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Lomitapide repurposing for treatment of malignancies: A promising direction

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ABSTRACT

The development of novel drugs from basic science to clinical practice requires several years, much effort, and cost. Drug repurposing can promote the utilization of clinical drugs in cancer therapy. Recent studies have shown the potential effects of lomitapide on treating malignancies, which is currently used for the treatment of familial hypercholesterolemia. We systematically review possible functions and mechanisms of lomitapide as an anti-tumor compound, regarding the aspects of apoptosis, autophagy, and metabolism of tumor cells, to support repurposing lomitapide for the clinical treatment of tumors.

1. Introduction

The incidence of malignancies is gradually increasing [1]. Among them, breast cancer is the most frequent malignant disease worldwide (2.26 million of new cases/year; 11.7 % of total malignancies), followed by lung cancer (2.20 million of new cases/year; 11.4 % of total malignancies), colorectal cancer (CRC) (1.93 million of new cases/year; 10.0 % of total malignancies) and prostate cancer (1.41 million of new cases/year; 7.30 % of total malignancies) [2]. The rapid increase in the global burden of cancer morbidity and mortality is reported to be associated with human economic and social development, with risk factors not limited to reproduction and hormones, but also lifestyles [3–5].

Cancer treatment encompasses various approaches, including surgery, radiotherapy, chemotherapy, immunotherapy, and more. Nevertheless, cancer treatment encounters significant challenges, including drug resistance, toxicity, side effects, recurrence, and metastasis. Hence, extensive research is necessary to investigate the mechanisms underlying tumor occurrence, molecular markers, novel drugs, and treatment strategies, aiming to enhance the quality of life and prognosis for patients with tumors. Therefore, the development of new anti-tumor drugs is increasingly urgent. Drug repurposing provides a very promising approach to address this need by screening 'old' clinically-used drugs for relevant disease targets, and expanding the therapeutic range of existing drugs for new application [6,7]. As the safety, toxicity, and side-effects of such drugs have been investigated already, drug repurposing ensures good bioavailability and suitable physicochemical properties, along with shortened time and reduced cost required for drug development

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Abbreviations				
CRC	Colorectal Cancer			
HoFH	Homozygous Familial Hypercholesterolemia			
MTTP	Microsomal Triglyceride Transfer Protein			
HBV	Hepatitis B Virus			
Apo B	Apolipoprotein B			
VLDL	Very Low-Density Lipoprotein			
LDL	Low-Density Lipoprotein			
LDL-C	Low-Density Lipoprotein Cholesterol			
CYP3A4	Cytochrome P450 Isoenzyme 3A4			
INR	International Normalized Ratio			
FDA	Food and Drug Administration			
SARS-Cov	<i>I-2</i> Severe Acute Respiratory Syndrome Coronavirus 2			
hACE2	Human Angiotensin-Converting Enzyme 2			
HTP	High-Throughput			
ATP	Adenosine Triphosphate			
IC50	Half Maximal Inhibitory Concentration			
ER	Estrogen ReceptorERα: Estrogen Receptor alpha			
VS	Virtual Screening			
mTOR	Mammalian Target of Rapamycin			
mLST8	Mammalian Lethal with SEC13 Protein 8			
DEPIOR	DEP Domain Containing MTOR-Interacting Protein			
PRAS40	Proline-Rich Ak I Substrate 40 KDa			
rigtor	Regulatory Associated Protein of MTOR			
mSin1	Mammalian Stress-Activated Protein Kinase Interacting Protein 1			
Protor	Protein Observed with Rictor			
PI3K	Phosphoinositide 3-Kinases			
PTEN	Phosphatase and Tensin Homolog			
HIF1-α	Hypoxia-Inducible Factor 1-alpha			
Rheb	Ras Homolog Enriched in Brain			
4E-BP1	Eukaryotic Translation Initiation Factor 4E-Binding Protein 1			
elF4E	Eukaryotic Translation Initiation Factor 4E			
ACC	Acetyl-CoA Carboxylase			
GLUT1/4	Glucose Transporter Type 1/4			
CPT1	Carnitine Palmitoyltransferase 1			
PP2A	Protein Phosphatase 2A			
ROS	Reactive Oxygen Species			
ADP	Adenosine Diphosphate			
MM	Multiple Myeloma			
DFG	Asp168-Phel69-Gly170			
ISC CTDece	Tuberous Scierosis Complex			
GIPase	Guanosine Tripnospitalase			
FCED	Fidermal Crowth Eactor Recentor			
BTK	Bruton's Tyrosine Kinase			
SREBP	Sterol Regulatory Element Binding Protein			
ATF4	Activating Transcription Factor 4			
CMA	Chaperone-mediated Autophagy			
LC3	Microtubule-Associated Protein Light Chain 3			
ULK1	Unc-51 Like Autophagy Activating Kinase 1			
PPM1D	Protein Phosphatase 1D Magnesium-Dependent, Delta Isoform			
PARP	Poly (ADP-Ribose) Polymerase			
ACD	Autophagy-Mediated Cell Death			
PD-1	Programmed Death-1			
PLD-1	Phospholipase D1			

[8]. For example, the anti-diabetic drug metformin exhibits anti-tumor effects, and is being investigated in phase II/III clinical trials [9], while the antiplatelet drug aspirin has potential therapeutic benefit for patients with prostate cancer [10]. In addition, the anti-allergic drug azelastine [11], antiseptic compound benzethonium chloride [12], anti-hepatitis B virus (HBV) drug adefovir dipivoxil [13], traditional Chinese herb daurisoline [14], and imperatorin [15] have all been used to inhibit malignant tumors.

Lomitapide, an inhibitor of microsomal triglyceride transfer protein (MTTP), has been used in the clinic for treatment of homozygous familial hypercholesterolemia (HoFH) [16]. Recently, lomitapide has been found to have anti-tumor effects in CRC [17]. However, the application potential and molecular mechanism of lomitapide in different types of malignancies is still unclear. To extend the utilization and uncover its mechanism, this article systematically reviews the clinical utilization of lomitapide and its potential mechanism and efficacy, in anti-tumor application, to provide evidence for further investigation of repurposing lomitapide in precision treatment of patients with malignancies.

2. Overview of lomitapide

2.1. Structure and pharmacodynamic of lomitapide

Lomitapide, was initially developed as a lipid-lowering agent, then used as a niche orphan drug for HoFH [18] (Fig. 1). Based on patient tolerance and response, the recommended dose is started from 5 mg once daily, gradually titrated to a maximum of 60 mg/day [19]. As an oral drug, lomitapide targets MTTP to prevent assembly of apolipoprotein B (Apo B)-containing lipoproteins in the liver and intestines [20]. It has been reported that MTTP is involved in the intracellular transfer of lipids required for the assembly and secretion of very low-density lipoprotein (VLDL) (Fig. 2). MTTP inhibition by lomitapide leads to decreased plasma lipid levels through suppressing the secretion of VLDL, and consequently of low-density lipoprotein (LDL) [21].

Lomitapide is primarily metabolized in the liver via cytochrome P450 isoenzyme 3A4 (CYP3A4) into inactive metabolites without MTTP inhibitory activity. Due to a high first-pass metabolism in the liver, the absolute bioavailability of lomitapide is approximately 7 % [22]. As a substrate of CYP3A4, lomitapide also acts as a CYP3A4 inhibitor to the accumulation of other CYP3A4 substrates, such as statins and warfarin. Normally, the time to reach maximum lomitapide concentration after a single dose of 60 mg is approximately 6 h. Lomitapide has a mean volume of distribution in plasma ranging from 985 to 1292 L, a serum half-life of 39.7 h, and is approximately 52.9–59.5 % excreted in the urine and 33.4–35.1 % in the feces [23–25].

Lomitapide can decrease the levels of low-density lipoprotein cholesterol (LDL-C) and very low-density lipoprotein cholesterol (VLDL-C) in the plasma of rabbits with hyperlipidemia, as well as reducing atherosclerotic plaques in Apo E knockout mice [26]. In a long-term (126-week) clinical trial, lomitapide treatment, combined with other lipid-lowering therapies, was shown to be highly effective in reducing the level of LDL-C in patients with HoFH. Meanwhile, the tolerability is acceptable without significant changes in glucose, insulin, homeostatic model assessment of estimated insulin resistance or increased high-sensitivity C-reactive protein [27]. Furthermore, in the clinical studies of up to 246 weeks, more than 70 % of patients received the maximum tolerated dose of the drug, and more than half of the patients benefited by keeping their LDL-C at a low level (<1.8 mmol/L) [20,27,28].

However, lomitapide produces a range of dose-dependent side effects including gastrointestinal disturbances, such as diarrhea, nausea, and dyspepsia [27,29], as well as elevated transaminases [20,28] and fat-soluble vitamin deficiency [20,28,30]. Despite these issues, adverse effects are usually manageable and can often be resolved with dose adjustments or temporary discontinuation [20, 27–30]. It is worth noting that the development of hepatic steatosis is an issue, and although more data are needed to support the effect of more than 5 years of medication on hepatic steatosis [27,29], it is still recommended that regular liver function tests and fat-soluble vitamin monitoring are needed during treatment [20,28].

Regarding special circumstances, such as use during pregnancy and lactation, animal studies have shown lomitapide to be potentially harmful to the fetus. The available human data are insufficient to conclude any drug-related risk of major birth defects or adverse fetal outcomes. Due to its potentially serious side effects and lack of extensive human data, caution is advised [31].

Importantly, lomitapide inhibits P-glycoprotein, an energy-dependent efflux pump responsible for reducing intracellular drug accumulation, thereby increasing the risk of multiple pharmacokinetic interactions and toxicity of co-administered drugs [32,33]. Considering the metabolism and pharmacology of lomitapide, the risks of lomitapide co-administered with certain drugs need to be carefully evaluated.

As lomitapide is metabolized by CYP3A4 enzymes, co-administration of strong or moderate CYP3A4 inhibitors (e.g., fluconazole) significantly increases the concentration of lomitapide in blood, which may result in serious adverse reactions. In addition, co-administration of lomitapide with other drugs that are metabolized by CYP3A4 enzymes (e.g., atorvastatin) may interfere with their metabolism and increase the concentrations of these drugs, which may increase the risk of adverse reactions. Close monitoring the international normalized ratio (INR) is required with concomitant use of warfarin, an oral anticoagulant, as lomitapide may result in an elevated INR [31].

In conclusion, lomitapide, characterized by its manageable side effects and significant reduction in LDL-C levels, is highlighted by long-term clinical experience and continuous post-marketing surveillance, which is consistent with the desirable attributes of the drug to be repurposed for the treatment of other diseases.

2.2. Utilization and potential applications of lomitapide

Lomitapide has been used primarily as a lipid-lowering drug in patients with HoFH, reducing the risk of cardiovascular events, such as myocardial infarction and stroke [24]. Since its approval, other applications of lomitapide have been investigated. Zheng et al.



Fig. 1. Structure of lomitapide. Compound ID: 9853053; Molecular Formula: C39H37F6N3O2; Molecular Weight: 693.7 [g/mol] [22].



