5
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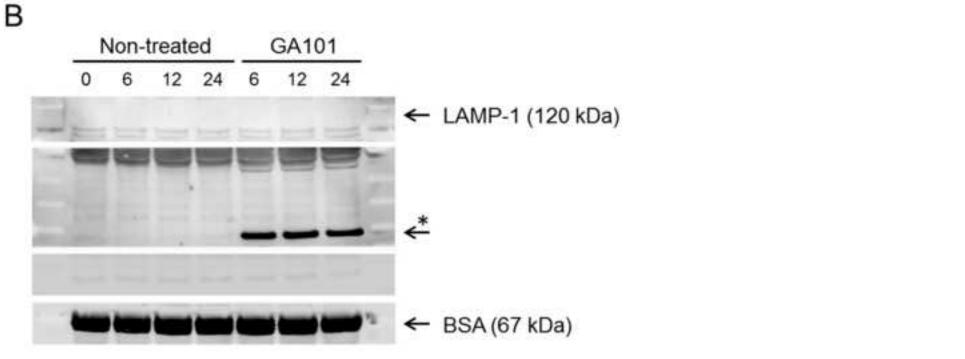


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*Statement of conflict of interest

Competing financial interests: AS is employee of Institut Roche. The remaining authors declare no competing financial interests.

Supplementary Material

Unexpected cross-reactivity of anti-cathepsin B antibodies leads to uncertainties regarding the mechanism of action of anti-CD20 monoclonal antibody GA101

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Supplementary Material and Methods

Protein array

Cells were treated with GA101 for 1 and 6h, and then subjected to protein array using PathScan® Stress and Apoptosis Signaling Antibody Array Kit and PathScan® Intracellular Signaling Array Kit (Cell Signaling), according to manufacturer's instruction. In brief, GA101-treated cells were lysed in 100 µl of PathScan Sandwich ELISA lysis buffer (Cell Signaling) containing ETDA-free anti-protease cocktail (Roche). The supernatants were collected after a centrifugation at 14000g for 2 min. Array slides were incubated in blocking buffer for 15 min. Lysate (75 µl, 0.6 mg/ml) was dispensed into wells of array slide for overnight incubation at 4°C. Incubation in Detection Antibody Cocktail solution (75 µl) for 1.5h and in HRP-linked Streptavidin solution (75 µl) for 45 min was then sequentially performed. Labeled proteins were detected by chemiluminescence using LumiGIO/Peroxide solution and recorded with LAS3000 software (Fujifilm). Spot intensities were analyzed using ImageJ Software.

Membrane protein extraction

5x10⁶ cells were harvested 4h after treatment with GA101 by centrifugation at 300g for 5 min. Untreated cells were used as controls. Cell pellets were washed with 3mL of Cell Wash Solution (Membrane Protein Extraction kit, Thermo scientific) and centrifuged at 300g for 5 min. Supernatants were carefully removed and discarded. Cells were resuspended in 1.5mL of Cell Wash Solution and transferred to a 2mL centrifuge tube. Cells were centrifuged at 300g for 5 min and supernatants were discarded. 0.75mL of Permeabilization Buffer (Membrane Protein Extraction kit, Thermo scientific) was added to the cell pellets. Cell suspension was then incubated 10min at 4°C with constant mixing. After incubation, cells were centrifuged for 15min at 16000g. Supernatants containing cytosolic proteins were transferred into a new

tube. 0.5mL of Solubilization buffer (Membrane Protein Extraction kit, Thermo scientific) was added to the pellets in order to resuspend the cells. Tubes were then incubated at 4°C for 30min with constant mixing. After incubation, cells were centrifuged at 16000g for 15min at 4°C. Supernatants containing solubilized membrane and membrane-associated proteins were collected into a new tube. The quantity of proteins in samples was estimated by Bradford assay using a Multiskan Spectrum plate reader at 595nm (Thermo Electro Corporation) and western blotting was performed.

Western blotting

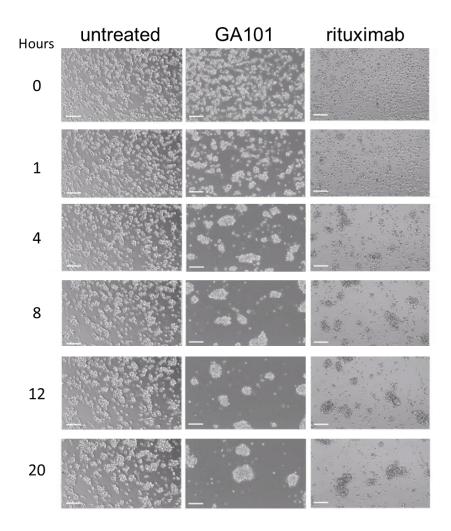
Total cell lysates were prepared using RIPA lysis buffer containing ETDA-free anti-protease cocktail. The quantity of proteins in samples was estimated by Bradford assay. For SDS-PAGE, 25-50µg of proteins were loaded onto NuPAGE 4-12% Bis-Tris (1.5 nm) gels (Novex, Life Technologies). Fractionation of cellular proteins was performed using MES buffer (Life technologies) at 200V for 40 min. Protein transfer was performed using iBlot Gel Transfer Stacks (nitrocellulose mini, Life Technologies). The protein bands were detected by chemiluminescence using Lumina Forte reagent (Millipore) and recorded with LAS3000 software (Fujifilm).

Immunocytochemistry

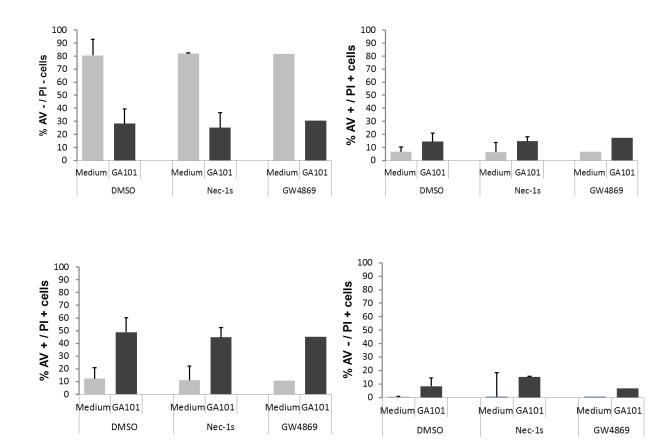
Cells were spun on glass slides by centrifugation at 650rpm for 5min. Fixed cells were dried overnight at room temperature and stored at -20°C. Fixation and permeabilization were performed using 4% paraformaldehyde (at room temperature) and acetone (-20°C) for 10min, respectively, followed by incubation in blocking buffer (5% BSA in PBS) overnight at 4°C with gentle agitation. The cells were then labeled using mouse anti-LAMP-1 (ab25630, Abcam) and rabbit anti-cathepsin B antibody (sc-13985 from Santa-Cruz or ab30443 from Abcam) at room temperature for 1h, followed by incubation with donkey anti-mouse-

Alexa568 (Invitrogen) and goat anti-rabbit-Alexa488 (Invitrogen) secondary antibodies, before a final wash in PBS containing 0.2% Tween-20. Fluorescence imaging microphotographs were taken using an Axiophot Zeiss epifluorescence microscope.

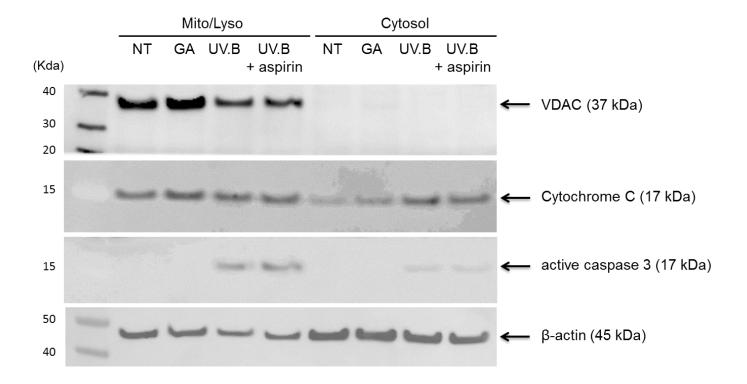
Supplementary Figures



Supplementary Figure 1: Homotypic adhesion of SUDHL-4 cells induced by GA101 or Rituximab. Microphotographs of untreated SUDHL-4 cells and cells treated with GA101 or Rituximab (10 μ g/ml) were taken at 1, 4, 8, 12 and 20h post-treatment using phase contrast microscopy (Objective: 10x, scale bar: 100 μ m).

