**PRDX1 Influences The Occurrence and Progression of Liver Cancer by Inhibiting Mitochondrial Apoptosis Pathway**

Hong-hua Sun, M.D.,¹, Yang-long Li, M.D.,¹, Hao Jiang, M.D.,¹, Xiang-hua Yin, M.D.,¹, Xing-lin Jin, M.D.²*

1. Department of Oncology, Yanbian University Hospital (Yanbian hospital), Yanji, China
2. Department of Hepatobiliary Surgery, Yanbian University Hospital (Yanbian hospital), Yanji, China

*Corresponding Address: Department of Hepatobiliary Surgery, Yanbian University Hospital (Yanbian hospital), Yanji, China
Email: jinxinglin_yuh@126.com

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Abstract

**Objective:** The aim of this study is to elucidate the role of PRDX1 in hepatocellular carcinoma using hepatoma cells.

**Materials and Methods:** In this experimental study, we elucidated role of PRDX1, using hepatoma cell lines.

**Results:** PRDX1 was upregulated in different types of cancers, including lung adenocarcinoma, breast cancer and liver cancer reported by several studies. Nevertheless, mechanism of inducing liver cell death by PRDX1 remains largely unknown. Here, we showed that PRDX1 expression is enhanced in different cell lines. Here, we used western blot, quantitative real time polymerase chain reaction (qRT-PCR) and different biochemical assays to explore the role of PRDX1. We observed that overexpression of PRDX1 significantly enhanced proliferation of hepatoma cell lines, while knock-down of this gene showed significant inhibitory effects. We found that knock-down of PRDX1 activated cleaved caspase-3, caspase-9 proteins and Poly [ADP-ribose] polymerase 1 (PARP-1), which further executed apoptotic process, leading to cell death. We found that PRDX1 knock-down significantly produced mitochondrial fragmentation. We showed that silencing PRDX1 led to the loss of B-cell lymphoma 2 (Bcl-2) and activated Bcl-2-like protein 11 (Bim) which further induced Bax activation. Bax further released cytochrome c from mitochondria and induced apoptotic proteins, suggesting a significant role of PRDX1 knock-down in apoptosis. Finally, we showed that knock-down of PRDX1 significantly activated expression of Dynein-related protein 1 (Drp1), fission 1 (Fis1) and dynamin-2 (Dyn2) suggesting a crucial role of PRDX1 in mitochondrial fragmentation and apoptosis conditions. This study highlighted an important role of PRDX1 in regulating proliferation of hepatoma cells and thus future studies are required to validate its effect on hepatocytes.

**Conclusion:** We propose that future works on PRDX1 inhibitors may act as a therapeutic candidate for treatment of liver cancer.

**Keywords:** Hepatocellular Carcinoma, Liver Cancer, Peroxiredoxins, PRDX1

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**Introduction**

Human hepatocellular carcinoma (HCC) is one of the most common types of liver cancer, which accounts for more than 70% of total liver cancer. It is known for the high mortality rate (>8%) worldwide. Peroxiredoxins are a large family of antioxidant enzymes that play an essential role in antioxidant defense and peroxide detoxification. **PRDX1** is a multifunctional protein involved in cell growth, differentiation and apoptosis (1). **PRDX1** is reported in different types of cancer, including lung adenocarcinoma, breast cancer, soft tissue sarcomas (2), colorectal cancer and prostate cancer. Most studies reported elevated level of **PRDX1** in pathological conditions.

