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PD-L1 Domain Organization, Signaling Motifs and Interactors in Cancer Immunotherapy

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Article

PD-L1 Domain Organization, Signaling Motifs and Interactors in Cancer Immunotherapy

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Simple Summary: Immune checkpoint blockade has transformed clinical oncology. However, much is unknown of the cellular and immunological mechanisms behind its success. In recent years, extensive research on the mechanisms of action of programmed death 1 ligand 1 (PD-L1) has uncovered the multiple facets of this immune checkpoint molecule on the biology of the cell. Here we review the current knowledge on PD-L1 structure, signaling motifs and interactors that provide a mechanistic insight into the functions of this key immune checkpoint.

Abstract: Programmed cell death 1 ligand-1 (PD-L1)/ programmed cell death-1 (PD-1) blockade immunotherapies have revolutionized oncology. These therapies consist of blocking the binding of PD-1 expressed in T cells to its ligand PD-L1 expressed by cancer cells using monoclonal antibodies administered systemically. When localized on the surface of cancer cells, PD-L1 delivers inhibitory signals to the T cell through PD-1, inactivating T cell effector functions. In addition to this mechanism of action, PD-L1 also delivers intracellular signals to the cancer cell, in a process termed “reverse signaling” or “intrinsic signaling”. This intrinsic signal transduction takes place both in the presence and in the absence of PD-1 binding, and contributes to the survival of cancer cells in response to pro-apoptotic stimuli. PD-L1 intrinsic signaling functions are much wider than originally suspected, and include protection from apoptosis, enhancement of cancer cell proliferation, regulating DNA damage responses and even acting as a co-transcriptional transactivator. The mechanisms governing these functions are currently under intensive research. In this review we provide a perspective on PD-L1 research from distinct points of view, but especially focusing on its structure, signaling motifs and interactors.

Keywords: cancer immunotherapy; B7-H1; immune checkpoint blockade; signal transduction pathways

1. Introduction

Not so long ago, cancer immunotherapies were not considered serious therapeutic options by most oncologists or researchers in oncology. Development of antineoplastic treatments was largely devoted to engineering small molecules and kinase inhibitors targeting cancer cell growth and survival pathways [1–4]. Cancer cells were the targets, and pharmaceutical companies invested significantly into research in cancer cell apoptosis, tumor angiogenesis and processes focusing on the cancer cell. But not centered in the patient's immune system unless in collaboration with academic groups. These strategies were strongly incentivized by the emergence of targeted therapies with small molecule inhibitors specifically targeting mutated variants of well-known oncogenes in cancer cells [5,6]. It could be safely said that immunotherapies were not on their radar.

Nevertheless, it has to be acknowledged that certain immunotherapies were already being given to some patients with limited success, those who did not respond to the standard care of treatments. For example, high-dose interleukin (IL)-2 and interferon (IFNs) therapies [7–11], T cell transfer of tumor-infiltrating T cell (TIL) clones expanded *ex vivo*, or even autologous T cells genetically modified to express recombinant T cell receptors (TCR) specific for well-known tumor-associated antigens [12–15].

Everything started to change when an anti-cytotoxic T-lymphocyte associated protein (CTLA)-4 antibody produced significant therapeutic efficacies in metastatic melanoma patients [16,17]. But the revolution came in 2012 after the publication of clinical trials evaluating anti-PD-1 and anti-PD-L1 in cancer patients [18,19]. Programmed cell death-1 (PD-1, CD279) was discovered in 1992 in apoptotic T-cells by the research team lead by Tasuku Honjo [20]. A few years later, programmed cell death-1 ligand-1 (PD-L1) was discovered by the team led by Lieping Chen and was named B7 homologue-1 (B7-H1, CD274), a novel member of the B7 family of immunomodulators [21]. PD-L1 turned out to be a negative regulator of immune responses [22–24]. Shortly after its discovery, B7-H1 was identified as the canonical ligand of PD-1 and renamed as PD-L1 [24,25]. Indeed, the PD-1/PD-L1 signaling axis was found to regulate inflammation and systemic tolerance [26–32]. But most importantly, this signaling axis was critical for the evasion of cancer cells from the immune system [23,33–35]. Disruption of PD-1/PD-L1 interactions through several experimental approaches including blockade with monoclonal antibodies targeting either PD-1 or PD-L1, led to an enhancement of anti-cancer immune responses in several tumor models [36–40].

Our team started to work on PD-1/PD-L1 signaling in 2005, and at the time these molecules were just two of many novel potential regulators of anti-cancer immune responses. Indeed, in agreement with the studies from our contemporary investigators, we found that PD-L1 silencing in antigen-presenting dendritic cells (DC) enhanced anti-tumor immunity specially in combination with DC activators [31,41]. In 2012 there was a turning point that took everybody by surprise. The oncology field was shaken after the publication of the first clinical trials with PD-1/PD-L1 blocking antibodies [18,19]. The results were truly unprecedented, with good tolerability and significant therapeutic responses in a wide variety of cancers, surpassing the therapeutic activities already observed with ipilimumab, a clinically approved anti-CTLA-4 antibody [17]. These results confirmed the therapeutic viability of treatments that instead of targeting the cancer cell, were directed towards the immune cell compartment. Within a couple of years, medical oncologists had to be retrained as immunologists, and pharmaceutical companies re-directed investments towards the development of antibodies targeting the so-called “immune checkpoints” [42]. Immunooncology as we understand it today had been born.