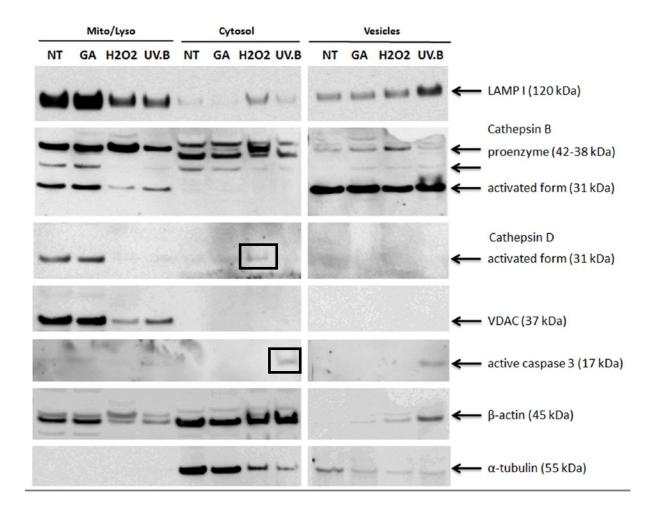


Supplementary Figure 2: Chemical inhibition of RIPK1 and sphingomyelinase does not prevent cell death after GA101 exposure. Raji cells were incubated in presence of 20 μM of RIPK inhibitor (Nec-1s) or 2 μM of sphingomyelinase inhibitor (GW4869) for 1h and then treated with 10 μg/ml of GA101 for 6h. Cells treated with DMSO were prepared as controls. Treated cells were analyzed by flow cytometry after dual Annexin V (AV) – Propidium iodide (PI) staining.



Supplementary Figure 3. Cytosolic release of Cytochrome C and caspase-3 activation are detectable in UVB-treated Raji cells.

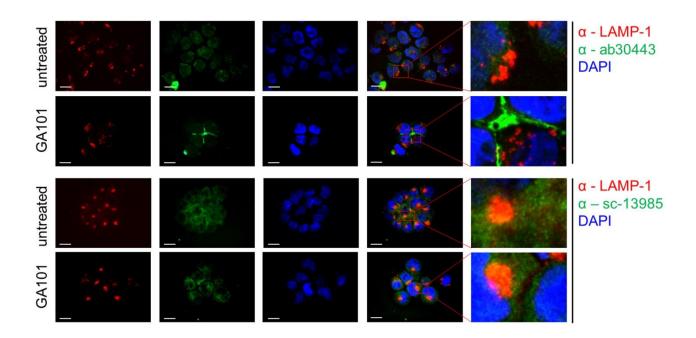
Cells were left untreated or treated with 10 µg/ml of GA101 for 16 h and subcellular fractionation was then performed. Cells exposed to 50 mJ/cm² UVB with or without 10 mM aspirin (Pique et al., 2000) were prepared as a positive control for apoptosis induction. Abundance of the assayed mitochondrial proteins in the mitochondria/lysosome (Mito/Lyso) fraction and in the cytosolic fraction was analyzed by western blotting. The MW (kDa) of each protein is indicated. VDAC is a mitochondrial membrane protein. The results indicate that in contrast to cells treated with GA101, cytosolic release of cytochrome C and cleavage of caspase-3 are observed in cells challenged with UBV or aspirin.



Supplementary Figure 4. Detection of cathepsin release in H₂O₂-treated cells.

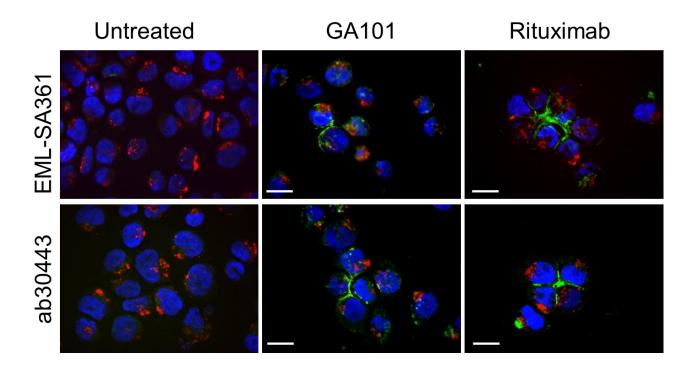
Raji cells were left untreated or treated with 10 μg/ml of GA101 or 0.05 mM H₂O₂ for 16 h, followed by subcellular fractionation. Abundance of lysosomal-associated membrane protein 1 (LAMP1), cathepsin B (labeled using antibody sc-13985) and cathepsin D in the mitochondria/lysosome (Mito/Lyso) fraction, in the cytosolic fraction and in the vesicle-rich fraction was analyzed by western blot. The MW (kDa) of each protein is indicated. NT: non-treated, GA: GA101. The presence of active cathepsin B and D proteins only in the Mito/Lyso fraction but not in the cytosol shows that LMP does not occur in response to GA101 treatment. H2O2 and UVB were used as positive controls for LMP and MMP respectively and produced

the expected outcome: cytosolic release of cathepsin D (see box in lane 7) and of active caspase-3 (box in lane 8), respectively.



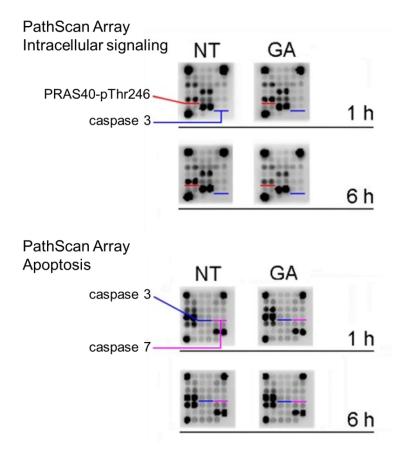
Supplementary Figure 5: Immunocytochemical staining using anti-cathepsin B antibodies ab30443 and sc-13985. Untreated and GA101-treated cells were cytospinned and subsequently subjected to immunofluorescent labeling using an antibody directed against the lysosomal marker LAMP1 (red) and either ab30443 or sc-13985 (green), two antibodies produced to detect cathepsin B. The nucleus was stained using DAPI (blue).

Microphotographs of labeled cells were taken under an Axiophot Zeiss epifluorescence microscope (Objective: 50 x Oil, scale bar: 15μM). These immunofluorescence data strongly suggest that ab30443 (as well as EML-SA36, see Supplementary Figure 6) recognizes GA101 itself, either localized at the cell surface after CD20 ligation or in the pericortical or subplasmalemmal region as a consequence of its cellular internalization. Note that staining was brighter at cell-cell junctions, suggesting that GA101-CD20 complexes actively participate to the HA process.



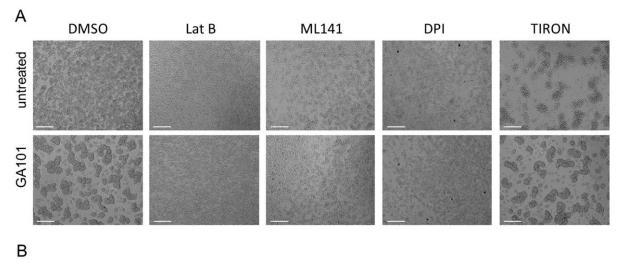
Supplementary Figure 6: Immunofluorescent labeling using the EML-SA361 antibody.