However, Fang et al. (3) showed the lower **PRDX1** expression in HCC cells. **PRDX1** is upregulated in cervical cancers and enhanced proliferation, migration and invasion by inhibiting apoptosis (4). Analysis of a disease model represented higher **PRDX1** expression level in brain, while it is associated with toll like receptor-4 (TLR-4) inflammation and apoptosis. Several studies reported its expression in tumor tissues of the liver (3). However, the cellular role of **PRDX1** in hepatocellular carcinoma and mechanism of this association with related protein remains unknown. Caspases are essential proteins. They are activated when cell death is required (5). Poly ADP-ribose polymerase 1 (PARP-1) has multiple functions involved in DNA repair, cell death and transcriptions of some essential genes involved in inflammatory processes (6). It is a well-known substrate of caspase proteins (7). Caspase-3 cleaves PARP-1 upon activation and therefore prevents PARP-1 from repairing the damage (8). It has been demonstrated that overexpression of human Mitochondrial fission 1 protein (hFis1) induced apoptosis, which may suggest a role of mitochondrial fission in apoptosis. Dynem-related protein 1 (Drp1) expression is upregulated in HCC cells and involved in autophagy (9).

Here, in this study, we elucidated role of **PRDX1**...
in hepatocellular carcinoma using hepatoma cells. The role of PRDX1 on hepatocytes cells was poorly known. We We reported for the first time that the mechanism by which PRDX1 acts on HCC cells via B-cell lymphoma 2 (Bcl-2).

Materials and Methods

RNA sequencing database

In this experimental study, the RNA sequencing data from more than 350 patients of liver cancer were obtained from TCGA database. The expression of PRDX1 mRNA were analyzed using the database. The Kaplan-Meier and Cox regression survival analysis was performed to see the relationship between PRDX1 levels and patient survival.

Cell culture

HCC cells were obtained from ATCC (Virginia, USA). Cell culture media and supplements were purchased from Gibco (Sigma, USA). HCC cells were cultured in DMEM high glucose medium supplemented with 2 mM glutamine, 100 units/ml penicillin (both from Gibco, USA), and 100 μg/ml streptomycin (Gibco, USA). Cells were grown at 37°C in the presence of 5% CO2. Cells were grown for 2-3 days. Following the confluency, the cells were proceeded for analysis of mRNA or protein expressions.

Quantitative reverse transcription polymerase chain reaction

Extraction of total RNA was done by Trizol reagent (Ambion, USA). Synthesis of cDNA was done by RevertAid cDNA Synthesis Kit (Thermo Fisher Scientific, USA) for that 1 μg of total RNA of each sample was used. The cDNA samples were kept at -20°C for quantitative reverse transcription PCR (qRT-PCR). The SYBR green dye (Invitrogen, USA) was used to bind to double stranded DNA and emit green light (λmax=520 nm), in terms of quantifying cDNA. For qRT-PCR, the master mix was used as the manufacturer’s instruction. Specific primers of PRDX1 and GAPDH were used (Table 1). Data was acquired and analyzed using comparative CT method.

| Table 1: Primer information |
|-----------------------------|
| Gene name | Primer sequence (5'-3') |
| PRDX1 | F: GCACCAUGUGUCAGAGTATG  \\
|  | R: GCAACACAGGGAGGTCATTAC  \\
| GAPDH | F: GGTGTAGAACATGAGAAGATGA  \\
|  | R: GAGTCCCTCCACGATACCAAG  \\

Cells transfection

The PRDX1-siRNA are 5’GCACCAUGUGUCAGAGTATG3’ which was synthesized by GenePharma (Shanghai, China). HepG2 Cells were seeded and transfected using Lipofectamine 2000 reagent (Invitrogen, USA) following manufacturer’s instructions. 3×104 cells were seeded and allowed to 70-90% confluency. Transfection mixture was prepared with 50 ng, 25 μl DNA dilution and 25 μl opti-MEM (Gibco, USA) dilution. Mixing Lipofectamine 2000 diluent and DNA diluent was performed in a centrifuge tube with a capacity of 1.5 ml, followed by 15 minutes incubation in hood. Optimum medium was removed and DNA/lipofectamine 2000 mixture was gently added dropwise into cells.

