The Role of PGC1α in Cancer Metabolism and its Therapeutic Implications

Zheqiong Tan1,2,3, Xiangjian Luo1,2,3, Lanbo Xiao1,2,3, Min Tang1,2,3, Ann M. Bode4, Zigang Dong4, and Ya Cao1,2,3

Abstract

PGC1α is a transcription factor coactivator that influences a majority of cellular metabolic pathways. Abnormal expression of PGC1α is associated with several chronic diseases and, in recent years, it has been shown to be a critical controller of cancer development. PGC1α acts as a stress sensor in cancer cells and can be activated by nutrient deprivation, oxidative damage, and chemotherapy. It influences mitochondria respiration, reactive oxygen species defense system, and fatty acid metabolism by interacting with specific transcription factors. The characteristic traits of PGC1α in maintaining metabolic homeostasis promote cancer cell survival and tumor metastasis in harsh environments. Not only does PGC1α act as a coactivator, but it is also itself controlled by oncogenes and transcription factors. PGC1α and these molecules can form signaling axes that include PML/PGC1α/MMR, MITF/PGC1α, and PGC1α/ERRα, which are important in regulating metabolic adaptation in specific cancer types. Some of these PGC1α-associated pathways are inherently activated in cancer cells, and others are induced by stress, which enable cancer cells to acquire resistance against therapy. Notably, certain therapeutic-resistant cancer cells are addicted to PGC1α-dependent metabolic activities. Suppression of PGC1α expression resensitizes these cells to therapeutic treatments, which implicates PGC1α as a promising target in cancer molecular classification and therapy. Mol Cancer Ther; 15(5); 774-82. ©2016 AACR.

Introduction

Metabolic reprogramming is considered to be a hallmark of cancer (1). Glycolysis, mitochondrial respiration, glutaminolysis, and fatty acid metabolism are important participants in cancer development (2–6). These processes provide cancer cells with an adaptable metabolic feature and afford survival opportunities for cancer cells undergoing stress (7–9). Among the numerous regulators or mediators of cancer metabolism, PPARγ coactivator-1 alpha (PGC1α) is emerging as an essential controller of multiple metabolic pathways (10, 11).

PGC1α is strongly activated by conditions causing energy limitation, including cold, exercise, and fasting, and is particularly abundant in tissues demanding large energy consumption (12–14). Once activated, PGC1α interacts with several transcription factors and affects various biologic activities under normal physiologic conditions (15). Induced by exercise, PGC1α can promote a functional fiber switch toward more oxidative types in skeletal muscle cells by interacting with muscle-specific myocyte enhancer factor 2 family transcription factors (16, 17). PGC1α also facilitates mitochondrial oxidative phosphorylation (OxPhos) by coactivating nuclear respiratory factor 1 and estrogen-related receptors (ERRs; refs. 18, 19). It has been identified to stimulate fatty acid oxidation (FAO) through interactions with several transcription factors including sirtuin 1 (SIRT1), PPARs, and hepatocyte nuclear factor 4 (20–25), and PGC1α also increases autophagy and thermogenesis through transcription factor EB and uncoupling protein-1, respectively, under stress condition (26–30). In addition, it has been shown to protect cells against oxidative damage through nuclear factor erythroid 2 (Nrf2) and forkhead box O3 (31–33). In all of these instances, PGC1α functions as a necessary adaptor for cells to maintain metabolic balance under harsh situations, and it plays a protective role in preventing chronic diseases, such as skeletal muscle atrophy, heart failure, neurodegeneration, obesity, diabetes, and hepatic steatosis, and some of these diseases are predisposing factors for cancer initiation (10, 11, 34, 35). Recently, several advances have shown that PGC1α expression is tightly associated with cancer progression (10, 11). The exceptional ability of PGC1α in manipulating cellular metabolism enables cancer cells to thrive under a constantly fluctuating energy status, and highlights the importance of PGC1α in effective cancer therapy (36).