2. Programmed Death 1 Ligand 1, PD-L1

PD-L1 is a transmembrane molecule belonging to the B7 family of co-stimulatory molecules. As such, its domain organization is typical to that of the B7 family [21] (**Figure 1**). PD-L1 is a type I transmembrane surface glycoprotein expressed constitutively by most cells of the myeloid lineage, although its expression can be induced in many cell types following responses to inflammatory stimuli. In cancer cells, PD-L1 expression can also be driven by some oncogenes. PD-L1 presents an immunoglobulin (Ig) variable (V)-like extracellular region, which contains complementary determining-like (CDR) regions constituting the PD-1 binding domain. This interaction is structurally similar to the binding of antigens to antibodies and to the TCR [43,44]. The hydrophobic transmembrane domain is followed by an intracellular region which shows poor sequence similarity to the domains from other B7 counterparts [45]. There is recent evidence suggesting that PD-L1 forms dimers and tetramers in the cell membrane, through association by residues in the transmembrane and intracellular domains [46]. Most importantly, its intracellular domain is critical for reverse signaling in different cell types including cancer cells, and for regulating the molecular stability of the molecule.

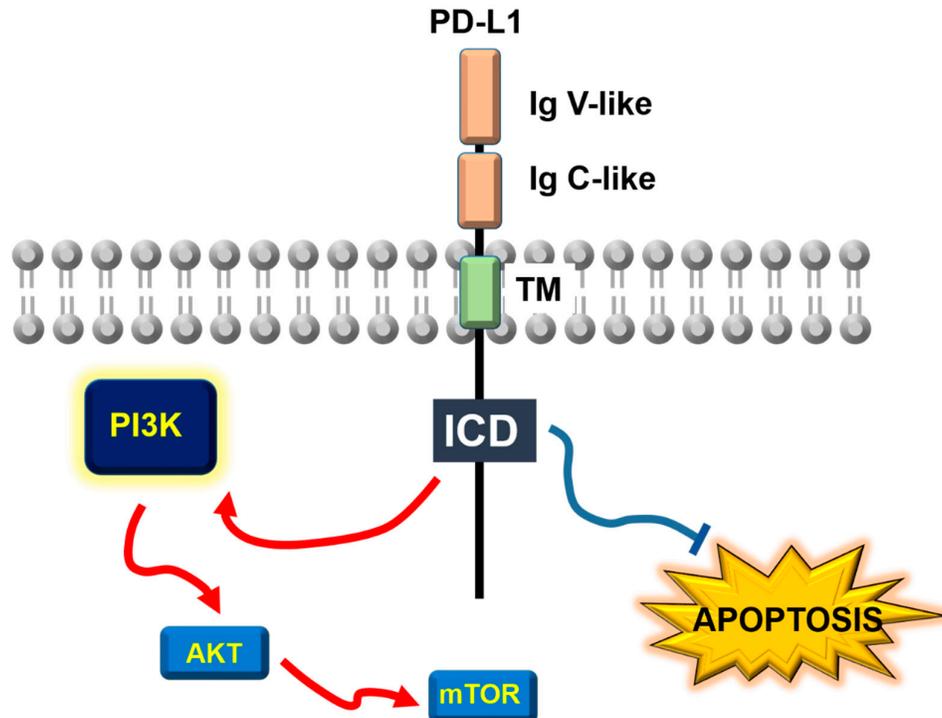


Figure 1. Overall structure and signal transduction functions by PD-L1. Schematic representation of the molecular organization of PD-L1 in the cell membrane. The reverse signaling activating the PI3K/AKT/mTOR pathway and counteracting apoptosis are indicated. Blue line, inhibitory relationship between PD-L1 reverse signaling and induction of apoptotic pathways. Red arrows, activating relationships between the indicated proteins. Ig V and Ig C, indicate immunoglobulin-like variable and conserved sequence motifs. TM, transmembrane domain; ICD, intracellular cytoplasmic domain.

PD-L1 is expressed constitutively in myeloid cells such as DCs, myeloid-derived suppressor cells (MDSCs) and macrophages [29,31,47–51]. Additionally, PD-L1 expression is upregulated in many cell types of different ontologies such as cancer cells, endothelial cells and T cells [27,52–54]. PD-L1 expression can be induced following stimulation with pro-inflammatory cytokines such as interferon gamma (IFN γ), IFN alpha (IFN α), tumor necrosis factor alpha (TNF α), IL-1 or IL-6 through direct or indirect pathways [55–59]. In cancer cells, transcriptional regulation of PD-L1 expression can differ depending on the tumor type or mutational profile in tumor cells [60–62]. In some cases, cancer cells may express PD-L1 constitutively due to the oncogenic activation of signaling pathways such as those controlled by rat sarcoma (RAS), epidermal growth factor receptor (EGFR), mitogen activated protein kinases (MAPK) among others [56,63–68]. PD-L1 expression is also regulated by other mechanisms which include control of its stability and membrane trafficking through ubiquitination, glycosylation, other protein modifications and epigenetic mechanisms [67,69–78].