Western blotting

Lysis buffer (200 μl/well) was used to lyse HepG2 cells. Lysis buffer was composed of Triton X-100 (1%), Tris (50 mM, pH=7.6) and NaCl (150 mM), with inhibitors of phosphatases and proteases. sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE, 7.5%) was used to separate 40 μg of the total extracted protein. Then Western blotting was done as demonstrated by Moeschel et al. (10). Following the application of antibodies for western blotting anti-PRDX1 (ab109498), anti-beta actin (ab115777), anti-caspase-3 (ab13847 and ab32042), anti-cleave caspase-9 (ab202068 and ab25758), anti-PARP-1 (ab191217), anti-Bim (ab7888), anti-Bcl-2 (ab115777), anti caspase-3 (ab13847 and ab32042), anti-cleave caspase-9 (ab202068 and ab25758), anti-PARP-1 (ab191217), anti-Bim (ab7888), anti-Bax (ab3191), anti-DRP1 (ab184247) and anti-Dyn2 (ab65556; all purchased from AbCam, UK). Nitrocellulose was blocked using skimmed milk (5%) or BSA (2%, both from Merck, Germany) for two hours. Subsequently, membranes were incubated with primary antibodies at 4°C overnight. Before incubation with secondary antibody, washing was performed (four times for 10 minutes), followed by appropriate conjugated secondary incubation for one hour. For visualizing expression level of proteins, enhanced chemiluminescence was performed.

Cell counting assay

For detecting proliferation, the number of living cells was determined with CCK-8 kit (ab228554, AbCam, UK), according to the manufacturer’s instructions. In 96-well plate HepG2 cells were cultivated (five thousands cells in each well). In the incubator, the cells were seeded for 24, 48 and 72 hours. After that, four hours incubation was performed on the cells containing CCK-8 reagent (10 μl). Lastly, optical density was determined at wave length of 450 nm.

Annexin V-FITC-PI staining analysis

HepG2 Cells were stained with Annexin V-FITC/PI
Critical. Higher-level expression was reported by several regulating oxidation reductions, its expression level is significant. Multiple groups differences were analyzed using one-

manner, we found that knock-down of PRDX1 significantly decreased proliferation of hepatoma cells. PRDX1 overexpression significantly enhanced proliferation of hepatoma cells (Fig.2F, middle panel) compared to control cells, while knock-down of PRDX1 showed significant inhibitory effects and reduced cell proliferations. Next, we were interested to see its effect on caspase proteins. Interestingly, we found that knock-down of PRDX1 induced cell death via activation of cleaved and active caspase-3 and caspase-9, which further executed an apoptotic process, leading to cell death and inhibited proliferation of hepatoma cells (Fig.2E, middle panel) compared to control cells, while knock-down of PRDX1 showed significant inhibitory effects and reduced cell proliferations. 

PRDX1 knock-down induced apoptosis in hepatoma cells

Based on the higher expression of PRDX1 in most of the cancerous tissues and cells, we were interested to see its cellular role. We overexpressed the PRDX1 construct in HCC cells and tested the efficiency of transfection. We found almost 3-fold higher mRNA and protein expression of PRDX1 using hepatoma cells, while using siRNA against PRDX1 (si-PRDX1) significantly inhibited its expression (Fig.2A, 2B). Figure 2C shows relative expression level of PRDX1, in the presence of si-RNA. Cell counting kit-8 (CCK-8) is a widely used colorimetric-based assay used to measure cells viability. We wanted to test the effect of PRDX1 on HCC cell proliferations. We found that knock-down of PRDX1 significantly decreased half maximal inhibitory concentration (IC_{50}) value of HCC cells, suggesting that Knock-down of PRDX1 possesses great anti-tumor activity (Fig.2D). This was further confirmed by clonal formation assay, which was used to assess effect of PRDX1 expression on the proliferation of hepatoma cells. PRDX1 overexpression significantly enhanced proliferation of hepatoma cells (Fig.2E, middle panel) compared to control cells, while knock-down of PRDX1 showed significant inhibitory effects and reduced cell proliferations.