Fig. 2. The lipid-lowering molecular mechanism of lomitapide. Abbreviation: Apo B-apolipoprotein B, MTTP-microsomal triglyceride transfer protein, VLDL-very low-density lipoprotein, LDL-low-density lipoprotein.

found that lomitapide increased patients' survival after middle cerebral artery occlusion, and reduced the neuronal tissue loss through promoting neuronal autophagy and inhibiting microglial migration, resulting in improved neurological function, suggesting repositioning lomitapide for the treatment of stroke [34]. For searching new anti-bacterial agents against multidrug-resistant Gram-positive bacterial infections, Zhang et al. reported that lomitapide displayed broad anti-microbial activities against Gram-positive bacteria, which may be related to cell wall destruction and the inhibition of surface proteins [35]. In addition, an anti-malarial activity of lomitapide was also revealed by inhibition of β -hematin formation and parasite growth [36]. To accelerate the development of COVID-19 treatment, the repurposing of food and drug administration (FDA)-approved drugs against COVID-19 was conducted, applying a new computational protocol against three severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) targets, including protease, papain-like protease and spike protein [37]. With encouraging results of binding between lomitapide and spike protein [37], Olotu et al. observed that allosteric binding of lomitapide perturbed the prefusion spike protein conformation, resulting in displacement of human angiotensin-converting enzyme 2 (hACE2) from the spike protein receptor-binding domain [38].

Lomitapide is supported by *in vitro* and *in vivo* preclinical experiments as a potential anti-tumor agent (Table 1). Lomitapide significantly inhibited the viability of CRC cell lines (HCT116, HT29), with no observed side effects of lomitapide, and normal human colonic mucosal epithelial cell (NCM460) viability was not affected [17]. In addition, Lee et al. utilized a high-throughput (HTP) cancer cell viability assay based on an adenosine triphosphate (ATP) assay to evaluate the effect of lomitapide on the viability of 22 other cell lines (Melanoma, Leukemia, Colon Cancer, Glioblastoma, Lung Cancer, Ovarian Cancer, Breast Cancer, MM, Prostate Cancer, Pancreatic Cancer, Sarcoma, Gastric Cancer, Endometrial Cancer, Lymphoma, Renal Cancer, Neuroblastoma, Esophageal Cancer, Myeloid Leukemia, Bladder Cancer, Liver Cancer, Cervical Cancer, and Thyroid Cancer) with reduced viability of all cancer cells with 1.5–5 µM as half maximal inhibitory concentration (IC50) [39]. The lower IC50 suggests greater sensitivity and selectivity of lomitapide, however, it is unknown whether other forms of necrosis or toxicity alterations occur in cells treated with effective concentrations of the drug.

Similarly, *in vivo* experiments have revealed the therapeutic effects of lomitapide in CRC, where the drug significantly inhibited tumor growth. Tumor mass and volume were significantly reduced after lomitapide treatment compared with control group [17,39]. In terms of safety, no significant drug toxicity of lomitapide was observed in a mouse model based on transplantation of human-derived CRC, and lomitapide treatment did not affect the body weight of mice after treatment with a safe and effective dose (20 mg/kg) [17]. It

Table 1

Anti-tumor effects and mode of action of lomitapide in various types of malignancies.

Mechanism	Malignancy types	Mode of action	References
In vivo			
Syngeneic			
Regulation of immune	CRC	Tumor growth↓, antitumor response by CD8 ⁺ T lymphocyte infiltration↑	Lee et al., 2022 [39]
functions			
Regulation of immune	Melanoma	Tumor growth↓, antitumor response by CD8 ⁺ T lymphocyte infiltration↑	
functions			
Xenograft			
Autophagy	CRC	Tumor growth↓,	Lee et al., 2022 [39]
Autophagy	CRC	Tumor growth↓, <i>p</i> -AMPK↑, LC3 I/II↑	Zuo et al., 2021 [17]
Apoptosis	CRC	Tumor growth↓, apoptosis↑	
In vitro			
Autophagy	CRC	Tumor growth↓, apoptosis↑, LC3-II↑, P-ULK1↑	Lee et al., 2022 [39]
Autophagy	CRC	mTORC1 \downarrow , Tumor growth \downarrow , autophagy \uparrow , P– S6K1 \downarrow , P–S6 \downarrow , P-4E-BP1 \downarrow	
Autophagy	Breast cancer	Tumor growth↓, P– S6K1↓, P–S6↓, LC3-II↑	
Autophagy	Melanoma	Tumor growth \downarrow , P– S6K1 \downarrow , P–S6 \downarrow , LC3-II \uparrow ,	
Autophagy	Gastric	Tumor growth \downarrow , P– S6K1 \downarrow , P–S6 \downarrow , LC3-II \uparrow ,	
	carcinoma		
Autophagy	CRC	PP2A↓, <i>p</i> -AMPK↑, Tumor growth↓, autophagy↑, LC3 I/II↑, p62↓, beclin 1↑, Vps34	Zuo et al., 2021 [17]
		↑, Atg14↑	
Autophagy	CRC	Mitochondrial destruction, Proportion of tubular mitochondria \uparrow , ATP \downarrow , ROS \uparrow , p-	
		AMPK \uparrow , <i>p</i> -ACC \uparrow	
Apoptosis	CRC	Apoptosis↑, cleaved PARP↑, cleaved caspase 3↑	
Inhibition of tumor	Lung cancer	Tumor growth↓	
proliferation			
Inhibition of tumor	Liver cancer	Tumor growth↓	
proliferation			
Inhibition of tumor	Esophageal	Tumor growth↓	
proliferation	cancer		
Apoptosis	MM	Tumor growth \downarrow , disruption of lipid raft microdomains, apoptosis \uparrow , cleaved PARP \uparrow , CD38 \downarrow , BTK \downarrow	Saeed et al., 2022 [178]
Cell Cycle Arrest	MM	G0/G1 cell cycle arrest, TP53↑, c-MYC↑	

Abbreviation: CRC-Colorectal Cancer; MM-Multiple Myeloma.

should also be emphasized that xenotransplantation models involve the transplantation of human tumor cells or tissues into immunodeficient mice, and therefore allow direct assessment of human tumor cell behavior *in vivo*, mimicking the microenvironment of human tumors to a certain extent. Although it is suitable for the screening of new drugs and assessment of anti-tumor effects, the limitation is significant with the insufficient immune response to tumors. Correspondingly, the homotransplantation model uses tumor cells and hosts within the same species. Thus, compared to the former, the growth rate and microenvironment of the homografted tumors more closely resemble those of naturally occurred tumors, while the host retains an intact immune system, making it more suitable for studying the tumor immune response. In mouse CRC and melanoma syngeneic tumor transplantation models, lomitapide treatment was similarly unaffected by body weight in mice and no toxic pathological changes were observed in the liver, kidney or lung [39]. However, it is not known what form of death occurs in cells treated with the drug, such as programmed apoptosis or pathological necrosis, and if necrosis occurs, whether it reaches very high levels of cytotoxicity.



Fig. 3. The molecular mechanism of lomitapide suppressing malignancies.

The use of lomitapide in the treatment of malignant tumors depends not only on its inhibition of tumor growth, but also on the tolerance of normal tissues to it (Fig. 3). Although FDA-approved drugs are usually considered relatively safe, drug toxicity testing during the development of new drugs is still necessary. Therefore, in the future, a series of *in vivo* and *in vitro* experiments need to be carried out to jointly validate the safety of the drug and expand it to more malignant tumors, and only those compounds that show convincing safety and tolerability will be considered further.

3. Underlying molecular mechanisms of the anti-tumor effects of lomitapide

3.1. Potential direct binding to estrogen receptor alpha by lomitapide

As the estrogen receptor (ER)-positive subtype comprises the majority of breast cancers, anti-estrogens and aromatase inhibitors are used in clinic to improve overall survival, but half of them fail [40]. Among the different types of ERs, estrogen receptor alpha (ER α) is expressed in less than 10 % of normal breast epithelial cells, but increases in appropriate 50%–80 % breast cancer patients [41], and has been used as a therapeutic target for breast cancer because of its important role in determining the sensitivity of breast cancer cells to chemotherapeutic agents [42]. In the field of drug discovery, techniques such as molecular docking and virtual screening (VS) have become valuable additions to time-consuming and costly HTP screening experiments [43]. The ability of computational screening libraries of compounds for similarity to known inhibitors (ligand-based) or complementarity to the target structure has been validated [44,45]. Notably, numerous clinical drugs have been identified or optimized with the assistance of computational approaches, such as imatinib [46], zanamivir [47], nelfinavir [48], and erlotinib [49].

To identify novel ER α inhibitory ligands, TilakVijay et al. screened FDA-approved drug molecules by docking pyrazole, bipyrazole, thiazole, thiadiazole and scaffold analogs, revealing that lomitapide showed higher binding affinity for ER α than tamoxifen, which is a clinically used endocrine therapeutic drug targeting ER-positive breast cancer [50]. It was found that the binding of lomitapide to ER α exhibited van der Waals interactions. Thus, ER α may be a key 'bridge' between lomitapide and breast cancer.

Discovery of lomitapide by VS provides new options for personalized breast cancer treatment and may improve the therapeutic efficacy of existing drugs, especially for those patients who perform resistance to tamoxifen endocrine therapy. Importantly, virtual docking initially obtained information on the type of interaction, affinity, selectivity, receptor conformation change, and site of action of lomitapide and ER α , which could help understand the effect of lomitapide on ER α expression and/or activity and the mechanism of interaction between them. Unfortunately, although VS is a powerful tool, there is a lack of relevant *in vitro* and *in vivo* experimental validation to ensure the actual effectiveness and selectivity of lomitapide in the treatment of breast cancer patients. Meanwhile, the study failed to delve into the specific mechanisms by which lomitapide affects ER α , including how it influences downstream signaling pathways and cellular behaviors, such as inhibiting proliferation, invasion and metastasis, or reversing drug resistance in breast cancer. Similarly, this study fails to mention the assessment of potential toxicity and side effects of lomitapide, which is crucial for drug suitability development and clinical application.

3.2. Direct binding to mammalian target of rapamycin by lomitapide

3.2.1. The mTOR signaling pathway in malignancies

The mammalian target of rapamycin (mTOR) is present in all eukaryotic cells [51–55]. It is well known that mTOR plays a key role in the regulation of cell growth, proliferation, motility, autophagy, and metabolism through two distinct complexes (mTORC1 and mTORC2) [56–59]. Both share components such as mammalian lethal with SEC13 protein 8 (mLST8) and DEP domain containing mTOR-interacting protein (DEPTOR) [60,61] but mTORC1 uniquely contains regulatory associated protein of MTOR (Raptor) and proline-rich AKT substrate 40 kDa (PRAS40), whereas mTORC2 contains rapamycin-insensitive companion of mTOR (Rictor), mammalian stress-activated protein kinase interacting protein 1 (mSin1), and protein observed with rictor (Protor) [62–67]. Interestingly, mTORC1 is therefore sensitive to rapamycin treatment, whereas mTORC2 is not [64]. Abnormal activity in mTOR signaling has been associated with oncogenicity and progression of a variety of malignant tumors [68–70]. In prostate intraepithelial neoplasia, inhibition of mTOR activity suppresses the phosphoinositide 3-kinases (PI3K) signaling pathway, while in phosphatase and tensin homolog (PTEN)-deficient cancers, the PI3K signaling pathway can be inhibited by blocking apoptosis and hypoxia-inducible factor 1-alpha (HIF1- α)-dependent pathways [71,72].

Ras homolog enriched in brain (Rheb) is a direct activator of mTOR, and Rheb overexpression promotes oncogenesis in skin epithelial carcinogenesis. These molecular alterations contribute to the promotion of multistage epithelial tumorigenesis, angiogenesis, cytokine production, and stromal-epithelial crosstalk, thereby inducing tumorigenesis and progression [73]. Therefore mTOR inhibitors are considered a promising therapeutic strategy for malignant tumors [74]. The mTOR inhibitor rapamycin has been used in the clinical treatment of a variety of cancers [75,76]. Currently, eight orally effective mTOR inhibitors are undergoing clinical trials (www.icoa.fr/pkidb/).

