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## Transcriptional regulation of effector and memory CD8<sup>+</sup> T cell fates

James E. D. Thaventhiran<sup>1</sup>, Douglas T. Fearon<sup>2,3</sup>, and Luca Gattinoni<sup>4</sup>

<sup>1</sup>Centre for Lung Infection, Papworth Hospital NHS Foundation Trust, Papworth Everard, Cambridge CB23 3RE, United Kingdom

<sup>2</sup>Department of Medicine, University of Cambridge School of Clinical Medicine, Cambridge CB2 2QH, United Kingdom

<sup>3</sup>Cancer Research UK Cambridge Research Institute, Li Ka Shing Centre, Cambridge CB2 0RE, United Kingdom

<sup>4</sup>Experimental Transplantation and Immunology Branch, National Cancer Institute, National Institutes of Health, Bethesda, Maryland, USA

### Abstract

Immunity to intracellular pathogens and cancer relies on the generation of robust CD8<sup>+</sup> T cell effector responses as well as the establishment of immunological memory. During a primary immune response CD8<sup>+</sup> T cells experience diverse extracellular environmental cues and cell-cell interactions that trigger downstream transcriptional programs ultimately guiding a CD8<sup>+</sup> T cell to undertake either an effector or a memory cell fate. Here, we discuss our current understanding of the signaling pathways and transcriptional networks that regulate effector and memory commitment in CD8<sup>+</sup> T lymphocytes.

### Introduction

CD8<sup>+</sup> T cells play a critical role in the immune responses to both intracellular pathogens and cancer [1;2]. Upon pathogen-antigen or tumor-antigen stimulation, naïve CD8<sup>+</sup> T cells (T<sub>N</sub>) undergo a massive clonal expansion to generate large numbers of effector T cells capable of eliminating cells bearing the target antigen. At the end of the primary response the majority of responding CD8<sup>+</sup> T cells will undergo apoptosis; however, a small fraction of activated cells will persist long-term establishing a memory T cell population [3]. Expression of killer cell lectin-like receptor G1 (KLRG1) and IL-7 receptor- $\alpha$  (IL-7R $\alpha$ ) on responding CD8<sup>+</sup> T cells can distinguish cells that are destined to die or survive as long-lived memory cells. Specifically, IL-7R $\alpha$ <sup>+</sup>KLRG1<sup>-</sup> CD8<sup>+</sup> T cells have a greater potential to enter into the memory pool, whereas IL-7R $\alpha$ <sup>-</sup>KLRG1<sup>+</sup> CD8<sup>+</sup> T cells represent terminally differentiated, short-lived effector T cells (SLEC) [4]. The transcriptional regulation of these cell-fate decisions has undergone much scrutiny over the past years. Early studies establishing the transcriptional regulators Eomesodermin (EOMES), T-BET (encoded by T-BOX 21), B-cell CLL/lymphoma 6 (BCL-6) and B lymphocyte induced maturation protein 1 (BLIMP-1, encoded by PRDM1) as critical determinants of CD8<sup>+</sup> T cell differentiation have been

Corresponding authors: Gattinoni, Luca (gattinol@mail.nih.gov) and Thaventhiran, James E. D. (jedt2@cam.ac.uk).

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reviewed in detail elsewhere [5;6]. Here, we discuss more recent advances that have shaped our understanding of the signaling pathways and transcriptional programs that regulate the formation of effector and memory CD8<sup>+</sup> T cells.

## STAT signaling

Signal transducer and activator of transcription (STAT) signaling pathways are central to the differentiation and long-term survival of CD8<sup>+</sup> T cells. Seven members of the STAT family have been described in mammals (STAT1, STAT2, STAT3, STAT4, STAT5A, STAT5B and STAT6) [7]. While a single cytokine receptor can activate downstream multiple STATs, most receptors function through a dominant STAT protein. For instance, interleukin (IL)-6, IL-10 and IL-21 preferentially act through STAT3 while IL-12 and IL-2 activate STAT4 and STAT5, respectively (Figure 1).

