

Review Article

L-type amino acid transport and cancer: targeting the mTORC1 pathway to inhibit neoplasia

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Abstract: The L-type amino acid transporter (LAT) family are Na⁺-independent transporters, which deliver neutral amino acids into cells. The four LATs, LAT1 (SLC7A5), LAT2 (SLC7A8), LAT3 (SLC43A1) and LAT4 (SLC43A2), are responsible for the majority of cellular leucine uptake. They show increased expression in many cancers, and are critical for control of protein translation and cell growth through the mTORC1 pathway. The increased transporter expression observed in cancers is regulated by transcriptional pathways such as hormone receptors, c-myc and nutrient starvation responses. We review the expression and function of the LAT family in cancer, as well as the recent development of specific inhibitors targeting LAT1 or LAT3. These LAT family inhibitors may be useful adjuvant therapeutics in multiple cancers.

Keywords: L-type amino acid, transport, cancer, mTORC1 pathway

Recent advances in therapeutics designed to target the PI3K/Akt/mTORC1 pathway have resulted in dozens of new anti-cancer compounds currently undergoing Phase I/II trials [1, 2]. This critical cell growth pathway is also regulated by nutrients, in particular the essential amino acid leucine, which is required for activation of the mTORC1/Ragulator complex. Leucine is the most common of the 20 proteinogenic amino acids present in proteins. It is thought that mTORC1 can only begin translation when sufficient levels of leucine, arginine or glutamine are available. The L-type amino acid transporters (LATs) are the major transporters that mediate uptake of leucine into cells, thereby regulating mTORC1 signaling and protein synthesis. This critical requirement for intracellular leucine is reflected in the increased expression of LATs in the majority of cancers, and in the diverse transcription factors that regulate their expression. The classification, structure and function of LAT family have been well reviewed recently [3, 4]. In our review, we provide an overview of recent studies focusing on the role and regulation of the four LAT family members (LAT1, LAT2, LAT3 and LAT4) in cancer. We have analyzed LAT family member

expression levels, correlations with disease state and metastasis, and their role in cancer cell growth through the mTORC1 pathway. Furthermore, we discuss targeting of the LAT family as a novel anti-cancer approach and the current state of LAT inhibitors.

L-type amino acid transporter family

The L-type amino acid transporter (LAT) family consists of four Na⁺-independent neutral amino acid transporters. The members of this family are grouped in two sub-families, namely, SLC7 (LAT1 and LAT2) and SLC43 (LAT3 and LAT4). Each member of the LAT family is believed to contain 12 transmembrane domains, however there are no current structures solved for any of the human LAT proteins. LAT1 (SLC7A5) and LAT2 (SLC7A8) associate with the 4F2hc (4F2 antigen heavy chain; CD98 heavy chain) glycoprotein, forming a heterodimeric obligatory exchanger with a high affinity [5-9]. LAT3 (SLC43A1) and LAT4 (SLC43A2) are facilitated diffusers of neutral amino acids with a low affinity, and do not appear to require a binding partner [10, 11]. LAT3 and LAT4 deliver a narrow range of neutral amino acids into cells, including leucine, isoleucine, valine, phenylalanine and

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Table 1. LAT expression and function

Protein	Gene	Substrates	Expression pattern
LAT1	SLC7A5	Leu, Ile, Phe, Met, Tyr, His, Trp, Val	Brain, spleen, placenta, ovary, testis, colon, blood-brain barrier, fetal liver, activated lymphocytes [5, 6]
LAT2	SLC7A8	Gly, Ala, Ser, Thr, Asn, Gln, Met, Leu, Ile, Val, Phe, Tyr, Trp, His	Jejunum, ileum, kidney, placenta, brain, liver, skeletal muscle, prostate, ovaries, fetal liver, testis and heart [7-9]
LAT3	SLC43A1	Met, Leu, Ile, Val, Phe	Pancreas, skin, muscle, liver, kidney podocytes, prostate [10, 20, 23, 25]
LAT4	SLC43A2	Met, Leu, Ile, Val, Phe	Placenta, kidney, peripheral blood leukocytes [11]

methionine [10, 11]. Similarly, LAT1 and LAT2 can transport these same neutral amino acids, including additional amino acids such as tyrosine, histidine and tryptophan [5, 7-9] (**Table 1**).