3.2.2. Binding to mTORC1

Currently, although rapamycin is still a promising anti-tumor agent [77–79], its derivatives mainly act on the mTORC1 isoform, and mTORC2 can reactivate mTOR signaling through other negative feedback pathways, resulting in the development of resistance to mTOR inhibitors through increasing expression of eukaryotic translation initiation factor [77,80]. The increased resistance to mTOR inhibitors limits the therapeutic use of rapamycin derivatives for malignant tumors [78,81].

To investigate the potential novel application of 'old drugs' in a cost-effective way, Lee et al. used a structure-based VS approach on

over 3000 FDA-approved drugs with mTOR druggable potential [39]. Interestingly, although lomitapide was originally not approved for cancer treatment, its specific binding to the ATP-binding catalytic core of mTORC1, including residues H2189, D2190, L2192, Q2194, D2195, D2338, and D2357, evoked further investigation of its anti-tumor activities. The reduced thermal stability of the recombinant mTOR kinase domain indicates that lomitapide selectively binds to the kinase domain of mTOR, disrupting the interaction between the kinase domain and its ligands and leading to a decrease in the thermal stability of the kinase domain [39]. Lomitapide inhibits mTOR activity by binding to the catalytic region of mTOR protein kinase in a manner competitive with ATP, which is different from the binding site of rapamycin-like mTOR inhibitors, targeting the FRB domain [39]. In a CRC animal model, lomitapide nearly completely eliminated the phosphorylation of eukaryotic translation initiation factor 4E-binding protein 1 (4E-BP1) and inhibited the viability of cancer cells *in vitro* and *in vivo*, while the anti-tumor effects of other mTOR inhibitors were reduced by eukaryotic translation initiation factor 4E (elF4E) overexpression [39], supporting the potential advantages of lomitapide as an mTOR inhibitor for the treatment of malignant tumors.

3.3. Activation of the AMPK signaling pathway by lomitapide

3.3.1. AMPK signaling in Malignancy

The AMPK signaling pathway is involved in the control of energy utilization through inhibition of anabolism and stimulation of catabolism, including the metabolism of lipid, glucose and protein [82–85], which is a key factor to ensure energy homeostasis and cell survival in times of energy scarcity [86].

The inhibition of anabolism by AMPK can be achieved through transcription-dependent and transcript-independent pathways [85, 86]. AMPK inhibits lipid and sterol synthesis through inactivating the regulatory enzymes in a rate-limiting step of both fatty acid and cholesterol biosynthesis, acetyl-CoA carboxylase (ACC), as well as suppressing the phosphorylation of β -reductase [87,88]. In addition, AMPK regulates biological metabolic processes mainly through mTOR to reduce the consumption of ATP during protein translation and cell growth [89]. Usually, under energy-deficient conditions, the activity of AMPK is increased, whereas mTOR is inactive, and increased AMPK activity could inhibit mTOR signaling pathway [90]. Further, the inhibition of mTOR activity reduces protein synthesis and induces the slowdown of cell growth [91,92]. However, under nutrient-sufficient conditions, mTOR inhibits AMPK activity, which can be considered as a more refined regulation of metabolism by organisms, reflecting the inseparable and close relationship between mTOR and AMPK [93].

To increase energy storage, AMPK stimulates the breakdown of macromolecules to generate ATP, including the utilization of glucose, mobilization of stored lipids and autophagy-induced degradation of macromolecules in yeast and mammalian cells [94–96]. During autophagy, AMPK phosphorylates proteins are involved in glucose transport, which increases plasma membrane localization of glucose transporter type 1/4 (GLUT1/4) and facilitates the uptake of glucose into cells [97,98]. In addition, AMPK also increases the utilization of cellular stored lipids through activating lipases and stimulating the release of fatty acids [99]. The released free fatty acids will be transported to mitochondria by carnitine palmitoyltransferase 1 (CPT1), which can be inhibited by the products of ACC [100–102].

3.3.2. Activation of AMPK to block lipid metabolism by lomitapide

Recently, Zou et al. conducted a screening of 1056 FDA-approved drugs from a small-molecule library with the aim of repurposing them for anti-tumor treatment. Interestingly, lomitapide was found to exhibit anti-tumor properties *in vitro* and *in vivo*, through stimulating mitochondrial dysfunction-mediated AMPK activation [17]. Protein phosphatase 2A (PP2A), a highly conserved and ubiquitous Ser/Thr phosphatase in eukaryotes, is the direct target of lomitapide in CRC cells [17]. AMPK is negatively regulated by PP2A, which mediates high nutrient-induced AMPK inhibition by dephosphorylating AMPK α and interfering with the interaction of the α 2 and γ 1 subunits of AMPK [103,104]. Not surprisingly, in PP2A-deficient CRC cells, the anti-tumor bioactivity of lomitapide was attenuated accordingly, indicating that the anti-tumor effect of lomitapide occurs in a PP2A-dependent manner, at least partially [17].

Lomitapide interferes with mitochondrial dynamics and increases the levels of reactive oxygen species (ROS), which in turn activates the AMPK signaling pathway [105–107]. Importantly, the activities of AMPK are closely related to the ATP/adenosine diphosphate (ADP) ratio, which is regulated by a variety of physiological conditions, including mitochondrial inhibition, nutritional starvation, and exercise [108,109]. Disruption of mitochondrial network structure, reduction in ATP levels and increases in ROS levels were found in lomitapide-treated CRC cells (HCT116 and HT29), corresponding to an upregulation of AMPK phosphorylation, which supports that the regulation of AMPK by lomitapide occurs through mitochondrial signaling.

In lomitapide-treated CRC cells, the increased AMPK activity phosphorylates and inhibits the activity of ACC, preventing the transport of fatty acids and blocking the energy supply of CRC cells, resulting in an inhibitory effect on the proliferation of cancer cells [17]. The interference of lipid metabolism by lomitapide may be the main mechanism by which lomitapide inhibits cancers.

3.4. Other factors involved in the effects of lomitapide on cancers

3.4.1. The P38 MAPK signaling pathway

P38 MAPK belongs to the MAPK family, an important family of intracellular signal transducers involved in the regulation of various intracellular responses, such as inflammation, cell cycle regulation, cell death, development, differentiation, senescence, and tumorigenesis [110]. Based on its structure, p38 can be divided into four isoforms, those being p38 α , p38 β , p38 γ and p38 δ [111]. Among them, p38 α is the most comprehensively investigated, and is mainly associated with the inflammatory response [112,113].

When tumor cells are subjected to extracellular stimuli, such as inflammation, cytokines and chemotherapeutic drugs, p38

pathways are activated to exert pro-apoptotic effects and inhibit tumor growth by phosphorylating p53, inducing the translocation of Bax, participating in Fas/FasL-induced apoptosis and enhancing *c-MYC* and *TNF-* α expression [114,115]. In glioblastoma, p38 activation can be attenuated by the small guanosine triphosphatase (GTPase) RND2 through reducing p38 phosphorylation, to inhibit autophagy and apoptosis of glioblastoma cells [116].

In another drug repositioning study, based on computerized virtual molecular docking and molecular dynamics simulations, Suriya et al. verified that lomitapide impedes the anti-tumor function of p38 by binding to the metastable regulatory site of p38 [117,118]. There is no structural overlap between the lomitapide- and ATP-binding sites on p38. The former is spatially distinct by approximately 60° from the ATP-binding site on p38 [119]. The conserved amino acid motif (Asp168-Phe169-Gly170) DFG for the lomitapide-binding site in p38 is allosteric between DFG-in and DFG-out conformations, revealing the potential binding ability of lomitapide with an alternative binding site on p38 [120]. The induced autophagy and apoptosis in CRC and multiple myeloma (MM) cells by lomitapide are indicative of the anti-tumor activity of lomitapide. However, the role of MAPK and its role under lomitapide treatment needs to be verified by further experiments [17,39,121].

3.4.2. Upstream regulators of mTORC1

As the main anti-tumor target of lomitapide, the expression and activity of mTORC1 is regulated by different factors, including growth factors, stress, energy status, oxygenation and amino acids. The tuberous sclerosis complex (TSC) plays a crucial role in inhibiting mTORC1 activities by interacting with and stabilizing the GTPase-activating protein, resulting in the conversion of small GTPase Rheb into an inactive state [122,123]. Activation of mTORC1 occurs primarily through PI3K/AKT signaling pathway, the downstream of growth factors, which phosphorylates and inactivates tuberous sclerosis complex 2 (TSC2) [124–126]. In contrast, the phosphatase PTEN, a tumor suppressor, counteracts the pathway by dephosphorylating PI3K substrates, exerting an inhibitory effect on mTOR [127]. However, the total and phosphorylated protein levels of mTOR upstream factors, such as AKT and PTEN, are not affected by lomitapide treatment [39]. Similarly, knockdown of TSC2 failed to interfere with the inhibitory effect of lomitapide on mTORC1 [91].

As mentioned above, the energy status also regulates mTORC1 through multiple mechanisms [128,129]. Among them, AMPK can directly inhibit mTORC1 activities via phosphorylating Raptor in response to energy depletion [92]. On the other hand, AMPK can phosphorylate and activate TSC2, which indirectly reduces the activation of mTORC1 [91,92,130].

4. The diverse anti-tumor effects of lomitapide

4.1. Disruption of lipid rafts

Lipid rafts are microstructural domains present in a variety of membrane structures consisting of cholesterol, saturated phospholipids, and sphingolipids, and containing a variety of signaling and transport proteins [131]. The composition of lipid rafts in the membrane is highly varied in tumor cells, and is crucial for proliferative signaling, due to processes such as recruiting epidermal growth factor receptor (EGFR) to the rafts [132]. Not surprisingly, lipid raft disruption by the alkyl phospholipid edelfosine displaces all AKT and mTOR from rafts, causing the inactivation of AKT signaling, resulting in apoptosis [133].

CD38, a glycoprotein highly enriched in and considered a biomarker for lipid rafts, and catalyzes the synthesis and degradation of cyclic adenosine diphosphate ribose [134,135]. Inhibition of CD38, which suppresses proliferation and promotes apoptosis of tumor cells, is an effective strategy against MM [136]. As a regulator of CD38, non-receptor bruton's tyrosine kinase (BTK) plays decisive roles in the development, differentiation and proliferation of B-lineage cells [137]. Saeed et al. screened 1230 FDA-approved drugs for targeting BTK, and validated 10 potential components, including lomitapide [121]. In a proliferation assay, more than 80 % of MM cells entered into late apoptosis following treatment with different concentrations of lomitapide. Lomitapide reduced levels of cholesterol, which is highly enriched in lipid raft microregions, leading to the disruption of membrane lipid rafts, and inhibition of death receptors [138–140]. To uncover the potential signaling pathways involved in lomitapide-treated MM cells, gene expression profiles were conducted, and showed that both CD38 and its regulator BTK were downregulated, as well as the genes involved in DNA damage, cell death, cell cycle, lipid metabolism, oxidative phosphorylation, and mitochondrial dysfunction [121].