There is now evidence indicating that STAT4 and STAT5 signaling drive T cells towards terminal differentiation, whereas STAT3 withholds differentiation favoring the establishment of CD8<sup>+</sup> T cell memory. Increased levels of Stat4 activity resulting from IL-12 signaling promoted the generation of SLEC [4] whereas memory responses were enhanced in mice deficient of IL-12 [8;9]. Sustained Stat5 signaling also favors terminal differentiation as cells perceiving prolonged IL-2 signals exhibited a more pronounced effector phenotype and increased amounts of KLRG1 [10]. By contrast, Stat3 signaling is critical for the generation of memory CD8<sup>+</sup> T cells as Stat3-deficient T cells underwent terminal differentiation and failed to form self-renewing T<sub>CM</sub> [11]. Moreover, disruption of IL-6, IL-10 or IL-21 signaling by genetic depletion of either the cytokine itself or the cytokine receptor resulted in the accumulation of SLEC and impaired memory responses [11–14]. Consistent with these findings, patients with autosomal-dominant hyper-IgE syndrome, a disease often caused by dominant-negative mutations in STAT3, form decreased numbers of T<sub>CM</sub> and exhibit defective immune responses against viral infections [15]

Mechanistically, the pro-differentiating activity of Stat4 and Stat5 appears to be secondary to the induction of key master regulators of effector differentiation such as T-bet [4;9], Blimp-1 [10;16–18] and, as discussed below, inhibitor of DNA-binding 2 (Id2) [19] (Figure 1). Stat3, instead, was found to control CD8<sup>+</sup> T cell differentiation by sustaining the expression of Eomes which is key for the long-term persistence of memory CD8<sup>+</sup> T cells as it regulates IL-15-dependent homeostatic turnover via the induction of IL-2R $\beta$  [20], as well as Bcl-6, a transcriptional repressor of Blimp-1 [11;21;22](Figure 1). Additionally, Stat3 can favor memory CD8<sup>+</sup> T cell formation by mitigating the activity of IL-12 through the induction of suppressor of cytokine signaling 3 (Socs3) [11] (Figure 1).

## WNT– $\beta$ -catenin signaling

WNT– $\beta$ -catenin signaling has recently emerged as a critical determinant of CD8<sup>+</sup> T cell differentiation. This signaling pathway revolves around  $\beta$ -catenin which in the absence of WNT signals is targeted for proteasomal degradation by a ‘destruction complex’ consisting of Axin, Adenomatosis Polyposis Coli (APC), and the serine/threonine kinases Casein Kinase 1 (CK1) and Glycogen-Synthase Kinase 3 $\beta$  (GSK-3 $\beta$ ) [23]. Binding of WNT to the Frizzled receptor and LRP5 or 6 co-receptors triggers a signaling cascade resulting in the disruption of the ‘destruction complex’ and subsequent accumulation and nuclear translocation of  $\beta$ -catenin which allows  $\beta$ -catenin to interact with T cell factor (TCF) and lymphoid enhancer-binding factor (LEF) family members to promote specific gene expression [23] (Figure 1).