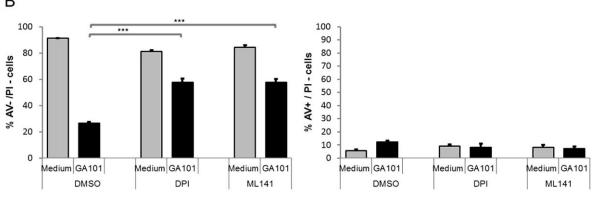
Untreated and GA101-treated cells were cytospinned and subsequently subjected to immunofluorescent labeling using an antibody directed against the lysosomal marker LAMP1 (red) and either EML-SA361 or ab30443 (green), two antibodies produced to detect cathepsin B. The nucleus was stained using DAPI (bleu). Microphotographs of labeled cells were taken under an Axiophot Zeiss epifluorescence microscope (Objective: 50 x Oil, scale bar: 15µM).

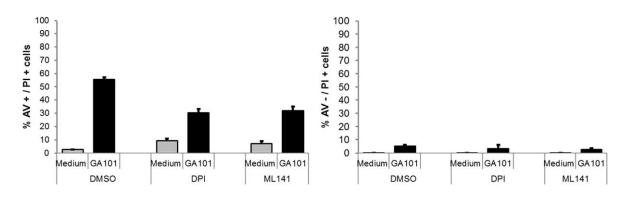


Supplementary Figure 7. The activation status of major signaling and apoptotic molecules remains stable upon GA101 exposure. Raji cells were left untreated or treated with 10 μg/ml of GA101 for 1 and 6h. Total cell lysates were prepared and subjected to intracellular signaling and apoptosis protein arrays using the PathScan® Intracellular and Apoptosis Signaling Antibody Array Kits. The expression of total or phosphorylated proteins was visualized using a chemiluminescent method. One negative (left-bottom) and three positive controls were set in the 4 corners of each membrane. NT: non-treated, GA: GA101. The pathways studied were: (1) MAPK-MEK/ERK (Erk1/2-Thr202/Tyr204); (2) MAPK-p38/JNK (TAK-Ser412, p38-Thr180/Tyr182, SAPK/JNK-Thr183/Tyr185; HSP27-Ser78); (3) Jak/Src (Stat1/3-Tyr701/Try705); (4) mTORC1 (S6 ribosomal protein-Ser235/236, p70 S6 kinase-Thr389); (5) mTORC2 (Akt-Thr308/Ser473, PRAS40-Thr246, Bad-Ser112/Bad136, GSK-3-Ser9); (6) AMPK (AMPKα-Thr172); (7) ATM/ATR (p53-Ser15, Chk1/Chk2-Ser345/Thr68; Smad2-Ser465/467); (8) caspase (caspase-3/7 and PARP cleavage; Survivin);

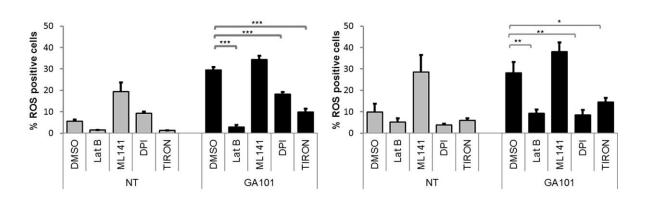
(9) NF- κ B/Rel (I κ B α -Ser32/36). Our results indicate that the binding of GA101 to CD20 does not provoke a significant modification in the assayed signaling pathways. Only Thr246-phosphorylated PRAS40 was reduced (by ~30%) in GA101-treated cells 6h after treatment. Of note, activation of caspases -3 and -7 was not detected in GA101-treated cells, confirming that GA101-induced cell death is caspase-independent.







C



Supplementary Figure 8: Involvement of Cdc42 GTPase and NOX activities in HA, ROS production and cell death induced in response to GA101. (A) Raji cells were incubated in presence of 20 μM of actin polymerization inhibitor (Latrunculin B, LatB), 20 mM of ROS scavenger (Tiron), 150 μM of NOX inhibitor DPI or 160 μM of cdc42 GTPase inhibitor ML141 for 2 h and then treated with 10 μg/ml of GA101 for 6 h. Cells treated with DMSO were prepared as controls. Microphotographs were taken using an inverted Leica microscope (objective: 10x, scale bar: 100 μm). (B) Raji cells were incubated in presence of 150 μM of NOX inhibitor DPI or 160 μM of Cdc42 GTPase inhibitor ML141 for 2 h and then treated with 10 μg/ml of GA101 for 6 h. Cells treated with DMSO were prepared as controls. Treated cells were analyzed by flow cytometry after dual AV/PI staining. (C) Raji cells were incubated in presence of 20 μM Lat B, 20 mM Tiron, 100 μM DPI or 160 μM ML141 for 2 h and then treated with 10 μg/mL of GA101 and the ROS marker carboxy-H2DCFDA (25mM) for 30min, 1h, 3h, 6h or left untreated. At each time point, cells were harvested to measure ROS production by flow cytometry.

Supplementary Table 1: Identification of the proteins recognized by the anti-cathepsin B antibody EML-SA361. A protein lysate of SUDHL-4 cells treated with 10 μ g/ml of GA101 was prepared and the EML-SA361 antibody was used to carry out immunoprecipitation. Proteins present in the immunoprecipitate were then analyzed by high-resolution mass spectrometry using a LTQ Velos mass spectrometer.