In 1998, two independent groups cloned LAT1 from cancer cells [5, 6]. LAT1 has 507 amino acids with a molecular weight of 55 kDa. LAT1 mRNA is strongly expressed in brain, spleen, placenta, testis and colon (**Table 1**) [5]. LAT2 was subsequently cloned due to its homology with LAT1 [7-9]. Human LAT2 and LAT1 shows an amino acid sequence identity of 50%. LAT2 has 535 amino acids with a molecular weight of 58 kDa [7]. LAT2 transcripts are strongly expressed in jejunum, ileum, kidney, placenta, brain, and also detected in liver, skeletal muscle, prostate, ovaries and heart [7-9, 12]. Both LAT1 and LAT2 transport capacity is independent of sodium or chloride. However, binding of 4F2hc at cysteine 163 (LAT1) is required for the normal function and membrane localization of LAT1 and LAT2 [5, 7, 8]. Leucine transport by LAT1 is also dependent on L-glutamine, which is delivered by other amino acid transporters including ASCT2 (SLC1A5) [13-16].

LAT3 transcript was originally cloned from prostate cancer and named prostate cancer overexpressed gene 1 (POV1) [17, 18]. Later, POV1 was identified as a transporter and named LAT3 by expression cloning from the hepatocarcinoma-derived cell line FLC [10]. Mouse LAT3 contains 564 amino acids with a molecular weight of 62.6 kDa [19], while human LAT3 has 559 amino acids. A long intracellular loop predicted to exist between transmembrane domains 6 and 7, contains putative protein kinase C-dependent phosphorylation sites and a tyrosine phosphorylation site [19]. Human LAT4 exhibits 57% identity to human LAT3 [11]. LAT3 and LAT4 have a broad expression pattern in human tissues. Northern blot analysis showed that LAT3 mRNA is expressed in pancreas, liver,

skeletal muscle and fetal liver at a high levels [10, 19] (**Table 1**). Human LAT4 mRNA is strongly expressed in placenta, kidney and peripheral blood leukocytes in human tissue. Mouse LAT4 is detected in intestine, kidney, brain, white adipose tissue, testis and heart, but not in liver [11] (**Table 1**). However, the physiologic functions of LAT3/LAT4 in these organs are still not fully understood. Although the expression of LAT3 in kidney is low, strong expression is detected at the apical plasma membrane of podocyte foot processes. LAT3 is important for the development and maintenance of podocyte function and structure [20, 21]. A recent study also showed that red blood cell development requires LAT3 expression for hemoglobin production. In LAT4 knockout mice, newborn mice are smaller than wild type mice [22], suggesting that LAT4 is important for growth and development.

LAT family expression and function in cancer

While the LAT family clearly play important roles in development and function of normal tissues, they are frequently increased in cancer samples. To effectively review this area, and highlight the important role of LAT family members in cancer, we have summarized publications across multiple cancers (**Table 2**). In addition, we have performed new analyses of Oncomine microarray/sequencing datasets to further highlight which cancers show a significant increase in LAT expression compared to normal tissue ($P < 0.05$, Fold change > 2 ; **Table 2**). These data clearly show that LAT1 is most commonly upregulated in multiple cancers, and accordingly LAT1 has been the most studied of the LAT family members. While the Oncomine data suggest that LAT2 is upregulated in 9 different cancer types, there are few studies that have validated its role in cancer cell growth. LAT3 and LAT4 show a more restricted expression pattern in 5 or 4 different cancer types

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Table 2. LAT expression in tumors