Studies employing a physiological WNT ligand, WNT3A, or inhibitors of GSK-3 $\beta$  to activate WNT- $\beta$ -catenin signaling revealed that this pathway withholds the differentiation of T<sub>N</sub> into SLEC while promoting the generation of long-lived memory stem cells (T<sub>SCM</sub>) and central memory T cells (T<sub>CM</sub>) [24–27]. These observations have recently been corroborated using gain- and loss-of function genetic approaches. Overexpression of a stabilized form of  $\beta$ -catenin in CD8<sup>+</sup> T cells hampered cell proliferation and the acquisition of effector functions [28]. Furthermore, constitutive activation of WNT signaling by transgenic expression of Tcf-1 and stabilized  $\beta$ -catenin resulted in reduced expansion of antigen-specific CD8<sup>+</sup> T cells and enhanced memory T cell formation [29]. Conversely, deletion of Tcf1 promoted CD8<sup>+</sup> T cell differentiation into SLEC and impaired the maintenance of IL-7R<sup>+</sup>KLRG1<sup>-</sup> memory precursors resulting in decreased T<sub>CM</sub> cells and impaired immune responses to pathogen re-challenge [30;31]. Lef-1 deficient CD8<sup>+</sup> T cells exhibit only minor alterations in the development of effector and memory responses, indicating functional redundancy in Lef-1 activity through Tcf-1 dependent mechanism[32]. Indeed, deletion of both Tcf-1 and Lef-1 caused virtually a complete loss of memory precursors and failure to mount recall responses [32]. Although deletion of  $\beta$ -catenin alone was insufficient to quench WNT signaling in CD8<sup>+</sup> T cells as indicated by WNT reporter activity [33] nor did it alter CD8<sup>+</sup> T cell effector and memory responses [34], several lines of evidence indicate that the phenotype of Tcf-1 and Lef-1 knockout cells is dependent on WNT- $\beta$ -catenin signaling. For instance, memory recall responses were impaired in CD8<sup>+</sup> T cells lacking both  $\beta$ -catenin and its homolog  $\gamma$ -catenin [30]. Perhaps more compelling, genetic complementation of Tcf-1 knockouts with Tcf1 p45, but not the p33 isoform which lacks the catenin-binding domain, rescued defective T cell memory responses [30].

How WNT- $\beta$ -catenin signaling affects CD8<sup>+</sup> T cell differentiation has just begun to be elucidated. Tcf-1 was found to partially act through the induction of Eomes [31]. Additional mechanisms might involve an indirect regulation of the pro-memory transcription STAT3 [35] and ID2 as discussed below [36] (Figure 1).

## ID proteins

ID proteins are a key family of transcription regulators that control effector and memory CD8<sup>+</sup> T cell development. These proteins, which lack a basic DNA-binding region, mainly function as negative regulators of E protein transcriptional activity by forming heterodimer through a helix-loop-helix (HLH) domain and preventing E proteins from binding to DNA [37]. Four ID proteins (ID1–ID4) have been described, but only the function of ID2 and ID3 has been investigated in the differentiation of mature CD8<sup>+</sup> T cells. Both Id2 and Id3 are found in naïve CD8<sup>+</sup> T cells, but following T cell activation their expression is dichotomously regulated [19;38]. While Id3 expression is actively repressed by Blimp-1 [38], Id2 is upregulated as cells differentiate into SLEC as the result of Stat4/Stat5 signaling [19] and possibly the Tcf-1 down-regulation that accompanies this process [36] (Figure 1). Id2 is required to support the survival of expanding effector CD8<sup>+</sup> T cells [39] and to induce sufficient levels of T-bet to sustain the accumulation of SLEC [40;41]. By contrast, Id3 is maintained in memory precursors and is critical for the maintenance of long-lived memory CD8<sup>+</sup> T cells [19;38]. Enforced expression of Id3 in SLEC was sufficient to confer long-term survival to these cells otherwise destined to die [38]. Consistently, deletion of the E proteins, E2a and HEB, led to long-term accumulation of KLRG1<sup>+</sup> T cells [42]. Both Id2 and Id3 partly operate through inhibition of E2A, but they clearly exert different functions in effector and memory T cells, perhaps as results of diverse binding affinities for E protein members or context-dependent interactions with additional molecules. For instance, Id2 restrained the expression of E2A-target genes *Tcf7*, *Socs3* and *Id3*, which are key for memory T cell development [41] (Figure 1), and altered the expression of pro- and anti-apoptotic genes such as *Bcl2l1*, *Bcl2* and *Serpin* peptidase inhibitor, clade B, member 9

(*Serpinb9*) [39]. Id3, instead, was found to affect a set of genes that control genome stability including forkhead box M1 (*Foxm1*), NIMA-related kinase 2 (*Nek2*) and members of the minichromosome maintenance and kinesin complexes [38]. Nevertheless, the activity of Id2 and Id3 appear to extend beyond the mere regulation of E proteins as T cells deficient of both E2A and HEB display a more subtle phenotype compared to those observed in the absence of Id2 and Id3 [42].