Réf. CCMP	Réf. Clients	Analyses LCMSMS (LTQ Velos)			Bases de données	
13 1144	Lysat GA101	1144.raw			SwissProt + sequences clients	
Accession P35579	Coverage 32.76	# Peptides 126	MW [kDa] 226.4	S core 3720.80	Description Myosin-9 OS=Homo sepiens GN=MYH9 PE=1 SV=4 - [MYH9_HUMAN]	
P08670	67,38	77	53,6	2180,26	Vimentin OS=Homo sepiens GN=VIM PE=1 SV=4 - [VIME_HUMAN]	
P60712	49,07	57	41,7	1803,90	Actin, cytoplesmic 1 OS=Bas teurus GN=ACTB PE=1 SV=1 - [ACTB_BOVIN]	
Q15149	4,46	19	531,5	715,93	Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3 - [PLEC_HUMAN]	
P04264 P00761	23,60 32,90	16 25	66,0 24,4	651,77 638,50	Keratin, type II cytoskeletal 1 OS=thomo sapiens GN=RRT1 PE=1 SV=6 - [K2C1_HUMAN] Trypsin OS=Sus scrofe PE=1 SV=1 - [TRYP_PIG]	
P35527	21,67	12	62,0	497,93	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 - [K1C9_HUMAN]	
Q3ZCH0	15,91	15	73,7	407,38	Stress-70 protein, mitochondrial OS=8os taurus GN=HSPA9 PE=2 SV=1 - [GRP75_80VIN]	
P33241	21,83	10	37,2	407,37	Lymphocyte-specific protein 1 OS=Homo sapiens GN=LSP1 PE=1 SV=1 - [LSP1_HUMAN]	
Q3ZCF3 P35908	55,83 21,91	12	18,6 65.4	390,14 375,46	S-phase kinase-associated protein 1 OS=Bos taurus GN=SKP1 PE=2 SV=1 - [SKP1_80VIN] Keratin, type II cytoskeletal 2 epidermal OS=Homo sepiera GN=KRT2 PE=1 SV=2 - [K22E_HUMAN]	
Q5R507	21,32	8	30,6	366,06	F-actin-capping protein subunit beta OS=Pongo abelii GN=CAPZ8 PE=2 SV=2 - [CAPZ8_PON48]	
P60661	33,11	7	16,9	357,46	Myosin light polypeptide 6 OS=Bos taurus GN=MYL6 PE=2 SV=2 - [MYL6_BOVIN]	
006967	7,81	5	64,5	353,48	Multidrug resistance ABC transporter ATP-binding/permease protein 8mrA OS=8acillus subtilis (strain 168) GN=bmrA PE=1 SV=1 - [8MRA_8ACSU]	
P13645 P16401	22,60 16.37	10	58,8 22.6	351,40	Keratin, type I cytoskeletal 10 OS=Homo sepiens GN=RRT10 PE=1 SV=6 - [KIC10_HUMAN]	
Q90YQ6	47.76	13	15,4	340,74 335,89	Historie Hi. 5 OS=Homo sepiens GN=HET1H18 PE=1 SV=3 - [H15_HUMAN] 405 ribosomel protein S17 OS=Idelurus punctatus GN=rps17 PE=2 SV=3 - [RS17_ETPU]	
P61284	33,33	8	17,8	328,67	60S ribosomal protein L12 OS=86s taurus GN=RPL12 PE=2 SV=1 - (RL12_80VIN)	
P09867	25,94	6	34,2	294,28	Heterogeneous nuclear ribonudeoprotein A1 OS=Bos taurus GN=HNRNPA1 PE=1 SV=2 - [ROA1_BOVIN]	
Q3T0R1	32,89	12	17,7 59.7	292,94	40S ribosomal protein S18 OS=Bos taurus GN=RPS18 PE=2 SV=3 - [RS18_BOV NI] ATO suphtharm subsult aliaba mitterbondisial OS=Res baurus GN=ATORA + DE=1 SV=1 - (ATORA BOVINI)	
P19483 O9ULV4	11,39 12,24	5	59,7 53,2	282,58 280,97	ATP synthase subunit algha, mitochondrial OS=Bes taurus GN=ATPSA1 PE=1 SV=1 - [ATPA_BOVIN] Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1 - [COR1C_HUMAN]	
P04406	18,81	4	36,0	274,95	Gycaraldehyde-3-pilosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 - [G3P_HUMAN]	
P14618	9,23	4	57,9	269,91	Pyruvete Knase isozymes M1/M2 OS=Homo sapiens GN=PKM PE=1 SV=4 - [KPYM_HJMAN]	
P15864	17,92	8	21,3	261,06	Historie H1.2 OS=Mus musculus GN=Histific PE=1 SV=2 - [H12_MOUSE]	
Q3T0F4 P62960	23,64 25.16	5	18,9 35,7	214,79 214,51	405 r basamel protein S10 OS=8as teurus GN=RPS10 PE=2 SV=1 - [RS10_BOV N] Nuclease-sereitive element-binding protein 1 OS=Mus musculus GN=Ybx1 PE=1 SV=3 - [YB0X1_MOUSE]	
P62960 P19338	20,70	7	35,7 76,6	214,51	Nuclease-sensione element-duraing protein 1 US=Mus musculus (aN=10x1 Pt=1 S V=3 - [YSUX1_MUUSc] Nuclealin OS=Hamo sepiens GN=NCL Pt=1 SV=3 - [NUCL_HUMAN]	
P53999	33,07	3	14,4	201,54	Activated RNA polymerase II transcriptional coactivator p15 OS=Homo sapiens GN=SUB1 PE=1 SV=3 - [TCP4_HUMAN]	
Q3T057	32,86	7	14,9	199,32	60S ribosomal protein L23 OS=Bos taurus GN=RPL23 PE=2 SV=2 - [RL23_BOVIN]	
P19378	9,91	6	70,8	199,17	Heat shock cognete 71 kDa protein OS =Cricatulus griseus GN=HSPAS PE=2 SV=1 - [HSP7C_CRISR]	
Q01082 P52907	2,28 17.13	6	274,4 32.9	197,94 190.17	Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTBN1 PE=1 SV=2 - [SPT82_HUMAN] F-actin-capping protein subunit alshe-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3 - (CAZA1_HUMAN)	
014974	3,69	8	115,2	188,10	Protein phosphatase 1 regulatory subunit 12A OS=Homo sepiens GN=CHZA1 rE=1 SV=3 - [CAZA1_TUMNIN] Protein phosphatase 1 regulatory subunit 12A OS=Homo sepiens GN=PPP1R12A PE=1 SV=1 - [NYPT1_HUMAN]	
A 507 D1	7,68	5	104,9	187,70	Alpha-actinin-4 OS=Bos teurus GN=ACTN4 PE=2 SV=1 - [ACTN4_BOVIN]	
Q3MIC0	32,61	3	10,3	184,20	60S r bosomel protein L37a OS=8os taurus GN=RPL37A PE=3 SV=3 - [RL37A_BOVIN]	
Q2H160 Q9TTV2	14,96 14,96	4	36,0 35.9	181,07 181,07	Heter ogeneous nuclear nibonudeoproteins A2/81 OS=8cs taurus GN=HNRNPA281 PE=2 SV=1 - [ROA2_80VIN] Heter ogeneous nuclear nibonudeoproteins A2/81 OS=Seguinus cedipus GN=HNRNPA281 PE=1 SV=1 - [ROA2_SAGOE]	
P20592	8,25	6	82,0	180,03	Interferon-induced GTP-binding protein Mx2 OS=Homo sepiens GN=MX2 PE=1 SV=1 - [MX2_HUMAN]	
P07910	12,75	6	33,6	176,42	Heter ogeneous nuclear ribonude oproteins C1/C2 OS=Homo sapiens GN=HNRNPC PE=1 SV=4 - [HNRPC_HUMAN]	
P18859	31,48	2	12,6	173,29	ATP synthase-coupling factor 6, mitochondrial OS=Homo sepiens GN=ATP53 PE=1 SV=1 - [ATP53_HUMAN]	
P29966	15,66	4	31,5	171,66	Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCKS PE=1 SV=4 - [MARCS_HUMAN]	
Q28009 P21333	14,04	3	52,3 280.6	169,13 167,86	RNA-binding protein FUS OS=Bos teurus GN=FUS PE=2 SV=2 - [FUS_BOVIN] Filamin-A OS=Homo sepiens GN=FLNA PE=1 SV=4 - [FLNA_HUMAN]	
