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## *Plasmodium berghei* Hsp90 contains a natural immunogenic I-A<sup>b</sup>-restricted antigen common to rodent and human *Plasmodium* species

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### ABSTRACT

Thorough understanding of the role of CD4 T cells in immunity can be greatly assisted by the study of responses to defined specificities. This requires knowledge of *Plasmodium*-derived immunogenic epitopes, of which only a few have been identified, especially for the mouse C57BL/6 background. We recently developed a TCR transgenic mouse line, termed PbT-II, that produces CD4<sup>+</sup> T cells specific for an MHC class II (I-A<sup>b</sup>)-restricted *Plasmodium* epitope and is responsive to both sporozoites and blood-stage *P. berghei*. Here, we identify a peptide within the *P. berghei* heat shock protein 90 as the cognate epitope recognised by PbT-II cells. We show that C57BL/6 mice infected with *P. berghei* blood-stage induce an endogenous CD4 T cell response specific for this epitope, indicating cells of similar specificity to PbT-II cells are present in the naïve repertoire. Adoptive transfer of *in vitro* activated T<sub>H</sub>1-, or particularly T<sub>H</sub>2-polarised PbT-II cells improved control of *P. berghei* parasitemia in C57BL/6 mice and drastically reduced the onset of experimental cerebral malaria. Our results identify a versatile, potentially protective MHC-II restricted epitope useful for exploration of CD4 T cell-mediated immunity and vaccination strategies against malaria.

### 1. Introduction

Malaria remains a major infectious disease threatening the health and livelihoods of hundreds of millions of people globally. Vaccination against malaria would improve the prospects for disease reduction, but a highly efficacious vaccine remains elusive (Cockburn and Seder, 2018). It is therefore essential to expand our understanding of the basic immunological mechanisms conducive to anti-malarial immunity to enable

generation of novel vaccines or to improve existing strategies (Fernandez-Ruiz et al., 2021). Identification of immunogenic epitopes remains a key area for further development.

CD4 T cells intervene in a broad variety of immunological processes and have been shown to play essential roles in immunity to different developmental stages of *Plasmodium* within their mammalian host. In mice vaccinated with radiation-attenuated sporozoites, CD4 T cells are necessary to enable CD8 T cell immunity (Carvalho et al., 2002), which

**Abbreviations:** DC, dendritic cells; cDC1, type I conventional DC; ECM, experimental cerebral malaria; Hsp, heat shock protein.

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controls liver stage *Plasmodium* infection (Fernandez-Ruiz et al., 2016; Schofield et al., 1987). CD4 T cells also contribute to the control of blood-stage infections with *P. chabaudi*, *P. yoelii* and *P. berghei* (Süss et al., 1988; Langhorne et al., 1990; Butler et al., 2011; Haque et al., 2011; Hirunpetcharat et al., 1999). This population of T cells is very diverse, able to differentiate into functionally distinct subtypes early upon activation by antigen presenting cells (APC) (Choi et al., 2013). Interactions with monocytes or B cells shortly after activation during *Plasmodium* infection polarises CD4 T cells into T<sub>H1</sub> or T<sub>FH</sub> cells respectively (Lonnberg et al., 2017). Depletion of CD4 T cells during acute *P. chabaudi* infection, but not later, prevents mice from making parasite-specific IgG and hinders subsequent parasite control (Langhorne et al., 1990), with antibody production facilitated by Tfh-B cell interactions (Perez-Mazliah et al., 2015, 2017). T<sub>H1</sub> cells are also reported to modulate the growth of acute *P. chabaudi* parasitemia (Wikenheiser et al., 2016). In addition to their contribution to immunity, CD4 T cells have been also involved in the development of severe malaria pathology, namely experimental cerebral malaria (ECM) (Amante et al., 2010). This form of severe malaria pathology is triggered by the accumulation of infected red blood cells (iRBC) and parasite-specific CD8 T cells in the brain of *P. berghei* infected mice (Belnoue et al., 2002; Lundie et al., 2008; Swanson et al., 2016). The latter are thought to respond to parasite antigen on brain endothelial cells, alter the blood brain barrier, increasing its permeability and causing fatal neurological damage (Howland et al., 2013; Ghazanfari et al., 2018). CD4 T cells promote inflammation and attract pathogenic CD8 T cells to the brain during blood stage *P. berghei* infection, triggering ECM (Villegas-Mendez et al., 2012).

Understanding of CD4 T cell biology in malaria has been greatly enhanced by the development of MHC-II restricted, *Plasmodium*-specific transgenic T cells (Stephens et al., 2005; Fernandez-Ruiz et al., 2017), which enabled detailed analyses of CD4 T cell responses during infection or after vaccination. Recently, we developed the PbT-II line, an MHC-II-restricted TCR transgenic line specific for *Plasmodium*, on the C57BL/6 background (Fernandez-Ruiz et al., 2017). This line was derived from a CD4 T cell isolated from the spleen of a *P. berghei* blood-stage-infected mouse, but its cognate epitope was unknown (Fernandez-Ruiz et al., 2017). PbT-II cells responded to *P. chabaudi*, *P. yoelii*, and even to *P. falciparum* blood stage parasites, indicating their specificity for a well conserved epitope. Moreover, PbT-II cells also responded to irradiated *P. berghei* sporozoites, and hence their specific target was broadly expressed. PbT-II cells were able to elicit protective immunity to *P. chabaudi* when adoptively transferred into CD40L-deficient mice, and were able to enhance priming of *Plasmodium*-specific CD8 T cells by cDC1 (Fernandez-Ruiz et al., 2017). These properties underscored the importance of identifying the cognate epitope of PbT-II cells to enable the study of endogenous CD4 T cell responses of the same specificity during infection, a more physiological scenario than use of PbT-II cells, and to enable exploration of CD4 T cell-based vaccination against *Plasmodium* in this system.

Here, we used a mass spectrometry-based approach to identify a peptide within *P. berghei* heat shock protein 90 (PbHsp90, PBANKA\_0805700), PbHsp90<sub>484-496</sub>, as the cognate epitope recognised by PbT-II cells. We incorporated this epitope in a vaccine platform and defined its potential for protection against blood-stage *P. berghei* infection. Knowledge of this epitope also enabled us to generate *in vitro* activated PbT-II cells polarised towards T<sub>H1</sub> or T<sub>H2</sub> subtypes, which revealed a highly protective capacity of these cells against ECM and blood stage *P. berghei* infection. We conclude that PbHsp90<sub>484-496</sub> is a valuable epitope for the study of CD4 T cells against malaria in the C57BL/6 background.

## 2. Results

### 2.1. PbT-II cells form long-lived memory

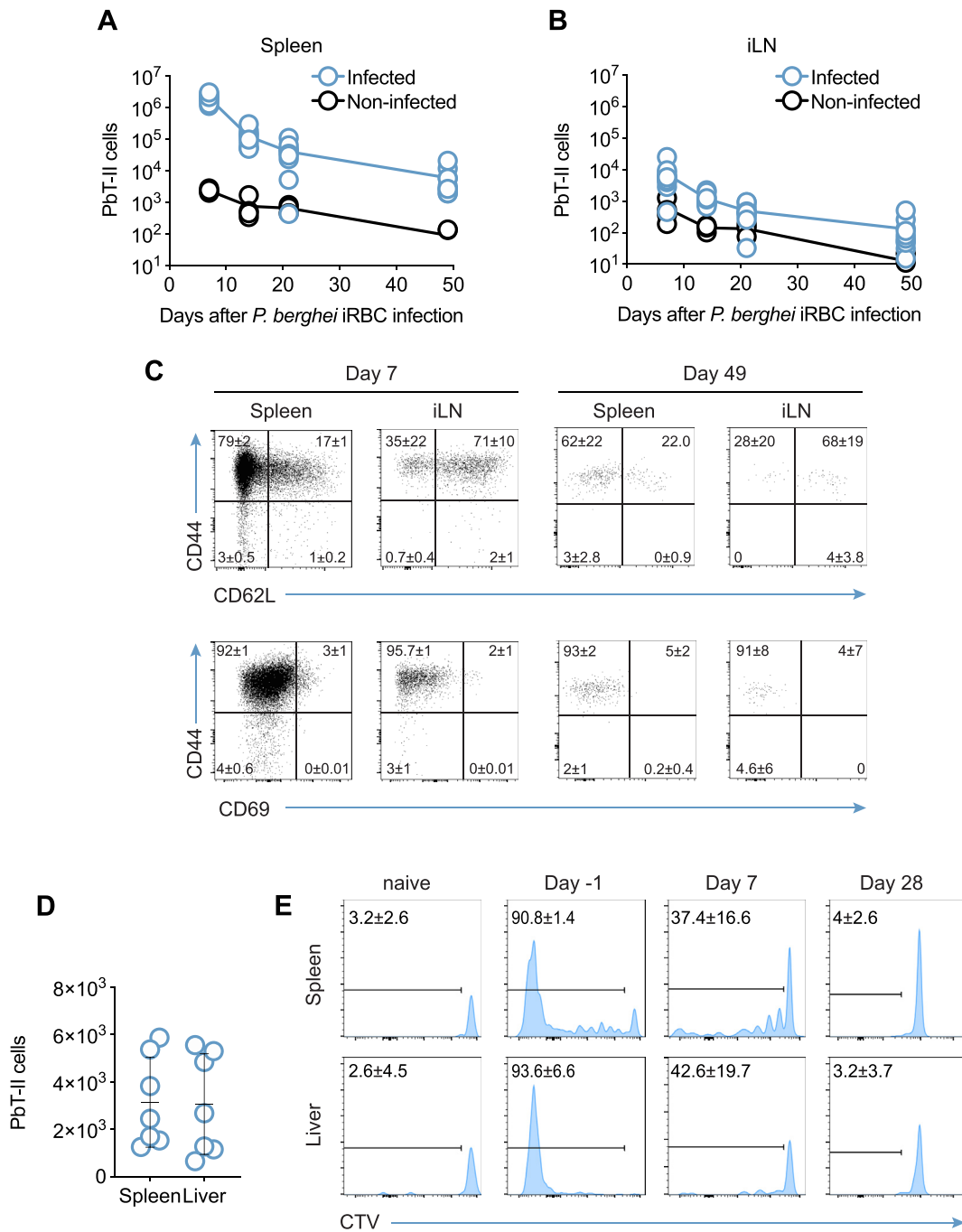
We recently described a novel MHC-II-restricted TCR transgenic

mouse line, termed PbT-II, that responds to a conserved, unidentified *Plasmodium* epitope (Fernandez-Ruiz et al., 2017). While acute responses had been measured, it was unclear whether cells of this specificity formed memory populations, an issue relevant to vaccine development. To address this issue, we adoptively transferred 50,000 PbT-II cells expressing GFP (PbT-II.GFP) into B6 host mice, infected these mice intravenously (i.v.) with 10<sup>4</sup> *P. berghei*-infected red blood cells (iRBC) and enumerated PbT-II cells in the spleen and inguinal lymph nodes (iLN) up to day 49 after infection (Fig. 1A–C, S1). In this type of experiment, ECM kills all mice within 2 weeks of infection. Consequently, mice were treated with chloroquine from day 5 to avoid development of ECM. Blood stage *P. berghei* infection induced extensive expansion of PbT-II cells and seeding of lymphoid organs by day 7. A progressive decline in numbers of PbT-II cells occurred thereafter, with significant numbers still remaining on day 49 (Fig. 1A and B). Virtually all effector and memory PbT-II cells expressed CD44 (Fig. 1C). In the spleen, most PbT-II cells (approximately 79% on average) were CD62L<sup>−</sup> at each time point examined, hence displaying a T<sub>EM</sub> phenotype (Fig. 1C). In the inguinal lymph node, as expected, the great majority of PbT-II cells (>70%) were CD62L<sup>+</sup>, as this marker is required for T cell entry to these lymphoid organs. We detected no expression of CD69 in either organ (Fig. 1C), suggesting cells were not continuously exposed to stimulation by antigen, nor formed resident memory populations in these tissues. Numbers of PbT-II cells transferred into naïve recipients remained low throughout the time course (Fig. 1A and B), with some of them showing CD44 expression early after transfer (Fig. S1C). Together, these data indicated that PbT-II cells could form memory populations in response to *P. berghei* blood-stage infection.