### PI3K–AKT–mTOR signaling pathway

The nutrient-sensing serine/threonine protein kinase mammalian target of rapamycin (mTOR) is a well-established regulator of cell growth and metabolism, but more recently has emerged as a pivotal modulator of CD8<sup>+</sup> T cell fate decisions. mTOR integrates signals from pro-inflammatory cytokines such as IL-2 and IL-12 through phosphoinositol 3-kinase (PI3K)–AKT signaling as well as Wnt proteins via GSK-3 $\beta$  (Figure 1). Sustained activation of AKT/mTOR activity by IL-12 [43], expression of a constitutively active form of AKT [44;45], and deletion of Tuberous sclerosis 1 (*Tsc1*) [46] all drive naive T cells towards a terminally differentiated effector state. Remarkably, modulation of mTOR activity with low doses of the mTOR inhibitor, rapamycin, increases the numbers of memory T cells as well as promotes the preferential formation of T<sub>CM</sub> [47–49]. Similarly, pharmacological blockade of AKT can augment CD8<sup>+</sup> memory T cells although through a different mechanism involving the rescue of SLEC survival [45].

The transcriptional mechanisms by which AKT/mTOR signaling favor CD8<sup>+</sup> T cell effector differentiation have recently been resolved and implicate Forkhead Box O1 (FOXO1) at the center stage [50]. Phosphorylation of FOXO1 by AKT facilitates its binding to cytosolic 14-3-3 scaffold proteins which prevents translocation of FOXO1 into the nucleus. The consequent loss of Foxo1 transcriptional activity resulted in reduced mRNA levels of the pro-memory transcription factors Eomes [43] and Bcl-6 [51] whereas indirectly augmented the expression T-bet [4;50] (Figure 1). Additionally, inhibition of Foxo1 causes down-regulation of Kruppel-like factor 2 (*Klf-2*), a key regulator of lymph node homing molecules which are critical for T<sub>CM</sub> and T<sub>SCM</sub> cell function [52].

### The Hippo signaling pathway

The Hippo pathway is an evolutionarily conserved intracellular signal transduction cascade that transduces cell-cell contact signals to trigger differentiation [53]. Recently this signaling pathway has also been demonstrated to affect the transcriptional regulation of differentiation of CD8<sup>+</sup> T cells. The core components of this serine/threonine kinase pathway consists of Mammalian sterile-20-like kinase (MST), MOB kinase activator (MOB), Salvador homolog 1 (SAV1) and Large tumor suppressor homolog (LATS) (only MST and LATS are kinases). In the original description of the pathway, it was noted that following cell-cell contact a wave of phosphorylation is initiated leading to activation of the serine kinase, LATS, which in turn phosphorylates the transcriptional co-activator Yes-associated protein (Yap) [53]. Phosphorylated Yap is excluded from the nucleus and is degraded, preventing Yap-dependent transcription. In CD8<sup>+</sup> T cells the Hippo pathway is assembled in response to the signals necessary for CD8<sup>+</sup> T cell differentiation, IL-2, and antigen, but in the absence of contact between activated CD8<sup>+</sup> T cells, Hippo signaling is prevented (Figure 2A) [54]. However, in conditions in which antigen/IL-2 activated CD8<sup>+</sup> T cells come into contact with each other, triggering of the Hippo pathway leads to the degradation of Yap, suggesting that a receptor/ligand pair is present on activated CD8<sup>+</sup> T cells that is absent on T<sub>N</sub> (Figure 2B) [54]. CTLA-4 and its ligand CD80, which are both induced upon antigen/IL-2 stimulation of T<sub>N</sub> were found to be the triggering receptor/ligand pair activating the Hippo pathway (Figure 2B) [54]. The recent *in vivo* demonstration that, following vaccination, activated