3. PD-L1 as an Anti-Apoptotic Receptor and AKT/mTOR Regulator

Just before 2012, most of the researchers in PD-1/PD-L1 signaling were focusing on the effects of PD-L1 binding to PD-1, and in the signaling pathways regulated by PD-1 that inhibited T-cells. Thus, among these where the pathways associated to the binding of Src homology region 2 domain-containing phosphatases (SHP) 1 and 2 to ITIM (immunoreceptor tyrosine-based inhibitory) and ITSM (immunoreceptor tyrosine-based switch) motifs in the intracellular domain of PD-1 [79–86], and the up-regulation of E3 ubiquitin ligases of the Casitas B cell lymphoma (CBL) family [31,87–89]. At this point, nobody was paying too much attention to a potential reverse signaling by PD-L1 on the

cancer cell itself, apart from a few studies pioneered by Lieping Chen's team. For several years, the protective role of PD-L1 was restricted to its action as a molecular brake to the effector activities of cancer-specific T cells through its binding with PD-1. In this model, PD-1 signaling into the T-cell was the main protective mechanism of tumors against the T cell attack. In 2004, a screening for T-cell inhibitory molecules expressed by melanoma B16-F10 cancer cells treated with IFN γ uncovered PD-L1 as a protective candidate. Antibody blockade of PD-L1/PD-1 interactions, or absence of PD-1 expression in T cells augmented tumor rejection, suggesting that PD-L1 represented a molecular shield protecting cancer cells from T cell cytotoxicity [34–36]. Surprisingly, in 2008, the Lieping Chen's group provided a molecular protection mechanism for cancer cells driven by PD-L1 independently on its PD-1-engaging activities. In this model, PD-L1 expression conferred cancer cells with resistance to different apoptotic stimuli by transmitting intracellular signals to cancer cells [90] (**Figure 1**). The authors of the study demonstrated that P815 mastocytoma and renal adenocarcinoma Renca cell lines required PD-L1 expression to resist T cell cytotoxicity. As expected, this resistance was abrogated by PD-L1 blocking antibodies. Then, the authors used T cells expressing a PD-1 molecule with its intracellular region replaced by GFP, rendering PD-1 signal-null. In these conditions, cancer cells remained resistant to the T cell attack as long as they expressed PD-L1. This protection was lost when cancer cells expressed a PD-L1 molecule with its intracellular domain replaced by GFP. This study concluded that PD-L1 intracellular signaling conferred resistance to cancer cells against pro-apoptotic stimuli, including first apoptosis signal receptor (Fas)-Fas ligand (FasL) interactions among others [90]. However, when the authors examined major anti-apoptotic and apoptotic pathways, they did not find significant differences between controls versus PD-L1-engaged cancer cells. This study concluded that PD-L1 may be providing an early signal to inhibit apoptotic pathways. Interestingly, the potential signal transduction properties of PD-L1 were described in other experimental contexts. One of such was metabolic competition between cancer cells and T cells. This mechanism is utilized by cancer cells by depleting glucose in the tumor microenvironment. Glucose depletion then interferes with T cell effector activities [91]. A study conducted by Palmer et al. in 2015 demonstrated that treatments with antibodies targeting immune checkpoints CTLA-4, PD-1 and PD-L1 restored glucose concentrations within the tumor microenvironment [92]. These results suggested that immune checkpoint molecules regulated glucose metabolism in mouse sarcoma cells. The authors continued evaluating the effects of PD-L1 blockade or its silencing over glucose metabolism, and demonstrated that PD-L1 blockade in the absence of T cells inhibited the AKR mouse T cell lymphoma (AKT, protein kinase B) / mammalian target of rapamycin (mTOR) pathway (**Figure 1**). This inhibition led to a reduction in transcription of glycolytic genes, decreasing glucose consumption without affecting cancer cell proliferation or tumor growth. This direct effect of PD-L1 expression over glucose metabolism was later confirmed in 2019 by Kim et al. in lung cancer cell lines [93]. Regulation of mTOR and autophagy pathways by PD-L1 expression in the absence of T cells was also demonstrated by Clark et al. in 2016 in two cancer models: mouse B16 melanoma and ovarian ID8 cells [94]. However in this case, reduction of PD-L1 expression inhibited proliferation of cancer cells, suggesting that these effects might be cell type-specific, as this was also observed in U87 glioblastoma cells [95]. Moreover, the same authors concluded in a follow-up study that PD-L1 signaling played a role in tumor initiating cells (TIC) and their resistance to pro-apoptotic treatments. PD-L1 silencing reduced TIC numbers and their associated functions. But unlike the findings by Chen's team and our own results [90,96], PD-L1 expression in TIC sensitized these cells to IFN γ and rapamycin [97].

A wide range of later studies have confirmed the activating role of PD-L1 intrinsic signaling over phosphatidylinositol 3-kinase (PI3K)-AKT-mTOR pathways, in most instances associated to promoting cancer cell survival and resistance to apoptosis [98–101] (**Figure 1**).