P22061	11,01	3	24,6	161,80	Protein-L-boaspartate(D-aspartate) 0-methyltransferase OS=Homo sapiens GN=PCMT1 PE=1 SV=4 - [PIMT_HUMAN]	
P62846	22,07	2	17,0	160,13	40S ribosomal protein S15 OS=Gallus gallus GN=RPS15 PE=2 SV=2 - [RS15_CHICK]	
Q2K3D0	16,44	6	49,6	157,58	Tubulin beta-5 chain OS=8os taurus GN=T U885 PE=2 SV=1 - [T885_8OV IV]	
P02533	7,63 12.85	4 3	51,5 28.6	154,23 153,57	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4 - [K1C14_HUMAN]	
Q5E995 Q6IP73	19,72	7	23,2	152,23	40S r basomal protein S6 OS=8ss taurus GN=RPS6 PE=2 SV=1 - [RS6_BOVIN] Nescent polypeptide-associated complex subunit alpha OS=Xenopus Isevis GN=nacs PE=2 SV=1 - [NACA_XENIA]	
Q99623	14,38	4	33,3	149,20	Prohibitin-2 OS=Homo sepiens GN=PH82 PE=1 SV=2 - [PH82_HUMAN]	
076N24 gi328877287	15.21	3	29.6 23,9	148.80	40.5 - 200 March 19 M	
9328677267 P23290	17,41	3	/0.1	144,18	Chein H, Epilape Cherecterization And Crystal Structure Of Ga101 Provide Insights Into The Molecular Basis For The Type I TYPE II Distinction Of Anti- Co20 Anti spincing ractor, promise- and glucemine-inch US=nomo septems (NESERY PCE) SY 22 - (SERY_HUMAN)	uoues
Q3T169	13,58	4	26,7	141,45	40S ribosomal protein S3 OS=8cs taurus GN=RPS3 PE=2 SV=1 - [RS3_80VIN]	
Q6P1L8	29,66	3	15,9	138,87	39S r basomal protein L14, mitadronárial OS=Homo sepiens GN=MRPL14 PE=1 SV=1 - [RM14_HUMAN]	
Q3SWW9	12,54	3	37,2	134,66	Serine/ threonine-protein phosphatase PP1-beta catalytic subunit OS=8cs taurus GN=PPP1C8 PE=2 SV=1 - [PP18_80VIN]	
8011T2 Q3SZF8	2,06 32.20	2	116,4 13,5	134,14 131,33	Unconventional myosin-1g OS=Homo sepiens GN=MYO1G PE=1 SV=2 - [MYO1G_HUMAN] Small nuclear ribonucleoprotein Sm D2 OS=Bos taurus GN=SNRPD2 PE=3 SV=1 - [SMD2_BOV3N]	
Q3SZF8 Q3ZCA2	24,67	3	26,2	131,33	Small nuclear notinucleoprotein 5m bit us note tautus Gilesinkhild years 5v=1 - [5vibiz_80v1vi] Cleavage and polyadarylation specificity factor subunit 5 OS=8bs taurus Gil=NUDT21 PE=2 SV=1 - [CPSFS_BOVIN]	
Q00715	20,00	2	14,0	128,92	Histone H2B type 1 OS=Ratitus norvegicus PE=1 SV=2 - [H2B1_RAT]	
Q563X5	16,00	3	13,7	125,61	40S r bosomal protein S25 OS=8os taurus GN=RPS25 PE=2 SV=1 - [RS25_80V IN]	
P62318	24,60 10.05	4	13,9	122,57	Small nuclear ribonucleoprotein Sm 03 OS =Homo sapiens GN=SNRP03 PE=1 SV=1 - [SM03_HUMAN]	
P40673 Q563U9	10,05 20,61	2	24,0 15,2	122,42 120,64	High mobility group protein 82 OS=80s taurus GN=HM682 PE=1 SV=3 - (HMG82_BOV3N) 405 r bosomal protein S24 OS=80s taurus GN=PSS24 PE=2 SV=2 - (RS24_BOV3N)	
P36604	4,22	2	73,2	120,46	78 KDe glucose-regulated protein fromolog OS=S chizoseccharomyces pombe (strain 972 / ATCC 24843) GN=bip1 PE=2 SV=2 - [GRP78_SCHP0]	
0270144	18,35	3	18,4	118,24	40S ribosomal protein S11 OS=8os taurus GN=RPS11 PE=2 SV=3 - [RS11_BOV N]	
Q3T0V4	31,30	2	11,7	116,36	60S acidic ribosomal protein P2 OS=8os taurus GN=RPLP2 PE=3 SV=1 - [RLA2_BOVIN]	
P42899	16,02 4,22	2	20,6 85.2	115,51 114,50	28 KDa heaf- and acid-stable phosphoprotein OS=Homo sepiens GN=PDAP1 PE=1 SV=1 - [HAP28_HUMAN] LIM domain and actin-binding protein 1 OS =Homo sepiens GN=LIMA1 PE=1 SV=1 - [LIMA1_HUMAN]	
P42899 Q13442	7,22	2	121,6		Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=1 - [LIMA1_TUMAN]	
P42899	2,63			113,47		
P42899 Q13442 Q9UHB6	2,63 6,05	3	28,5	113,47 108,38	Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2 - [TPM4_HORS E]	
P42899 Q13442 Q9UH86 Q00159 P02561 Q76181	6,05 26,52	3	14,5	108,38 107,52	Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2 - [TRM4_HDRS E] 405 ribasomal protein 512 OS=Bos taurus GN=RP512 PE=2 SV=1 - [RS12_BOV30]	
P42899 Q13442 Q9UHB6 O00159 P02561 Q76I81 P14317	6,05 26,52 5,97	3 2	14,5 54,0	108,38 107,52 105,88	Tropomyosin algine 4 dnen OS=Equus cabellus GN=TPM4 PE=1 SN=2 - [TPM4_HDRSE] 495 ribosomal protein 510 OS=Bot Issuns GN=R912 PE=2 SN=1 - [RS12_50/19] Hersbeppicific Integra cell-specific protein GS=Heros septem GN=HSLS1 PE=1 SN=3 - [HCLS1_HUMM]	
P42899 Q13442 Q9UHB6 O00159 P02561 Q76I81 P14317 A4FUH0	6,05 26,52	3	14,5 54,0 14,5	108,38 107,52	Tropomysin sighe-4 chain OS=Equus caballus GN=TPMP RE=1 SV=2 - [TRM4_HORS E] 405 r bosomal probin SIZ OS=Bot Starus GN=RSPI2 RE=2 SV=1 - [RSI2_BOVIN] Hemalopoidic lineage cell-specific probin OS=Homo septem GN=HCLS1 RE=1 SV=3 - [HCLS1_HLMMN] 605 r bosomal probin LIZ -lile 1 OS=Bot Sarus GN=RSI2.1 PE=2 SV=1 - [RIZ2_BOVIN]	
P42899 Q13442 Q9UHB6 O00159 P02561 Q76I81 P14317	6,05 26,52 5,97 31,97	3 2 3	14,5 54,0	108,38 107,52 105,88 105,43	Tropomyosin algine 4 dnen OS=Equus cabellus GN=TPM4 PE=1 SN=2 - [TPM4_HDRSE] 495 ribosomal protein 510 OS=Bot Issuns GN=R912 PE=2 SN=1 - [RS12_50/19] Hersbeppicific Integra cell-specific protein GS=Heros septem GN=HSLS1 PE=1 SN=3 - [HCLS1_HUMM]	
P42899 Q13442 Q9UH86 O00159 P02561 Q76181 P14317 A 4FUH0 Q75XW6	6,05 26,52 5,97 31,97 12,69	3 2 3 4	14,5 54,0 14,5 44,6	108,38 107,52 105,88 105,43 103,44	Tropom josin algine 4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2 - [TPM4_HORS E] 405 r bosomal probin S12 OS=Bos tauna GN=R951 PE=2 SV=1 - [R512_BOVN] 405 r bosomal grobin S12 OS=Bos tauna GN=R951 PE=2 SV=1 - [R512_BOVN] 605 r bosomal grobin 12 - R05 sebos tauna GN=R92_R12 PE=2 SV=1 - [R212_BOVN] Action-related probin 12 A OS=OS=Bos tauna GN=R952 PE=3 SV=1 - [R872_BOVNE] 405 r bosomal probin 12 A OS=OS=Bos tauna GN=R952 PE=3 SV=2 - [R52_BOVN] 584 domain-combining ribonudesprobin OS=Bros source GN=R952 PE=3 SV=2 - [S52_BOVN] 584 domain-combining ribonudesprobin OS=Bros source GN=R952 PE=0 SV=2 - [S52_BOVN]	