CD8<sup>+</sup> cells in lymph nodes form aggregated synapses with each other, provides visually striking evidence of how this signalling may occur [55]. Hippo activation increases the generation of SLEC in response to infectious challenge [54]. The pro-differentiating effects of Hippo signaling appear to be dependent on suppression of Eomes, and induction of Blimp-1. Indeed, overexpression of a Yap isoform not subject to Hippo-mediated negative regulation enhanced expression of Eomes, suppressed the induction of Blimp-1 and promoted the maintenance of IL-7Rα<sup>+</sup> and KLRG1<sup>-</sup> memory precursors [54].

The realization that CD8<sup>+</sup> T cell differentiation could be influenced not only by the inflammatory environment but also by the relative density of responding CD8<sup>+</sup> T cells has provided new insights to resolve seemingly ambiguous observations in the field such as the relationship between IL-2 and terminal differentiation. The role of IL-2 in CD8<sup>+</sup> terminal differentiation has remained controversial. Studies on its transcriptional effects have demonstrated that it both leads to expression of senescence-associated Blimp-1 [56] and memory-associated Eomes [57]. Furthermore, separate *in vivo* studies have revealed that antigen-specific cells expressing IL-2 receptor-α, the high affinity IL-2 receptor, have a continued proliferative advantage [58] and are more prone to terminally differentiate [10]. Confusingly, in certain infections, IL-2 signaling appears to be essential for maintenance of a normal proliferative secondary responses [59–61], while for other infection models, IL-2 signaling correlates with loss of secondary responses [62]. A way to resolve these conflicting results is offered by the recent investigations into the Hippo pathway detailed above. IL-2 signaling, in the context of an inactive Hippo pathway, promotes Yap dependent expression of Eomes, which prevents differentiation (Figure 2A). However, in the context of Hippo activation, Yap dependent transcription of Eomes is terminated and IL-2 signaling leads to Blimp-1 expression and terminal differentiation (Figure 2B). Kinetic consideration of the primary immune response suggests when these two different contexts occur. At initiation of the CD8<sup>+</sup> T cell response, antigen-specific frequency is low and the chance of activated cell-cell contact is correspondingly low (Figure 2A). However, after clonal expansion, activated cell frequency increases and, with this, there is an increase in the likelihood of activated cell-cell contact triggering the Hippo pathway and so of terminal differentiation (Figure 2B). These findings could provide a mechanism for the important question of how the CD8<sup>+</sup> T cell links terminal differentiation to the size of clonal expansion that is reminiscent of quorum sensing in bacteria and yeast, in which population size is sensed by the detection of soluble factors. The advantage of the Hippo pathway is that activation by cell-cell contact is a more direct means for sensing population size than is the concentration of a soluble surrogate of clonal expansion.

## Concluding remarks

Over the past decade our understanding of the signaling pathways and transcriptional programs that control effector and memory CD8<sup>+</sup> T cell fates has advanced considerably. It is becoming increasingly appreciated that between pathways regulating self-renewal and effector differentiation exist a significant amount of cross-talk such that the net influence of each pathway is finely balanced and tuned. For example, observations in other systems have demonstrated links between WNT and mTOR [63], Hippo and WNT [64;65], STAT3 and WNT [35], and Hippo and mTOR signaling [66]. Moreover, additional complexity is present at the transcriptional level whereby transcription factors that favor memory formation appear to be mutually enhancing and at the same time reciprocally antagonistic to the transcriptional network regulating effector differentiation, and *vice versa*. In summary, investigations of each pathway individually has provided great insight into what extracellular cues regulate each independently. Future work needs to address which extracellular context selects for the particular pathway that will exert dominant control over the transcriptional regulation of CD8<sup>+</sup> T cell differentiation.