PbT-II cells have also been shown to respond to *P. berghei* radiation attenuated sporozoites (RAS) (Fernandez-Ruiz et al., 2017), and vaccination of mice adoptively transferred with PbT-II.GFP cells revealed memory cells persisting in the spleen 50 days post-infection (Fig. 1D). To confirm that these PbT-II cells were not simply effectors responding to persisting antigen, we evaluated the persistence of the antigen recognised by PbT-II cells after RAS infection. To do this, we transferred CTV-coated, naïve PbT-II cells at different time points (day −1, 7 or 28) after RAS vaccination and measured their proliferation in the spleen and the liver (Fig. 1E). We detected some proliferation of PbT-II cells transferred on day 7 after RAS infection, indicating that their cognate antigen was still present at this time point. However, no proliferation was detected on PbT-II cells transferred on day 28. This suggested that the PbT-II cells identified on day 50 after RAS infection were memory T cells maintained independently of continuous antigenic stimulation.

### 2.2. Discovery of the cognate antigen of PbT-II cells

While PbT-II cells are highly useful to study CD4 T cell responses against malaria, their cognate antigen was unknown. This prevented us from studying endogenous CD4 T cell responses of the same specificity, limiting the scope of applicability of this new tool. We therefore sought to define the cognate epitope of PbT-II cells using a mass spectrometry-based approach. To do this, we cultured large numbers of DC (obtained from C57BL/6 mice treated with Flt3 ligand-producing cells (Mach et al., 2000)) with blood stage *P. berghei* parasites for 8 h (Valencia-Hernandez et al., 2020). We then eluted MHC-II (I-A<sup>b</sup>)-bound peptides from these DC and used high resolution mass spectrometry to identify *P. berghei*-derived peptides in the eluate. Using this workflow, we identified a total of 1187 epitopes derived from *P. berghei* alongside 26,578 epitopes of murine origin. 75 of these *P. berghei*-derived peptides fulfilled the following criteria and were selected for further analysis: (i) they were between 13 and 20 amino acids in length, (ii) they had been assigned a Byonic search engine score of at least 185 (which reflects the quality of peptide-spectrum matches), (iii) they were absent from naïve DC control samples, (iv) they showed either 100% sequence identity in *P. yoelii*, *P. chabaudi* and *P. falciparum*, or >90% sequence identity in *P. falciparum*. These peptides were chemically synthesised. To test their capacity to activate PbT-II cells, we enriched PbT-II.GFP cells from the spleen of a

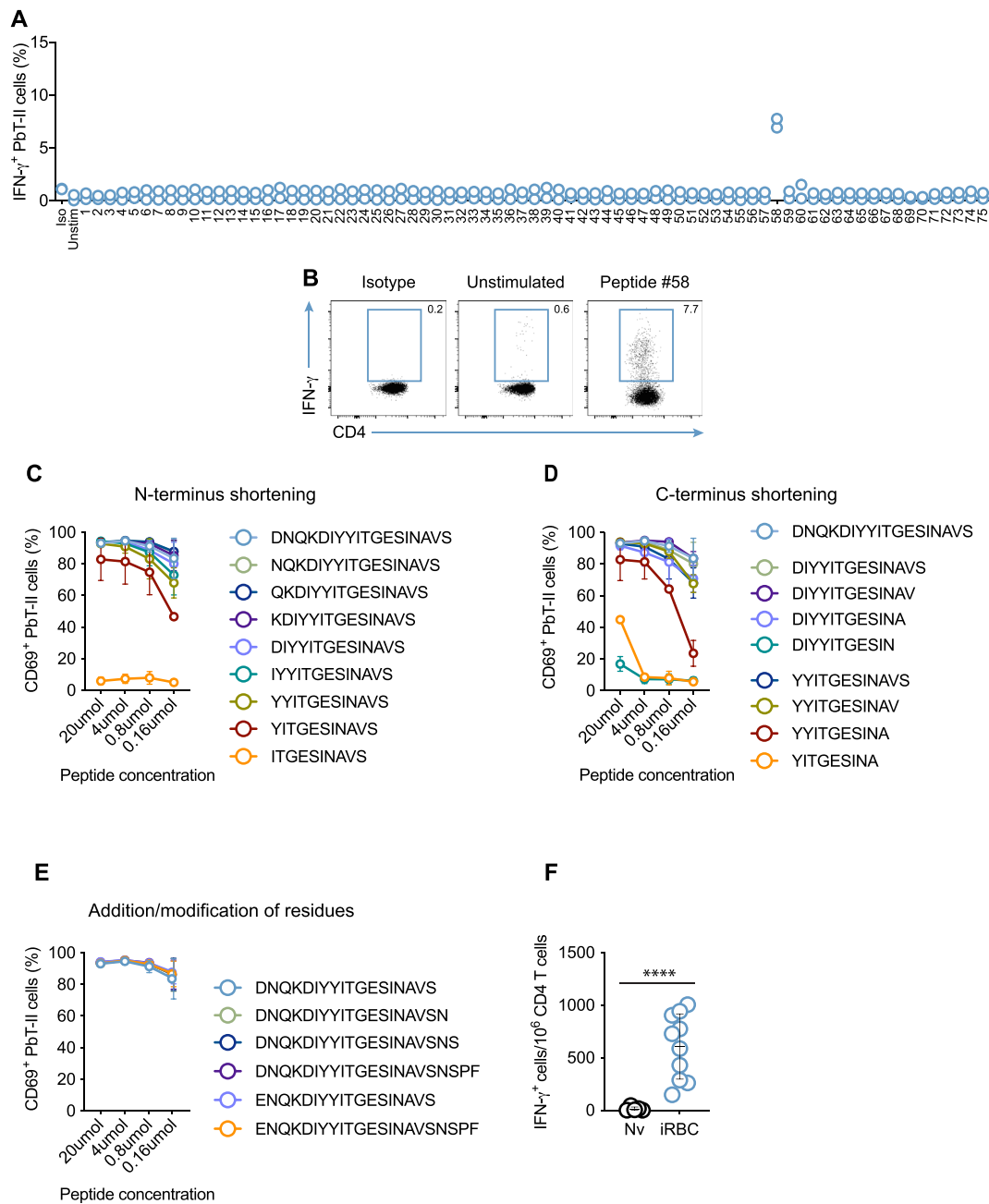


**Fig. 1. Hsp90-specific CD4 T cells form stable memory. A-B. PbT-II cell expansion and memory formation after *P. berghei* iRBC infection followed by chloroquine treatment.** Naïve, WT C57BL/6 mice received  $5 \times 10^4$  PbT-II.GFP cells, were injected (blue) or not (black) with  $10^4$  *P. berghei* iRBC i.v. on the next day and were treated with chloroquine from day 5. PbT-II cells were enumerated in the spleen (A) and inguinal lymph nodes (B) on the indicated days. Data were pooled from 2 independent experiments; each one with 5 infected and 1–2 non-infected mice. **C. Representative FACS plots of PbT-II cells** from panels A and B, gated on days 7 or 49. Numbers represent average percentages  $\pm$  SD of total CD4 T cells. **D. Memory PbT-II cell generation after RAS immunisation.** Mice received  $5 \times 10^4$  PbT-II.GFP cells and were infected with  $5 \times 10^4$  *P. berghei* RAS i.v. on the next day. PbT-II cells were enumerated in the spleen and the liver 50 days after immunisation. Data were pooled from 2 independent experiments, with 2–4 mice per group and experiment. Error bars represent mean  $\pm$  SD. **E. Proliferation of PbT-II cells upon transfer into RAS immunised mice.** Mice received  $5 \times 10^4$  *P. berghei* RAS i.v. on day 0, and  $5 \times 10^5$  CTV-coated PbT-II.GFP cells on days -1, 7 or 28 after RAS injection. Proliferation of PbT-II cells in the spleen and the liver was determined 5 days after injection of RAS. Representative histograms are shown. Numbers represent mean percentages of total CD4 T cells  $\pm$  SD. Data are representative for 2 independent experiments, each one with 3 mice/group.

PbT-II mouse infected with *P. berghei* iRBC 8 days earlier and treated with chloroquine from day 4. We restimulated these PbT-II cells *in vitro* with a small amount of each of the chemically synthesised peptides and performed intracellular staining for IFN- $\gamma$ . Peptide 58 (DNQKDIYYITGESI-NAVS) induced a significant upregulation of IFN- $\gamma$  production in PbT-II cells (Fig. 2A and B). This peptide originates from the heat shock protein

90 (Hsp90) of *P. berghei* (PBANKA\_0805700). Hsp90 is one of the most abundant chaperons and shares 94% sequence identity with its ortholog in *P. falciparum*, PfHsp90.