4. PD-L1 Non-Classical Signaling Motifs and Resistance to Interferons in Immunotherapy

In 2017, the research team led by Antoni Ribas published a ground-breaking study demonstrating a mechanism by which some melanoma tumors become resistant to PD-1 blockade

Figure 2. Conserved motifs in the cytoplasmic domain of PD-L1. (a) On top, transmembrane and intracellular region of PD-L1, with the conserved signaling motifs RMLD(VEKC), DTSSK and QFEET highlighted in boxes. Below, multialignment of selected PD-L1 sequences from the species indicated on the left, or with the indicated bacterial DNA-dependent RNA polymerase σ subunit conserved motifs. Red arrows, arginine and lysine residues involved in PD-L1 stability; Blue arrows, lysine residues with IFN-regulating activities. Residues in red, highly-conserved aminoacids; residues in green, conserved aminoacids; the region binding mRNAs is indicated; Numbers indicate aminoacid positions. (b) Selection of mutations in PD-L1 found in human carcinomas. On top, human PD-L1 sequence including the homologous RMLD(VEKC), DTSSK and QFEET motifs. Below, mutations found in biopsies from human patients. In red, disruptive mutations; in green, conserved mutations.

Using a classical deletion approach, the “RMLDVEKC” motif was absolutely required to inhibit type I and II IFN-driven apoptosis (**Figure 3**). In contrast, removal of “DTSSK” potentiated the anti-IFN activities of PD-L1, strongly suggesting a function as a negative regulator for this specific motif. The expression of cell surface proteins is frequently regulated by ubiquitination. Hence, the lysine residues in “RMLDVEKC” and “DTSSK” motives were mutated to eliminate this possibility. Their mutations also potentiated the anti-IFN activities of PD-L1, again suggesting that these lysine residues were negative regulators [96], although no apparent changes in PD-L1 cell surface expression were observed in our study. Interestingly, later studies have demonstrated a key role for residue modifications in the carboxy-terminus of PD-L1 that regulate its stability and degradation. For example, arginines R260, R262 and R265, just upstream of the RMLDVEKC motif, were shown to be critical for PD-L1 dimerization and for its complex glycosylation (**Figure 2a**) [46]. Acetylation of K263 regulates its nuclear localization [105,106]. Additionally, R260 and K263 are critical for huntingtin interacting protein 1 related (HIP1R) binding, which targets PD-L1 for degradation [107]. Interestingly, we had previously found mutations within some residues of these motifs selected in skin cancers and other carcinomas [96], highlighting their critical role in carcinogenesis (**Figure 2b**). Other modifications in the carboxy-terminus have been shown to regulate PD-L1 stabilization. For example palmitoylation in C272 by zinc finger DHHC-type containing 3 (DHHC3) stabilizes PD-L1, allowing cancer cell escape from the T cell attack [108]. This palmitoylation inhibits ubiquitination of C272 that causes PD-L1 degradation [109]. Surprisingly, we did not find specific functions for the “QFEET” motif [96].

Overall, IFN signaling pathways constitute a major mechanism for response to PD-1/PD-L1 blockade [45,89,96,110–112]. Hence, it is no wonder that one of the key functions of PD-L1 in cancer cells is to counteract IFN signaling and reduce IFN-induced apoptosis, although the specific pathway may be cancer type-dependent [113]. To shed some light about a possible mechanism, we then studied IFN signal transduction and caspase-dependent regulation of apoptosis in melanoma cells [96] (**Figure 3**). Melanoma cells responded to IFN β stimulation by enhancing STAT3 upregulation, but not STAT1 or STAT2. The elimination of PD-L1 selectively induced signal transducer and activator of transcription (STAT)3 phosphorylation in tyrosine 705, but not serine 727 phosphorylation. Abrogation of PD-L1 expression in melanoma cells sensitized them to IFN-driven apoptosis through a pathway dependent on caspases 7 and 9. Overall, our results indicated that the “RMLDVEKC” motif, negatively regulated by the “DTSSK” motif, inhibited STAT3 Y705 phosphorylation and IFN receptor signaling, truncating apoptosis dependent on caspase 7 and 9. Indeed, PD-L1 abrogation in macrophages was shown to potentiate STAT3 activation leading to IL6 production [114]. Something similar was observed in MDSCs [115]. Interestingly, a different mechanism involving phospho-STAT3 was described whereby Y705-STAT3 physically associates with PD-L1, facilitating its nuclear transport and pyroptosis induction in cancer cells through caspase 8 [116]. In other tumor models, the relationship between PD-L1 expression and regulation of JAK-STAT signaling pathways may differ. For example, JAK-STAT-activation has been shown to occur in NSCLC cells caused by PD-L1 reverse signaling in the context of enhancement of angiogenesis, as recently shown by Cavazzoni et al [117].