Structure and Regulation Mechanism of PGC1α

The PGC1α gene is located on chromosome 4 in human and encodes a protein containing 798 amino acids (29). When activated, PGC1α can be recruited as a transcriptional coactivator to subsequently dock or bind with transcription factors or nuclear receptors (NR; refs. 15, 37). The N-terminal activation domain and LXXLL motifs of PGC1α interact with various transcription factors (19, 37, 38). Proteins, such as CREB-binding protein, p300 and steroid receptor that acetylate histones, can be sequentially acylated at their LXXLL motifs through a histone acetyltransferase (HAT) reaction catalyzed by p300/CBP-associated factor (p/CAF) and transcriptional coactivator with CDC5L-like/pterin acetyltransferase (ACAT). PGC1α also contains two conserved LXXLL motifs, which can be acetylated by HATs, such as p300/CBP, CREB-binding protein, and p/CAF. The LXXLL motifs can then interact with several transcription factors, including NF-κB, c-Myb, CREB, and PPARs.

Corresponding Author: Ya Cao, Cancer Research Institute, Xiangya School of Medicine, Central South University, Hunan, China. 2Key Laboratory of Carcinogenesis of Chinese Ministry of Public Health, Central South University, Hunan, China. 3Key Laboratory of Chinese Ministry of Public Health, Central South University, Hunan, China. 4The Hormel Institute, University of Minnesota, Austin, Minnesota.
recruited to the PGC1α transcriptional activator complex, to remodel the chromatin structure and provide optimal biochemical conditions for target gene transactivation (39). The C-terminal of PGC-1α is believed to recruit the thyroid receptor–associated protein/vitamin D receptor–interacting protein/mediator complex that facilitates transcription initiation and interferes with RNA processing through Ser/Arg-rich or RNA-binding domains (40, 41).

Notably, PGC1α is controlled by several posttranslational modifications. Because PGC1α is markedly sensitive to cellular energy status, it is tightly regulated by stress sensors such as AMP-activated protein kinase (AMPK) and SIRT1. Both AMPK-mediated phosphorylation and SIRT1-mediated deacetylation activate PGC1α under energy deprivation conditions (42, 43). In addition, the p38 MAPK stabilizes the PGC1α protein by increasing its phosphorylation state (44). On the other hand, methylation of the arginine residues at the C-terminal region by protein arginine methyltransferase 1 (PRMT1) decreases PGC1α stability whereas phosphorylation of PGC-1α by Akt/protein kinase B and SUMOylation at the conserved lysine residue 183 attenuate PGC1α activity (44–46). These diverse posttranslational modifications direct PGC1α to different target genes. In addition to posttranslational modifications, PGC1α is also influenced by cellular calcium (Ca2+) and cyclic adenosine monophosphate signaling (47, 48). Notably, some transcription factors coactivated by PGC1α can, in turn, regulate PGC1α, comprising autoregulatory loops that augment target gene transcription (17).

PGC1α and Cancer Metabolism

PGC1α has been shown to be a promoter of carcinogenesis in chemical-induced colon and liver carcinoma mouse models (49). Ectopic expression of PGC1α has been observed in several cancer types (50–53), and it is regulated by several oncogenes and signaling pathways (Fig. 1; refs.54–57). Similar to its normal physiological functions, PGC1α primarily regulates mitochondrial respiration and detoxification of reactive oxygen species (ROS) in cancer cells through specific signaling pathways and transcription factors (Table 1). In addition, the involvement of PGC1α in regulating FAO and glucose- or glutamine-derived lipogenesis in cancer cells has become clearer in recent years (Fig. 2; refs.49, 51, 58).

MITF/PGC1α Axis in Melanoma

Among all its functions, PGC1α-dependent regulation of OxPhos is best studied in cancer, especially in melanoma. On the basis of PGC1α expression levels, melanomas have been defined into two subsets with different biologic phenotypes (53, 59, 60). The PGC1α-positive cells exhibit elevated mitochondrial oxidative metabolism and substantial ROS detoxifying capacities. In contrast, the PGC1α-negative cells are dependent on glycolysis for survival and are more sensitive to ROS-induced apoptosis (53). In this context, PGC1α is transactivated by the oncogenic melanocyte lineage specification transcription factor (MITF), and the PGC1α-negative cells seldom express MITF (57, 61). These findings indicate that melanomas classified by the expression of MITF/PGC1α have different metabolic capacities, resulting in distinct destinies following ROS-inducing treatments (53, 57).