MHC-II molecules have an open groove from which peptides can protrude (Chicz et al., 1992), and so we next sought to define the minimal epitope capable of stimulating PbT-II cells. Smaller versions of peptide 58



**Fig. 2. Discovery of the cognate peptide of PbT-II cells. A,B. Identification of a Plasmodium peptide recognised by PbT-II cells.** Splenocytes from a PbT-II.GFP mouse infected with  $10^4$  *P. berghei* iRBC i.v. 8 days earlier and treated with chloroquine from day 4 were cultured for 5 h with brefeldin A and candidate peptides at a concentration of 2.5  $\mu$ M, and intracellularly stained. Cells were gated as CD4<sup>+</sup> V $\alpha$ 2<sup>+</sup> GFP<sup>+</sup> and IFN- $\gamma$ <sup>+</sup>. **A.** Percentages of IFN- $\gamma$ <sup>+</sup> PbT-II cells. Data were pooled from two independent experiments. **B.** Representative FACS plots of samples in A. **C-E. Identification of the minimal epitope recognised by PbT-II cells.** Splenocytes from a naïve PbT-II.GFP mouse were cultured overnight with the titrated amounts of the indicated peptides and expression of CD69 was measured by flow cytometry. Data were pooled from 2 independent experiments. **C.** Subtraction of residues at the N-terminus of DNQKDIYYITGESINAVS. **D.** Subtraction of residues at the C-terminus of DNQKDIYYITGESINAVS. **E.** Responsiveness of PbT-II cells to Hsp90 epitopes larger than DNQKDIYYITGESINAVS and to their *P. falciparum* versions. Data in C-E were pooled from 2 independent experiments; error bars represent mean  $\pm$  SD. **F. Detection of Hsp90-specific endogenous CD4 T cell responses in mice exposed to blood stage *P. berghei* infection.** Naïve WT C57BL/6 mice were infected with  $10^4$  *P. berghei* iRBC i.v. and were treated with chloroquine from day 5. On day 7 after infection, splenocytes were enriched for CD4 T cells and incubated with the DIY peptide for 18 h. ELISpot was performed to detect IFN- $\gamma$  producing cells. Data were log transformed and compared using a Student's t-test. Two values of "0" in the control group were transformed to "1" to enable log transformation. Data are representative for two experiments, each one with 2–3 naïve and 5 infected mice per group. Error bars represent mean  $\pm$  SD.

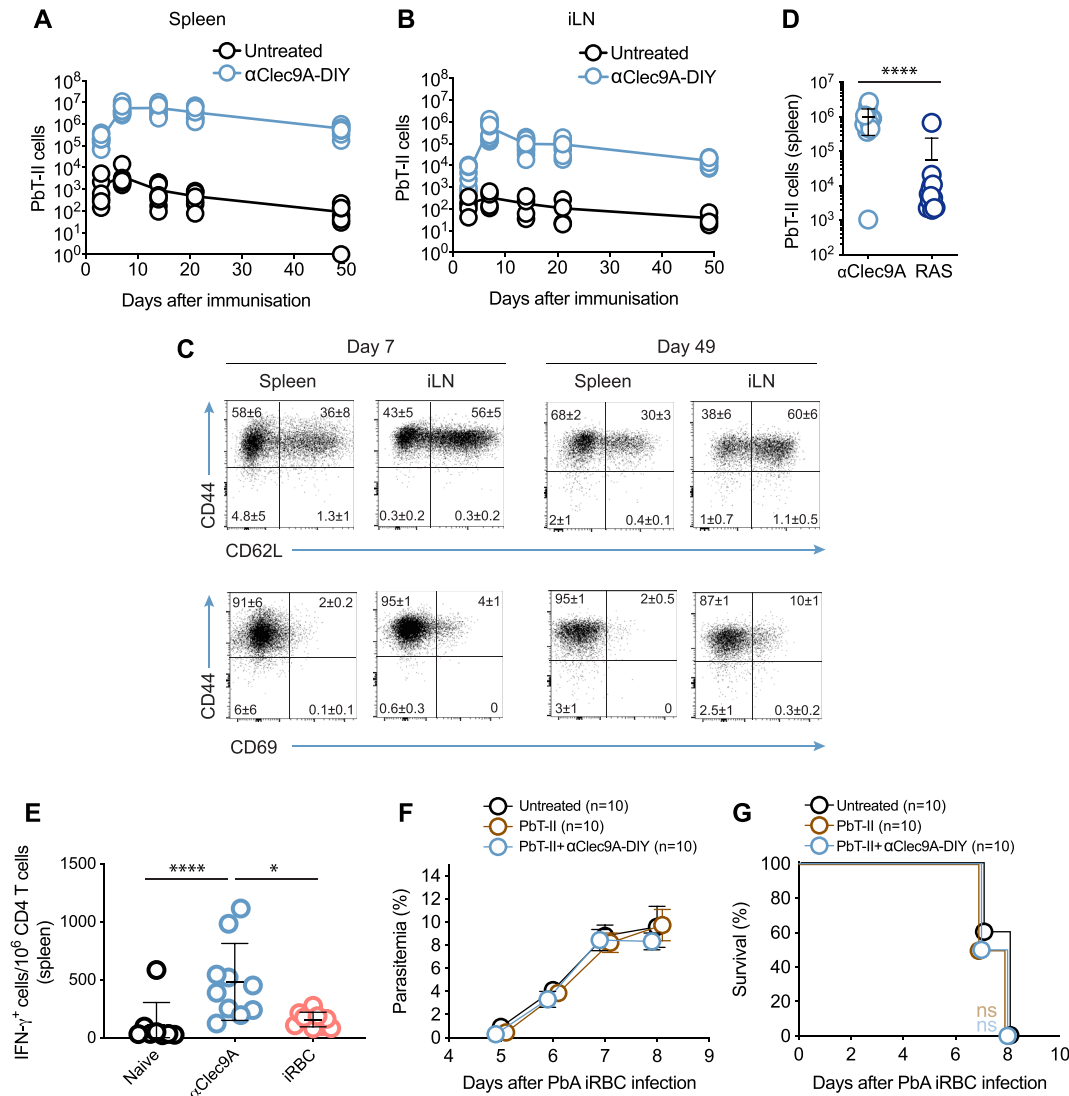
shortened at their N-terminus (Fig. 2C) were synthesised and tested for their capacity to induce CD69 upregulation in naïve PbT-II cells. Peptide variant DIYYITGESINAVS provided maximal response, comparable to that elicited by peptide 58, and YYITGESINAVS was the shortest peptide version to provide a substantial response. We then tested the responsiveness of peptide variants shortened at their C-terminus. On the basis of

our previous result, we used shortened versions of DIYYITGESINAVS and YYITGESINAVS. While removal of the C-terminal serine had minimal impact on the stimulatory capacity of these peptides, removal of the valine significantly diminished PbT-II responses (Fig. 2D). We conclude that the minimum epitope required for maximal stimulation of PbT-II cells is DIYYITGESINAV, or PbHsp90<sub>484-496</sub> (termed hereafter DIY for

simplicity), with YYITGESINAV still inducing substantial responses. We next evaluated the stimulatory capacity of Hsp90-derived peptides longer than peptide 58. Addition of at least four extra residues to the C-terminus of peptide 58 still resulted in maximal PbT-II stimulation (Fig. 2E). The sequence of peptide 58 in the *P. falciparum* ortholog of *P. berghei* Hsp90 differs from the latter in the first residue at its N-terminus, which changes from aspartic acid in *P. berghei* to glutamic acid. We found PbT-II cells to respond equally strongly to either peptide (Fig. 2E). Identification of the optimal epitope recognised by PbT-II cells allowed examination of the

endogenous CD4 T cell response to this epitope. An ELISpot assay revealed splenic IFN- $\gamma$  producing T cells specific for the DIY epitope were induced on day 7 after *P. berghei* blood-stage infection of B6 mice (Fig. 2F), establishing that *PbHsp90*-specific endogenous CD4 T cells responded to this infection.

Knowledge of the cognate peptide recognised by PbT-II cells also enabled us to target this epitope through vaccination, and to study its potential as a target for immunisation against malaria. Because CDC1 are the main antigen presenting cell for CD4 T cells in malaria



**Fig. 3.  $\alpha$ Clec9A vaccination targeting the DIY epitope of Hsp90 induces potent memory formation.** A-C. **Immunisation with  $\alpha$ Clec9A-DIY induces strong PbT-II cell memory formation.** Naïve C57BL/6 mice received  $5 \times 10^4$  PbT-II.GFP cells and were immunised with  $8 \mu\text{g}$   $\alpha$ Clec9A-DIY mAb and  $5 \text{ nmol}$  CpG. Numbers of PbT-II cells were measured in the spleen (A) and inguinal lymph node (B) at the indicated time points after immunisation. Data were pooled from two independent experiments, each one with 2–4 untreated and 5 vaccinated mice per group. C. **Representative FACS plots of PbT-II cells** from panels A and B, gated on days 7 or 49. Numbers represent average percentages  $\pm$  SD of total CD4 T cells. D.  **$\alpha$ Clec9A vaccination induces more potent PbT-II memory than RAS.** Mice received  $5 \times 10^4$  PbT-II.GFP cells and were injected with either  $2 \mu\text{g}$   $\alpha$ Clec9A-DIY and  $5 \text{ nmol}$  CpG or  $5 \times 10^4$  RAS. Numbers of memory PbT-II cells were measured in the spleen on day 28 after immunisation. Data were log-transformed and compared using a Student's t-test. Data were pooled from 2 independent experiments; with 3–10 mice/group. Error bars represent mean  $\pm$  SD. E. **Induction of a specific endogenous CD4 T cell response to the DIY epitope by  $\alpha$ Clec9A-DIY vaccination.** Mice were immunised with  $2 \mu\text{g}$   $\alpha$ Clec9A-DIY and  $5 \text{ nmol}$  CpG or infected with  $10^4$  *P. berghei* iRBC and cured from day 5. On day 35 after immunisation/infection, splenocytes (including  $250,000$  CD4 T cells/well) were restimulated *in vitro* with the DIY peptide and ELISpot was performed to detect IFN- $\gamma$  producing cells. Data were log-transformed and compared using one-way ANOVA and Tukey's Multiple Comparisons test. Data were pooled from 2 independent experiments; each one with 4–5 mice per group. Error bars represent mean  $\pm$  SD. F, G. **Protective capacity of  $\alpha$ Clec9A-DIY vaccination against blood stage *P. berghei* infection.** Mice received  $5 \times 10^4$  PbT-II.GFP cells and were immunised with  $2 \mu\text{g}$   $\alpha$ Clec9A-DIY and  $5 \text{ nmol}$  CpG one day later. They then were infected with  $10^4$  *P. berghei* iRBC 7–14 days after priming. F. **Course of *P. berghei* parasitaemia.** Data were log-transformed and analysed using One-Way ANOVA and Dunnett's Multiple Comparisons tests comparing each group's parasitemia with that of the untreated group. No significant differences were found. G. **Survival.** Statistical analysis of survival was carried out by performing pairwise comparisons between the different groups using log-rank tests and adjusting for multiple comparisons by performing a Bonferroni correction for the total number of groups (significance level was  $P < 0.016$ ; n.s.,  $P > 0.016$ ). Data in F, G were pooled from 2 independent experiments, each one with 5 mice/group.