Cancer	LAT1 (SLC7A5)		LAT2 (SLC7A8)		LAT3 (SLC43A1)		LAT4 (SLC43A2)		4F2hc (SLC3A2)	
	REF	ONC	REF	ONC	REF	ONC	REF	ONC	REF	ONC
Bladder	[92-94]	2/12								
Brain/CNS	[30, 42]									3/35
Breast	[34, 77, 95-97]	15/52		10/50				1/45	[34]	1/53
Cervical	[98]									
Cholangiocarcinoma	[66]									
Colorectal	[34]	23/34		4/34		2/34	[99]		[34]	6/37
Esophageal	[100]					3/9		1/6		1/9
Gastric	[36]	1/23								
Head and Neck	[34, 42, 99, 101]	7/32		2/32			[99]		[34]	3/32
Kidney		1/24				1/20		1/10		1/24
Leukemia	[87, 102]	4/28		4/27	[103]					2/31
Liver	[102, 104-107]				[108]				[33]	
Lung	[26, 35, 37, 67]	14/31							[37, 67]	
Lymphoma		8/30		1/29				2/21		
Melanoma	[15, 109]	3/7		1/7						1/7
Myeloma	[110-112]	1/8	[110]							
Ovarian	[113, 114]	3/14								
Pancreatic	[32, 115, 116]									
Pleural mesothelioma	[28]									
Prostate	[24, 25, 39]			1/20	[17, 18, 24, 25]	4/20				1/21
Sarcoma	[34, 42]	1/20							[34]	
Tongue cancer	[31]								[31]	
Thymic carcinomas	[29]									
Urinary tract	[92, 117]									
Uterine leiomyoma	[118]		[79]						[79]	
Other (seminoma)						3/3				
Other (skin)		4/4		4/4						1/4
Other (parathyroid)				3/3						

Expression of LAT family members in a variety of cancers was assessed using Pubmed to find published references (REF) and Oncomine (ONC) to detect significant upregulation ($P < 0.05$, fold change > 2) for each transporter. Oncomine numbers represent Datasets with Significant Upregulation/Total Number of Datasets.

respectively, with multiple publications on the critical role of LAT3 in prostate cancer [17, 18, 23-25]. **Table 2** shows the potential utility of targeting the LAT family in a variety of cancers, as well as highlighting a number of cancers that require further analysis of LAT family expression and function.

Immunohistochemical analysis in patient cohorts have shown that LAT1 is overexpressed in cancer and its expression correlates with cell proliferation and cancer progression. LAT1 is highly expressed in 52% of the large cell neuroendocrine carcinomas of the lung [26, 27], 50% of pleural mesothelioma [28], 75% of thymic carcinomas [29], 25% of high-grade gliomas [30], 61% of tongue cancer [31], 53% of pancreatic cancer [32] and 61% in hepatocellular carcinoma [33]. In these studies, a significant correlation was found between LAT1 expression and proliferation marker Ki-67, suggesting that

LAT1 is important for proliferation in cancer cells [27, 29, 31-37].

LAT1 has also been used as biomarker for malignant cancer. Using Kaplan-Meier analysis of patients, low LAT1 expression patients showed a significant longer overall survival compared to high LAT1 expression patients, indicating that LAT1 could be a prognostic marker for predicting poor outcome after surgery [32, 33, 38]. In prostate cancer, LAT1 expression is correlated with prognosis in poor survival patients [39]. In breast cancer, LAT1 (SLC7A5) is also part of the 5 gene Mammostrat™ immunohistochemistry panel, where high expression is used to predict recurrence in ER+ breast cancer during endocrine therapy [40, 41].

Studies determining the function of LAT1 in cancer have utilized a well characterized LAT family inhibitor, BCH (2-aminobicyclo-(2,2,1)-

heptane-2-carboxylic acid). BCH can inhibit all members of LAT family at a concentration above 10 mM. BCH treatment decreases leucine transport and suppresses mTORC1 signaling [13, 24]. Expression of cell cycle regulators is altered, such as up-regulation of p21 in glioma cells [30] and p27 in prostate cancer cells [24], down-regulation of CDK1, CDC20 and E2F1 [25]. Therefore, cell proliferation and DNA synthesis are suppressed.

When LAT1 is blocked by BCH, several studies also showed that apoptosis was enhanced in glioma cells [30], oral epidermoid carcinoma cells, osteogenic sarcoma cells [42]. Cleaved caspase 3 and cleaved PARP levels are increased after BCH treatment [30]. However, no apoptosis was observed using either BCH or knockdown LAT1 or LAT3 in prostate cancer cell lines [24]. This suggests that LAT-related cell apoptosis may be dependent on the cell type.