The V600E BRAF mutation plays a critical role in melanogenesis by constitutively activating the MAPK signaling pathways (62, 63). Although the BRAF inhibitor, vemurafenib, and the MEK inhibitor, selumetinib, have achieved superior clinical effects to treat BRAF V600E–positive individuals, de novo and acquired
resistance are still prevalent (64–67). PGC1α and MITF are induced in both melanoma cell lines and patient biopsies following BRAF or MEK inhibition (57). MITF/PGC1α signaling promotes OxPhos and protects drug-resistant cells from BRAF inhibitor–induced apoptosis. Encouragingly, a genome-wide siRNA screen and mRNA expression profile of resistant melanoma cell lines showed that resistance can be abrogated by inhibiting mTORC1/2 (68). Inhibition of mTORC1/2 decreases MITF nuclear localization and PGC1α expression. The combination inhibition of MEK and mTORC1/2 markedly reduces xenograft tumor proliferation in MEK inhibitor–resistant mice (Fig. 3). This finding supports the idea that PGC1α could be a candidate biomarker to determine therapeutic strategies. At the very least, blocking mitochondria respiration genes or mTORC1/2 signaling could re sensitize cancer cells to BRAF or MEK inhibition in melanomas harboring activated MITF/PGC1α/OxPhos signaling.

PGC1α/ERRα axis in breast cancer

ERRα is a ligand-independent NR that regulates a number of metabolic genes in the presence of a coactivator, such as PGC1α (69). PGC1α and ERRα are both downstream proteins of the kinase suppressor of RAS1 (KSR1), a molecular supporting Ras microenvironments (76). Disruption of PGC1α expression and patient outcome. Even though this study did not identify the target transcription factor of PGC1α in CCCs, the data illustrated that PGC1α is essential in cancer metastasis.

Overall, the PGC1α/ERRα signaling axis is responsible for altering cellular metabolic status and guarantees cancer cell survival under limited nutrient supply and high-energy demanding microenvironments (76). Disruption of PGC1α expression and patient outcome. Even though this study did not identify the target transcription factor of PGC1α in CCCs, the data illustrated that PGC1α is essential in cancer metastasis.

Another group demonstrated that PGC1α and ERRα are overexpressed in brain metastatic breast cancer cells, with enhanced mitochondria respiration, FAO, glycolysis, and elimination of ROS (74). These changes give brain metastatic cells a considerable growth advantage, which is accompanied by resistance to therapeutic drugs. Recently, a study also confirmed that PGC1α expression is markedly upregulated in circulating cancer cells (CCC) in a breast cancer metastatic mouse model (75). These cells relied on PGC1α to maintain mitochondria activity during their transition to target organs. Clinical analysis in this research also indicated that PGC1α is enriched in invasive ductal breast cancer patients with bone marrow dissemination, and illustrated a significant negative correlation between PGC1α expression and patient outcome. Even though this study did not identify the target transcription factor of PGC1α in CCCs, the data illustrated that PGC1α is essential in cancer metastasis.

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Table 1. A summary of PGC1α-dependent signaling in cancer

<table>
<thead>
<tr>
<th>Signaling axis</th>
<th>Cancer type</th>
<th>Metabolic pathways</th>
<th>Function</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>MITF/PGC1α</td>
<td>Melanoma</td>
<td>OxPhos, ROS clearance</td>
<td>Resistance to BRAF or MEK inhibitors</td>
<td>(53, 57, 68)</td>
</tr>
<tr>
<td>PGC1α/ERRα</td>
<td>Breast cancer</td>
<td>OxPhos, Glycolysis</td>
<td>Support anchorage independent growth</td>
<td>(70)</td>
</tr>
<tr>
<td>PGC1α/ERRα</td>
<td>ERBB2/Neu-induced breast cancer</td>
<td>Glutamine-derived lipogenesis</td>
<td>Promote cell growth in hypoxia</td>
<td>(51)</td>
</tr>
<tr>
<td>PML/PGC1α/PPARα</td>
<td>Breast cancer</td>
<td>FAO</td>
<td>Promote cell growth and luminal filling</td>
<td>(58)</td>
</tr>
<tr>
<td>Androgen/AR/AMPK/PGC1α</td>
<td>Prostate cancer</td>
<td>OxPhos, Glucose and FAO</td>
<td>Promote cell growth</td>
<td>(52, 93, 94)</td>
</tr>
<tr>
<td>p53/PGC1α</td>
<td>Lung and liver cancer</td>
<td>OxPhos, ROS clearance</td>
<td>Contribute to p53 target selection; Resistance to transient starvation</td>
<td>(96)</td>
</tr>
<tr>
<td>SIRT1/PGC1α/Nrf2</td>
<td>Breast, ovarian, colon, lung cancer</td>
<td>ROS clearance</td>
<td>A target axis of mrt-34 and metformin analogs</td>
<td>(102)</td>
</tr>
<tr>
<td>RIP1/PGC1α</td>
<td>Lung cancer</td>
<td>OxPhos, Glycolysis</td>
<td>Maintain DNA integrity and promote cell growth</td>
<td>(98)</td>
</tr>
<tr>
<td>PGC1α/ACLY-FASN</td>
<td>Colon and liver cancer</td>
<td>Glucose-derived lipogenesis</td>
<td>Promote tumor growth</td>
<td>(49)</td>
</tr>
<tr>
<td>MYC/PGC1α</td>
<td>PDAC</td>
<td>OxPhos, glycolysis</td>
<td>Resistance to metformin treatment</td>
<td>(56)</td>
</tr>
<tr>
<td>HIF-Dec/PGC1α</td>
<td>ccRCC</td>
<td>OxPhos, ROS</td>
<td>Promote tumor growth</td>
<td>(55)</td>
</tr>
</tbody>
</table>