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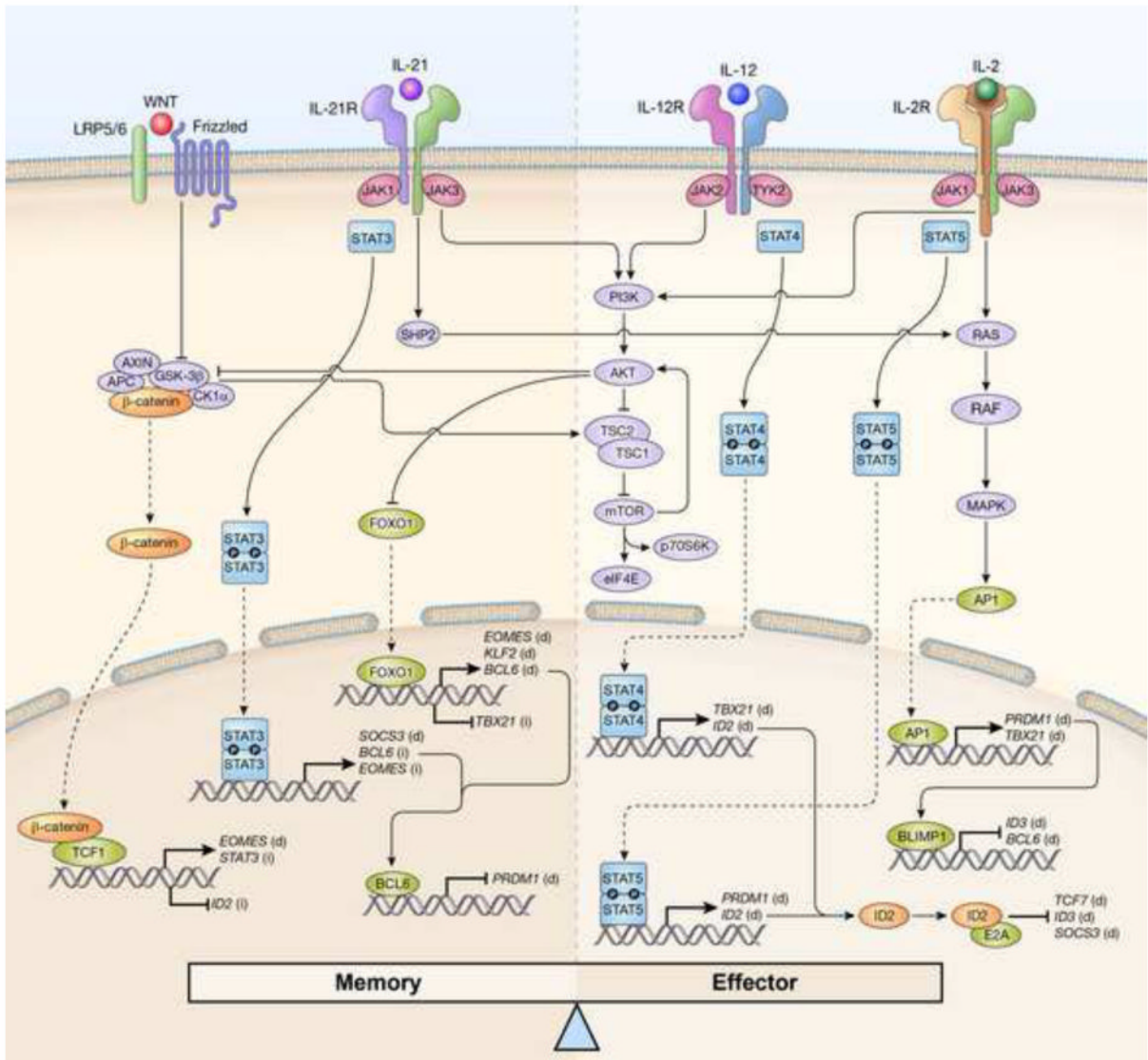
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### Review Highlights