Results

**PRDX1 is upregulated in liver cancers cells**

Given the role of PRDX1 as an antioxidant system and regulating oxidation reductions, its expression level is critical. Higher-level expression was reported by several studies in different malignancies, including lung (12), cervical (13), prostate (14) and liver cancers (4). However, limited studies reported PRDX1 expression in human specimens. Significant difference in PRDX1 expression using TCGA public database was observed, we found that transcripts of PRDX1 had a significant differences between cancerous and paracancerous tissues of liver cancer patients (Fig.1A). PRDX1 mRNA expression was found to have a higher expression of 1.3 fold in cancerous tissues compared to control (15). PRDX1 transcript and protein expression levels were significantly higher in different cancerous cell lines (HepG2, Huh-7, Hep-3B) compared to control cells (Fig.1B-D), which are consistent with the other studies. The highest PRDX1 mRNA and protein level were found in HepG2 cells with 3-fold higher expression compared to control.
**Fig. 1:** Expression of peroxiredoxin 1 (PRDX1) in different cell lines of liver cancers. 

- **A.** Box diagram of PRDX1 expression, with significant difference between cancerous and paracancerous tissues of liver cancer patients.
- **B.** PRDX1 mRNA expression was significantly higher in cancerous cells.
- **C.** Western blot results showed an increased expression of PRDX1 protein in cancerous cells, with the highest expression level observed in hepatoma (HepG2) cells.
- **D.** Quantifications of protein levels. The experiment was repeated three times. Data represent mean ± SEM. *; P<0.05, **; P<0.01, and ***; P<0.001.

**Fig. 2:** PRDX1 knock-down induced cell death via apoptosis in HCC cells.

- **A.** Significant increase of PRDX1 mRNA expression level when overexpressed in hepatoma cells.
- **B.** Western blot showed that PRDX1 overexpression enhanced expression level of PRDX1, while knock-down of this gene substantially reduced the expression.
- **C.** Quantification of the protein levels.
- **D.** CCK-8 assay showed a significant reduction in the IC50 value of hepatoma cells.
- **E.** Clonal formation assay demonstrated effect of PRDX1 expression on the proliferation of hepatoma cells. Knock-down of PRDX1 showed a significant inhibitory effect on cell proliferation.
- **F.** Quantification of the number of colonies.
- **G.** Western results showed the effect of knock-down of PRDX1 protein on caspase proteins in hepatoma cells.
- **H.** Quantification of the protein levels. The experiment was repeated three times. Data represent mean ± SEM. **; P<0.01, and ***; P<0.001.
PRDX1 knock-down induced apoptosis via Bax activation

PRDX1 mediated apoptosis in hepatoma cells was unknown. We wanted to explore effect of PRDX1 in hepatoma cells. We found that PRDX1 overexpression significantly increased Bcl-2 expression, while knock-down of this gene showed a significant reduction of Bcl-2 and enhanced Bax expression (Fig.3A), suggesting an apoptotic condition. Mitochondrial function is essential which is required for normal cellular metabolism. Mitochondrial fragmentation is associated with increased fission (16). Next, we assessed mitochondrial morphology using mitotracker, whether or not PRDX1 regulate mitochondrial morphology. We found that PRDX1 knock-down significantly produced mitochondrial fragmentation (Fig.3B). All of these cellular events are closely associated with each other. These results indicated that higher expression of Bax may induce apoptosis via dysregulating mitochondrial membrane potential and induced fragmentation. While increased mitochondrial fragmentation and expression of Bax suggested a favorable condition of cellular death. Taken together, these results implied that PRDX1 played a crucial role in inducing cell death of hepatoma cells via regulating Bcl-2 and Bax (Fig.3A).

![Fig.3](image-url)

**Fig.3:** PRDX1 knock-down reduced mitochondrial transmembrane potential in HCC cells. A. Western blot results depicted that PRDX1 knock-down substantially reduced expression of Bcl-2 and increased Bax expression. The lower bottom showed quantifications of protein levels. B. Mitotracker red assay was used to see the effect of si-PRDX1 expression on mitochondrial morphology of hepatoma cells. PRDX1 knock-down induced significantly increased filamentous mitochondrial morphology, assessed by fluorescent intensity. Representative graphs show quantifications. The experiment was repeated three times. Data represent mean ± SEM. **; P<0.01, and ***; P<0.001.
**PRDX1** knock-down induces apoptosis via activation of mitochondrial fission