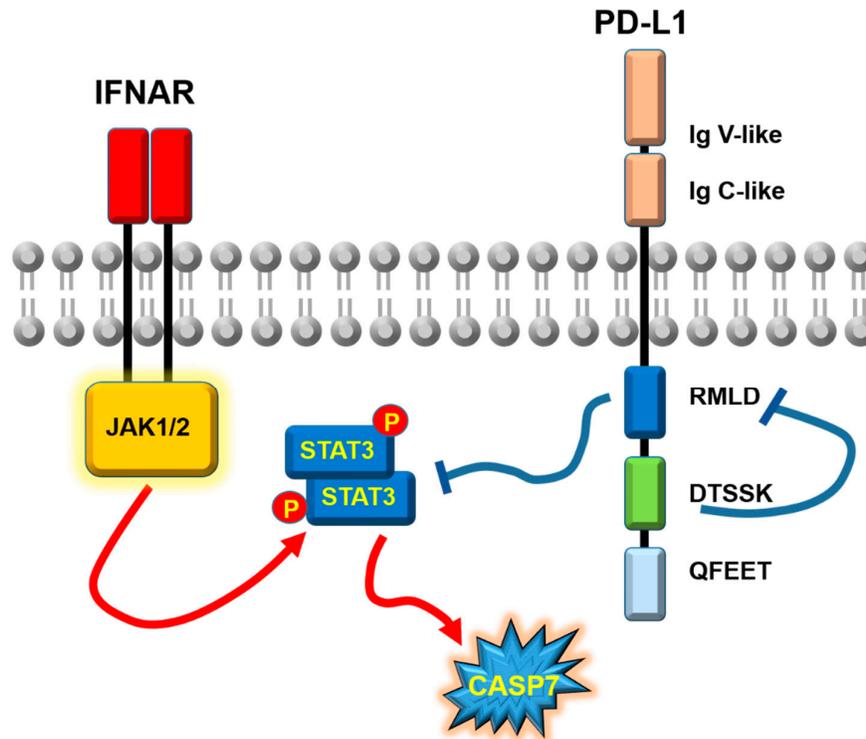


Figure 3. Structure, conserved motifs and anti-IFN activities of PD-L1. Schematic representation of the molecular organization of PD-L1 (right) in the cell membrane, with the main conserved sequence motifs indicated in the figure. The reverse signaling pathway counteracting IFN-driven apoptosis is also depicted. On the left, IFNs signal through JAK1/2 leading to STAT3 phosphorylation and CASP7-dependent apoptosis. Blue lines, inhibitory relationships between the indicated sequence motifs and molecules. Red arrows, activating relationships between the indicated proteins. Ig V and Ig C, indicate immunoglobulin-like variable and conserved sequence motifs. IFNAR, interferon receptor.

Melanoma B16-derived tumors were more sensitive to IFN β when PD-L1 expression was reduced, a feature dependent on PD-L1 intracellular signal transduction in B16 cells. Indeed, we also found that the human homologue of the “DTSSK” motif was selectively enriched in mutations in several human carcinomas (**Figure 2b**). These mutations were tested *in vitro*, demonstrating that they enhanced the anti-IFN capacities of human PD-L1 [96]. Importantly, antibody blockade of PD-L1 decreased cancer cell proliferation and enhanced sensitivity to IFN β in murine and human melanoma cancer cells [96], a mechanism later confirmed in other tumor types [118,119]. The role of PD-L1 as a factor favoring cancer cell proliferation is also supported by studies in other tumor models, in which agonistic PD-L1 antibodies induce cell growth and survival, such as in Hodgkin lymphoma [120]. Thus, apart from inactivating mutations of the IFN signal transduction pathway and antigen presentation, other mutations directly in PD-L1 can be selected in human carcinomas that protect cancer cells from IFN-induced apoptosis.

5. The PD-L1 Interactome

We continued with a follow-up study taking advantage that the human interactome had been published [121]. These data was obtained by mass spectrometry analyses in human embryonic kidney (HEK)-293T cells after antibody-based affinity purification of targets of interest bound to their interacting proteins. An interactome associated to human PD-L1 was constructed for the first time with proteins associated to affinity-purified PD-L1 [45]. This interactome can be divided in three

functional groups: (1) DNA-damage response; (2) nuclear protein and RNA import/export group; (3) and Golgi- endoplasmic reticulum (ER) interactors (**Figure 4**).

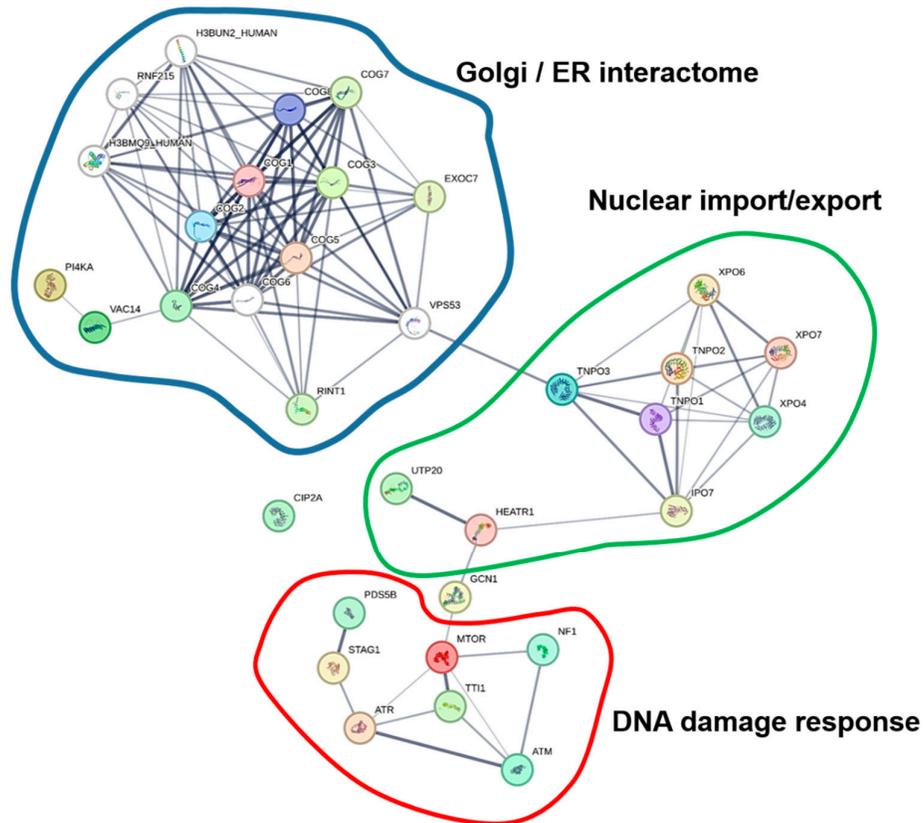


Figure 4. Interactome associated to human PD-L1. Interactors detected experimentally in [121] are shown and arranged reconstructing their interactions with STRING (<https://string-db.org/>) [45]. Predicted nodes are shown in white. Interactomes have been grouped in three main classes according to their associated functions, as indicated in the figure.