(Fernandez-Ruiz et al., 2017), we generated a reagent to shuttle the PbT-II epitope to this DC subtype for maximal responses: we conjugated the DIY epitope to a monoclonal antibody (mAb) that targets Clec9A, a canonical surface receptor of cDC1. Optimal CD4 T cell priming does not necessarily require an adjuvant (Lahoud et al., 2011), and thus we first compared the capacity of this reagent to induce the expansion of PbT-II cells, with or without CpG adjuvant, which was previously shown to be optimal for the expansion of CD8 T cells through  $\alpha$ Clec9A mAb (Fernandez-Ruiz et al., 2016). Indeed, maximal PbT-II proliferation was achieved even at lower doses of  $\alpha$ Clec9A-DIY when this mAb was administered together with CpG adjuvant (Fig. S2). We therefore decided to utilise the  $\alpha$ Clec9A-DIY reagent in combination with CpG adjuvant for subsequent experiments.

We next sought to determine the kinetics of PbT-II cell expansion and persistence after  $\alpha$ Clec9A-DIY immunisation. Mice received 50,000 PbT-II.uGFP cells and were immunised with 8  $\mu$ g  $\alpha$ Clec9A-DIY and 5 nmol CpG, and PbT-II cells were enumerated and phenotyped in the spleen and inguinal lymph node up to day 49 after immunisation (Fig. 3A–C, S3). This revealed a large expansion of PbT-II cells and the formation of memory T cells in vaccinated mice (Fig. 3A and B). These cells showed a phenotype similar to that of PbT-II cells generated after iRBC infection (Figs. 3C and 1C). However, compared to blood-stage infection, the proportion of T<sub>CM</sub> cells was somewhat higher in the spleen and lower in the LN (Figs. 3C and 1C), and a small but consistent population of LN PbT-II cells (~10%) expressed CD69 (Fig. 3C). The total number of memory PbT-II cells in the spleen on day 27 after immunisation using 2  $\mu$ g  $\alpha$ Clec9A-DIY and 5 nmol CpG was significantly higher than that obtained in mice vaccinated with 50,000 RAS (Fig. 3D). In the absence of PbT-II cell adoptive transfer, vaccination with  $\alpha$ Clec9A-DIY also expanded an endogenous population of specific CD4 T cells and generated a significant number of memory cells (Fig. 3E). Again,  $\alpha$ Clec9A-DIY vaccinated mice generated significantly higher numbers of Hsp90-specific memory CD4 T cells than iRBC infected mice (Fig. 3E).

We showed previously that PbT-II cells can compensate for the lack of functional endogenous CD4 T cells in CD40L KO mice and, partially, in RAG KO mice, provide immunity against *P. chabaudi* infection (Fernandez-Ruiz et al., 2017). The development of the  $\alpha$ Clec9A-DIY reagent enabled us to test whether immunisation expanding these cells could improve immunity against blood stage *Plasmodium* infection. To assess this question, PbT-II.uGFP cells were adoptively transferred into B6 mice prior to vaccination with  $\alpha$ Clec9A-DIY and CpG adjuvant, and then these mice were challenged 7–14 days later with 10,000 *P. berghei* iRBC. This vaccination regime did not provide protection, however, based neither on reduced parasitaemia levels (Fig. 3F) nor the onset of ECM (Fig. 3G).

### 2.3. Generation of different helper phenotypes of PbT-II cells

CD4 T cells are highly heterogeneous, with modes of immunisation and adjuvants potentially inducing different types of helper phenotypes in activated effector cells. We reasoned that the failure of  $\alpha$ Clec9A-DIY vaccination in inducing protection from blood stage *P. berghei* infection might be due to the generation of effector CD4 T cell phenotypes of suboptimal efficacy against this type of infection, particularly as this approach primarily induces cells of a T<sub>FH</sub> phenotype (Kato et al., 2015). The identification of the cognate epitope of PbT-II cells provided the opportunity to *in vitro* activate these cells under specific polarising conditions to generate populations of helper cells of particular phenotypes. Thus, *in vitro* activation of PbT-II cells under T<sub>H1</sub>-polarising conditions induced approximately 90% of the activated cells to produce either IFN- $\gamma$  or TNF, with 70% producing both cytokines, 7 days after transfer into recipient mice (Fig. 4A–C). In contrast, PbT-II activation under T<sub>H2</sub>-polarising conditions induced >70% of cells to produce IL-4 or IL-13, with nearly 50% of these cells producing both cytokines. A substantial proportion of T<sub>H2</sub>-polarised cells (above 40%) also expressed TNF. Both T<sub>H1</sub> and T<sub>H2</sub>-polarised cells contained similar frequencies (approximately 55%) of IL-2 producing cells. Importantly, Th1- and Th2-polarised cells

maintained their phenotype in naïve recipient mice for at least 35 days after transfer (Fig. S4).

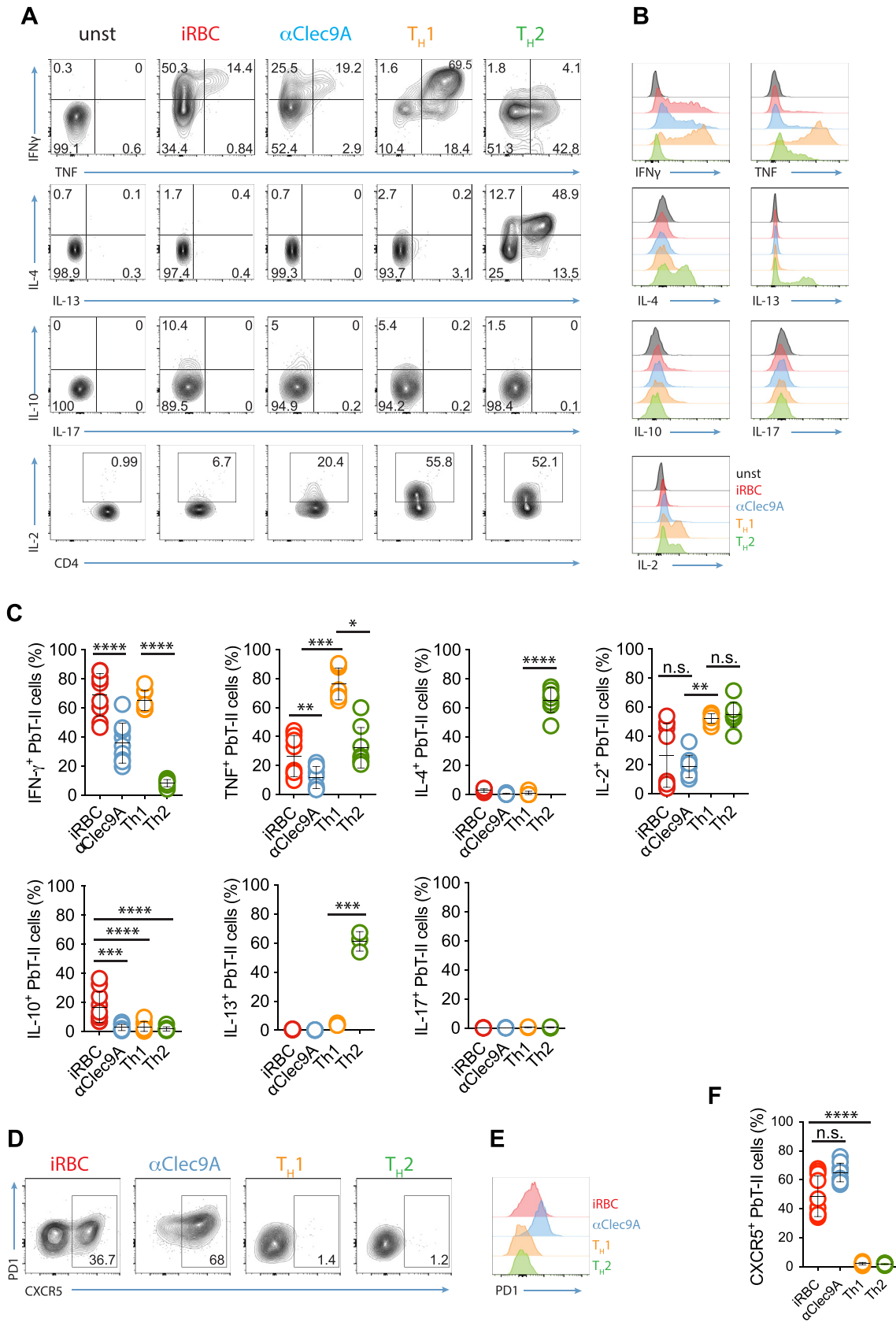
In comparison with *in vitro*-polarised cells, PbT-II cells expanded *in vivo* by  $\alpha$ Clec9A-DIY immunisation displayed a T<sub>H1</sub>-like phenotype on day 7, with high expression of IFN- $\gamma$ , but a low percentage of these cells expressed TNF compared to T<sub>H1</sub>-polarised cells activated *in vitro*. The phenotype of the PbT-II cells expanded after  $\alpha$ Clec9A-DIY immunisation was indeed similar to that induced by blood stage *P. berghei* infection, with the latter inducing higher percentages of IFN- $\gamma$ - and TNF-producing PbT-II cells, but a similar percentage of IL-2-producing PbT-II cells. Only iRBC infection induced moderate IL-10 expression in PbT-II cells, and none of the strategies used to activate PbT-II cells induced IL-17 expression (Fig. 4A–C). In agreement with previous reports (Fernandez-Ruiz et al., 2017), a significant proportion of PbT-II cells activated during blood stage *P. berghei* infection adopted a T<sub>FH</sub> phenotype (Fig. 4D–F). Indeed, this was also the case for cells activated using  $\alpha$ Clec9A-DIY, with close to 70% of the PbT-II cells expressing increased levels of CXCR5 and PD1 (Fig. 4D–F). This proportion was however not significantly higher than that induced by *P. berghei* iRBC infection (Fig. 4F). PbT-II cells activated *in vitro* under T<sub>H1</sub> or T<sub>H2</sub>-polarising conditions did not develop into a T<sub>fh</sub> phenotype (Fig. 4D–F).

We next sought to determine whether *in vitro* activated T<sub>H1</sub> or T<sub>H2</sub> PbT-II cells would differ from those generated by  $\alpha$ Clec9A-DIY immunisation in their capacity to protect mice from blood stage *P. berghei* infection. Mice received 10<sup>7</sup> *in vitro* activated T<sub>H1</sub> or T<sub>H2</sub> PbT-II or gDT-II cells and were challenged with 10<sup>4</sup> *P. berghei* iRBC 7 days after transfer. Mice that received either type of PbT-II cells developed lower levels of parasitaemia (Fig. 5A) and were significantly protected from ECM (Fig. 5B). Similar results were obtained when mice were challenged 35 days after T cell transfer (Fig. 5C and D). In this case, however, T<sub>H2</sub> PbT-II cells provided better protection against ECM than T<sub>H1</sub> cells. *In vitro* activated CD4 T cells of an irrelevant specificity (gDT-II cells) did not alter the course of parasitaemia nor influenced ECM development (Fig. 5A–D).