Next, we assessed expression level of proteins which are crucial for mitochondrial fission, whether or not accumulation of these proteins regulate mitochondrial fragmentation (Fig.3B). We found that silencing **PRDX1** greatly enhanced expression of Drp1, Fis1 and Dyn2 proteins, reflecting the abnormal function of mitochondria and initiation of apoptosis process. Inhibition of GTPase activity of Drp1 by dominant-negative protein (Drp1K38A) has been shown to delay cell death (17). They demonstrated that overexpression of hFis1 induced apoptosis, suggesting a role of mitochondrial fission in apoptosis. Next, to investigate effect of PRDX1 knock-down on mitochondrial fission machinery, we found that expression of Drp1, Fis1 and Dyn2 were significantly activated (Fig.4A), proposing mitochondrial fragmentation and apoptosis conditions.

Reduction of Bcl-2 in PRDX1 knocked-down cells (Fig.3B) reflected release of cytochrome c, followed by activation of downstream caspase signaling. Therefore, we checked expression of cytochrome c, Apaf-1 and BH3-only proteins (Bim) to confirm its correlation with PRDX1 knock-down (Fig.4B). Silencing **PRDX1** led to the loss of Bcl-2 and activated Bim protein, which further induced Bax protein activation. Bax further released cytochrome c from mitochondria for the induction of apoptotic proteins. Taken together, these data suggested that knock-down of PRDX1 facilitated mitochondrial fission and activated caspase proteins, i.e. release of cytochrome c, Bim and Apaf-1, to induce death of hepatoma cells.

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**Fig.4:** Effect of PRDX1 knock-down on apoptosis and mitochondrial fission machinery of HCC cells. **A.** Western results showed that knock-down of PRDX1 significantly enhanced expression of Drp1, Fis1 and Dyn2 in hepatoma cells. **B.** Images and graphs showed that overexpression of PRDX1 decreased apoptotic proteins (Bim, cytochrome C and Apaf-1) expression level, while knock-down of this gene significantly enhanced expression of caspase proteins. The right panel shows quantifications of protein levels. The experiment was repeated three times. Data represent mean ± SEM. **; P<0.01, and ***; P<0.001.
Discussion

In this study, we explored effect of silencing PRDX1 in hepatoma cells. Several studies showed that PRDX1 is upregulated in different types of cancer, including lung adenocarcinoma (19, 20), soft tissue sarcoma (2) and prostate cancer (14, 21). However, cellular role of PRDX1 in liver cells remains to be understood. Sun et al. analyzed RNA sequences from the TCGA database and reported that PRDX1 mRNA expression level was increased 1.3 fold in the malignant compared to the control tissues (15). We tested PRDX1 expression and found an increased expression of PRDX1 in different HCC cell lines, which is in line with the other studies and suggested a vital role in cellular proliferation. We found relatively higher PRDX1 mRNA and protein expression levels in HepG2 cells.

There are studies which reported role of PRDX1 in cellular proliferation. Gong et al. (22) demonstrated that PRDX1 regulated proliferation of esophageal squamous cell carcinoma. Lu et al. (4) reported overexpression of PRDX1 in cervical cancer and found that PRDX1 enhanced proliferation, migration and invasion by inhibiting apoptosis. Next, we were interested to explore association between PRDX1 and hepatoma cells. We found that knock-down of PRDX1 significantly decreased the IC50 value of hepatoma cells, suggesting that knockdown of PRDX1 possessed great anti-tumor activity. We assessed proliferation effect by clonal formation assay and found that PRDX1 overexpression significantly enhanced proliferation of the hepatoma compared to control cells, while knock-down of this gene showed significant inhibitory effects and reduced proliferation of cells, suggesting an important role of PRDX1 silencing in hepatoma cells. Next, we were interested to explore molecular mechanism of cell death. We asked question whether silencing PRDX1 is associated with caspase activation? We found that knock-down of PRDX1 induced cell death via activation of active and cleaved caspase-3 and caspase-9 proteins, which further executed apoptotic process, leading to cell death.