LATs and mTORC1 signaling

Perhaps the most important role of LATs is to transport neutral amino acids for protein synthesis. One of the major LAT substrates, leucine, is not only an essential amino acid, but also a regulator of mTORC1 (mammalian target of rapamycin complex 1) signaling. mTOR is a member of the phosphoinositide-3-kinase related kinase (PIKK) family that possess catalytic activity as a protein serine-threonine kinase. mTOR is present within the cell bound in two major complexes, mTORC1 and mTORC2. mTORC1 is formed by mTOR complexed with mLST8, RAPTOR, PRAS40 and DEPTOR, activating S6 kinase while repressing eIF-4E-binding protein (4E-BP1), thereby regulating protein translation [43, 44]. mTORC2 is formed by mTOR complexed with mLST8, RICTOR and mSin1, which can phosphorylate and activate Akt at Ser473 [45-47].

Both PI3K/Akt signaling and amino acids (especially leucine, arginine and glutamine) are required to activate mTORC1 signaling [13, 44, 48]. While the PI3K/Akt signaling pathway is well understood, the exact mechanism by which amino acids are sensed and activate mTORC1 remains unclear. Activated Akt phosphorylates TSC2 leading to the suppression of TSC2 activity. The inactivated TSC2 dissociates from the surface of lysosomes, releasing Rheb, a small

GTPase, to activate mTORC1 on the lysosomal surface [49-53]. Recent studies have suggested that the intracellular level of leucine can be detected by a leucyl-tRNA synthetase (LRS), which can then catalyze the ATP-dependent ligation of L-leucine to leucyl-tRNA during protein synthesis [54, 55]. In the leucine rich environment, LRS with leucine may then interact and activate the Rag GTPase complex. Rag proteins are Ras-related small GTP-binding proteins that include four mammalian members, RagA, RagB, RagC and RagD. They form heterodimers consisting of RagA or RagB with RagC or RagD [56, 57]. Recent work showed that Rag GTPases are only essential for leucine- or arginine-activated mTORC1 signaling [58]. Glutamine-activated mTORC1 activation depends on adenosine diphosphate ribosylation factor-1 GTPase (Arf1) [58]. LRS may also bind to RAPTOR to activate mTORC1 signaling on the surface of lysosome [54, 55]. While the mechanism of leucine sensing remains unclear, low levels of intracellular amino acids lead to Rag heterodimer binding and recruitment of the TSC complex to the lysosome, thereby inhibiting Rheb and mTORC1 signaling [52, 53].

Another study has suggested that glutaminolysis and α -ketoglutarate are involved in glutamine and leucine sensing to activate mTORC1 signaling [48]. The enzyme glutaminase releases the amide group of glutamine to form glutamate. Leucine can directly bind and activate glutamate dehydrogenase, which subsequently converts glutamate to α -ketoglutarate (α -KG) [59]. α -KG is sufficient to stimulate recruitment of mTORC1 to the lysosome by activating RagB. The activated LRS or α -KG stimulates the transition of RagA/RagB GDP-RagC/RagD GTP to RagA/RagB GTP-RagC/RagD GDP [48].

Lysosomal membrane proteins, vacuolar adenosine triphosphatase (v-ATPase) and SLC36A1, have been shown to interact with Rag GTPases, and may be necessary for mTORC1 activation by amino acids [60]. Lysosomal membrane amino acid transporter SLC38A9 was recently shown to interact with Regulator/LAMTOR complex, four RAG GTPases and VAOD1 of the v-ATPase [61, 62]. Purified SLC38A9 directly interacts with arginine making it a potential amino acid sensor for mTORC1 signaling [62]. When arginine binds to SLC38A9 substrate-binding site, SLC38A9 may undergo a

conformational change which affects its interactors, such as v-ATPase, RAG GTPases and Ragulator.