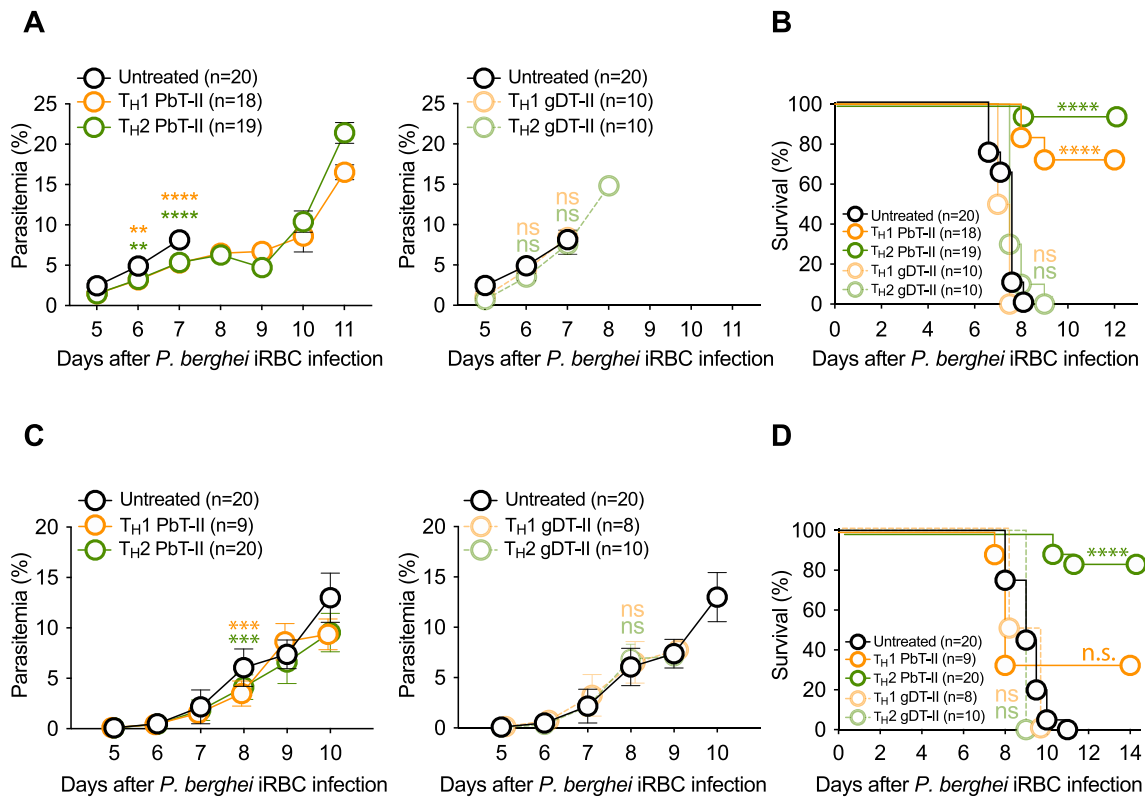
### 3. Discussion

Here, we identified PbHsp90<sub>484-496</sub> as the cognate antigen of PbT-II cells, opening new ways to utilise a versatile tool for the study of CD4 T cells in malaria, and enabling the study of endogenous CD4 T cells of the same specificity. Identification of this epitope enabled us to target CD4 T cells for vaccination against blood stage *Plasmodium* infection, and to generate populations of polarised PbT-II cells and test their protective capacity, revealing a protective role for T<sub>H2</sub> cells, and moderately for T<sub>H1</sub> cells, against blood stage infection.

The immunogenic epitope within *P. berghei* Hsp90 initially identified here using mass spectrometry as capable of activating PbT-II cells (peptide 58) is an 18-mer peptide (DNQKDIYYITGESINAVS) eluted from MHC-II molecules (I-A<sup>b</sup>) of parasite-exposed DC. MHC-II molecules have an open peptide-binding groove that enables loading of large peptides, which can protrude from both sides of the cleft (Hunt et al., 1992; Brown et al., 1993). Binding of the peptide to the MHC-II molecule occurs through via a core of 9 residues containing critical anchor points. But this core 9-mer is not necessarily fixed. For instance, in some cases the same peptide can bind to MHC-II molecules in different registers, thus using different 9-mer cores (McFarland et al., 1999). However, flanking residues of the 9-mer core can influence MHC-II stability and the peptide conformation in the cleft, as well as make contact with the TCR, playing a role in its affinity for MHC-II (McFarland et al., 1999; Landais et al., 2009; Nelson et al., 1994; Holland et al., 2013). It was therefore important to identify the minimal epitope within the PbHsp90-derived 18-mer peptide initially identified by mass spec (DNQKDIYYITGESINAVS), and to determine whether additional flanking residues influenced PbT-II cell responsiveness. We conclude that the 9-mer core that mediates binding to MHC-II is YITGESINA, as deletion of any further residues on either side drastically reduced PbT-II cell stimulation. However, the 14-mer



(caption on next page)



**Fig. 5. Hsp90-specific  $T_H2$  cells induce partial immunity to blood stage *Plasmodium* spp. infection, and ECM protection. A-D. Protective capacity of in vitro polarised  $T_H1$  or  $T_H2$  effector Hsp90-specific CD4 T cells on the course of *P. berghei* iRBC infection.** Naïve C57BL/6 mice received  $10^7$  in vitro activated,  $T_H1$ - or  $T_H2$ -polarised PbT-II or control gDT-II cells and were infected with  $10^4$  *P. berghei* iRBC 7 days later (A, B) or 100 *P. berghei* iRBC 35 days later (C, D). A, C. Course of *P. berghei* parasitaemia. For clarity, test and control groups are shown in separate graphs (PbT-II, left panels; gDT-II, right panels). Data were log-transformed and analysed using One-Way ANOVA and Dunnett's Multiple Comparisons tests comparing each group's parasitemia with that of the untreated group (n.s. = not significant,  $P > 0.05$ ; \*\*,  $P < 0.01$ ; \*\*\*,  $P < 0.001$ ; \*\*\*\*,  $P < 0.0001$ ). B, D. Survival. Survival was analysed by performing pairwise comparisons between the different groups using log-rank tests and adjusting for multiple comparisons by performing a Bonferroni correction for the total number of groups (significance level was  $P < 0.01$ ; n.s.,  $P > 0.01$ ; \*\*\*\*,  $P < 0.0001$ ). Data were pooled from 2 to 3 independent experiments for the untreated, Th1- and Th2-PbT-II groups, and 1–2 experiments for Th1- and Th2-gDT-II groups, with 4–10 mice/group.

DIYYITGESINAVS, including extra residues at both the N- and the C-termini of the 9-mer core peptide, provided the highest stimulation of PbT-II cells. Remarkably, addition of further residues to this 14-mer, either to the N- or the C-termini, up to a total of at least 22 residues, still resulted in maximal PbT-II cell responsiveness, suggesting that these residues likely protrude outside the region of interaction between the MHC-II molecule and the TCR and neither are necessary, nor obstruct, PbT-II recognition of Hsp90. Also, post administration digestion of these larger peptides may contribute to their stimulatory capacity. In any case, this feature has broader implications in vaccination seeking to generate *Plasmodium*-specific CD4 T cell responses. As shown here for *P. falciparum* Hsp90, residue variation outside the 9-mer core between orthologs across different parasites does not appear to affect immunogenicity, enabling the target of multiple *Plasmodium* species through subunit vaccination containing relatively small epitopes, as long as the MHC-binding core epitope is maintained. Moreover, larger peptides may contain multiple

core registers presentable by different HLA molecules, thus broadening immunogenicity in human populations.

Hsp90 is an essential, highly conserved and abundant protein in all eukaryotic organisms, including *Plasmodium* parasites, which consists of different subtypes. *PbHsp90* (PBANKA\_0805700) has a relatively high sequence identity (66%) with both mouse Hsp90 $\alpha$  (*Hsp90aa1*) and Hsp90 $\beta$  (*Hsp90ab1*). The peptide DIYYITGESINAVS in *PbHsp90* changes to HIYFITGETKDQVA in mouse Hsp90 $\alpha$  (50% identity) and to SIYYITGESKEQVA in mouse Hsp90 $\beta$  (64% identity). Similarly, *P. falciparum* Hsp90 (Pf3D7\_0708400) has 68% and 64% sequence identity with human Hsp90 $\alpha$  and Hsp90 $\beta$  respectively (PlasmoDB). Hsp90 is conserved across several parasitic protists such as *Plasmodium*, *Toxoplasma*, *Trypanosoma* or *Leishmania* and this is reflected in the fact that growth of parasites as diverse as *P. falciparum*, *P. berghei*, *Toxoplasma gondii*, and *Trypanosoma evansi* can be inhibited by geldanamycin, a structural analog of ATP that interferes with Hsp90 function (Pallavi et al., 2010;

**Fig. 4. Phenotype of PbT-II cells activated in vitro or generated after *P. berghei* iRBC infection or  $\alpha$ Clec9A immunisation. A-C. Characterisation of activated PbT-II cells.** Naïve C57BL/6 mice received  $5 \times 10^4$  PbT-II.GFP cells and were infected with  $10^4$  *P. berghei* iRBC, or immunised with 2  $\mu$ g  $\alpha$ Clec9A-DIY and 5 nmol CpG one day later ( $\alpha$ Clec9A), or received  $2 \times 10^6$  PbT-II cells activated in vitro under  $T_H1$ - or  $T_H2$ -polarising conditions. IFN- $\gamma$ , TNF, IL-4, IL-13, IL-10, IL-17 and IL-2 levels in PbT-II cells from the spleen were examined by intracellular staining on day 7 after infection/immunisation/adoptive cell transfer. Unst = unstained intracellularly. A. Representative dot plots. B. Representative histograms. C. Percentages of PbT-II cells expressing the indicated cytokines. D-F. Determination of the proportion of Tfh cells. Additional samples were stained for CXCR5 and PD1 to estimate proportions of Tfh cells generated. D. Representative contour plots. E. Representative histograms for PD1 expression. F. Proportions of Tfh cells generated. Fig. 4A and B are representative for the data shown in Fig. 4C. Fig. 4D and E are representative for the data shown in Fig. 4F. Data in Fig. 4C and F were pooled from 2 independent experiments for IL-2, IL-4, IFN- $\gamma$  and IL-10. IL-17 and IL-13 expression was examined in one experiment. Each experiment included 3–5 mice per group. Error bars in 4C and 4F denote mean  $\pm$  SD. Data were log-transformed and analysed using one-way ANOVA and tukey's Multiple Comparisons tests. n.s. = not significant,  $P > 0.05$ ; \*,  $P < 0.05$ ; \*\*,  $P < 0.01$ ; \*\*\*,  $P < 0.001$ ; \*\*\*\*,  $P < 0.0001$ .