4.2. Inhibition of cellular proliferation

Metabolic reprogramming of tumor cells is an important sign of tumorigenesis, which is characterized by increased intracellular activities, such as protein synthesis, lipid synthesis, carbohydrate metabolism and mitochondrial biosynthesis [141]. It is well known that mTORC1 is a key regulator of energy metabolism [86]. During protein synthesis, mTOR phosphorylates and activates downstream kinases to initiate mRNA translation [142–144]. To investigate the effects of lomitapide on mTOR downstream targets, Lee et al. examined total protein and phosphorylated protein levels, finding that only mTORC1 and its substrates were decreased following lomitapide treatment, while no significant change was found in the phosphorylation and activation of AKT by mTORC2 [39], indicating an inhibitory role of lomitapide on the mTORC1 signaling pathway, which in turn suppressed protein biosynthesis.

Lipids are the basic component of the cell membrane, the formation of which is regulated by mTORC1 activity. De novo synthesis of lipid is promoted by mTORC1, through activating the transcription factor, sterol regulatory element binding protein (SREBP), to meet the needs of membrane formation during cell growth [145–147]. On the other hand, mTORC1 also promotes the synthesis of nucleotides required for DNA replication and ribosome synthesis through promoting the expression of activating transcription factor 4

(ATF4), providing carbon units for purine synthesis [148]. The inhibition of cellular proliferation by lomitapide was also found in skin cancer and gastric cancer cell lines, which was also confirmed to be through inhibiting mTORC1 and its downstream factors [39].

4.3. Induction of cellular autophagy

Autophagy is a lysosome-mediated process of protein degradation that removes damaged organelles, denatured proteins and invading pathogens in cells to meet the requirements of organelle renewal and cell metabolism [149]. Based on the capturing of cargoes to be degraded, autophagy can be divided into three major categories, macroautophagy, microautophagy and chaperone-mediated autophagy (CMA) [150]. Among them, macroautophagy is the predominant and well-studied type, and is the autophagy discussed below.

Microtubule-associated protein light chain 3 (LC3) is recognized as the typical biomarker of autophagy, and is present in the membrane of autophagic vesicles [150]. Currently, it is found that autophagy plays opposite roles in different stages of diverse malignances. At early stages, autophagy inhibits the malignant transformation of cells through maintaining stability of the genome, preventing cell damage from chronic tissue damage or inflammation, and reducing the accumulation of harmful substances. However, in the late stage, autophagy enables tumor cells to cope with hypoxia, malnutrition, and even radiocherapy and/or chemotherapy, resulting in the progression of tumors and chemo-radioresistance [151].

It is noteworthy that lomitapide increased the level of LC3-II in CRC cells, indicating increased autophagy in treated malignant cells [17]. Lee et al. showed that lomitapide decreased mTORC1-mediated phosphorylation of S757 on unc-51 like autophagy activating kinase 1 (ULK1) [39]. The extent of autophagy induction in different cellular environments depends on the relative activities of mTORC1 and AMPK. Under nutrient-sufficient conditions, mTORC1 mediates site-specific phosphorylation of ULK1 via Raptor to prevent the formation of the ULK1-Atg13-FIP200 complex, a key autophagy regulatory complex, which can be reversed by rapamycin through dephosphorylating ULK1 [152]. During periods of starvation and cellular stress, AMPK plays a dual role by inhibiting mTORC1 activity while also phosphorylating ULK1 to activate the enzyme. As a result of AMPK's inhibition of mTORC1 activity, ULK1, PP2A, and the protein phosphatase 1D magnesium-dependent, delta isoform (PPM1D) undergo dephosphorylation [153,154]. Then, the activated ULK1 complex is transferred to the isolated membrane of the endoplasmic reticulum, initiating the autophagy process [153,154].

It is reported that the regulation of lysosomal biogenesis by mTORC1 indirectly inhibits autophagy. For example, nuclear translocation and activity of transcription factor EB, a major transcriptional regulator of lysosomal biogenesis and autophagy genes, is prevented by mTORC1 under normal nutrient conditions [155–157], and is also a potential target for lomitapide treatment in malignancies. In CRC, lomitapide inhibits the progression of tumor cells through promoting cellular autophagy through the AMPK-mTOR signaling pathway. In addition, Zuo et al. showed that lomitapide can also induce autophagy in tumor cells through an AMPK-mTOR-independent transduction pathway in which a large accumulation of ROS in tumor cells is induced to interfere with normal mitochondrial function, along with the induced apoptosis [17].

4.4. Induction of cell apoptosis

Induction of apoptosis is one of the important strategies to inhibit the development of malignancies, and involves changes in nuclear morphology, DNA fragmentation and caspase 3 activation [158]. During apoptosis, the nuclear poly ADP-Ribose polymerase (PARP), a post-translational modification enzyme in base excision repair, nucleotide excision repair and single-stranded base repair, is cleaved by caspases, disrupting cellular DNA repair [159]. Following lomitapide treatment, apoptosis was induced in CRC cells in a dose-dependent manner with increased cleaved caspase 3 and PARP. PP2A, an effective therapeutic target in malignancies [160,161], is suppressed in lomitapide-treated CRC cells, achieving anti-tumor effects through disrupting cellular DNA repair, and inducing apoptosis [17]. In MM cells, the increased apoptosis was also induced by lomitapide treatment, and involved dysregulation of p53 gene [121].

However, in another investigation, the induction of caspase 3/7 activity in CRC cells treated with 2.5 μ M and 5 μ M lomitapide was negligible, indicating that no significant induction of apoptosis had occurred [39]. Potential variations in experimental conditions between the two studies, such as the cell lines of CRC, cell culture conditions, treatment duration, and the purity and quality of lomitapide, may account for the observed differences in apoptosis induction. It is plausible that lomitapide may exhibit efficacy in inducing apoptosis of CRC cells at higher concentrations. Consequently, lower concentrations of lomitapide may not be sufficiently effective in activating caspase 3/7 and inducing apoptosis. Furthermore, lomitapide might impact the survival or proliferation of CRC cells through alternative mechanisms such as cell cycle regulation, cell migration, and cell differentiation, rather than primarily relying on apoptosis. To gain a more comprehensive understanding of the mechanism of lomitapide action on CRC cells, further investigations are warranted. These investigations should encompass a broader range of lomitapide concentrations, exploration of different CRC cell lines, assessment of alternative apoptosis indicators, and the replication of experiments under varying experimental conditions.

4.5. Induction of cell cycle arrest

Control of the cell cycle is the key regulator during cell growth, differentiation, senescence and even cell death, while uncontrolled cycle progression is one of the hallmarks of tumorigenesis [162]. Studies have demonstrated that treatment with lomitapide induces a significant cell cycle arrest at the G0/G1 phase, thereby impeding cell cycle progression in MM cells [121]. Gene expression profiling showed that lomitapide triggers dysregulation of the tumor suppressor gene p53 and the proto-oncogene *c-MYC*. Downregulation of

c-MYC induced cell cycle arrest and impaired the mitogenic response [163], while p53 responded to a variety of cellular stresses, inducing cell cycle arrest and apoptosis, to inhibit malignant transformation [164]. It is worth noting that different tumor cell lines exhibit varying responses to cell cycle arrest. For instance, the CRC cell line HCT-116 does not show significant cell cycle arrest, while the metastatic melanoma cell line UACC62 undergoes apoptosis when arrested in S phase. On the other hand, no significant apoptosis was observed in the SK-Mel-5 and osteosarcoma cell line HT1080 when they arrested at G2/M phase, but their proliferation was inhibited [165]. Exploring the molecular mechanisms underlying these effects, such as the regulation of cell cycle regulators and apoptotic pathways, will offer valuable insights into the therapeutic potential of lomitapide.

It is worth considering that mTOR also assists regulating cell cycle progression and cell proliferation [166]. mTOR and its downstream factors not only regulate cell growth and tumor size, but also are involved in regulating cell cycle progression [167]. However, Lee et al. did not find any change in cell cycle-related genes in CRC treated with lomitapide [39], although activated AMPK and inhibited mTOR was detected [17,39]. The intricate nature of cell cycle regulation, the heterogeneity of cell types, and the interplay between signaling pathways may contribute to the lack of changes in cell cycle-related genes observed in CRC cells treated with lomitapide. Future studies could investigate the impact of these factors and shed light on the mechanisms by which lomitapide regulates the cell cycle.

4.6. Increased sensitivity to chemotherapy

As lomitapide shows effective anti-tumor activity in diverse malignancies, combined therapeutic strategies with chemotherapeutic drugs are emerging as promising treatment methods. The role of autophagy in the development of tumors is controversial, either protecting tumor cells from harmful conditions or inducing autophagy-mediated cell death (ACD) [168–171]. Exploring the regulatory mechanisms of autophagic pathway-related molecules in different types of tumor cells could help the development of targeted drugs. As the role of autophagy in tumor development continues to be clarified, new diagnostic and therapeutic targets could provide new ideas for the study of tumor pathogenesis.

Programmed death-1 (PD-1) is an immune-inhibitory receptor expressed in activated T cells, which plays a critical role in induction



Fig. 4. The graphic abstract of lomitapide in malignancies.

and maintenance of immune tolerance, contributing to the inhibition of effective anti-tumor and anti-microbial immunity [172]. PD-1 blockage is proved to be a prominent anti-tumor immunotherapy [173–175]. However, it is noted no significant improvement during disease progression in the majority of patients who only received anti-PD-1 therapy [173–175]. The improved tumor suppression after co-administration with mTOR inhibitors provides a rationale for the therapeutic strategies of mTOR inhibitors combined with immunosuppressive therapy [176,177]. In mouse colon cancer models, the inhibition of tumor growth was more pronounced in experimental groups treated with lomitapide in combination with anti-PD-1 antibodies than that in single treatment groups [39]. Immunohistochemical staining of tumor tissues revealed that the combination treatment increased the infiltration of CD8⁺ T cells into tumor. With treatment at a safe concentration of lomitapide at an effective dose of 20 mg/kg, neither significant changes in body weight nor hepatic/renal toxicity was detected, indicating that lomitapide is well tolerated for increasing therapeutic efficacy of other anti-tumor drugs [17,39].

5. Conclusion and perspectives

The anti-tumor efficacy of lomitapide appears promising in preclinical studies, especially for targeting certain molecular subtypes of cancer, and to a lesser extent, for combating drug resistance, as well as synergism with anti-tumor regimens that are already widely used. In conclusion, lomitapide has significant potential as an anti-tumor therapeutic agent in the following areas (Fig. 4).

Molecular docking and VS showed the direct binding of lomitapide to multiple protein receptors, such as BTK, ER- α and p38 MAPK, revealing its potential targets and multiple pharmacological effects, as well as providing new options for the treatment of specific molecular types of cancer. The results of *in vivo* experiments or *in vitro* experiments revealed that lomitapide has the potential to bind or inhibit multiple targets or pathways, such as ER- α , mTOR, AMPK, PP2A, and CD38, and this multi-targeting mechanism of action is of great significance for the treatment of malignant tumors. Meanwhile, preclinical studies of lomitapide with anti-phospholipase D1 (PLD-1) synergistic therapy revealed its clinical application as a novel anti-tumor synergistic drug.

Importantly, the shortcomings and gaps should not be ignored, such as the high-risk situations and side effects of pharmacological interactions with lomitapide still need to be revealed by more *in vivo* experiments and clinical studies. The effect of lomitapide on malignancies includes angiogenesis, invasion and distant metastasis, gene mutation, inflammation-promoted tumors, metabolism, epigenetic reprogramming, tumor microenvironment, antiaging, and immune escape, etc. The mechanisms underlying the effects of lomitapide on these aspects are unclear, and these issues warrant further studies to more fully assess the potential of lomitapide in antitumor therapy.