The first group of proteins included mTOR, several kinases that regulate ancho-independent cell growth, and surprisingly, key regulators of the DNA damage response pathway including ATM (ataxia telangiectasia mutated) and ATR (ataxia telangiectasia and Rad3-related protein) (**Figure 4**) [45]. It had already been experimentally demonstrated at the time that PD-L1 was regulating signaling through mTOR/AKT pathways [99], as extensively described above. However, the association of ATM and ATR proteins to PD-L1 was unexpected, strongly suggesting a direct link between PD-L1 and regulation of the DNA damage response pathway [45]. Indeed, radiotherapy had been found to induce PD-L1 upregulation in cancer cells through the activity of ATM/ATR [122]. Later on in 2021, Ozawa et al. showed that IFN-mediated PD-L1 upregulation was associated to the double-strand breaks (DSB) repair pathway in patients with colitic cancer, mainly by immunofluorescence microscopy techniques [123]. Indeed, PD-L1 upregulation was shown to be associated to resistance of cancer cells to radiotherapy in a genome-wide CRISPR/Cas9-based screening, by accelerating DBS repair. Interestingly, this mechanism was dependent on PD-L1 N219 deglycosylation and its translocation to the cell nucleus. PD-L1 translocation was mediated by CMTM6, one of PD-L1's known interactors [69,70] (**Figure 5**). In the nucleus, PD-L1 was shown to bind KU (X-Ray repair cross complementing 6 and 5 dimer, XRCC6/XRCC5) through its IgC-like domain and facilitate non-homologous end joining recombination (NHEJ) [124]. Further research supported that nuclear PD-L1 was not an artefact as suggested by other authors [125], and confirmed that PD-L1 can translocate to the nucleus [106,124,126,127]. Hou et al. showed in a study that PD-L1

translocated to the nucleus through an interaction of its carboxy terminus with Y705-phosphorylated STAT3, where PD-L1/STAT3 regulated gasdermin C (GSDMC) transcription in cancer cells in response to hypoxia [116] (**Figure 5**). Similar links between PD-L1 and DNA repair mechanisms have been also published by other authors [128,129]. Very recently, a direct association between nuclear PD-L1 and ATR which regulates DNA damage response was demonstrated [130] (**Figure 5**). A role for regulation of DNA repair mechanisms through binding to BRCA1 associated RING domain 1 (BARD1) was also described in several cancer types [128]. The authors of this study suggested that PD-L1 may be promoting BARD1 translocation into the nucleus, favouring breast cancer 1 (BRCA1) nuclear foci formation and homologous recombination. However, the authors of this study did not map the potential binding site for BARD1.

The second group of interactors that we originally described were associated to mRNA import/export and protein nuclear import/export pathways (**Figure 4**) [45]. At that time, we did not consider these results to be relevant, but since then, many research teams have demonstrated the nuclear import/export of PD-L1 associated to glycosylation and deglycosylation pathways, binding to phosphorylated STAT-3, CKLF like MARVEL transmembrane domain containing 6 (CMTM6) binding or by other mechanisms (**Figure 5**). As mentioned above, it turned out that nuclear PD-L1 is related to key and very relevant functions in cancer cell biology, inflammation and immunity [54,106,123,124,126–128,130].

The third group of interactors included Golgi and ER proteins, as would be expected for a transmembrane glycoprotein. Indeed, the regulation of PD-L1 transport, ubiquitination and degradation turned out to be a major immunoregulatory mechanism in tumor biology [31,69–71,73–78,124,126,131–133].

In 2021, a PD-L1-associated metabolic interactome was also obtained and its relationship with choline kinase (CHK) α was established by analysing breast cancer (MDA-MB-231 and SUM-149) and pancreatic ductal adenocarcinoma (Pa09C and Pa20C) cell lines [134]. The authors used high resolution magnetic resonance spectroscopy, following PD-L1 and CHK α silencing with small-interfering RNAs. An inverse correlation in expression between both proteins was demonstrated. Inverse changes in metabolites were identified regulated by both proteins, as well as lipid profiles, which were mediated through CHK α , cyclooxygenase 2 (COX2) and transforming growth factor beta (TGF β).

A later study by Nieto et al. defined PD-L1's intracellular interactome and the role of its carboxy-terminus in mediating signal transduction in a head and neck squamous cell carcinoma model [135]. Interestingly, there were some differences between the interactome in the absence and presence of PD-1 binding to PD-L1. The authors of the study also demonstrated a physical association between PD-L1, interleukin enhancer binding factor (ILF)2, ILF3, family with sequence similarity 129 member B (FAM129B) and protein tyrosine phosphatase non-receptor type 1 (PTPN1) by co-immunoprecipitation (**Figure 5**). Interestingly, ILF2 and ILF3 associated to PD-L1 in the absence and in the presence of PD-1 interaction. In this experimental model, ILF2-ILF3 binding to PD-L1 preceded and induced STAT3 phosphorylation, favoring cancer cell progression.