Echeverria et al., 2005; Banumathy et al., 2003). PfHsp90 associates with other proteins, such as Hsp70, via an adaptor protein (Banumathy et al., 2003; Gitau et al., 2012) to function as an ATP-dependent chaperon, contributing to the folding of newly synthesised proteins and cell growth, and to mediating signal transduction (Pratt, 1997; Daniyan et al., 2019). Interestingly, Hsp90 stabilises ribosomal subunit components (Kim et al., 2006), another abundant group of *Plasmodium* proteins that coincidentally contain protective CD8 T cell epitopes (Valencia-Hernandez et al., 2020). PfHsp90 is predominantly present in the cytoplasm of the parasite (Gitau et al., 2012), and, unlike other heat shock proteins, it has not been found within the exportome to the host's RBC (Sargeant et al., 2006). Nevertheless, this does not diminish its immunogenic properties, as APC can take up parasites and present internal proteins to CD4 T cells via MHC-II molecules (Fernandez-Ruiz et al., 2017; Arroyo and Pepper, 2020). Indeed, while the intracellular location of Hsp90 impedes its targeting by antibodies, PbHsp90-specific PbT-II cells can still activate B cells of other specificities for isotype switching and the production of high affinity, protective antibodies (Fernandez-Ruiz et al., 2017). Importantly, the immunogenicity of PbHsp90<sub>484-496</sub> upon natural iRBC infection seems moderate (approximately 0.05% of total endogenous splenic CD4 T cells in *P. berghei* infected mice specific for this epitope, Fig. 2F) compared to that previously established for dominant MHC-II *P. berghei* epitopes such as ENTRAMP, GADPH or EF1 $\alpha$  (roughly 0.1–0.5% of total CD4 T cells in *P. berghei* infected mice) (Draheim et al., 2017). This could reflect differences in the expression of these antigens (Draheim et al., 2017), or may reflect a relative scarcity of PbHsp90<sub>484-496</sub>-specific precursors in the naïve CD4 T cell repertoire of B6 mice compared to these other specificities. However, this did not hinder our capacity to efficiently expand PbHsp90<sub>484-496</sub>-specific cells and generate robust memory through  $\alpha$ Clec9A vaccination, supporting the suitability of this antigen as a target for vaccination studies.

CD4 T cells are important mediators of immunity against blood stage *Plasmodium* infection (Perez-Mazliah and Langhorne, 2014). Subpopulations of parasite-specific T<sub>H1</sub> and T<sub>H2</sub> CD4 T cells form shortly after blood stage *P. berghei* and *P. chabaudi* infection (Lonnberg et al., 2017; Fernandez-Ruiz et al., 2017). T<sub>H1</sub> cells appear to contribute to the modulation of the peak of *P. chabaudi* parasitemia during acute infection (Wikenheiser et al., 2016; James et al., 2018) and also reduce *P. berghei* parasitemia (Oakley et al., 2013), although impaired capacity to generate T<sub>H1</sub> cells translates into better control of non-lethal *P. yoelii* parasitemia (Oakley et al., 2014; Salles et al., 2017). While modulation of *P. berghei* parasitemia by CD4 T cells in C57BL/6 mice does not impede lethality early after infection, *P. chabaudi* parasitaemia progresses to a persistent stage in WT mice once a prominent first peak is reduced to almost undetectable levels. T<sub>H2</sub> cells, acting during the acute stage of infection, are essential for the generation of efficient humoral responses capable of eliminating persistent infection (Perez-Mazliah et al., 2015, 2017). Similarly, T<sub>H2</sub> cells are also critical for control of persistent parasitemia by non-lethal *P. yoelii* infections (Zander et al., 2015). Here, we tested the protective capacity of vaccination targeting Clec9A against *P. berghei*, using recombinant mAb linked to the PbHsp90 epitope, combined with a CpG-based adjuvant. This form of vaccination is known to elicit strong T<sub>FFH</sub> and humoral responses (Lahoud et al., 2011), and we indeed achieved strong formation of T<sub>FFH</sub> cells, as well as moderate generation of T<sub>H1</sub> cells capable of co-expressing IFN- $\gamma$  and TNF (Fig. 4A, D). This vaccination strategy did not exert any detectable protection of B6 mice infected with *P. berghei*.  $\alpha$ Clec9A vaccination perhaps generated insufficient numbers of T<sub>H1</sub> cells for substantial protection, and T<sub>FFH</sub> formation through vaccination may not have provided a substantial advantage of over natural, endogenous T<sub>FFH</sub> formation during the course of infection.

Identification of the PbHsp90 epitope enabled us to generate highly enriched populations of T<sub>H1</sub>-polarised PbT-II cells *in vitro* and explore their protective capacity upon adoptive transfer in a scenario in which these cells were present at high numbers, in the absence of other T<sub>H</sub> cell populations. Production of IFN- $\gamma$  (Su and Stevenson, 2000; van der Heyde et al., 1997) and TNF (Amante et al., 2010; Li and Langhorne, 2000)

contributes to the control of acute *P. berghei* and *P. chabaudi* parasitemia and, in agreement with these studies, we found that adoptive transfer of high numbers of T<sub>H1</sub> cells expressing these cytokines significantly improved parasitemia control in the *P. berghei* blood stage infection model. Vaccination strategies that promote strong T<sub>H1</sub> bias, as shown for example through induction of OX-40 signalling in effector CD4 T cells (Zander et al., 2015), may hence be more effective in controlling parasitemia than  $\alpha$ Clec9A+CpG. However, as mentioned, a T<sub>FFH</sub> component is likely still necessary, as excessive T<sub>H1</sub> bias and prevention of T<sub>FFH</sub> formation can abrogate parasitemia control (Zander et al., 2015).

Unexpectedly, T<sub>H1</sub>-polarised PbT-II cells reduced development of ECM. IFN- $\gamma$ -producing CD4 T cells have been implicated in promoting ECM in *P. berghei*-infected B6 mice by attracting effector CD8 T cells to the brain (Villegas-Mendez et al., 2012). Lack of expression of the T<sub>H1</sub> transcription factor Tbet results in lower accumulation of CD4 and CD8 T cells in the brain and no ECM (Oakley et al., 2013). While ECM can occur in B6 mice in the absence of CD4 T cells (Nitcheu et al., 2003), and hence these cells are not essential, it is possible that additional numbers of T<sub>H1</sub> cells in the spleen retained CD8 T cells in this organ through the production of IFN- $\gamma$  and prevented their migration to the brain (Teo et al., 2018). Improved control of parasitemia by T<sub>H1</sub> PbT-II T cells may have reduced parasite accumulation in the brain, hindering ECM development, as previously reported for mice in which absence of type I IFN signalling resulted in enhanced T<sub>H1</sub> generation (Haque et al., 2011).

Improved control of *P. berghei* parasitemia, as well as reduction of ECM rates, was also found after adoptive transfer of T<sub>H2</sub>-polarised PbT-II cells. T<sub>H2</sub> cells have been long known to form during *P. chabaudi* infection (Langhorne et al., 1989). Interactions with B cells promote T<sub>H2</sub> polarization in this model, and an absence of B cells results in the exclusive generation of T<sub>H1</sub> cells (Taylor-Robinson and Phillips, 1994; Langhorne et al., 1998). T<sub>H2</sub> cells were found to mediate *P. chabaudi* parasitemia control (Taylor-Robinson et al., 1993), and IL-4 KO mice, while able to control parasitemia, suffered a higher peak of acute parasitemia and a more prolonged chronic infection than their WT counterparts (von der Weid et al., 1994). Our data aligns with these studies, supporting a protective role for T<sub>H2</sub> cells in control of *P. berghei* blood stage infection. As for T<sub>H1</sub> cells, enhanced control of parasitemia by T<sub>H2</sub> cells, may have resulted in ECM impairment by reducing parasite loads in the brain. *P. berghei* infection does not seem to naturally induce substantial T<sub>H2</sub> cell polarization ((Fernandez-Ruiz et al., 2017); Fig. 4A–C), and hence adoptive transfer of *in vitro* polarised cells, or vaccination studies, remain the best strategies to study these cells in the context of *P. berghei* infection. While, as for blood stage infection,  $\alpha$ Clec9A vaccination combined with CpG adjuvant did not promote T<sub>H2</sub> formation, use of T<sub>H2</sub>-promoting adjuvants or antigen targeting to cDC2, which favour the generation of these cells (Kasahara and Clark, 2012; Sponaas et al., 2006), may enable exploiting the protective capacity of T<sub>H2</sub> cells against *Plasmodium* spp. parasitemia. Alternatively, antigen specificity can bias *Plasmodium*-specific CD4 T cell development towards T<sub>H1</sub> or T<sub>H2</sub> (Quin and Langhorne, 2001) and, while PbHsp90<sub>484-496</sub> does not appear to naturally favour the formation of T<sub>H2</sub> cells, other T cell specificities or antigen formulations may be easily harnessed through vaccination for T<sub>H2</sub>-mediated protection.

An aspect, not explored here, that presents a potential advantage of targeting *Plasmodium* Hsp90 for CD4 T cell immunity derives from the fact that this protein is expressed during both the liver and the blood stage of the infection (Fernandez-Ruiz et al., 2017; Howick et al., 2019). In addition to their aforementioned effects on blood stage immunity, CD4 T cells can directly kill liver stage parasites (Tsuji et al., 1990), and are required for the generation of protective memory CD8 T cell responses in the liver after RAS vaccination (Carvalho et al., 2002; Weiss et al., 1993). Therefore, vaccination aimed at stimulating CD4 T cells in combination of CD8 T cells may strengthen immunity against *Plasmodium* in the liver, while additionally protecting against blood stage infection, thus providing broader protection.

In summary, we identified here an immunogenic I-A<sup>b</sup>-restricted

epitope in *PbHsp90* that is highly conserved across *Plasmodium* species. This epitope joins a growing list of known *Plasmodium* epitopes (Draheim et al., 2017) to improve understanding of the role of CD4 T cells in malaria immunity.

#### 4. Materials and methods

##### 4.1. Mice

All procedures were performed in strict accordance with the recommendations of the Australian code of practice for the care and use of animals for scientific purposes. The protocols were approved by the Melbourne Health Research Animal Ethics Committee, University of Melbourne (ethic project IDs: 1112347, 1513505, 1714302, 1814522).