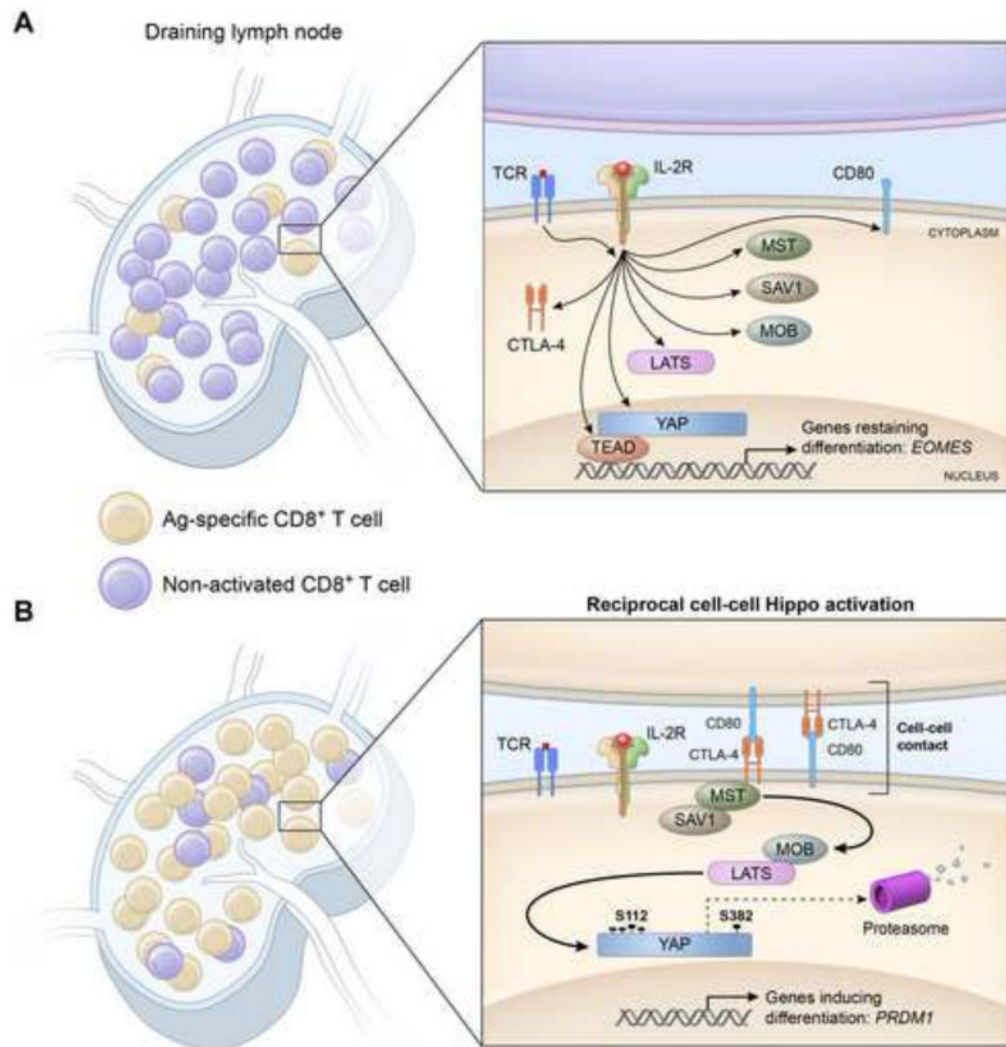
- Evolutionarily conserved signaling pathways such as WNT, STAT3, mTOR and Hippo regulate effector and memory T cell fate decisions.
- Cross-talk exists between signaling pathways governing CD8<sup>+</sup> T cell differentiation.
- Transcription factors controlling memory T cell fates are often self-reinforcing and antagonistic to the transcriptional program regulating effector differentiation.
- CD8<sup>+</sup> T cell fate is influenced by both the inflammatory environment and the relative density of responding cells