P42899 Q13442 Q9UH86 O00159 P02561 Q7681 P14317 A 4FUH0 Q75XW6 P62276 P82979 Q63610	6,05 26,52 5,97 31,97 12,69 33,93 13,33 10,48	3 2 3 4 2 2 2	14,5 54,0 14,5 44,6 6,7 23,7 29,0	108,38 107,52 105,88 105,43 103,44 103,30 102,56	Tropomysein algine 4 chain OS-Efquus cabellus (Bit TPM RE-1 SVs-2 - [TPM4_HXSE] Membalpoide (intege cell-specific probin GS-thoma specific GHRSL12_60V3) Membalpoide (intege cell-specific probin GS-thoma specific GHRSL13_FR-1 SVs-3 - [HLSL_HMMN] 605 r bosomal probin 122 He 1 OS-8bs taurus GHRSL21. PR-2 SVs-1 - [R222_B0V1N] Addiversible of public AD-Si-Bellor record GHRSL21. PR-2 SVs-1 - [R222_B0V1N] 405 r bosomal probin 529 OS-8bs taurus GHRSL221 PR-3 SVs-2 - [R529_B0V1N] 528 domain-containing ribonadesprobin OS-thoma specific GHRSL218 FR-1 SVs-2 - [SARIP_HMMN] Tropomysein spiral - dam OS-8bs taurus consiguin GHRSL218 FR-1 SVs-2 - [TRSL_RAT]	
P42899 Q13442 Q9UH86 Q00159 P02561 Q76181 P14317 A 4FUH0 Q75XW6 P62276 P82979 Q63610 Q6EWQ7	6,05 25,52 5,97 31,97 12,69 33,93 13,33 10,48 22,73	3 2 3 4 2 2 2 2	14,5 54,0 14,5 44,6 6,7 23,7 29,0 16,8	108,38 107,52 105,88 105,43 103,44 103,30 102,56 102,36	Tropomyosin algine 4 chain OS=Equus caballus GN=TPM4 RE=1 SV=2 - [TPM4_HORS E] 405 r bosomal probin S12 DS=Bot Saurus GN=RP31 RE=2 SV=1 - (RS121_80VN) 405 r bosomal probin S2 DS=Bot Saurus GN=RP312 RE=2 SV=1 - (RS121_80VN) 405 r bosomal probin L22-H8 i OS=Bot Saurus GN=RP221 PE=2 SV=1 - [R222_80VN) Action-related or delin 2 A OS=Denin rerio GN=setzla RE=2 SV=1 - [R822_B0VN] 546 bosomal probin S20 GS=Bot Saurus GN=RP32 RE=2 SV=1 - [R822_B0VN] 546 bosomal-probin S20 GS=Bot Saurus GN=RP32 RE=2 SV=2 - [S832_B0VN] 546 bosomal-probin S20 GS=Bot Saurus GN=RP32 RE=2 SV=2 - [S832_B0VN] 547 bosomal-probin S20 GS=Bot Saurus GN=RP32 RE=2 SV=2 - [S832_B0VN] 548 bosomal-probin S20 GS=Bot Saurus GN=RP32 RE=2 SV=3 - [TPM3_B0VN] 548 bosomal-probin GS=Bot Saurus GN=RP32 RE=2 SV=3 - [TPM3_B0VN] 548 bosomal-probin GS=Bot Saurus GN=RP32 RE=2 SV=3 - [TPM3_B0VN] 548 bosomal-probin GS=Bot Saurus GN=RP32 RE=2 SV=3 - [TPM3_B0VN]	
P42899 Q13442 Q9UH86 Q00159 P02561 Q7681 P14317 A 4FUH0 Q75XW6 P62276 P82979 Q63610	6,05 26,52 5,97 31,97 12,69 33,93 13,33 10,48	3 2 3 4 2 2 2	14,5 54,0 14,5 44,6 6,7 23,7 29,0	108,38 107,52 105,88 105,43 103,44 103,30 102,56	Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM PE=1 SV=2 - [TPM4_HORS E] 405 r bosomal probin S12 OS=Bot Saurus GN=RS12 PE=2 SV=1 - [RS12_BOVIN] **Tema biopalicii (image coll-specific probin io Serbino sapen GN=RS12X1 PE=2 SV=1 - [RS12_BOVIN] 605 r bosomal probin 122 Hille 1 OS=Bot Saurus GN=RS12X1 PE=2 SV=1 - [RS22_BOVIN] Actin-related probin 12-0 SO=Bot Saurus GN=RS12X1 PE=2 SV=1 - [RS22_BOVIN] 515 r bosomal probin 529 OS=Bot Saurus GN=RS229 PE=3 SV=2 - [RS23_BOVIN] 526 domain-containing ribonudesprobin OS=Boto Saurus GN=RS22 PE=3 SV=2 - [RS23_BOVIN] 527 domain-containing ribonudesprobin OS=Boto Saurus GN=RS22 PE=3 SV=2 - [RS13_BOVIN] Tropomyosin alpha-3 chain OS=RS41a non regious GN=Tpm3 PE=1 SV=2 - [TPM3_BAT] Eukaryolic Variation initiation factor SA-1 OS=Bot Saurus GN=RS42 RE=2 SV=3 - [TPS1_BOVIN] Complement comprisent 1 Q subcompoment binding protein, milborhordinal OS erbino sapiens GN=CSP= SV=1 - [CQ8P_HUMAN]	
P42899 Q13442 Q9UB6 000159 P02561 Q76181 P14317 A 4FUH0 Q75XW6 P62276 P82979 Q63610 Q6EWQ7 Q07021	6,05 25,52 5,97 31,97 12,69 33,93 13,33 10,48 22,73 9,93	3 2 3 4 2 2 2 2 2 2	14,5 54,0 14,5 44,6 6,7 23,7 29,0 16,8 31,3	108,38 107,52 105,88 105,43 103,44 103,30 102,56 102,36 100,58 98,96	Tropomyosin algine 4 chain OS=Equus caballus GN=TPM4 RE=1 SV=2 - [TPM4_HORS E] 405 r bosomal probin S12 DS=Bot Saurus GN=RP31 RE=2 SV=1 - (RS121_80VN) 405 r bosomal probin S2 DS=Bot Saurus GN=RP312 RE=2 SV=1 - (RS121_80VN) 405 r bosomal probin L22-H8 i OS=Bot Saurus GN=RP221 PE=2 SV=1 - [R222_80VN) Action-related or delin 2 A OS=Denin rerio GN=setzla RE=2 SV=1 - [R822_B0VN] 546 bosomal probin S20 GS=Bot Saurus GN=RP32 RE=2 SV=1 - [R822_B0VN] 546 bosomal-probin S20 GS=Bot Saurus GN=RP32 RE=2 SV=2 - [S832_B0VN] 546 bosomal-probin S20 GS=Bot Saurus GN=RP32 RE=2 SV=2 - [S832_B0VN] 547 bosomal-probin S20 GS=Bot Saurus GN=RP32 RE=2 SV=2 - [S832_B0VN] 548 bosomal-probin S20 GS=Bot Saurus GN=RP32 RE=2 SV=3 - [TPM3_B0VN] 548 bosomal-probin GS=Bot Saurus GN=RP32 RE=2 SV=3 - [TPM3_B0VN] 548 bosomal-probin GS=Bot Saurus GN=RP32 RE=2 SV=3 - [TPM3_B0VN] 548 bosomal-probin GS=Bot Saurus GN=RP32 RE=2 SV=3 - [TPM3_B0VN]	