Amino acid-activated signaling is also tightly regulated by proteins which interact with Rag GTPase or Ragulator. For example, folliculin and its interacting partner FNIP1/2 form a complex to activate RagC/D as a GTPase activating protein (GAP) [63]. Sestrins also bind to the heterodimeric Rag complexes and negatively regulate the activity of Rag complexes [64]. GATOR complexes interact with the Rag GTPase complex to negatively regulate leucine signaling. GATOR is composed of two subcomplexes named GATOR1 (DEPDC5, Npr12 and Npr13) and GATOR2 (Mios, WDR24, WDR59, Seh1L and Sec13) [65]. GATOR1 has GTPase-activating protein activity for RagA and RagB. GATOR1 components, such as NPRL2 and DEPDC5, contain deletion or mutation in multiple cancer cell lines, leading to hyperactivation of mTORC1 signaling and insensitivity to amino acid deprivation [65].

The role of LAT in metastasis

Several studies have suggested that LAT1 expression also correlates with metastasis. These data are across a range of cancers, including colon, breast, prostate, head and neck, lung, genital as well as soft-tissue sarcomas, all showing that LAT1 expression is significantly higher in the metastatic sites than in the primary sites [24, 27, 34]. LAT1 transport function may be critical in providing nutrients for metastatic cancer cells, as BCH treatment or knock-down of LAT1 expression by shRNA has been shown to decrease cell migration and invasion in cholangiocarcinoma cells *in vitro* [66]. This was also seen in prostate cancer, where LAT1 or LAT3 shRNA significantly inhibited metastasis *in vivo*, however this was confounded by a significant reduction in tumor size [25]. These effects were likely due to the transport function of the LATs, as microarray analysis showed significant downregulation of genes involved in cell cycle regulation, including CDK1, CDC20 and transcription factors E2F1 and E2F2 [25]. These same genes are highly expressed in metastatic prostate cancer, suggesting inhibition of LAT transporters may suppress metastatic prostate cancer proliferation [25].

LAT1 expression closely correlates with 4F2hc expression in human cancers, and has been

shown to have a critical role in the metastatic process of diverse human neoplasms [31, 33, 34, 37, 67]. Apart from the transport activity of LAT1, regulation of metastasis may be mediated through integrin signaling, since 4F2hc has been shown to interact with β 1-integrin and regulate β 1-integrin affinity [68] and expression [69]. It was shown that the amino acid transporter function of LAT1 is not required for this effect of 4F2hc on integrin function. Further studies showed that 4F2hc interacts with the cytoplasmic domain of β 1A integrin to reverse the suppression of integrin activation [70, 71]. The 4F2hc transmembrane domain also binds to integrin $\alpha_v\beta_3$ [72], suggesting that perhaps LAT1/4F2hc may be important in interactions with the metastatic niche. It is also possible that 4F2hc binding to integrins allows the cell to use LAT1 to “probe” the environment for nutrients.

Induction of LAT expression

Several factors, such as hormone stimulation, Myc/Rb oncogenic transcription, nutrient starvation and environmental stress have been shown to induce LAT expression, thereby providing the neutral amino acids required for cancer cell growth, survival and progression. The diverse nature of these stimuli highlight the critical requirement for nutrient supply to the cancer cell. For example, in prostate cancer LAT3 expression is driven by androgen receptor (AR) signaling, leading to high expression in primary prostate cancer [24, 25]. This is driven by direct AR transcription, confirmed by chromatin immunoprecipitation (ChIP) and promoter luciferase assays [24]. However, during anti-androgen therapies, LAT3 levels decrease, causing nutrient starvation. The reduction of amino acid levels activate the ATF4 nutrient stress signaling pathway through uncharged tRNAs in the cytoplasm. The general control non-derepressible 2 (GCN2) kinase binds to uncharged tRNAs, leading to phosphorylation of the eukaryotic translation initiation factor 2 α (eIF2 α) on Serine 51 [73]. Activated eIF2 α initiates the rapid translation of ATF4, which translocates to the nucleus, driving an adaptive response that includes transcription of amino acid transporters. The ATF4 knockout mice showed decreased expression of a number of amino acid transporters, with recent ChIP and promoter luciferase assays used to confirm ATF4 binding to amino acid response elements (AAREs) in LAT1,

4F2hc, ASCT2, ASCT1 and xCT [24, 25, 74-76]. Therefore, the ATF4 adaptive response to anti-androgen therapies restores intracellular amino acid levels through transporters including LAT1, allowing further protein translation and cell growth.