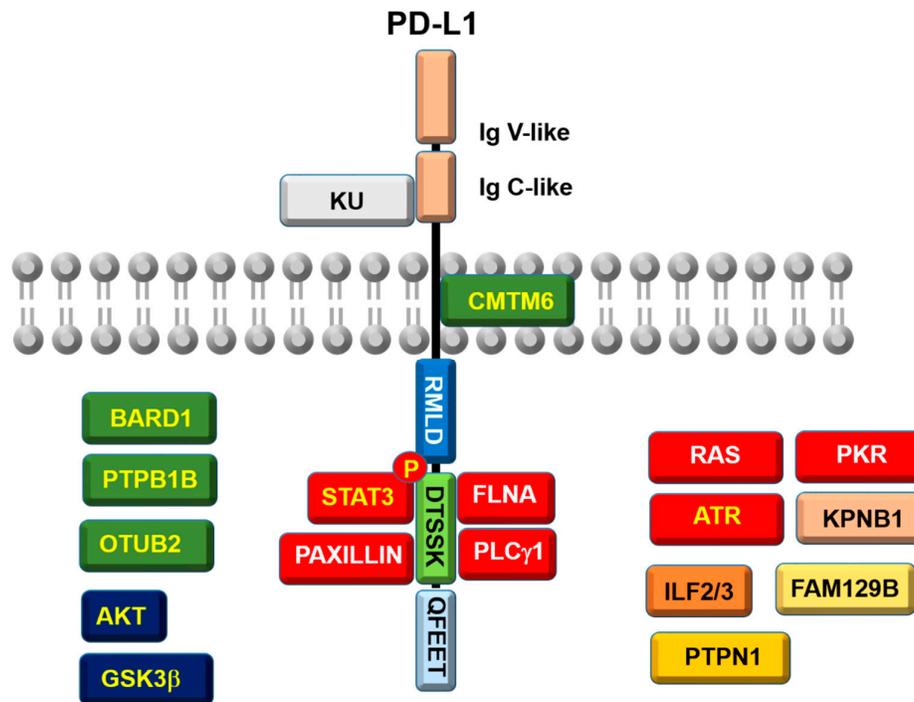


Figure 5. PD-L1 interacting proteins. In the figure, the PD-L1 structure is represented with its conserved sequence motifs as indicated. Experimentally identified binding partners other than the originally published [45] are indicated in the figure. Those in close contact correspond to interactors for which the interacting domain in PD-L1 is known, as schematically shown in the figure. *Interactome associated to human PD-L1.*

Other direct interactors identified to date include glycogen synthase kinase 3 beta (GSK3 β) in head and neck squamous carcinoma [136] (**Figure 5**). Upregulated PD-L1 following irradiation in radioresistant cancer cells enhanced its association with GSK3 β , leading to its inactivation by phosphorylation and subsequent increase in cell proliferation and survival. AKT was also found to be a direct interactor at least by coimmunoprecipitation with PD-L1 in platelets, sustaining its activation [100] (**Figure 5**).

In triple-negative breast cancer cells, PD-L1 was shown to co-immunoprecipitate with the tyrosine phosphatase PTP1B through PD-L1's carboxy terminus (**Figure 5**). However, the specific motifs mediating this binding were not identified in this study. The authors of the study proposed a mechanism by which PD-L1 binding to PTP1B prevented GSK3 β -mediated phosphorylation and subsequent degradation by ubiquitination of Snail, promoting epithelial to mesenchymal transition (EMT) in cancer cells [137].

The deubiquitinating enzyme OTU deubiquitinase ubiquitin aldehyde binding 2 (OTUB2) was also shown to be a direct interactor with cytoplasmic PD-L1 in many cancer cell types [138]. Interestingly, this interactor, at least its catalytically active form, was shown to bind to PD-L1's intracellular domain both in vivo and also in vitro with purified proteins (**Figure 5**). However, the specific motif mediating this interaction was not mapped. The authors of this study proposed that catalytically active OTUB2 binds to PD-L1 and prevents its degradation.

Intriguingly, karyopherin subunit beta 1 (KPNB1) has been shown to associate to PD-L1 and mediate its translocation to the nucleus, where it cooperates with specificity protein 1 (SP1) to transactivate growth arrest specific 6 (GAS6) transcription, leading to enhanced non-small cell lung cancer (NSCLC) proliferation [127] (**Figure 5**). Likewise, nuclear PD-L1 has been shown to associate to epidermal growth factor receptor 1 (EGFR) promoter, leading to its transcription by association

with phospho-STAT3 [106]. These results extend PD-L1's role to that of transcriptional co-activator, if not a transcription factor by itself.