PARP-1 has multiple functions, involved in DNA repair, cell death and transcriptions of some essential genes involved in inflammatory processes (6). It is a well-known substrate of caspase proteins (7, 23). Caspase-3 cleaves PARP-1 upon activation and prevents PARP-1 from repairing the damage (8, 24). Our results showed that knock-down of PRDX1 increased PARP-1 expression, suggesting depletion of NAD+ levels, thereby induced cellular death.

Bcl-2, as an essential protein, is a member of the Bcl-2 family, which act as a negative regulator of apoptosis. Moreover, Bcl-2 has shown to be protective and Bax up-regulation has pro-apoptotic role (25, 26). Several evidences reported that Bcl-2 regulate cytochrome c and therefore prevented activation of apoptotic genes (27, 28). Overactivation of Bcl-2 inhibited release of cytochrome c and initiation of apoptosis (29). Lu et al. (4) found that PRDX1 overexpression increased Bcl-2 expression, while down-regulated Bax expression. This is in line with our findings, representing that PRDX1 overexpression significantly increased Bcl-2 expression, while knock-down of this gene showed a significant reduction of Bcl-2 and enhanced Bax expression in hepatoma cells, suggesting a vital role of PRDX1 knock-down in cancerous cells. Once cytochrome is released in the cytosol, cytosolic cytochrome c further mediates apoptosis- protease activating factor 1 (Apaf-1) to induce activation of the other caspase proteins (30). Researchers reported the role of Bax protein in facilitating release of cytochrome c from mitochondria to induce apoptosis process (31, 32). While, the other studies demonstrated that Bim protein directly activated Bax protein. This may suggest that BIM protein plays an indirect role by antagonizing Bcl-2 proteins, thereby allowing Bax activation to proceed (33, 34). In our study, we found that silencing PRDX1 led to the loss of Bcl-2 and activated Bim protein which further induced activation of Bax protein. We showed that Bax further released cytochrome c from mitochondria to induce apoptotic proteins, suggesting a significant role of PRDX1 knock-down in apoptosis. Researchers reported the role of PRDX1 and found that overexpression of PRDX1 enhanced Bcl-2 expression, while at the same time down-regulated Bax expression (4). Our findings showed that PRDX1 overexpression significantly increased Bcl-2 expression, while knock-down of this gene enhanced Bax expression in hepatoma cells. This is consistent with studies previously reported in different cell lines.

Next, we asked question whether PRDX1 has any role in regulating mitochondrial fission proteins of HCC cells. Drp1, Fis1 and Dyn2 played a role as fission mediators (35). The mitochondrial fission machinery played a vital role in mitochondrial function. Disruption in fission machinery led to the abnormal division of mitochondrial membrane. It was required to produced new mitochondria to induce apoptotic proteins, suggesting a significant role of mitochondrial fission in apoptosis in yeast cells (18). There are other studies demonstrating the role of Drp1 and Fis1. Thus, they have been shown to inhibit mitochondrial fission and prevent apoptosis (38). In our findings, we analyzed that PRDX1 knock-down significantly activated mitochondrial fission proteins (Drp1, Fis1 and Dyn2), which may suggest its role in inducing apoptosis. We also showed that mitochondrial fission, induced by silencing PRDX1, resulted in mitochondrial fragmentation. These results suggested a significant role of silencing PRDX1 on mitochondrial fragmentation and fission associated proteins, thereby leading to apoptosis conditions.

Conclusion

A little attention has been given to study effect of PRDX1 on live cancer via inhibiting mitochondrial apoptosis.
pathway. We reported that PRDX1 acted via Bcl-2 to inhibit cell death and apoptosis in hepatoma cells. Furthermore, silencing PRDX1 simulated apoptosis pathways by activating Bax protein, which facilitated release of cytochrome c from the mitochondria followed by activation of the other related apoptotic proteins to induce cell death. Future studies targeting PRDX1 inhibitors are required, which may act as a therapeutic candidate for the treatment of liver cancer.