Other LAT family members also appear to be regulated by hormone receptors. In breast cancer cells, LAT1 expression is increased in response to estradiol which activates estrogen receptor (ER) [77]. LAT2 has been shown to increase expression in the presence of dihydrotestosterone (DHT), which activates AR [78]. Progesterone also activates ER to induce LAT2 mRNA level increase in primary human uterine leiomyoma smooth muscle (LSM) cells and tissues from premenopausal women [79]. These hormone driven responses are likely important drivers of proliferation during development, and their reactivation during oncogenic transformation is critical for subsequent cancer cell growth.

In addition to nutrient deprivation, oxygen-tension may also contribute to LAT1 expression. HIF2 α binds to the SLC7A5 proximal promoter, increasing expression of LAT1 and activating mTORC1 signaling in renal carcinoma cells, as well as in normal liver and lung tissues [80]. These studies indicate that LAT1 is a key environmental sensor to regulate mTORC1 signaling.

The development of a LAT1 knockout mouse has provided further clues to regulation of LAT1 expression. Knockout T cells do not respond to antigen stimulation, thereby preventing T cell clonal expansion or effector cell differentiation [81]. Wild type T cells, however, respond to antigen or PKC activation (phorbol ester) by upregulating expression of LAT1 [81, 82]. Conditional knockdown of LAT1 in activated T cells suppressed c-Myc translation but not transcription. This is an mTORC1 independent process, as rapamycin did not prevent TCR-mediated elevation of c-Myc expression [81]. Since c-Myc has a short half-life (~15 min) [83], sustained expression is required for the maintenance of c-Myc protein. Therefore, LAT1 is critical in sustaining c-Myc levels. c-Myc is also important for metabolic processes including glycolytic switch and regulation of glutaminolysis, as well as for cell proliferation [84].

LAT family inhibitors

Amino acids such as leucine (**Figure 1A**) contain amine and carboxylic acid groups, as well as side chains, which are recognized by substrate binding sites of transporters. Generation of LAT inhibitors has therefore focused primarily on compounds that mimic LAT substrates, and can therefore compete for amino acid binding. However, this strategy has in general resulted in high effective concentrations of inhibitors, as is seen with the leucine analogue BCH (**Figure 1B**; ~10 mM). Furthermore, since the LAT family shares the majority of substrates, BCH targets all members of LAT family, which is undesirable for clinical development. Recently, several new inhibitors were developed to more potently target LAT1 and/or LAT3 (**Figure 1**).

JPH203 (also called KYT-0353; (S)-2-amino-3-(4-((5-amino-2-phenylbenzo[d]oxazol-7-yl)methoxy)-3,5-dichlorophenyl) propanoic acid; **Figure 1C**) is a novel tyrosine analog, which selectively inhibits LAT1 transport activity [85]. JPH203 showed a dramatic inhibition of leucine uptake (IC_{50} =0.06 μ M) and cell growth (IC_{50} =4.1 μ M) in human colon cancer cells (HT-29) [85], human oral cancer cells (YD-38) [86] and leukemic cells [87]. In nude mice, significant inhibitory effects on tumor growth were observed after 7 days treatment with 12.5 mg/kg of this compound [85]. JPH203 suppressed activation of mTORC1 and Akt, decreased expression of c-myc in T-ALL (T-cell acute lymphoblastic leukemia) and T-LL (T-cell lymphoblastic lymphoma) [87]. JPH203 induced ATF4 translation initiation and an unfolded protein response mediated by CHOP (the C/EBP homologous protein), followed by cell death [87]. Importantly, JPH203 had no toxic effect on normal murine thymocytes, lymphocytes, erythrocytes, platelets, bone marrow mature cells, stem cells and early progenitors. Preclinical data from four patients showed no apoptotic effects of JPH203 on normal peripheral blood lymphocytes cells or cord blood mononuclear cells *ex vivo* [87]. Therefore, therapies targeting LAT1 in T-ALL is an attractive strategy that appears to have little side effects in normal cells. However, JPH203 biotransformation via phase II metabolism produces *N*-acetyl-JPH203 (NAc-JPH203), which may accumulate in the liver and kidney, and will need to be considered for future pre-clinical testing [88, 89]. Combined with chemotherapeutic drugs, such as rapamycin, dexametha-