P 42 899 Q13442 Q94486 O001 59 P02 561 Q76181 P14317 A 4FUHD Q75XW6 P62 276 P82 979 Q6 36 10 Q6 8W Q7 Q70 72 1 P40 926	6,05 26,52 5,97 31,97 12,69 33,93 13,33 10,48 22,73 9,93 10,36 27,73 8,38	3 2 3 4 2 2 2 2 2 2 3	14,5 54,0 14,5 44,6 6,7 23,7 29,0 16,8 31,3 35,5 13,3 36,6	108,38 107,52 105,88 105,43 103,44 103,30 102,56 102,36 100,58 98,96 96,04 95,38	Tropomysein algine 4 chain OS-Eduus cabellus (Bit TPM RE-1 SVe2 - (TPM4_HXSE) 405 r Boomal probin 51:00 S-Bobs tearus GilleRP51 PE-2 SVe1 - (1812_50/19) (Membalpoidic lineage cell-specific probin Gis-Homo specific GilleRS12.1 PE-2 SVe1 - (HLSL_HUMM) 605 r Boomal probin 122 He 1 OS-Bob tearus GilleRS2.1 PE-2 SVe1 - (R222_80/19) Addiversible of public AD-Si-Bob tearus GilleRS2.2 PE-2 SVe1 - (R222_80/19) Addiversible of public 32 OS-Bob tearus GilleRS2.2 PE-2 SVe1 - (R222_80/19) 605 r Boomal probin 529 OS-Bob tearus GilleRS2.2 PE-3 SVe2 - (R329_80/19) 605 r Boomal probin 529 OS-Bob tearus GilleRS2.2 PE-3 SVe2 - (R329_80/19) 605 r Boomal probin 529 OS-Bob tearus GilleRS2.2 PE-3 SVe2 - (R329_80/19) 605 r Boomal probin 529 OS-Bob tearus GilleRS2.2 PE-3 SVe2 - (R329_90/19) 606 r Boomal-containing ritionadesprobin Gis-thomo specific GilleRS2.2 SVe3 - (IP54_80/19) 607 Tropomysein signific ration 54-1 OS-Bob tearus GilleRS2.2 SVe3 - (IP54_80/19) 608 r Boomal probin 529 OS-Bob tearus GilleRS2.2 SVe3 - (IP54_90/19) 609 r Boomal probin 529 OS-Bob tearus GilleRS2.2 SVe3 - (IP54_90/19) 609 r Boomal probin 529 OS-Bob tearus GilleRS2.2 SVe3 - (IP54_90/19) 609 r Boomal probin 529 OS-Bob tearus GilleRS2.2 SVe3 - (IP54_90/19) 609 r Boomal probin 529 OS-Bob tearus GilleRS2.2 SVe3 - (IP54_90/19) 609 r Boomal probin 529 OS-Bob tearus GilleRS2.2 SVe3 - (IP54_90/19) 609 r Boomal probin 529 OS-Bob tearus GilleRS2.2 SVe3 - (IP54_90/19) 609 r Boomal probin 529 OS-Bob tearus GilleRS2.2 SVe3 - (IP54_90/19) 609 r Boomal probin 529 OS-Bob tearus GilleRS2.2 SVe3 - (IP54_90/19) 609 r Boomal probin 529 OS-Bob tearus GilleRS2.2 SVe3 - (IP54_90/19) 609 r Boomal probin 529 OS-Bob tearus GilleRS2.2 SVe3 - (IP54_90/19) 609 r Boomalpool 122 Boomalpool 122 SVe3 - (IP54_90/19) 609 r Boomalpool 122 Boomalpool 122 SVe3 - (IP54_90/19) 609 r Boomalpool 122 Boomalpool 122 SVe3 - (IP54_90/19) 609 r Boomalpool 122 Boomalpool 122 SVe3 - (IP54_90/19) 609 r Boomalpool 122 Boomalpool 122 SVe3 - (IP54_90/19) 609 r Boomalpool 122 Boomalpo	
P42899 Q13442 Q9UH86 Q00159 P00251 Q76181 P14317 A 4FUH0 Q75XW6 P62276 P82979 Q63610 Q65WQ7 Q07021 P49926 Q32C10 P07195 P01840	6,05 25,52 5,97 13,97 12,69 33,93 10,48 22,73 9,93 10,36 27,73 83,83	3 2 3 4 4 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	14,5 54,0 14,5 44,6 6,7 23,7 29,0 16,8 31,3 35,5 13,3 36,6 11,0	108,38 107,52 105,88 105,43 103,44 103,30 102,56 102,36 100,58 98,96 96,04 95,38 94,14	Tropomyosin algine 4 chain OS=Equas caballus GN=TPM4 PE=1 SV=2 - [TPM4_HORS E] 495 r Bosomal probin 532 OS=Bot Savus GN=RP31 PE=2 SV=1 - [R312_BOVN] Herabopiotic Impage cell-species probin GS-thoro sepano GNH=LSS PE=1 SV=3 - [HCLS1_HUMM] 595 r Bosomal probin 122-lile 1 OS=Bot Savurus GN=RP323 PE=2 SV=1 - [R322_BOVN] Addin-relabilat probin 52 OS=Bot Savurus GN=RP323 PE=2 SV=1 - [R322_BOVN] 495 r Bosomal probin 52 OS=Bot Savurus GN=RP329 PE=2 SV=2 - [R328_BOVN] 584 domesi-corabining ribonudesprobin OS=thoro septems GN=SARP PE=1 SV=3 - [SARP_HUMM] Tropomyosin glidar 3 clinic OS=Botta nor regious GN=Pp=3 PE=1 SV=3 - [FSN=1_GNN] Eukaryolic translation initiation factor 5A-1 OS=Bot Savurus GN=E53 PE=2 SV=3 - [FSN1_BOVN] Complement component 1 Q subcomponent-Briding probin, mibichondrial OS=thoro sapiems GN=CARP PE=1 SV=1 - [C1Q8P_HUMM] Simal nuclear ribonucleoprobin is m 01 OS=Bot Savurus GN=E5RP01 SV=1 SV=1 (SNP0_BOVN) L-leatable delphydogeness Bridgenia OS=thoro sapiems GN=DNPO2 PE=1 SV=1 - [ROPH_HUMM] Simal nuclear ribonucleoprobin is m 01 OS=Bot Savurus GN=E5RP01 SV=1 SV=1 (SNP0_BOVN) L-leatable delphydogeness B clinic OS=thoro sapiems GN=E1RP01 SV=1 SV=1 (SNP0_BOVN) L-leatable delphydogeness B clinic OS=thoro sapiems GN=E1RP01 SV=1 SV=1 (SNP0_BOVN) L-leatable delphydogeness B clinic OS=thoro sapiems GN=E1RP01 SV=1 SV=1 SV=1 (SNP0_BOXN) [J speptible 4 clinic region OS=thoropatiems collected PE=1 SV=1 SV=1 (SNP0_BOXN) [J speptible 4 clinic region OS=thoropatiems collected PE=1 SV=1 SV=1 SV=1 SV=1 SV=1 SV=1 SV=1 SV	
P42899 Q13442 Q4U-86 Q4U-86 Q4U-86 Q4U-86 Q40561 Q4561	6.05 26.52 5.57 31.97 12.59 33.93 12.33 10.48 22.73 9.93 10.36 27.73 8.38	3 2 2 3 4 4 2 2 2 2 2 2 2 2 2 2 3 3 2 2 2 2	14,5 54,0 14,5 44,6 6,7 23,7 29,0 16,8 31,3 35,5 13,3 36,6 11,0 12,5	108,38 107,52 105,88 105,43 103,44 103,30 102,56 100,58 98,96 96,04 95,38 94,14 92,94	Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SVs2 - [TPM4_HDRS E] 405 r bosomal probin S12 DS=Bs taurus GN=RP31 PE=2 SVs1 - (RS121_ROVIN) Membalopiatic Image call-specifs prohio dis-throw aspecia GN=LS12 PE=1 SVs1 - [RLS12_ROVIN] 605 r bosomal probin L12-like 1 OS=Bso taurus GN=RR128.1 PE=2 SVs1 - [R222_ROVIN] Actin-related or detain 2-A OS=Dseno rerio GN=extria PE=1 SVs1 - [R222_ROVIN] Actin-related or detain 2-A OS=Dseno rerio GN=extria PE=1 SVs1 - [R222_ROVIN] 540 formalin-combining riborus/deoprotein OS=Ptom septems GN=SARIP PE=1 SVs3 - [SARIP_HUMAN] Tropomyosin alpha-3 chain OS=Ratta non regious GN=Rp3 PE=1 SVs3 - [TPM3_RAT] Eukaryoto terralistion initiation factor 5-1 OS=Bso taurus GN=Fp3 PE=2 SVs3 - [TPM3_RAT] Eukaryoto terralistion initiation factor 5-1 OS=Bso taurus GN=Fp3 PE=2 SVs3 - [TPM3_RAT] Small nucker information prohion initiation factor 5-1 OS=Bso taurus GN=Rp3 PE=1 SVs3 - [MDM1_HMAN] Small nucker information prohion initiation factor 5-1 OS=Bso taurus GN=Rp3 PE=1 SVs3 - [MDM1_HMAN] Small nucker informatioprohion initiation (Sni-Sni-Sni-Sni-Sni-Sni-Sni-Sni-Sni-Sni-	