*PGC1α is suppressed by the oncogene or signaling pathway in this context.
emerge during treatment. The resistant cells display an intermediate metabolic phenotype with reduced OxPhos but enhanced glycolysis, as a result of increased MYC/PGC1α ratio, compared with metformin-sensitive CSCs (56), and MYC inhibition increases the sensitivity to metformin in resistant CSCs. These data indicated MYC/PGC1α balance determines the metabolic plasticity and sensitivity to metformin of pancreatic CSCs.

Figure 2. Biologic function of PGC1α in cancer cells. Once induced by stress, PGC1α interacts with specific transcription factors and promotes mitochondrial respiration, fatty acid metabolism, or ROS detoxification, which facilitates cancer metabolic adaptation.

Figure 3. Involvement of the MITF/PGC1α signaling in melanoma therapy. A, mechanism of the MITF/PGC1α signaling axis in melanoma therapeutic resistance. MITF can be activated by BRAF or MEK inhibition and then transactivate PGC1α, which promotes mitochondrial respiration and ROS detoxification, leading to drug tolerance of BRAF/MEK inhibition. B, combinatory suppression of BRAF/MEK and mTORC1/2 contributes to melanoma cell death. mTORC1/2 inhibition can decrease nuclear localization of MITF, then suppress PGC1α expression and mitochondrial respiration, which resensitizes melanoma to BRAF/MEK inhibition.
Another research study performed in a mouse model of pancreatic tumor also highlighted the importance of PGC1α in PDAC therapeutic resistance. Tumor cells which survive the genetic or pharmacologic ablation of KRAS, overexpress PGC1α (79). Although PGC1α expression is closely related to therapeutic resistance of PDAC in both models, mechanisms of how PGC1α influences tumor relapse are different. The former study emphasized the regulation of MYC on PGC1α in a KRas-independent manner (56). It is the increased MYC/PGC1α ratio reduces the reliance of CSCs on OxyPhos, leading to metformin resistance. While, in KRas ablation-resistant mouse model, it is the strong reliance on OxyPhos ensures resistant cells survival (79), and this phenomenon might be restricted to KRas-ablated dormant pancreatic tumor cells.

PML/PGC1α/PPARα axis in breast cancer

Even though mitochondrial respiration has been considered as the main biologic function of PGC1α, the crucial role of PGC1α in regulating FAO has received more attention in recent years. FAO is activated in several type of cancers, and the transcription factor, PPARα, is the main regulator of this process (80–83). PPARα can be activated by endogenous fatty acid, fatty acid derivatives or fibrates, and is coregulated by PGC1α (84, 85). In breast cancer cells, PGC1α is controlled by the promyelocytic leukemia (PML) gene which is enhanced in a subset of breast cancers and especially enriched in triple-negative cases (58, 86). PGC1α is deacetylated by PML, leading to transactivation of PPARα and FAO activation. The PML/PGC1α/PPARα/FAO signaling pathway provides ATP to promote cell survival and luminal filling in breast cancer (58). Furthermore, this pathway is also involved in hematopoietic stem cell maintenance (87, 88). Although only a small number of studies reported the involvement of PGC1α in cancer stem cells, the metabolic profile of hematopoietic stem cells and cancer stem cells could have some common traits in stemness maintenance (79, 89–91). These studies provided evidence indicating that PML/PGC1α/PPARα signaling is essential for maintaining cellular metabolic homeostasis with potential therapeutic implications.