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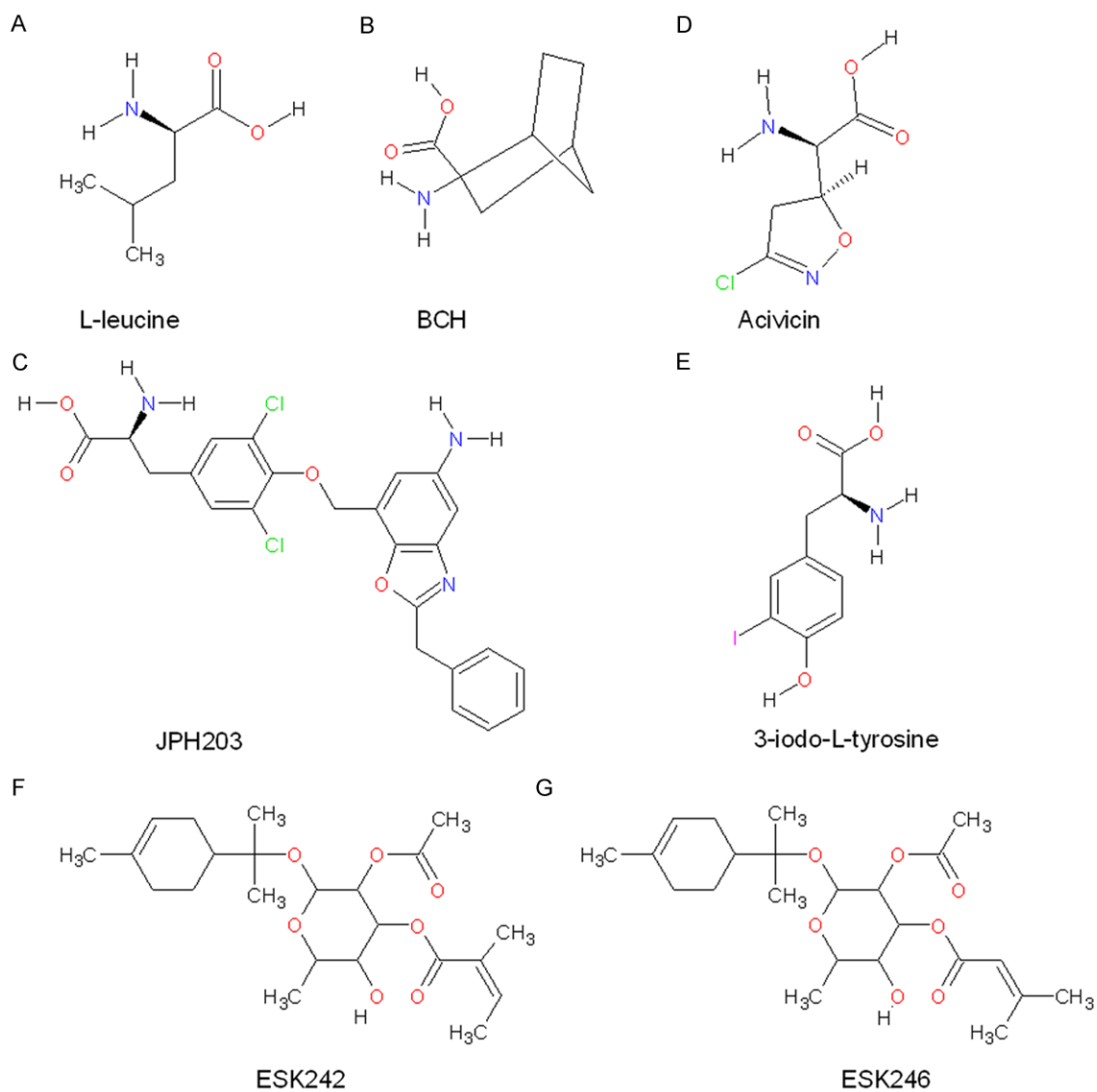