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Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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References

- [1] R.L. Siegel, K.D. Miller, H.E. Fuchs, A. Jemal, Cancer statistics, 2022, CA Cancer J Clin 72 (1) (2022) 7–33.
- [2] J. Ferla, M. Colombet, I. Soerjomataram, D.M. Parkin, M. Pineros, A. Znaor, et al., Cancer statistics for the year 2020: an overview, Int. J. Cancer 149 (2021) 778–789.
- [3] H. Sung, J. Ferlay, R.L. Siegel, M. Laversanne, I. Soerjomataram, A. Jemal, et al., Global cancer statistics 2020: GLOBOCAN estimates of incidence and mortality worldwide for 36 cancers in 185 Countries, CA Cancer J Clin 71 (3) (2021) 209–249.
- [4] L.A. Torre, F. Islami, R.L. Siegel, E.M. Ward, A. Jemal, Global cancer in women: burden and trends, Cancer Epidemiol. Biomarkers Prev. : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology 26 (4) (2017) 444–457.
- [5] C. Mattiuzzi, F. Sanchis-Gomar, G. Lippi, Concise update on colorectal cancer epidemiology, Ann. Transl. Med. 7 (21) (2019) 609.
- [6] N. Novac, Challenges and opportunities of drug repositioning, Trends Pharmacol. Sci. 34 (5) (2013) 267-272.
- [7] T.I. Oprea, J.E. Bauman, C.G. Bologa, T. Buranda, A. Chigaev, B.S. Edwards, et al., Drug repurposing from an academic perspective, Drug Discov. Today Ther. Strat. 8 (3–4) (2011) 61–69.
- [8] T.T. Ashburn, K.B. Thor, Drug repositioning: identifying and developing new uses for existing drugs, Nat. Rev. Drug Discov. 3 (8) (2004) 673-683.
- [9] L.G. Ferreira, A.D. Andricopulo, Drug repositioning approaches to parasitic diseases: a medicinal chemistry perspective, Drug Discov. Today 21 (10) (2016) 1699–1710.
- [10] S.N. Joshi, E.A. Murphy, P. Olaniyi, R.J. Bryant, The multiple effects of aspirin in prostate cancer patients, Cancer treatment and research communications 26 (2021) 100267.
- [11] H.F. Hu, W.W. Xu, Y.J. Li, Y. He, W.X. Zhang, L. Liao, et al., Anti-allergic drug azelastine suppresses colon tumorigenesis by directly targeting ARF1 to inhibit IQGAP1-ERK-Drp1-mediated mitochondrial fission, Theranostics 11 (4) (2021) 1828–1844.
- [12] X.H. Huang, Y. Wang, P. Hong, J. Yang, C.C. Zheng, X.F. Yin, et al., Benzethonium chloride suppresses lung cancer tumorigenesis through inducing p38mediated cyclin D1 degradation, Am. J. Cancer Res. 9 (11) (2019) 2397–2412.
- [13] J. Yang, W.W. Xu, P. Hong, F. Ye, X.H. Huang, H.F. Hu, et al., Adefovir dipivoxil sensitizes colon cancer cells to vemurafenib by disrupting the KCTD12-CDK1 interaction, Cancer Lett. 451 (2019) 79–91.
- [14] X.H. Huang, X. Yan, Q.H. Zhang, P. Hong, W.X. Zhang, Y.P. Liu, et al., Direct targeting of HSP90 with daurisoline destabilizes beta-catenin to suppress lung cancer tumorigenesis, Cancer Lett. 489 (2020) 66–78.
- [15] W.W. Xu, Z.H. Huang, L. Liao, Q.H. Zhang, J.Q. Li, C.C. Zheng, et al., Direct targeting of CREB1 with imperatorin inhibits TGFbeta2-ERK signaling to suppress esophageal cancer metastasis, Adv. Sci. 7 (16) (2020) 2000925.
- [16] A. Pirillo, A.L. Catapano, Understanding the efficacy and safety of lomitapide in homozygous familial hypercholesterolaemia, Eur J Prev Cardiol 29 (5) (2022) 829–831.
- [17] Q. Zuo, L. Liao, Z.T. Yao, Y.P. Liu, D.K. Wang, S.J. Li, et al., Targeting PP2A with lomitapide suppresses colorectal tumorigenesis through the activation of AMPK/Beclin1-mediated autophagy, Cancer Lett. 521 (2021) 281–293.
- [18] C. Stefanutti, C. Morozzi, S. Di Giacomo, New clinical perspectives of hypolipidemic drug therapy in severe hypercholesterolemia, Curr. Med. Chem. 19 (28) (2012) 4861–4868.
- [19] A. Nohara, Y. Otsubo, K. Yanagi, M. Yoshida, K. Ikewaki, M. Harada-Shiba, et al., Safety and efficacy of lomitapide in Japanese patients with homozygous familial hypercholesterolemia (HoFH): results from the AEGR-733-301 long-term extension study, J Atheroscler Thromb 26 (4) (2019) 368–377.
- [20] M. Cuchel, L.T. Bloedon, P.O. Szapary, D.M. Kolansky, M.L. Wolfe, A. Sarkis, et al., Inhibition of microsomal triglyceride transfer protein in familial hypercholesterolemia, N. Engl. J. Med. 356 (2) (2007) 148–156.
- [21] M.M. Hussain, P. Rava, M. Walsh, M. Rana, J. Iqbal, Multiple functions of microsomal triglyceride transfer protein, Nutr. Metab. 9 (2012) 14.
- [22] E. Khoury, D. Brisson, N. Roy, G. Tremblay, D. Gaudet, Review of the long-term safety of lomitapide: a microsomal triglycerides transfer protein inhibitor for treating homozygous familial hypercholesterolemia, Expert Opin Drug Saf 18 (5) (2019) 403–414.
- [23] Drug Information Handbook2016-2017 25th edition.
- [24] R. Alonso, A. Cuevas, P. Mata, Lomitapide: a review of its clinical use, efficacy, and tolerability, Core Evid. 14 (2019) 19-30.
- [25] C.M. Perry, Lomitapide: a review of its use in adults with homozygous familial hypercholesterolemia, Am. J. Cardiovasc. Drugs : drugs, devices, and other interventions 13 (4) (2013) 285–296.
- [26] D.J. Rader, J.J. Kastelein, Lomitapide and mipomersen: two first-in-class drugs for reducing low-density lipoprotein cholesterol in patients with homozygous familial hypercholesterolemia, Circulation 129 (9) (2014) 1022–1032.
- [27] D.J. Blom, M.R. Averna, E.A. Meagher, H. du Toit Theron, C.R. Sirtori, R.A. Hegele, et al., Long-term efficacy and safety of the microsomal triglyceride transfer protein inhibitor lomitapide in patients with homozygous familial hypercholesterolemia, Circulation 136 (3) (2017) 332–335.
- [28] M. Cuchel, E.A. Meagher, H. du Toit Theron, D.J. Blom, A.D. Marais, R.A. Hegele, et al., Efficacy and safety of a microsomal triglyceride transfer protein inhibitor in patients with homozygous familial hypercholesterolaemia: a single-arm, open-label, phase 3 study, Lancet (London, England) 381 (9860) (2013) 40–46.
- [29] D. Blom, M. Averna, E. Meagher, H. du Toit Theron, C. Sirtori, R. Hegele, et al., Abstract 12450: long-term efficacy and safety of lomitapide for the treatment of homozygous familial hypercholesterolemia: results of the phase 3 extension trial, Circulation 132 (suppl_3) (2015) A12450–A.
- [30] C.E. Chandler, D.E. Wilder, J.L. Pettini, Y.E. Savoy, S.F. Petras, G. Chang, et al., CP-346086: an MTP inhibitor that lowers plasma cholesterol and triglycerides in experimental animals and in humans, J. Lipid Res. 44 (10) (2003) 1887–1901.
- [31] Juxtapid [package insert], Cambridge, MA, Aegerion Pharmaceuticals, 2020.
- [32] Z. Reiner, Resistance and intolerance to statins, Nutr Metab Cardiovasc Dis 24 (10) (2014) 1057–1066.
- [33] R. Kerb, S. Hoffmeyer, U. Brinkmann, ABC drug transporters: hereditary polymorphisms and pharmacological impact in MDR1, MRP1 and MRP2, Pharmacogenomics 2 (1) (2001) 51–64.
- [34] Y. Zheng, Y. Hu, Z. Han, F. Yan, S. Zhang, Z. Yang, et al., Lomitapide ameliorates middle cerebral artery occlusion-induced cerebral ischemia/reperfusion injury by promoting neuronal autophagy and inhibiting microglial migration, CNS Neurosci. Ther. 28 (12) (2022) 2183–2194.
- [35] Y. Zhang, Y. Zhang, C. Chen, H. Cheng, X. Deng, D. Li, et al., Antibacterial activities and action mode of anti-hyperlipidemic lomitapide against Staphylococcus aureus, BMC Microbiol. 22 (1) (2022) 114.
- [36] A.C.C. de Sousa, K. Maepa, J.M. Combrinck, T.J. Egan, Lapatinib, nilotinib and lomitapide inhibit haemozoin formation in malaria parasites, Molecules 25 (7) (2020).
- [37] S. De Vita, M.G. Chini, G. Lauro, G. Bifulco, Accelerating the repurposing of FDA-approved drugs against coronavirus disease-19 (COVID-19), RSC advances 10 (67) (2020) 40867–40875.
- [38] F.A. Olotu, K.F. Omolabi, M.E.S. Soliman, Leaving no stone unturned: allosteric targeting of SARS-CoV-2 spike protein at putative druggable sites disrupts human angiotensin-converting enzyme interactions at the receptor binding domain, Inform. Med. Unlocked 21 (2020) 100451.
- [39] B. Lee, S.J. Park, S. Lee, J. Lee, E. Lee, E.S. Yoo, et al., Lomitapide, a cholesterol-lowering drug, is an anticancer agent that induces autophagic cell death via inhibiting mTOR, Cell Death Dis. 13 (7) (2022) 603.
- [40] R. Clarke, J.J. Tyson, J.M. Dixon, Endocrine resistance in breast cancer–An overview and update, Mol. Cell. Endocrinol. 418 (0 3) (2015) 220–234. Pt 3.
 [41] B. Huang, Y. Omoto, H. Iwase, H. Yamashita, T. Toyama, R.C. Coombes, et al., Differential expression of estrogen receptor alpha, beta1, and beta2 in lobular
- and ductal breast cancer, Proc Natl Acad Sci U S A 111 (5) (2014) 1933–1938. [42] H.H. Lee, Y. Zhu, K.M. Govindasamy, G. Gopalan, Downregulation of Aurora-A overrides estrogen-mediated growth and chemoresistance in breast cancer cells,
- Endocr. Relat. Cancer 15 (3) (2008) 765–775.[43] F. Stanzione, I. Giangreco, J.C. Cole, Use of molecular docking computational tools in drug discovery, Prog. Med. Chem. 60 (2021) 273–343.