AR/PGC1α axis in prostate cancer

The androgen receptor (AR) is a ligand-activated transcription factor that is substantially modulated by coregulators (92). Among the coactivators, PGC1α interacts with AR to orchestrate central metabolism and cell survival in prostate cancer (93). PGC1α can bind to the N-terminal domain of the AR and promote the formation of AR homodimer, which increases the transcription of AR target genes, such as PSA (52). Inhibition of PGC1α causes cell-cycle arrest at the G2-phase and suppresses growth of either AR-positive or castration-resistant prostate cancer cells. These findings indicated that disruption of PGC1α expression could be useful for treating AR-positive prostate cancer and also might be more efficient in castration-resistant prostate cancer, which depends more on AR signaling (52).

More than a coactivator of AR, PGC1α can be simultaneously regulated by AR signaling. Both mRNA and protein levels of PGC1α can be induced by androgens in prostate cancer in an AMPK-dependent manner (94). The androgen/AR/AMPK/PGC1α signaling axis increases mitochondria biogenesis, glucose oxidation, and FAO to generate building blocks and ATP for cancer cell growth. The positive feedback regulation provides a great advantage to sustain PGC1α expression and augment its influence on cancer metabolism.

p53/PGC1α axis in cell fate determination

p53 can either be a tumor suppressor or an oncogene in cancer. Its biologic function is tightly regulated by translation modifications and interaction with other proteins (95). PGC1α acts as a contributor to wild-type p53 target selection in cancer cells in response to glucose deprivation (96). When PGC1α is induced by transient starvation and binds to p53, Lys120 acetylation of p53 is prevented, and p53 preferentially transactivates genes associated with ROS clearance and mitochondrial metabolism. However, in prolonged or chronic starvation, PGC1α undergoes degradation by ring finger protein 2-mediated ubiquitin–proteasome pathway. This process facilitates Lys120 acetylation of p53, leading to p53-dependent apoptosis (96). In this case, p53 has both cytoprotective and cytotoxic functions under nutrient-limited conditions. PGC1α performs as an essential switch in modulating stress-dependent transcription of p53, and directs the stress response of p53 toward prosurviving outcomes (97).

In addition to the interaction of PGC1α and wild-type p53, other studies suggested that PGC1α expression can be influenced by wide-type p53. Gene expression analysis in 28 human lung adenocarcinoma cell lines with different p53 mutational status showed that the mRNA level of PGC1α is higher in p53 wild-type cell lines compared with cell lines with p53 loss or missense mutation (50). Suppression of PGC1α inhibits the growth of p53 wild-type lung adenocarcinoma cells, implicating that PGC1α might be a potential target of wild-type p53 in lung adenocarcinoma, and the direct transcription regulation of wild-type p53 on PGC1α has been demonstrated in neuroblastoma cells and myoblasts (54). Similar to the AR/PGC1α axis, an autoregulatory loop might also exist between p53 and PGC1α.

As well as the direct regulatory mechanism between PGC1α and p53, the receptor-interacting protein 1 (RIP1)/PGC1α signaling axis indirectly affects the control of p53-dependent cell proliferation (98). This signaling pathway maintains metabolic homeostasis in lung cancer cells. Loss of RIP1 suppresses PGC1α expression and OxyPhos, resulting in accelerated glycolysis. However, excessive glycolysis decreases cellular NAD+ levels and impairs DNA repair, which activates p53-mediated cell growth inhibition (98, 99). These data provide additional evidence supporting a reciprocal regulation between metabolic adaptation and wild-type p53 in cancer cell fate determination.