6. The DNA-Dependent RNA Polymerase-Like Domain

A surprising result from our original bioinformatic analyses on PD-L1 was the identification of a conserved sequence in the intracytoplasmic domain corresponding to a highly conserved bacterial DNA-dependent RNA polymerase β subunit motif (**Figure 2b**) [45,96]. This result was completely unexpected. The RNAPol motif encompassed part of the RMLD and the complete DTSSK sequences (**Figure 2b**). We demonstrated that these sequences contributed to the anti-IFN response, but the relevance of an RNAPol motif in PD-L1's carboxy terminus was unclear at the time. However, in 2019 Tu et al. demonstrated that PD-L1 could act as an RNA-binding protein [139], mapping the interacting domain (aminoacids 270-279) to most of the RNAPol-like motif (**Figure 2b**). The authors of this study showed that intracellular PD-L1 stabilized several mRNAs including those coding for nibrin (NBS1) and BRCA1 in HCT116 and MDA-MD-231 cell lines. PD-L1 protected mRNAs from degradation and increased resistance to DNA damage. It is tempting to speculate that the RNAPol-like motif contributes to DNA/RNA binding and participate in transcriptional regulation and DNA repair as already shown [69,70,116,124,127–130].

7. Other Pathways Regulated by PD-L1 Reverse Signaling

Since the early publications on PD-L1 intrinsic signaling in cancer cells, subsequent research has reinforced its critical role in a plethora of biological regulatory mechanisms. Theivanthiran et al. highlighted the role played by PD-L1 associated to the inflammasome to drive granulocytic MDSC recruitment into the tumor, which caused resistance to PD-1 blockade immunotherapy [140]. Indeed, anti-PD-L1 antibody plus IFN treatment of BRAFV600E PTEN^{-/-} melanoma cells was shown to activate NOD-like receptor protein 3 (NLRP3) through protein kinase R (PKR) binding (**Figure 5**). This effect was shown to take place in LLC mouse lung adenocarcinoma cells. This mechanism was driven by PD-L1 crosslinking and STAT3 suppression, which seems to be a central common mechanism in PD-L1 intrinsic signaling in several cancer cell models [96,140].

Intrinsic PD-L1 reverse signaling is not restricted to cancer cells or exclusively linked to immune escape. Lucas et al. demonstrated a critical role for PD-L1 reverse signaling in regulating the migration of conventional activated DCs from the skin to the draining lymph node [141]. This mechanism was shown to be required for proper T cell priming, and relied on activation of c-c chemokine receptor type 7 (CCR7) signaling through the DTSSK domain of PD-L1. Most importantly, the DTSSK domain in PD-L1 was found also critical in lymphatic endothelial cells (LECs) for lymphatic remodelling following immune stimulation with polyIC, TNF α and IFN β [142]. Inactivating mutations in the DTSSK domain by replacing the TSS motif with alanines impeded actin polymerization and LEC movement. Interestingly, these mutations reduced the binding of PD-L1 to paxillin and phosphorylated S727 and Y705 STAT3, required for protein assembly at focal adhesions (**Figure 5**). In this study, the authors further characterized PD-L1 interactors and phospho-interactors after immunoprecipitation, finding 5 differential proteins between wild-type PD-L1 and DTSSK-mutated PD-L1 [142]. Binding of PD-L1 to H-RAS was shown by co-immunoprecipitation in 293T and LN229 cells by Qiu et al., although the specific domain regulating this interaction was not described in their study [143] (**Figure 5**). The authors showed that PD-L1 promoted RAS activation leading to EMT in glioblastoma multiforme. A similar mechanism was observed in colorectal cancer cells, regulated through ERK/AKT signal transduction pathway after binding to KRAS, as shown by co-immunoprecipitation [101]. In this study, PD-L1/PD-L1 interactions were mediated extracellular signal-mediated kinase (ERK)/AKT activation, although the specific domain of PD-L1 associated to KRAS was not identified (**Figure 5**). EMT was recently shown to be induced by PD-L1 intrinsic signaling, but in this study a MAPK p38-dependent mechanism was involved [144]. Hence, PD-L1 expression activated the MAPK ERK pathway, accelerating cancer cell growth and tumor

progression. STAT3-dependent signaling in CD4 T cells was also triggered by PD-L1 binding, and induced an anergic phenotype in CD8 T cells and a regulatory phenotype in CD4 T cells [145,146].

PD-L1 has been shown to directly bind phospholipase C in an EGFR-dependent manner in several lung cancer cell variants, regulating Rho GTPases, which enhanced tumorigenicity [119]. PD-L1 interactors were probed in a yeast 2-hybrid assay, finding filamin A (FLNA) and phospholipase C gamma 1 (PLC γ 1). The authors of this study concluded that PD-L1 associated with PLC which enhanced its transphosphorylation by EGFRs, and mapped the interacting domain at the region containing the DTSSK motif (**Figure 5**).

8. Conclusions

The clinical use of PD-L1/PD-1 blockade immunotherapies came fast and developed faster. Much faster than research into the molecular and cellular mechanisms of PD-1 and PD-L1 functions. Nevertheless, the extraordinary success of these therapies ignited research into the functions of these immune checkpoint inhibitors. During the last 10 years, we have discovered multiple facets of PD-L1 in cell biology. Not only as the so-called T-cell break in immunotherapy, but also as a molecule actively participating in cell proliferation, survival and in DNA damage responses. The importance of nuclear PD-L1 has also arisen recently, suggesting that PD-L1 can function as a co-transcriptional activator as well. The knowledge acquired on its structural organization, functions and interactors will help us in the identification of novel targets, and design improved therapies that can be used in combination with standard immune checkpoint blockade immunotherapies.

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