- [44] I.D. Kuntz, J.M. Blaney, S.J. Oatley, R. Langridge, T.E. Ferrin, A geometric approach to macromolecule-ligand interactions, J. Mol. Biol. 161 (2) (1982) 269–288.
- [45] P. Ripphausen, B. Nisius, L. Peltason, J. Bajorath, Quo vadis, virtual screening? A comprehensive survey of prospective applications, J. Med. Chem. 53 (24) (2010) 8461–8467.
- [46] B.J. Druker, N.B. Lydon, Lessons learned from the development of an abl tyrosine kinase inhibitor for chronic myelogenous leukemia, J. Clin. Invest. 105 (1) (2000) 3–7.
- [47] M. von Itzstein, W.Y. Wu, G.B. Kok, M.S. Pegg, J.C. Dyason, B. Jin, et al., Rational design of potent sialidase-based inhibitors of influenza virus replication, Nature 363 (6428) (1993) 418–423.
- [48] S.W. Kaldor, V.J. Kalish, J.F. Davies 2nd, B.V. Shetty, J.E. Fritz, K. Appelt, et al., Viracept (nelfinavir mesylate, AG1343): a potent, orally bioavailable inhibitor of HIV-1 protease, J. Med. Chem. 40 (24) (1997) 3979–3985.
- [49] M. Squires, G. Ward, G. Saxty, V. Berdini, A. Cleasby, P. King, et al., Potent, selective inhibitors of fibroblast growth factor receptor define fibroblast growth factor dependence in preclinical cancer models, Mol Cancer Ther 10 (9) (2011) 1542–1552.
- [50] J. Tilak Vijay, K. Vivek Babu, A. Uma, Virtual screening of novel compounds as potential ER-alpha inhibitors, Bioinformation 15 (5) (2019) 321–332.
- [51] J. Heitman, N.R. Movva, M.N. Hall, Targets for cell cycle arrest by the immunosuppressant rapamycin in yeast, Science 253 (5022) (1991) 905–909.
- [52] D.M. Sabatini, R.K. Barrow, S. Blackshaw, P.E. Burnett, M.M. Lai, M.E. Field, et al., Interaction of RAFT1 with gephyrin required for rapamycin-sensitive signaling, Science 284 (5417) (1999) 1161–1164.
 [53] E.J. Brown, M.W. Albers, T.B. Shin, K. Ichikawa, C.T. Keith, W.S. Lane, et al., A mammalian protein targeted by G1-arresting rapamycin-receptor complex,
- [53] E.J. Brown, M.W. Albers, T.S. Shini, K. Ichikawa, C.T. Kehn, W.S. Lane, et al., A mammanan protein targeted by G1-arresting rapamycin-receptor complex, Nature 369 (6483) (1994) 756–758.
- [54] D.M. Sabatini, H. Erdjument-Bromage, M. Lui, P. Tempst, S.H. Snyder, RAFT1: a mammalian protein that binds to FKBP12 in a rapamycin-dependent fashion and is homologous to yeast TORs, Cell 78 (1) (1994) 35–43.
- [55] C.J. Sabers, M.M. Martin, G.J. Brunn, J.M. Williams, F.J. Dumont, G. Wiederrecht, et al., Isolation of a protein target of the FKBP12-rapamycin complex in mammalian cells, J. Biol. Chem. 270 (2) (1995) 815–822.
- [56] L.C. Kim, R.S. Cook, J. Chen, mTORC1 and mTORC2 in cancer and the tumor microenvironment, Oncogene 36 (16) (2017) 2191-2201.
- [57] H. Zhang, J.P. Stallock, J.C. Ng, C. Reinhard, T.P. Neufeld, Regulation of cellular growth by the Drosophila target of rapamycin dTOR, Genes Dev. 14 (21) (2000) 2712–2724.
- [58] J.O. Lipton, M. Sahin, The neurology of mTOR, Neuron 84 (2) (2014) 275-291.
- [59] N. Hay, N. Sonenberg, Upstream and downstream of mTOR, Genes Dev. 18 (16) (2004) 1926–1945.
- [60] T.R. Peterson, M. Laplante, C.C. Thoreen, Y. Sancak, S.A. Kang, W.M. Kuehl, et al., DEPTOR is an mTOR inhibitor frequently overexpressed in multiple myeloma cells and required for their survival, Cell 137 (5) (2009) 873–886.
- [61] H. Yang, D.G. Rudge, J.D. Koos, B. Vaidialingam, H.J. Yang, N.P. Pavletich, mTOR kinase structure, mechanism and regulation, Nature 497 (7448) (2013) 217–223.
- [62] K. Hara, Y. Maruki, X. Long, K. Yoshino, N. Oshiro, S. Hidayat, et al., Raptor, a binding partner of target of rapamycin (TOR), mediates TOR action, Cell 110 (2) (2002) 177–189.
- [63] D.H. Kim, D.D. Sarbassov, S.M. Ali, J.E. King, R.R. Latek, H. Erdjument-Bromage, et al., mTOR interacts with raptor to form a nutrient-sensitive complex that signals to the cell growth machinery, Cell 110 (2) (2002) 163–175.
- [64] D.H. Kim, D.D. Sarbassov, S.M. Ali, R.R. Latek, K.V. Guntur, H. Erdjument-Bromage, et al., GbetaL, a positive regulator of the rapamycin-sensitive pathway required for the nutrient-sensitive interaction between raptor and mTOR, Mol Cell 11 (4) (2003) 895–904.
- [65] D.D. Sarbassov, S.M. Ali, D.H. Kim, D.A. Guertin, R.R. Latek, H. Erdjument-Bromage, et al., Rictor, a novel binding partner of mTOR, defines a rapamycininsensitive and raptor-independent pathway that regulates the cytoskeleton, Curr. Biol. 14 (14) (2004) 1296–1302.
- [66] E. Jacinto, V. Facchinetti, D. Liu, N. Soto, S. Wei, S.Y. Jung, et al., SIN1/MIP1 maintains rictor-mTOR complex integrity and regulates Akt phosphorylation and substrate specificity, Cell 127 (1) (2006) 125–137.
- [67] L.R. Pearce, X. Huang, J. Boudeau, R. Pawlowski, S. Wullschleger, M. Deak, et al., Identification of Protor as a novel Rictor-binding component of mTOR complex-2, Biochem. J. 405 (3) (2007) 513–522.
- [68] J.R. Cantor, D.M. Sabatini, Cancer cell metabolism: one hallmark, many faces, Cancer Discov. 2 (10) (2012) 881-898.
- [69] D.A. Guertin, D.M. Sabatini, Defining the role of mTOR in cancer, Cancer Cell 12 (1) (2007) 9-22.
- [70] D.M. Sabatini, mTOR and cancer: insights into a complex relationship, Nat. Rev. Cancer 6 (9) (2006) 729–734.
- [71] P.K. Majumder, P.G. Febbo, R. Bikoff, R. Berger, Q. Xue, L.M. McMahon, et al., mTOR inhibition reverses Akt-dependent prostate intraepithelial neoplasia through regulation of apoptotic and HIF-1-dependent pathways, Nat. Med. 10 (6) (2004) 594–601.
- [72] J. Blando, M. Portis, F. Benavides, A. Alexander, G. Mills, B. Dave, et al., PTEN deficiency is fully penetrant for prostate adenocarcinoma in C57BL/6 mice via mTOR-dependent growth, Am. J. Pathol. 174 (5) (2009) 1869–1879.
- [73] Z.H. Lu, M.B. Shvartsman, A.Y. Lee, J.M. Shao, M.M. Murray, R.D. Kladney, et al., Mammalian target of rapamycin activator RHEB is frequently overexpressed in human carcinomas and is critical and sufficient for skin epithelial carcinogenesis, Cancer Res. 70 (8) (2010) 3287–3298.
- [74] C. Magaway, E. Kim, E. Jacinto, Targeting mTOR and metabolism in cancer: lessons and innovations, Cells 8 (12) (2019).
- [75] R. Roskoski Jr., Properties of FDA-approved small molecule protein kinase inhibitors: a 2020 update, Pharmacol. Res. 152 (2020) 104609.
- [76] Z. Zou, T. Tao, H. Li, X. Zhu, mTOR signaling pathway and mTOR inhibitors in cancer: progress and challenges, Cell Biosci. 10 (2020) 31.
- [77] T. Alain, M. Morita, B.D. Fonseca, A. Yanagiya, N. Siddiqui, M. Bhat, et al., eIF4E/4E-BP ratio predicts the efficacy of mTOR targeted therapies, Cancer Res. 72 (24) (2012) 6468–6476.
- [78] J. Li, S.G. Kim, J. Blenis, Rapamycin: one drug, many effects, Cell Metab. 19 (3) (2014) 373-379.
- [79] M. Moschetta, A. Reale, C. Marasco, A. Vacca, M.R. Carratu, Therapeutic targeting of the mTOR-signalling pathway in cancer: benefits and limitations, Br. J. Pharmacol. 171 (16) (2014) 3801–3813.
- [80] C.L. Cope, R. Gilley, K. Balmanno, M.J. Sale, K.D. Howarth, M. Hampson, et al., Adaptation to mTOR kinase inhibitors by amplification of eIF4E to maintain cap-dependent translation, J. Cell Sci. 127 (Pt 4) (2014) 788–800.
- [81] A.Y. Choo, S.O. Yoon, S.G. Kim, P.P. Roux, J. Blenis, Rapamycin differentially inhibits S6Ks and 4E-BP1 to mediate cell-type-specific repression of mRNA translation, Proc Natl Acad Sci U S A. 105 (45) (2008) 17414–17419.
- [82] Y. Li, S. Xu, M.M. Mihaylova, B. Zheng, X. Hou, B. Jiang, et al., AMPK phosphorylates and inhibits SREBP activity to attenuate hepatic steatosis and atherosclerosis in diet-induced insulin-resistant mice, Cell Metab. 13 (4) (2011) 376–388.
- [83] S.H. Koo, L. Flechner, L. Qi, X. Zhang, R.A. Screaton, S. Jeffries, et al., The CREB coactivator TORC2 is a key regulator of fasting glucose metabolism, Nature 437 (7062) (2005) 1109–1111.
- [84] M.M. Mihaylova, D.S. Vasquez, K. Ravnskjaer, P.D. Denechaud, R.T. Yu, J.G. Alvarez, et al., Class IIa histone deacetylases are hormone-activated regulators of FOXO and mammalian glucose homeostasis, Cell 145 (4) (2011) 607–621.
- [85] W. Yang, Y.H. Hong, X.Q. Shen, C. Frankowski, H.S. Camp, T. Leff, Regulation of transcription by AMP-activated protein kinase: phosphorylation of p300 blocks its interaction with nuclear receptors, J. Biol. Chem. 276 (42) (2001) 38341–38344.
- [86] E.A. Dunlop, A.R. Tee, The kinase triad, AMPK, mTORC1 and ULK1, maintains energy and nutrient homoeostasis, Biochem. Soc. Trans. 41 (4) (2013) 939–943.
 [87] D. Carling, V.A. Zammit, D.G. Hardie, A common bicyclic protein kinase cascade inactivates the regulatory enzymes of fatty acid and cholesterol biosynthesis, FEBS Lett. 223 (2) (1987) 217–222.
- [88] M.R. Munday, D.G. Campbell, D. Carling, D.G. Hardie, Identification by amino acid sequencing of three major regulatory phosphorylation sites on rat acetyl-CoA carboxylase, Eur. J. Biochem. 175 (2) (1988) 331–338.
- [89] A. Gonzalez, M.N. Hall, S.C. Lin, D.G. Hardie, AMPK and TOR: the Yin and Yang of cellular nutrient sensing and growth control, Cell Metab. 31 (3) (2020) 472–492.