SIRT1/PGC1α axis in stress adaptation

SIRT1 is the main regulator of PGC1α and activates PGC1α through the deacetylation of PGC1α at specific lysine residues (20). SIRT1/PGC1α signaling is required to transactivate FAO genes under nutrient restriction in skeletal muscle cells (100). The switch from glucose to fatty acid utilization benefits cell survival under stress conditions, and SIRT1/PGC1α signaling also mediates Nrf2 expression to antagonize oxidative damage (101). It was identified as a targeted pathway of metformin in p53 wild-type cancer cells (102). Metformin suppresses this signaling through miR-34a in a p53-dependent manner and then sensitizes cancer cells to oxidative stress. These research findings provide new evidence for the effectiveness of metformin in cancer therapy (103).

Therapeutic Implications

As noted above, cells with high expression of PGC1α have an advantage to survive under metabolic stresses, including oxidative...
damage, energy deprivation, and even cancer therapy. The therapeutic resistant cancer cells especially have a strong reliance on metabolic activities mediated by PGC1α. On the basis of the evidence, PGC1α is believed to have an emerging role in cancer therapeutic resistance (57, 68, 75).

Whereas specific inhibitors of PGC1α are not yet available, the major methods to disrupt PGC1α signaling have been focused on suppressing key enzymes of PGC1α-dependent metabolic pathways or targeting-related transcription factors. OxPhos, FAO, or ERα inhibitors were all observed to reduce cell growth in PGC1α-positive cancer cells (51, 68, 75, 87).

Metabolic intervention significantly limits adaptive responses in cancer therapy as discussed above. However, suppressing a single metabolic node might not be fatal to certain cancer cells, because alternative metabolic paths still could be engaged to compensate for the deficiencies. In melanoma, suppressing PGC1α expression or OxPhos resensitize therapeutic-resistant cells to oxidative damage (53). However, these treatments simultaneously activate alternate metabolic fluxes in a small set of cancer cells (104). The increased ROS production caused by PGC1α inhibition stabilizes HIF1α protein, and HIF1α induces a metabolic switch from OxPhos to glycolysis which promotes cell survival (105). Surprisingly, even a combinatorial suppression of PGC1α and HIF1α could not eradicate tumors in mice. Instead, this process promotes glutamine utilization to offset the energy crisis. Only blocking all of these pathways can maximize tumor destruction (111). Mechanically, induction of cell death is the conclusion of the interactions are also elusive. More. over, except for PML and MYC, few oncogenes have been reported conclusively to regulate PGC1α (56, 58). Whether changes in PGC1α expression are due to oncogene control or a nongenetic metabolic adaptation might depend on cellular context. Elucidating these issues would be very helpful in understanding the function of PGC1α in cancer.

For the reason that certain chemotherapeutically resistant cancer cells are extremely addicted to PGC1α-dependent metabolic activities, targeting PGC1α-associated pathways could be a desirable means to resensitize cancer cell to therapy. However, even more than chemotherapy, radiotherapy is also a necessary strategy against some tumor types. The relationship between radiotherapy and PGC1α needs to be further studied. According to the evidence discussed earlier, disruption of PGC1α target genes and the potential compensatory pathways, combined with traditional chemotherapy/radiotherapy should be the best strategies to achieve maximized therapeutic efficiency in the future.

**Conclusion and Further Perspectives**

According to the abovementioned discussion, PGC1α facilitates a flexible metabolic profile in cancer cells and contributes to cancer survival and therapeutic resistance. (15, 114, 115). Even though mitochondrial respiration is identified as a predominant biologic function of PGC1α in cancer, a few studies also underscore PGC1α as a promoter of FAO and glucose- or glutamine-derived lipogenesis in recent years (49, 51, 58). The discoveries indicated that PGC1α can not only enhance ATP production, but also affect carbon flux. On the basis of a deeper understanding of FAO and autophagy in cancer therapy, more attention should be paid on the role of PGC1α in the regulation of lipid metabolism in the future (116–119).

Despite PGC1α can interact with various transcription factors under physiologic conditions, research studies focusing on PGC1α-targeted transcription factors in cancer cells are still limited, and mechanisms of the interactions are also elusive. Moreover, except for PML and MYC, few oncogenes have been reported conclusively to regulate PGC1α (56, 58). Whether changes in PGC1α expression are due to oncogene control or a nongenetic metabolic adaptation might depend on cellular context. Elucidating these issues would be very helpful in understanding the function of PGC1α in cancer.

**Disclosure of Potential Conflicts of Interest**

No potential conflicts of interest were disclosed.

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