Female C57BL/6 (B6), GFP (Okabe et al., 1997), PbT-II (Fernandez-Ruiz et al., 2017), gDT-II (Bedoui et al., 2009), were used between 6 and 12 weeks of age. Unless otherwise specified in the figure legends, naïve WT C57BL/6 mice were used as recipients of cells, immunisation or infection in the experiments described. Mice were maintained at the specific pathogen free (SPF) Bioresources Facility (BRF) at the Department of Microbiology and Immunology (DMI), The University of Melbourne. Mice were bred onsite or purchased from the Animal Resources Center (Canning Vale, Australia). The health status of mouse lines was routinely checked by the DMI's BRF staff. Mice were housed with littermates of the same sex (up to 5 mice per box) in Tecniplast Green Line™ independently ventilated cages (IVC system; Tecniplast, Buguggiate, Italy) and kept on a regular 12-h light/dark cycle at a temperature ranging from 19 to 22 °C. Barastoc Irradiated food pellets (Ridley, Melbourne, Australia) and reverse osmosis (RO) purified water were available *ad libitum*, with water provided by a central system integrated into the rack or by sipper sacks™ (Avidity Science, Waterford, USA). Corn cob or alpha-dry were used as bedding material and environmental enrichment for nesting and play was provided. Cages were cleaned fortnightly. Experiments were carried out under pathogen-free conditions and mice were randomly assigned to experimental groups. Experimental mice were routinely monitored for appearance and behavior throughout experiments. Animals used for the generation of the sporozoites were 4–5-week-old male Swiss Webster mice purchased from the Monash Animal Services (Melbourne, Victoria, Australia) and maintained at the School of Botany, The University of Melbourne, Australia.

##### 4.2. Mosquitoes

*Anopheles stephensi* mosquitoes (strain STE2/MRA-128 from BEI Resources, The Malaria Research and Reference Reagent Resource Center) were reared as described (Benedict, 1997): They were maintained at 27 °C and 75%–80% humidity with a 12 h light and dark photo-period in filtered drinking water (Frantelle beverages, Australia). The larvae were bred in plastic food trays (P.O.S.M Pty Ltd, Australia) containing 300 larvae, each with regular water changes every 3 days, and fed with Sera Vipfan Baby fish food (Sera, Heinsberg, Germany). Upon eclosion, the adult mosquitoes were transferred to aluminium cages (BioQuip Products, Inc., Rancho Dominguez, CA, USA) and kept in a secure incubator (Conviro, Winnipeg, Canada), in the insectary at the same temperature and humidity and maintained on 10% sucrose.

##### 4.3. Parasites and infections

*Plasmodium berghei* ANKA (BEI Resources, MRA-871) were used for infections. Sporozoites were generated for RAS vaccination as follows: Infections of naïve Swiss mice were carried out by i.p. inoculation of *P. berghei*-infected RBCs obtained from a donor mouse between the first and fourth passages from a cryopreserved stock. Parasitemia was monitored by Giemsa smear and exflagellation quantified 3 days post infection. 1 µL of tail prick blood was mixed with 100 µL of exflagellation media (RPMI, [ThermoFisher] supplemented with 10%v/v fetal calf

serum [FCS], pH 8.4), incubated for 15 min at 20 °C, and exflagellation events per 10<sup>4</sup> red blood cells were counted. *A. stephensi* mosquitoes were allowed to feed on anaesthetised mice once the exflagellation rate reached 12–15 events per 10<sup>4</sup> red blood cells. 22 days after blood meal, salivary glands were dissected and checked for the presence of sporozoites. Sporozoites were resuspended in cold PBS and irradiated using 20,000 Rad, and were injected intravenously (i.v.) as indicated in the figure legend.

For blood stage infections, donor mice were injected with frozen stabilates of blood stage parasites. 3–7 days later, these mice were bled, their parasitemia was measured and recipient mice were injected i.v. with the indicated amount of *P. berghei* infected red blood cells (iRBC) diluted in 0.2 mL PBS. Parasitemia was assessed by microscopic analysis of blood smears or by flow cytometry (see below).

For curing, mice were injected intraperitoneally with 0.8 mg chloroquine for 5 consecutive days, starting on the day after infection indicated in the figure legend, followed by provision of drinking water containing 600 mg/L chloroquine for 3 extra days.

##### 4.4. Generation and monitoring of ECM

Mice infected with blood-stage *P. berghei* and left untreated were monitored daily for the development of ECM. Mice were considered to have ECM when showing signs of neurological symptoms such as ataxia and paralysis, evaluated as the inability of mice to self-right.

##### 4.5. Adoptive transfer of CD4<sup>+</sup> T cells

PbT-II and gDT-II CD4<sup>+</sup> T cells were negatively enriched from the spleens and lymph nodes of PbT-II/uGFP or gDT-II mice as described (Smith et al., 2003). Briefly, tissues were disrupted by passage through 70 µm cell strainers and red cells were lysed. Single cell suspensions were labelled with a cocktail of rat monoclonal antibodies (WEHI Antibody Services, Melbourne, Australia) specific for CD8 (clone 53-6.7), MHC Class II (clone M5/114), macrophages and dendritic cells (clones BM8 [anti-F4/80] and M1/70 [anti-CD11b]) granulocytes (clone RB6-8C5 [anti-Gr1]) and red blood cells (clone Ter119 [anti-Ter-119]) prior to incubation with BioMag goat anti-rat IgG magnetic beads (Qiagen, Hilden, Germany) and separation of labelled, non-CD4 T cells using a magnet. Enriched naïve PbT-II CD4<sup>+</sup> T cells were counted and their purity was analysed by staining with anti-CD4, anti-Vα2 and anti-Vβ12 TCR antibodies. Negatively enriched gDT-II/uGFP cells were then positively enriched using the Invitrogen Dynabeads/DETAChA bead Mouse CD4 Kit (Life Technologie AS, Oslo, Norway) following the manufacturer's instructions. Cell counts were adjusted to 2.5 × 10<sup>5</sup>/mL in PBS and 0.2 mL were injected i.v. into recipient mice. In some instances, cells were labelled with CellTrace Violet (Thermo Fisher) prior to transfer following the manufacturer's instructions.

##### 4.6. Dendritic cell isolation

Dendritic cells were purified from the spleens of mice as previously described (Vremec et al., 2000): spleens were finely minced and digested in 1 mg/ml collagenase 3 (Worthington Biochemical Corporation, Lakewood, NJ, USA) and 20 µg/ml DNase I (Roche Diagnostics Deutschland, Mannheim, Germany) under intermittent agitation for 20 min at room temperature (RT). DC-T cell complexes were then disrupted by adding EDTA (pH 7.2) to the digest to a final concentration of 7.9 mM and continuing the incubation for an additional 5 min. After removing undigested fragments by filtering through a 70 µm mesh, cells were resuspended in 5 ml of 1.077 g/cm<sup>3</sup> isosmotic nycodenz medium (Nycodem Pharma AS, Oslo, Norway), layered over 5 ml nycodenz medium, overlaid with 1–2 ml of FCS, then centrifuged at 1700×g at 4 °C for 12 min. DC were resuspended in complete RPMI medium supplemented with 10% FCS before use in functional assays.

#### 4.7. $\alpha$ Clec9A vaccination

B6 mice were injected i.v. with the indicated doses of rat  $\alpha$ Clec9A mAb (clone 24/04-10B4) genetically fused to KDNQKDIYYITGESINAVSNSPFLEA, containing the PbHsp90<sub>484-496</sub> epitope, highlighted in bold) via a 4 Alanine linker to make the  $\alpha$ Clec9A-DIY mAb construct.  $\alpha$ Clec9A was injected with 5 nmol of a CpG oligonucleotide (CpG) generated by linking (5' to 3') CpG-2006 to CpG-21798 (Krieg, 2006; Samulowitz et al., 2010) (Integrated DNA Technologies, Coralville, IA, USA).

#### 4.8. *In vitro* activation and polarization of PbT-II cells

$10^6$  PbT-II or gDT-II splenocytes were cultured *in vitro* for 4–5 days together with  $10^7$  naive B6 DC enriched as above. These DC had been coated for 30 min at 37 °C with 2  $\mu$ M PbHsp90<sub>484-496</sub> (DIYYITGESINAV) or gDT-II<sub>315-327</sub> (IPPNWHIPSIQDA) peptide (Genscript) in complete media (RPMI containing 10% FCS, 2 mM L-glutamine, 5 mM HEPES and 50 mM 2-mercaptoethanol (Sigma Aldrich, Castle Hill, NSW, Australia), in the presence of 1  $\mu$ g/ml LPS (Sigma). Polarization was done as follows: T<sub>H</sub>1 polarization was induced by adding 1  $\mu$ g/ml LPS (Sigma), 10 U/ml IL-2 (Peprotech, Mt Waverly, VIC, Australia), 5  $\mu$ g/ml  $\alpha$ IL-4 mAb (11B11; Bio X Cell), and 5 ng/ml IL-12 (Biolegend) to the culture media. T<sub>H</sub>2 polarization was induced by adding 10 U/ml recombinant human IL-2 (Peprotech, Mt Waverly, VIC, Australia), 60 ng/ml IL-4 (Biolegend), and 5  $\mu$ g/ml  $\alpha$ IFN- $\gamma$  (XMG1.2, Bio X Cell) to the culture media. On day 3 of culture 15 ml of fresh complete media, including the polarization reagents as described, were added to the cultures.

Prior to transfer, cells were washed extensively with PBS to remove any excess LPS, counted and their purity analysed by staining with antibodies against CD4 and V $\alpha$ 2, V $\beta$ 12, V $\alpha$ 3.2, Tbet and Gata3. Activated cells were adjusted to the required concentration and injected in a volume of 0.2 mL of PBS via the tail vein.

#### 4.9. Organ processing for T cell analysis

Tissues were pushed through 70  $\mu$ m strainers to generate single cell suspensions. For spleen cell preparations, red blood cells were lysed and remaining cells were filtered through a 70  $\mu$ m mesh. Liver cell suspensions were passed through a 70  $\mu$ m mesh and resuspended in 35% isotonic Percoll. Cells were then centrifuged at 500 g for 20 min at room temperature (RT), the pellet harvested and then red cells lysed before further analysis.

#### 4.10. Flow cytometry

CD4 (RM4-5), PD1 (J43) CXCR5 (2G8), IFN- $\gamma$  (4S.B3), IL-10 (JES5-16E3), IL-17 (TC11-18H10.1), IL-2 (JES6-1A12), V $\beta$ 12 (MR11-1), Tbet (4B10) purchased from BioLegend (BioLegend, San Diego, CA, USA), CD8 $\alpha$  (53-6.7), TCR $\beta$  (H57-597) CD44 (IM7), V $\alpha$ 2 (B20.1), IL-4 (11B11), TNF (MP6-XT22), GATA3 (L50-823) were purchased from Becton Dickinson (BD, Franklin Lakes, NJ, USA); CD62L (MEL-14), CD69 (H1.2F3), V $\alpha$ 3.2 (RR3-16), IL-13 (eBio13A) from ThermoFisher Scientific (Waltham, MA, USA).