- [90] Y. Shi, H.M. Shen, V. Gopalakrishnan, N. Gordon, Epigenetic regulation of autophagy beyond the cytoplasm: a review, Front. Cell Dev. Biol. 9 (2021) 675599.
- [91] K. Inoki, T. Zhu, K.L. Guan, TSC2 mediates cellular energy response to control cell growth and survival, Cell 115 (5) (2003) 577-590.
- [92] D.M. Gwinn, D.B. Shackelford, D.F. Egan, M.M. Mihaylova, A. Mery, D.S. Vasquez, et al., AMPK phosphorylation of raptor mediates a metabolic checkpoint, Mol Cell 30 (2) (2008) 214–226.
- [93] N.X.Y. Ling, A. Kaczmarek, A. Hoque, E. Davie, K.R.W. Ngoei, K.R. Morrison, et al., mTORC1 directly inhibits AMPK to promote cell proliferation under nutrient stress, Nat. Metab. 2 (1) (2020) 41–49.
- [94] Z. Wang, W.A. Wilson, M.A. Fujino, P.J. Roach, Antagonistic controls of autophagy and glycogen accumulation by Snf1p, the yeast homolog of AMP-activated protein kinase, and the cyclin-dependent kinase Pho85p, Mol. Cell Biol. 21 (17) (2001) 5742–5752.
- [95] D. Meley, C. Bauvy, J.H. Houben-Weerts, P.F. Dubbelhuis, M.T. Helmond, P. Codogno, et al., AMP-activated protein kinase and the regulation of autophagic proteolysis, J. Biol. Chem. 281 (46) (2006) 34870–34879.
- [96] M. Hoyer-Hansen, L. Bastholm, P. Szyniarowski, M. Campanella, G. Szabadkai, T. Farkas, et al., Control of macroautophagy by calcium, calmodulin-dependent kinase kinase-beta, and Bcl-2, Mol Cell 25 (2) (2007) 193–205.
- [97] J.A. Chavez, W.G. Roach, S.R. Keller, W.S. Lane, G.E. Lienhard, Inhibition of GLUT4 translocation by Tbc1d1, a Rab GTPase-activating protein abundant in skeletal muscle, is partially relieved by AMP-activated protein kinase activation, J. Biol. Chem. 283 (14) (2008) 9187–9195.
- [98] N. Wu, B. Zheng, A. Shaywitz, Y. Dagon, C. Tower, G. Bellinger, et al., AMPK-dependent degradation of TXNIP upon energy stress leads to enhanced glucose uptake via GLUT1, Mol Cell 49 (6) (2013) 1167–1175.
- [99] M. Ahmadian, M.J. Abbott, T. Tang, C.S. Hudak, Y. Kim, M. Bruss, et al., Desnutrin/ATGL is regulated by AMPK and is required for a brown adipose phenotype, Cell Metab. 13 (6) (2011) 739–748.
- [100] J.D. McGarry, G.F. Leatherman, D.W. Foster, Carnitine palmitoyltransferase I. The site of inhibition of hepatic fatty acid oxidation by malonyl-CoA, J. Biol. Chem. 253 (12) (1978) 4128–4136.
- [101] J.A. McCubrey, M.M. Lahair, R.A. Franklin, Reactive oxygen species-induced activation of the MAP kinase signaling pathways, Antioxid Redox Signal 8 (9–10) (2006) 1775–1789.
- [102] A.S. Dhillon, S. Hagan, O. Rath, W. Kolch, MAP kinase signalling pathways in cancer, Oncogene 26 (22) (2007) 3279-3290.
- [103] J.V. Gimeno-Alcaniz, P. Sanz, Glucose and type 2A protein phosphatase regulate the interaction between catalytic and regulatory subunits of AMP-activated protein kinase, J. Mol. Biol. 333 (1) (2003) 201–209.
- [104] K. Ravnskjaer, M. Boergesen, L.T. Dalgaard, S. Mandrup, Glucose-induced repression of PPARalpha gene expression in pancreatic beta-cells involves PP2A activation and AMPK inactivation, J. Mol. Endocrinol. 36 (2) (2006) 289–299.
- [105] Q.W. Shen, M.J. Zhu, J. Tong, J. Ren, M. Du, Ca2+/calmodulin-dependent protein kinase kinase is involved in AMP-activated protein kinase activation by alpha-lipoic acid in C2C12 myotubes, Am J Physiol Cell Physiol 293 (4) (2007) C1395–C1403.
- [106] E.Q. Toyama, S. Herzig, J. Courchet, T.L. Lewis Jr., O.C. Loson, K. Hellberg, et al., Metabolism. AMP-activated protein kinase mediates mitochondrial fission in response to energy stress, Science 351 (6270) (2016) 275–281.
- [107] E.C. Hinchy, A.V. Gruszczyk, R. Willows, N. Navaratnam, A.R. Hall, G. Bates, et al., Mitochondria-derived ROS activate AMP-activated protein kinase (AMPK) indirectly, J. Biol. Chem. 293 (44) (2018) 17208–17217.
- [108] P. Grumati, L. Coletto, P. Sabatelli, M. Cescon, A. Angelin, E. Bertaggia, et al., Autophagy is defective in collagen VI muscular dystrophies, and its reactivation rescues myofiber degeneration, Nat. Med. 16 (11) (2010) 1313–1320.
- [109] V. Soubannier, G.L. McLelland, R. Zunino, E. Braschi, P. Rippstein, E.A. Fon, et al., A vesicular transport pathway shuttles cargo from mitochondria to lysosomes. Curr. Biol. 22 (2) (2012) 135–141.
- [110] H.J. Schaeffer, M.J. Weber, Mitogen-activated protein kinases: specific messages from ubiquitous messengers, Mol. Cell Biol. 19 (4) (1999) 2435–2444.
- [111] S. Lee, J. Rauch, W. Kolch, Targeting MAPK signaling in cancer: mechanisms of drug resistance and sensitivity, Int. J. Mol. Sci. 21 (3) (2020).
- [112] S. Kumar, J. Boehm, J.C. Lee, p38 MAP kinases: key signalling molecules as therapeutic targets for inflammatory diseases, Nat. Rev. Drug Discov. 2 (9) (2003) 717–726.
- [113] B. Canovas, A.R. Nebreda, Diversity and versatility of p38 kinase signalling in health and disease, Nat. Rev. Mol. Cell Biol. 22 (5) (2021) 346–366.

[114] M.J. Robinson, M.H. Cobb, Mitogen-activated protein kinase pathways, Curr. Opin. Cell Biol. 9 (2) (1997) 180-186.

- [115] T.S. Lewis, P.S. Shapiro, N.G. Ahn, Signal transduction through MAP kinase cascades, Adv. Cancer Res. 74 (1998) 49-139.
- [116] Y. Xu, Q. Sun, F. Yuan, H. Dong, H. Zhang, R. Geng, et al., RND2 attenuates apoptosis and autophagy in glioblastoma cells by targeting the p38 MAPK signalling pathway, J. Exp. Clin. Cancer Res. 39 (1) (2020) 174.
- [117] U. Suriya, P. Mahalapbutr, T. Rungrotmongkol, Integration of in silico strategies for drug repositioning towards P38alpha mitogen-activated protein kinase (MAPK) at the allosteric site, Pharmaceutics 14 (7) (2022).
- [118] A. Astolfi, G. Manfroni, V. Cecchetti, M.L. Barreca, A comprehensive structural overview of p38alpha mitogen-activated protein kinase in complex with ATPsite and non-ATP-site binders, ChemMedChem 13 (1) (2018) 7–14.
- [119] C. Pargellis, L. Tong, L. Churchill, P.F. Cirillo, T. Gilmore, A.G. Graham, et al., Inhibition of p38 MAP kinase by utilizing a novel allosteric binding site, Nat. Struct. Biol. 9 (4) (2002) 268–272.
- [120] D. Suplatov, K. Kopylov, Y. Sharapova, V. Svedas, Human p38alpha mitogen-activated protein kinase in the Asp168-Phe169-Gly170-in (DFG-in) state can bind allosteric inhibitor Doramapimod, J. Biomol. Struct. Dyn. 37 (8) (2019) 2049–2060.
- [121] M.E.M. Saeed, J.C. Boulos, S.B. Mucklich, E. Leich, M. Chatterjee, S.M. Klauck, et al., Disruption of lipid raft microdomains, regulation of CD38, TP53, and MYC signaling, and induction of apoptosis by lomitapide in multiple myeloma cells, Cancer genomics & proteomics 19 (5) (2022) 540–555.
- [122] K. Inoki, Y. Li, T. Xu, K.L. Guan, Rheb GTPase is a direct target of TSC2 GAP activity and regulates mTOR signaling, Genes Dev. 17 (15) (2003) 1829–1834.
 [123] A.R. Tee, B.D. Manning, P.P. Roux, L.C. Cantley, J. Blenis, Tuberous sclerosis complex gene products, Tuberin and Hamartin, control mTOR signaling by acting as a GTPase-activating protein complex toward Rheb, Curr. Biol. 13 (15) (2003) 1259–1268.
- [124] K. Inoki, Y. Li, T. Zhu, J. Wu, K.L. Guan, TSC2 is phosphorylated and inhibited by Akt and suppresses mTOR signalling, Nat. Cell Biol. 4 (9) (2002) 648–657.
 [125] B.D. Manning, A.R. Tee, M.N. Logsdon, J. Blenis, L.C. Cantley, Identification of the tuberous sclerosis complex-2 tumor suppressor gene product tuberin as a
- target of the phosphoinositide 3-kinase/akt pathway, Mol Cell 10 (1) (2002) 151–162.
- [126] L. Ma, Z. Chen, H. Erdjument-Bromage, P. Tempst, P.P. Pandolfi, Phosphorylation and functional inactivation of TSC2 by Erk implications for tuberous sclerosis and cancer pathogenesis, Cell 121 (2) (2005) 179–193.
- [127] Y. Feng, M. Spezia, S. Huang, C. Yuan, Z. Zeng, L. Zhang, et al., Breast cancer development and progression: risk factors, cancer stem cells, signaling pathways, genomics, and molecular pathogenesis, Genes & diseases 5 (2) (2018) 77–106.
- [128] A. Efeyan, R. Zoncu, S. Chang, I. Gumper, H. Snitkin, R.L. Wolfson, et al., Regulation of mTORC1 by the Rag GTPases is necessary for neonatal autophagy and survival, Nature 493 (7434) (2013) 679–683.
- [129] A. Kalender, A. Selvaraj, S.Y. Kim, P. Gulati, S. Brule, B. Viollet, et al., Metformin, independent of AMPK, inhibits mTORC1 in a rag GTPase-dependent manner, Cell Metab. 11 (5) (2010) 390–401.
- [130] R.J. Shaw, N. Bardeesy, B.D. Manning, L. Lopez, M. Kosmatka, R.A. DePinho, et al., The LKB1 tumor suppressor negatively regulates mTOR signaling, Cancer Cell 6 (1) (2004) 91–99.
- [131] E.J. Pavon, P. Munoz, M.D. Navarro, E. Raya-Alvarez, J.L. Callejas-Rubio, F. Navarro-Pelayo, et al., Increased association of CD38 with lipid rafts in T cells from patients with systemic lupus erythematosus and in activated normal T cells, Mol. Immunol. 43 (7) (2006) 1029–1039.
- [132] R. Zidovetzki, I. Levitan, Use of cyclodextrins to manipulate plasma membrane cholesterol content: evidence, misconceptions and control strategies, Biochim. Biophys. Acta 1768 (6) (2007) 1311–1324.
- [133] M. Reis-Sobreiro, G. Roue, A. Moros, C. Gajate, J. de la Iglesia-Vicente, D. Colomer, et al., Lipid raft-mediated Akt signaling as a therapeutic target in mantle cell lymphoma, Blood Cancer J. 3 (5) (2013) e118.
- [134] H.C. Lee, Enzymatic functions and structures of CD38 and homologs, Chem. Immunol. 75 (2000) 39–59.