P-1899 Q3-149 Q3-149 Q40-186 Q	6,05 25,52 5,97 13,97 12,69 33,93 10,48 22,73 9,93 10,36 27,73 83,83	3 2 3 4 4 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	14,5 54,0 14,5 44,6 6,7 23,7 29,0 16,8 31,3 35,5 13,3 36,6 11,0 12,5 38,2	108,38 107,52 105,88 105,43 103,44 103,30 102,56 102,36 100,38 98,64 95,38 94,14 92,84 90,93 90,90	Tropomyosin algine 4 chain OS=Equas caballus GRETPMA PE-1 SVs2 - [TPM4_HXRS E] 405 r bosomal protein 51: 02=Bot taurus GRERP12 PE-2 SVs1 - [KS12_50VN] Hembalpoisicii Inage cell-specile protein GS+thoro saperis GRH-LS1; PE-2 SVs1 - [K12_5], 20VNI) 405 r bosomal protein 122-Rei 1 OS=Bot taurus GRERP12 PE-2 SVs1 - [K12_5], 20VNI) 405 r bosomal protein 123-Rei 1 OS=Bot taurus GRERP12 PE-2 SVs1 - [K12_5], 20VNI) 405 r bosomal protein 239 OS=Bot taurus GRERP12 PE-2 SVs2 - [K12_5], 20VNI) 528 domant-combining rithous desprotein OS=Homo saperis GRERP12 PE-1 SVs2 - [SARP_HAMM] 7 tropomyosin glish 2-3 chain OS=Reita no revigus GRETP3 PE-1 SVs2 - [VE-3], 20VNI) 528 domant-combining rithous factor 5A-1 OS=Bot taurus GRETP3 PE-1 SVs2 - [VE-3], 20VNI) 528 domant-combinent 1 Q subcomponent binding protein, milochondrial OS erbon sapiens GRETP3 PE-1 SVs2 - [VE-3], 20VNI) 629 domant-combinent 1 Q subcomponent binding protein, milochondrial OS erbon sapiens GRETP3 PE-1 SVs2 - [VE-3], 20VNI) 75 mall nucles rithous deprotein 50 OS=Bot taurus GRETP3 PE-1 SVs2 - [VE-1], 20VNI) 75 mall nucles rithous deprotein 50 OS=Bot taurus GRETP3 PE-1 SVs2 - [VE-1], 20VNI) 75 mall nucles rithous deprotein 50 OS=Bot taurus GRETP3 PE-1 SVs2 - [VE-1], 20VNI) 75 mall nucles rithous deprotein 50 OS=Bot taurus GRETP3 PE-1 SVs2 - [VE-1], 20VNI) 75 kepte-6 chain 1 region GS=Chychlogos aurinus PE-1 SVs2 - [VE-1], 20VAI, 20	
P42899 Q13442 Q4U-86 Q4U-86 Q4U-86 Q4U-86 Q40561 Q4561	5,52 5,57 31,97 12,89 33,53 10,48 22,73 9,93 10,36 27,73 8,83 38,81 17,39 7,37	3 2 2 3 4 4 2 2 2 2 2 2 2 2 2 2 2 2 2 2	14,5 54,0 14,5 44,6 6,7 23,7 29,0 16,8 31,3 35,5 13,3 36,6 11,0 12,5	108,38 107,52 105,88 105,43 103,44 103,30 102,56 100,58 98,96 96,04 95,38 94,14 92,94	Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SVs2 - [TPM4_HDRS E] 405 r bosomal probin S12 DS=Bs taurus GN=RP31 PE=2 SVs1 - (RS121_ROVIN) Membalopiatic Image call-specifs prohio dis-throw aspecia GN=LS12 PE=1 SVs1 - [RLS12_ROVIN] 605 r bosomal probin L12-like 1 OS=Bso taurus GN=RR128.1 PE=2 SVs1 - [R222_ROVIN] Actin-related or detain 2-A OS=Dseno rerio GN=extria PE=1 SVs1 - [R222_ROVIN] Actin-related or detain 2-A OS=Dseno rerio GN=extria PE=1 SVs1 - [R222_ROVIN] 540 formalin-combining riborus/deoprotein OS=Ptom septems GN=SARIP PE=1 SVs3 - [SARIP_HUMAN] Tropomyosin alpha-3 chain OS=Ratta non regious GN=Rp3 PE=1 SVs3 - [TPM3_RAT] Eukaryoto terralistion initiation factor 5-1 OS=Bso taurus GN=Fp3 PE=2 SVs3 - [TPM3_RAT] Eukaryoto terralistion initiation factor 5-1 OS=Bso taurus GN=Fp3 PE=2 SVs3 - [TPM3_RAT] Small nucker information prohion initiation factor 5-1 OS=Bso taurus GN=Rp3 PE=1 SVs3 - [MDM1_HMAN] Small nucker information prohion initiation factor 5-1 OS=Bso taurus GN=Rp3 PE=1 SVs3 - [MDM1_HMAN] Small nucker informatioprohion initiation (Sni-Sni-Sni-Sni-Sni-Sni-Sni-Sni-Sni-Sni-	
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P-42899 Q3344 Q3448 O00159 P002561 Q76181 P14317 A-4**LHD Q755W6 P52576 Q55610 Q65610 Q65610 Q407021 P00156 P01595 P01595 P01596	5,52 5,57 11,97 12,89 13,93 13,33 10,48 22,73 9,92 10,36 27,73 8,38 39,81 17,39 7,37 25,58 11,83 9,47 15,00	3 2 2 3 4 4 2 2 2 2 2 2 2 2 2 2 2 2 2 2	14,5 54,0 14,5 44,6 6,7 23,7 29,0 16,8 31,3 35,5 13,3 36,6 11,0 12,5 38,2 10,1 31,3 30,8 26,7	108,38 107,52 105,88 105,40 105,58 105,40 105,40 105,40 105,56 105,26 10	Tropomyosin digitie 4 diskin OS=Equat caballus GN=TPM4 PE=1 SV=2 - [TPM4_HDRS E] 405 r Bosomal probin S12 DS=Bs taurus GN=R912 PE=2 SV=1 - (R512_BOVN) Methodological Control of the Control of Section 2014 CN=1 SV=1 - (R121_BOVN) Activities belief probin 12-24-11 DS=Bs taurus GN=R912 PE=2 SV=1 - (R212_BOVN) Activities belief probin S2 DS=Bs taurus GN=R912 PE=1 SV=1 - (R872_BOVN) Activities belief probin S2 DS=Bs taurus GN=R912 PE=1 SV=1 - (R872_BOVN) S46 formal probin S2 DS=Bs taurus GN=R912 PE=1 SV=2 - (R512_BOVN) S46 formal-combining ribon undesprobin OS=Mnon suplems GN=SARP PE=1 SV=3 - (R512_BOVN) S46 formal-combining ribon desprobin OS=Mnon suplems GN=SARP PE=1 SV=3 - (R512_BOVN) Tropomyosin digita - 3 dian OS=R814 taurus GN=R912 PE=3 SV=2 - (R781_BOVN) Extensive transition initiation factor S3-1 OS=dos taurus GN=E588P PE=1 SV=3 - (R781_BOVN) Complement component 1 Q subcomponet-bilding probin, milbochonida IOS elbomo suplems GN=CQRP PE=1 SV=1 - (C1QRP_HMMI) Small nuclear ribonucleoprobin Sm D1 OS=R85 taurus GN=SNRPD1 PE=3 SV=1 - (SND1_BOVN) Lestatic deliydrogenese S claim OS=Mnon suplems GN=LBNRPD1 PE=3 SV=1 - (SND1_BOVN) Lestatic deliydrogenese Sc claim OS=Mnon suplems GN=LBNRPD1 PE=3 SV=1 - (SND1_BOVN) Mac ophage migration inhibitor factor OS=Mnon suplems GN=LBNRPD1 PE=1 SV=1 - (RNDH_MMMI) Mac ophage migration inhibitor factor OS=Mnon suplems GN=R878 PE=1 SV=2 - (RNP_HMMI) Mac ophage migration inhibitor factor OS=Mnon suplems GN=R878 PE=1 SV=1 SV=1 SV=1 SV=1 SV=1 SV=1 SV=1 SV	
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Supplementary references

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