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Authors’ Contributions

H.h., X.I.J.; Contributed to conception and design. H.h.S.; Were responsible for overall supervision, and drafted the manuscript. H.h.S., X.I.J., Y.I.L., H.J., X.h.Y.; Contributed to all experimental works, data and statistical analyses and interpretation of data. All authors read and approved the final manuscript.

References

1. Ding C, X Fan, G Wu. Peroxiredoxin 1 - an antioxidant enzyme in cancer. J Cell Mol Med. 2017; 21(1): 193-202.
2. Takahashi A, Nakayama R, Ishibashi N, Doi A, Ichinohe R, Ikuyo T. PRDX1 and Liver Cancer. Cell J, Vol 24, No 11, November 2022.
3. Fang Y, He J, Janssen HLA, Wu J, Dong L, Shen XZ. Peroxiredoxin 1 regulates mitochondrial dynamics and regulates apoptosis in hepatoma cells. Further studies show that PRDX1 silencing cell death and apoptosis in hepatoma cells. Furthermore, PRDX1 and Liver Cancer. Cell J, Vol 24, No 11, November 2022.
4. Galluzzi L, Jaova N, Taisdemir E, Mauri MC, Hengartner M, Abrams JM, et al. Analysis of gene expression profiles of soft tissue sarcoma using a combination of knowledge-based filtering with integration of multiple statistics. PLoS One. 2014; 9(9): e106801.
5. Fang Y, He J, Janssen HLA, Wu J, Dong L, Shen XZ. Peroxiredoxin 1 regulates mitochondrial dynamics and regulates apoptosis in hepatoma cells. Further studies show that PRDX1 silencing cell death and apoptosis in hepatoma cells. Furthermore, PRDX1 and Liver Cancer. Cell J, Vol 24, No 11, November 2022.
6. Decker P, Muller S. Modulating poly (ADP-ribose) polymerase activity: potential for the prevention and therapy of pathogenetic path-ways. PLoS One. 2014; 9(9): e106801.
7. Decker P, Muller S. Modulating poly (ADP-ribose) polymerase activity: potential for the prevention and therapy of pathogenetic path-ways. PLoS One. 2014; 9(9): e106801.
8. Galluzzi L, Jaova N, Taisdemir E, Mauri MC, Hengartner M, Abrams JM, et al. Analysis of gene expression profiles of soft tissue sarcoma using a combination of knowledge-based filtering with integration of multiple statistics. PLoS One. 2014; 9(9): e106801.
9. Decker P, Muller S. Modulating poly (ADP-ribose) polymerase activity: potential for the prevention and therapy of pathogenetic path-ways. PLoS One. 2014; 9(9): e106801.
10. Galluzzi L, Jaova N, Taisdemir E, Mauri MC, Hengartner M, Abrams JM, et al. Analysis of gene expression profiles of soft tissue sarcoma using a combination of knowledge-based filtering with integration of multiple statistics. PLoS One. 2014; 9(9): e106801.
11. Decker P, Muller S. Modulating poly (ADP-ribose) polymerase activity: potential for the prevention and therapy of pathogenetic path-ways. PLoS One. 2014; 9(9): e106801.
12. Galluzzi L, Jaova N, Taisdemir E, Mauri MC, Hengartner M, Abrams JM, et al. Analysis of gene expression profiles of soft tissue sarcoma using a combination of knowledge-based filtering with integration of multiple statistics. PLoS One. 2014; 9(9): e106801.
13. Galluzzi L, Jaova N, Taisdemir E, Mauri MC, Hengartner M, Abrams JM, et al. Analysis of gene expression profiles of soft tissue sarcoma using a combination of knowledge-based filtering with integration of multiple statistics. PLoS One. 2014; 9(9): e106801.
14. Galluzzi L, Jaova N, Taisdemir E, Mauri MC, Hengartner M, Abrams JM, et al. Analysis of gene expression profiles of soft tissue sarcoma using a combination of knowledge-based filtering with integration of multiple statistics. PLoS One. 2014; 9(9): e106801.