- [135] R. Lande, F. Urbani, B. Di Carlo, G. Sconocchia, S. Deaglio, A. Funaro, et al., CD38 ligation plays a direct role in the induction of IL-1beta, IL-6, and IL-10 secretion in resting human monocytes, Cell. Immunol. 220 (1) (2002) 30–38.
- [136] S. Liao, S. Xiao, H. Chen, M. Zhang, Z. Chen, Y. Long, et al., CD38 enhances the proliferation and inhibits the apoptosis of cervical cancer cells by affecting the mitochondria functions, Mol. Carcinog. 56 (10) (2017) 2245–2257.
- [137] T. Robak, E. Robak, Tyrosine kinase inhibitors as potential drugs for B-cell lymphoid malignancies and autoimmune disorders, Expet Opin. Invest. Drugs 21 (7) (2012) 921–947.
- [138] J.H. Jeon, S.K. Kim, H.J. Kim, J. Chang, C.M. Ahn, Y.S. Chang, Lipid raft modulation inhibits NSCLC cell migration through delocalization of the focal adhesion complex, Lung Cancer 69 (2) (2010) 165–171.
- [139] A.C.S. Alves, R.A. Dias, L.P. Kagami, G.M. das Neves, F.C. Torres, V.L. Eifler-Lima, et al., Beyond the "lock and key" paradigm: targeting lipid rafts to induce the selective apoptosis of cancer cells, Curr. Med. Chem. 25 (18) (2018) 2082–2104.
- [140] C. Gajate, E. Del Canto-Janez, A.U. Acuna, F. Amat-Guerri, E. Geijo, A.M. Santos-Beneit, et al., Intracellular triggering of Fas aggregation and recruitment of apoptotic molecules into Fas-enriched rafts in selective tumor cell apoptosis, J. Exp. Med. 200 (3) (2004) 353–365.
- [141] I. Martinez-Reyes, N.S. Chandel, Cancer metabolism: looking forward, Nat. Rev. Cancer 21 (10) (2021) 669–680.
 [142] M.K. Holz, B.A. Ballif, S.P. Gygi, J. Blenis, mTOR and S6K1 mediate assembly of the translation preinitiation complex through dynamic protein interchange and ordered phosphorylation events, Cell 123 (4) (2005) 569–580.
- [143] G.J. Brunn, C.C. Hudson, A. Sekulic, J.M. Williams, H. Hosoi, P.J. Houghton, et al., Phosphorylation of the translational repressor PHAS-I by the mammalian target of rapamycin, Science 277 (5322) (1997) 99–101.
- [144] A.C. Gingras, S.P. Gygi, B. Raught, R.D. Polakiewicz, R.T. Abraham, M.F. Hoekstra, et al., Regulation of 4E-BP1 phosphorylation: a novel two-step mechanism, Genes Dev. 13 (11) (1999) 1422–1437.
- [145] T. Porstmann, C.R. Santos, B. Griffiths, M. Cully, M. Wu, S. Leevers, et al., SREBP activity is regulated by mTORC1 and contributes to Akt-dependent cell growth, Cell Metab. 8 (3) (2008) 224–236.
- [146] K. Duvel, J.L. Yecies, S. Menon, P. Raman, A.I. Lipovsky, A.L. Souza, et al., Activation of a metabolic gene regulatory network downstream of mTOR complex 1, Mol Cell 39 (2) (2010) 171–183.
- [147] T.R. Peterson, S.S. Sengupta, T.E. Harris, A.E. Carmack, S.A. Kang, E. Balderas, et al., mTOR complex 1 regulates lipin 1 localization to control the SREBP pathway, Cell 146 (3) (2011) 408–420.
- [148] I. Ben-Sahra, G. Hoxhaj, S.J.H. Ricoult, J.M. Asara, B.D. Manning, mTORC1 induces purine synthesis through control of the mitochondrial tetrahydrofolate cycle, Science 351 (6274) (2016) 728–733.
- [149] A. Schmoldt, H.F. Benthe, G. Haberland, Digitoxin metabolism by rat liver microsomes, Biochem. Pharmacol. 24 (17) (1975) 1639–1641.
- [150] N. Mizushima, B. Levine, A.M. Cuervo, D.J. Klionsky, Autophagy fights disease through cellular self-digestion, Nature 451 (7182) (2008) 1069–1075.
- [151] R.K. Amaravadi, A.C. Kimmelman, J. Debnath, Targeting autophagy in cancer: recent advances and future directions, Cancer Discov. 9 (9) (2019) 1167–1181.
 [152] N. Hosokawa, T. Hara, T. Kaizuka, C. Kishi, A. Takamura, Y. Miura, et al., Nutrient-dependent mTORC1 association with the ULK1-Atg13-FIP200 complex required for autophagy. Mol. Biol. Cell 20 (7) (2009) 1981–1991.
- [153] P.M. Wong, Y. Feng, J. Wang, R. Shi, X. Jiang, Regulation of autophagy by coordinated action of mTORC1 and protein phosphatase 2A, Nat. Commun. 6 (2015) 8048.
- [154] S. Torii, T. Yoshida, S. Arakawa, S. Honda, A. Nakanishi, S. Shimizu, Identification of PPM1D as an essential Ulk1 phosphatase for genotoxic stress-induced autophagy, EMBO Rep. 17 (11) (2016) 1552–1564.
- [155] J.A. Martina, Y. Chen, M. Gucek, R. Puertollano, MTORC1 functions as a transcriptional regulator of autophagy by preventing nuclear transport of TFEB, Autophagy 8 (6) (2012) 903–914.
- [156] A. Roczniak-Ferguson, C.S. Petit, F. Froehlich, S. Qian, J. Ky, B. Angarola, et al., The transcription factor TFEB links mTORC1 signaling to transcriptional control of lysosome homeostasis, Sci. Signal. 5 (228) (2012) ra42.
- [157] C. Settembre, R. Zoncu, D.L. Medina, F. Vetrini, S. Erdin, S. Erdin, et al., A lysosome-to-nucleus signalling mechanism senses and regulates the lysosome via mTOR and TFEB, Embo j 31 (5) (2012) 1095–1108.
- [158] T. Li, N. Kon, L. Jiang, M. Tan, T. Ludwig, Y. Zhao, et al., Tumor suppression in the absence of p53-mediated cell-cycle arrest, apoptosis, and senescence, Cell 149 (6) (2012) 1269–1283.
- [159] G.V. Chaitanya, A.J. Steven, P.P. Babu, PARP-1 cleavage fragments: signatures of cell-death proteases in neurodegeneration, Cell Commun. Signal. : CCS 8 (2010) 31.
- [160] K.E. Chang, B.R. Wei, J.P. Madigan, M.D. Hall, R.M. Simpson, Z. Zhuang, et al., The protein phosphatase 2A inhibitor LB100 sensitizes ovarian carcinoma cells to cisplatin-mediated cytotoxicity, Mol Cancer Ther 14 (1) (2015) 90–100.
- [161] D. Wei, L.A. Parsels, D. Karnak, M.A. Davis, J.D. Parsels, A.C. Marsh, et al., Inhibition of protein phosphatase 2A radiosensitizes pancreatic cancers by modulating CDC25C/CDK1 and homologous recombination repair, Clin. Cancer Res. : an official journal of the American Association for Cancer Research 19 (16) (2013) 4422–4432.
- [162] H.K. Matthews, C. Bertoli, R.A.M. de Bruin, Cell cycle control in cancer, Nat. Rev. Mol. Cell Biol. 23 (1) (2022) 74–88.
- [163] G. Bretones, M.D. Delgado, J. Leon, Myc and cell cycle control, Biochim. Biophys. Acta 1849 (5) (2015) 506–516.
- [164] B. Vogelstein, D. Lane, A.J. Levine, Surfing the p53 network, Nature 408 (6810) (2000) 307–310.
- [165] H. Wang, S. Mannava, V. Grachtchouk, D. Zhuang, M.S. Soengas, A.V. Gudkov, et al., c-Myc depletion inhibits proliferation of human tumor cells at various stages of the cell cycle, Oncogene 27 (13) (2008) 1905–1915.
- [166] R.T. Abraham, G.J. Wiederrecht, Immunopharmacology of rapamycin, Annu. Rev. Immunol. 14 (1996) 483–510.
- [167] D.C. Fingar, C.J. Richardson, A.R. Tee, L. Cheatham, C. Tsou, J. Blenis, mTOR controls cell cycle progression through its cell growth effectors S6K1 and 4E-BP1/eukaryotic translation initiation factor 4E, Mol. Cell Biol. 24 (1) (2004) 200–216.
- [168] J.M. Gump, A. Thorburn, Autophagy and apoptosis: what is the connection? Trends Cell Biol. 21 (7) (2011) 387-392.
- [169] K. Jing, K. Lim, Why is autophagy important in human diseases? Exp. Mol. Med. 44 (2) (2012) 69–72.
- [170] S.W. Ryter, K. Mizumura, A.M. Choi, The impact of autophagy on cell death modalities, Int J Cell Biol 2014 (2014) 502676.
- [171] M. Su, Y. Mei, S. Sinha, Role of the crosstalk between autophagy and apoptosis in cancer, J Oncol 2013 (2013) 102735.
- [172] T. Shimauchi, K. Kabashima, D. Nakashima, K. Sugita, Y. Yamada, R. Hino, et al., Augmented expression of programmed death-1 in both neoplastic and nonneoplastic CD4+ T-cells in adult T-cell leukemia/lymphoma, Int. J. Cancer 121 (12) (2007) 2585–2590.
- [173] J.M. Pitt, M. Vetizou, R. Daillere, M.P. Roberti, T. Yamazaki, B. Routy, et al., Resistance mechanisms to immune-checkpoint blockade in cancer: tumor-intrinsic and -extrinsic factors, Immunity 44 (6) (2016) 1255–1269.
- [174] N.A. Rizvi, M.D. Hellmann, A. Snyder, P. Kvistborg, V. Makarov, J.J. Havel, et al., Cancer immunology. Mutational landscape determines sensitivity to PD-1 blockade in non-small cell lung cancer, Science 348 (6230) (2015) 124–128.
- [175] S.L. Topalian, F.S. Hodi, J.R. Brahmer, S.N. Gettinger, D.C. Smith, D.F. McDermott, et al., Safety, activity, and immune correlates of anti-PD-1 antibody in cancer, N. Engl. J. Med. 366 (26) (2012) 2443–2454.
- [176] A. El Hage, O. Dormond, Combining mTOR inhibitors and T cell-based immunotherapies in cancer treatment, Cancers 13 (6) (2021).
- [177] H. Li, X. Li, S. Liu, L. Guo, B. Zhang, J. Zhang, et al., Programmed cell death-1 (PD-1) checkpoint blockade in combination with a mammalian target of rapamycin inhibitor restrains hepatocellular carcinoma growth induced by hepatoma cell-intrinsic PD-1, Hepatology 66 (6) (2017) 1920–1933.
- [178] M.E.M. Saeed, J.C. Boulos, S.B. Mücklich, E. Leich, M. Chatterjee, S.M. Klauck, et al., Disruption of lipid raft microdomains, regulation of CD38, TP53, and MYC signaling, and induction of apoptosis by lomitapide in multiple myeloma cells, Cancer Genomics Proteomics 19 (5) (2022) 540–555.