Peptides were purchased from GenScript (Piscataway, NJ, USA). Dead cells were excluded by propidium iodide, Ghost Dye<sup>TM</sup>Red 780 (Tonbo Biosciences) or LIVE/DEAD<sup>TM</sup> Fixable Near-IR Dead cell Stain Kit (Thermo Fisher Scientific) staining following the manufacturer's instructions. For the analysis of memory CD4<sup>+</sup> T cell populations in the spleen and the iLN, PbT-II CD4<sup>+</sup> CD44<sup>hi</sup> cells were subdivided into T<sub>CM</sub> or T<sub>EM</sub> based on CD62L expression (T<sub>CM</sub> CD62L<sup>+</sup>, T<sub>EM</sub> CD62L<sup>-</sup>).

Parasitaemia was assessed by incubating ~2  $\mu$ l tail blood with a 5 pg/mL Hoechst 33258 solution (ThermoFisher Scientific) in FACS buffer for 1 h at 37 °C. Parasites were discriminated from uninfected RBC using a 405 violet laser and a 450/50 filter. Cells were analysed by flow cytometry on a FACS Canto or Fortessa (BD Immunocytometry Systems,

San Jose, CA, USA), using FACSDiva (BD Immunocytometry Systems) or Flowjo software (Tree Star, Ashland, OR, USA).

Intracellular transcription factor staining was performed using the BD Pharmingen<sup>TM</sup> Transcription Factor Buffer set, following the manufacturer's instructions. Intracellular cytokine staining was performed using the BD Cytofix/Cytoperm<sup>TM</sup> Fixation/Permeabilization Kit, following the manufacturer's instructions, on *in vitro* restimulated cells.  $1-2 \times 10^6$  cells/well were restimulated *in vitro* for 5 h at 37 °C in the presence of 2  $\mu$ M PbHsp90<sub>484-496</sub> peptide. Brefeldin A (10  $\mu$ g/mL) was added 1 h after the start of the culture. Intracellular staining was performed at 4 °C overnight.

#### 4.11. Assessment of PbT-II activation *in vitro*

PbT-II cells enriched from the spleens and lymph nodes of PbT-II mice as explained before were adjusted to  $10^7$  cells/mL in PBS containing 0.1% BSA (Sigma). CellTrace<sup>TM</sup> violet (CTV, ThermoFisher) was then used to coat PbT-II cells: 40  $\mu$ L DMSO/vial were used to reconstitute lyophilised CTV stock. Then, 0.5  $\mu$ L CTV per mL of cells were added, and cells were incubated for 10 min at 37 °C, followed by two washes in RPMI containing 2.5% FCS.

DC ( $6.5 \times 10^5$ ) were incubated with the indicated amounts of peptide, or with 6  $\mu$ L of each of the fractions generated by liquid chromatography, for 1 h prior to adding 50,000 CTV-coated PbT-II.GFP cells per well. Upregulation of CD69 overnight were measured in PbT-II cells using flow cytometry.

#### 4.12. Generation of Plasmodium-derived epitopes for LC-MS/MS analysis

Generation of *Plasmodium*-derived peptides was done as described before (Valencia-Hernandez et al., 2020). B6 mice were treated with FMS-like tyrosine kinase 3 receptor ligand (Flt3-L) to promote cDC1 formation. Flt3-L was given by subcutaneous injection of  $10^6$  Flt3-L-expressing B6 myeloma cells (Mach et al., 2000) 11 days prior to harvesting spleens and enriching for DC as explained above. Blood stage malaria parasites were used as an abundant source of antigen that is known to be recognised by PbT-II cells (Fernandez-Ruiz et al., 2017): donor B6 mice were infected with *P. berghei* iRBC and heart bleed when parasitaemia levels were >15%.  $2.22 \times 10^9$  splenic cells from Flt3-L-treated mice (containing 63% DC, defined as CD11c<sup>hi</sup> MHC-II<sup>hi</sup> cells) were cultured with  $19.88 \times 10^9$  blood stage *P. berghei* parasites in complete RPMI media containing 10% FCS for 8 h at 37 °C and 6.5% CO<sub>2</sub> in T175 flasks (ThermoFisher). The uninfected sample was generated in the same way, by culturing  $1.66 \times 10^9$  splenic cells from Flt3-L-treated mice (containing 65.1% CD11c<sup>hi</sup> MHC-II<sup>hi</sup> cells) with  $57 \times 10^9$  RBC from naive B6 mice. Cells were then snap frozen prior to further analysis.

#### 4.13. Analysis of MHC bound epitopes by LC-MS/MS

MHC class II bound peptides were isolated from DC by immunoaffinity chromatography and RP-HPLC essentially as described before (Schittenhelm et al., 2015). In brief, the cells were lysed in 0.5% IGEPAL, 50 mM Tris-HCl pH 8.0, 150 mM NaCl and protease inhibitors (Complete Protease Inhibitor Cocktail Tablet; Roche Applied Science, Penzberg, Germany) for 45 min at 4 °C and lysates were cleared by ultracentrifugation at 40,000 g. MHC I-A<sup>b</sup> molecules were immunoaffinity purified using the Y-3P mouse monoclonal antibody bound to protein A sepharose. The peptides were eluted under mild acetic conditions and separated on a 50 mm monolithic C18 reverse-phase high-performance liquid chromatography (HPLC) column (Chromolith SpeedROD; Merck, Kenilworth, NJ, USA) using an EttanLC HPLC system (GE Healthcare). 90 individual fractions were collected and equidistantly pooled into 10 samples, which were vacuum concentrated and reconstituted to 15  $\mu$ l with 0.1% formic acid (FA).

Using a Dionex UltiMate 3000 RSLCnano system equipped with a Dionex UltiMate 3000 RS autosampler, the fractions were loaded via an

Acclaim PepMap 100 trap column (100  $\mu\text{m} \times 2\text{ cm}$ , nanoViper, C18, 5  $\mu\text{m}$ , 100  $\text{\AA}$ ; Thermo Scientific) onto an Acclaim PepMap RSLC analytical column (75  $\mu\text{m} \times 50\text{ cm}$ , nanoViper, C18, 2  $\mu\text{m}$ , 100  $\text{\AA}$ ; Thermo Scientific). The peptides were separated by increasing concentrations of 80% ACN/0.1% FA at a flow of 250 nl/min for 95 min and analysed with a QExactive Plus mass spectrometer (Thermo Scientific). In each cycle, a full ms1 scan (resolution: 70,000; AGC target: 3e6; maximum IT: 50 ms; scan range: 375–1600 m/z) preceded up to 12 subsequent ms2 scans (resolution: 17,500; AGC target: 2e5; maximum IT: 150 ms; isolation window: 1.8 m/z; scan range: 200–2000 m/z; NCE: 27). To minimize repeated sequencing of the same peptides, the dynamic exclusion was set to 15 s and the ‘exclude isotopes’ option was activated.

Acquired mass spectrometric raw files were searched against a combined UniProtKB/SwissProt database containing both mouse and *P. berghei* protein sequences. The search engine Byonic (Protein Metrics) was used to obtain peptide sequence information. Only peptides, which fell below at a false discovery rate (FDR) of 5% based on a decoy database were considered for further analysis.

#### 4.14. Detection of PbHsp90-restricted responses by ELISpot

B6 mice were injected with  $10^4$  *P. berghei* iRBC and cured by chloroquine treatment from day 5, or with 2  $\mu\text{g}$   $\alpha\text{Clec9A-DIY}$  plus 5 nmol CpG, 7 or 35 days before splenocytes were collected for ELISpot analysis. 0.45  $\mu\text{m}$  MultiScreen-IP sterile, clear Filter Plates (Merck) were coated overnight with 3  $\mu\text{g}/\text{mL}$  IFN- $\gamma$  capture Ab (clone AN-18; WEHI Antibody Services) in PBS and blocked with RPMI containing 10% FCS for 30 min at RT. Then,  $2 \times 10^5$  enriched CD4 T cells (day 7; cells were enriched as explained above; see PbT-II cell enrichment) or unenriched splenocytes containing  $2.5 \times 10^5$  CD4 T cells (day35) from the spleens of immunised mice were plated and cultured 18 h at 37 °C and 5% CO<sub>2</sub> in a humidified incubator in the presence or absence (day7) of DIY peptide (*PbHsp90*<sub>484-496</sub>) or HSV-1 peptide (*gD*<sub>315-327</sub>) (day35).

Plates were then incubated for 2 h with 1  $\mu\text{g}/\text{mL}$  biotin-conjugated detection mAb (clone R4-6A2; WEHI Antibody Services) diluted in PBS containing 0.5% FCS, followed by incubation with Streptavidin-HRP (MabTech, Stockholm, Sweden) for 1 h at RT and with TMB substrate (MabTech) for 15 min. Plates were washed after each incubation step. An AID ELISpot reader (Advanced Imaging Devices GmbH, Strassberg, Germany) was used to enumerate spots.

#### 4.15. Statistical analyses

Figures were generated using GraphPad Prism 8 (GraphPad Software, San Diego, CA, USA). Data are shown as mean values  $\pm$  standard deviation (SD), unless otherwise stated. Statistical analyses were performed using GraphPad Prism 8. Unless otherwise indicated, data shown in the figures were pooled from all independent experiments performed. Unless otherwise stated, statistical comparisons of cell numbers in different groups were performed by log-transforming the data and using a Student's t-test (2 groups) or one-way ANOVA followed by Tukey's multiple comparisons test (>2 groups).  $P < 0.05$  was considered to indicate statistical significance. \*,  $P < 0.05$ ; \*\*,  $P < 0.01$ ; \*\*\*,  $P < 0.001$ ; \*\*\*\*,  $P < 0.0001$ ; n.s., not significant ( $P > 0.05$ ).

#### Credit author statement

Investigation: MHE, GB, SG, YCC, RM, RBS, LB, DFR; Conceptualization: DFR, WRH, LB, RBS, AWP, MHL, IC; Funding Acquisition: DFR, WRH, AWP; Resources: PST, AC, VM, GIM, MHL, IC; Supervision: MHL, IC, KY, AWP, LB, WRH, DFR; Writing original draft: DFR; Writing – review and editing: MHE, YCC, GIM, AWP, MHL, IC, LB, WRH, DFR

#### 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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## Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.crimmu.2021.06.002>.

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