Figure 1. Structure of L-leucine and LAT family inhibitors. A. L-leucine; B. BCH; C. JPH203; D. Acivicin; E. 3-iodo-L-tyrosine; F. ESK242; G. ESK246.

son, doxorubicin, Velcade and L-asparaginase, JPH203 showed synergistic effects, decreasing cell survival. The highest synergy was observed in combination with rapamycin [87]. Therefore, JPH203 could be an adjuvant therapeutic strategy to treat hematopoietic malignancies. However, the specificity of this compound was only examined for LAT1 and LAT2 in human colon cells HT-29 and mouse renal proximal tubule cells S2. It remains to be determined whether JPH203 can also inhibit LAT3 or LAT4 [85].

Recent structural analysis of membrane proteins have led to a number of publications modelling transporter structures [90]. The LAT1

structure was modelled based on the crystal structure of the arginine/agmatine transporter AdiC from *E. coli* in the outward-facing conformation. Virtual screening was then performed using DOCK3.5.54, to filter compounds from KEGG (Kyoto Encyclopedia of Genes and Genomes) DRUG and KEGG LIGAND COMPOUND database against the LAT1 model. The top-scoring compounds were validated *in vitro*, discovering two novel LAT1 ligands, acivicin (**Figure 1D**) and 3-iodo-L-tyrosine (**Figure 1E**) [90]. The IC_{50} of 3,5-diiodo-L-tyrosine (similar to 3-iodo-L-tyrosine) and acivicin is 7.9 μ M and 340 μ M, respectively. Both 3-iodo-L-tyrosine

and acivicin were shown to suppress GBM cancer proliferation [90].

Other than these *in silico* screening approaches, conventional high throughput screening strategies have also led to the discovery of novel LAT inhibitors. Using a natural compounds library (Nature Bank), two new monoterpene glycosides ESK242 (Figure 1F) and ESK246 (Figure 1G) were isolated, which inhibit LATs with a low IC_{50} [91]. These compounds were screened from more than 4500 fractions of biota samples, and specificity was determined using *Xenopus* oocytes expressing LAT1/4F2hc, LAT2/4F2hc, LAT3 or LAT4. ESK242 was found to inhibit LAT1 and LAT3 mediated leucine uptake, while ESK246 preferentially inhibits LAT3. So far, ESK246 is the first reported LAT3 specific inhibitor, which may be used to study the physiological function of LAT3 in the future. Comparison of these new inhibitors with BCH (IC_{50} =4060 μ M in LNCaP prostate cancer cells), showed they are ~2 orders of magnitude more effective at inhibiting leucine uptake, with ESK246 and ESK242 having IC_{50} values of 8.1 μ M and 29.6 μ M respectively. ESK246 was also shown to significantly suppress LNCaP cell proliferation and cell cycle regulator expression at 50 μ M [91]. While these compounds do not contain distinct amine and carboxylic acid groups, ESK242 has a side chain similar to isoleucine and ESK246 similar to leucine. Further studies are required to determine if these side chains mediate binding to LAT1/3. These data would assist in the development of more drug-like inhibitors in the absence of LAT family structural information.

Conclusion

Over recent years, there has been substantial progress made on both the understanding of LAT family regulation and function in cancer, as well as the development of new inhibitors for this family of transporters. However, despite these advances, analysis of Oncomine data clearly shows that there are many more cancers where LAT family proteins may play an important role. Furthermore, a number of questions remain to be answered: 1) Since LAT1 and ASCT2 cooperate to regulate leucine transport, is it possible to target both transporters to more effectively suppress tumor growth? 2) Are there any proteins (other than 4F2hc) that directly interact with LATs to regulate amino

acid transport? 3) Are there post-translational modifications, such as phosphorylation, that can regulate the LAT family? The answer to these questions may provide additional avenues for therapeutic strategies modulating LAT functions. In conclusion, while increased expression of the L-type amino acid transporter family is important for cancer growth and progression, further development of current inhibitors are required in order to reach their full therapeutic potential.

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No potential conflicts of interest were disclosed.

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