**Figure 1. Signaling pathways modulating memory and effector CD8<sup>+</sup> T cell fates**

CD8<sup>+</sup> T cell memory and effector differentiation are tightly regulated by opposite signals received from inflammatory cytokines and developmental modulators. CD8<sup>+</sup> T cell memory is promoted by binding of WNT ligands to Frizzled/Low-density lipoprotein receptor related protein (LRP) 5/6 complexes and by interleukin-21 (IL-21) or other cytokines signaling through signal transducer and activator of transcription 3 (STAT3). Activation of these signaling pathways result in the expression of transcriptional regulators and molecules that favor self-renewal and memory formation, including STAT3, Eomesodermin (EOMES), B-cell CLL/lymphoma 6 (BCL6), Kruppel-like factor 2 (KLF2) and suppressor of cytokine signaling 3 (SOCS3). At the same time, these signaling pathways inhibit the expression of transcriptional regulators that promote CD8<sup>+</sup> T cell effector differentiation and senescence, such as T-BET (encoded by T-box 21 (TBX21)), B-lymphocyte-induced maturation protein 1 (BLIMP1, encoded by PRDM1) and inhibitor of DNA-binding 2 (ID2). Conversely, pro-inflammatory cytokines such as IL-2 and IL-12 drive CD8<sup>+</sup> T cell differentiation by triggering STAT4 and STAT5 as well as the phosphoinositide-3-kinase (PI3K)/AKT/ mammalian target of rapamycin (mTOR) pathway

and the RAS/RAF/ mitogen-activated protein kinase (MAPK) pathway. These signaling pathways induce the expression of the pro-effector molecules T-BET, BLIMP1 and ID2, as well as the inhibition of pro-memory transcription modulators such as forkhead box O1 (FOXO1), BCL6 and ID3. Between these self-renewal and pro-differentiation pathways there is a considerable amount of cross-talk such that the net effect of each pathways is precisely balanced. APC, adenomatous polyposis coli; CK1 $\alpha$ , casein kinase 1, alpha 1; GSK-3 $\beta$ , glycogen synthase 3 $\beta$ ; TCF, T cell factor; JAK, janus kinase; SHP2, SH2 domain-containing protein tyrosine phosphatase-2; TSC, tuberous sclerosis; eIF4E, eukaryotic translation initiation factor 4E; p70S6K, p70 ribosomal protein S6 kinase 1; TYK2, tyrosine kinase2; AP1, activator protein 1. (d), direct regulation; (i) indirect regulation.



**Figure 2. Differentiation of clonally expanding CD8<sup>+</sup> T cells is triggered by cell-cell contact between activated cells**

(A) In the initial stages of the primary response, stimulation of CD8<sup>+</sup> T cells by antigen and interleukin-2 (IL-2) leads to transcription and translation of the components of the Hippo pathway as well as cytotoxic T-lymphocyte-associated protein 4 (CTLA-4), and its ligand, CD80. However, contact between antigen-specific cells is unlikely, and intra-nuclear Yes-associated protein (Yap) is maintained because the Hippo pathway is not activated. This circumstance enables Yap-dependent transcription to suppress a commitment to terminal differentiation, which may be mediated by the ‘memory’ associated transcription factor, Eomesodermin (EOMES). (B) As clonal expansion increases the frequency of activated antigen-specific T cells, contact between these cells is more likely to occur, leading to surface expression of CTLA-4 and its ligation by CD80, thereby triggering the Hippo signaling cascade. Ultimately, this activates the serine/threonine kinase, Large Tumor Suppressor Homolog (LATS), which phosphorylates Yap at 5 serine residues, one of which, pS112, leads to Yap being trapped in the cytosol, and another, pS382, causes its ubiquitinylation and proteasomal degradation. This loss of Yap is associated with the expression of PR domain containing 1, with ZNF domain (PRDM1) and terminal



differentiation. SAV1, salvador homolog 1; MST, mammalian sterile-20-like kinases MOB, MOB kinase activator; TEAD, TEA domain family member.