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Marion Haas, Thierry Fest

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HAL Id: hal-04125746 https://hal.science/hal-04125746

Submitted on 29 Jun 2023

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5 Marion Haas^{1,2}, and Thierry Fest^{1,2,*}

- ⁶ ¹ Université de Rennes 1, INSERM, Établissement Français du Sang de Bretagne,
- 7 Team B_DEVIL, UMR_S1236, Rennes, France.
- ⁸ ² Laboratoire d'Hématologie, Centre Hospitalier Universitaire, Rennes, France.

9 * Correspondence:

- 10 Thierry Fest, MD, PhD
- 11 E-mail: thierry.fest@univ-rennes1.fr

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13 Abstract word count: 174

- 14 Main text word count: 3803
- 15 Reference count: 65
- 16

17 Keywords: B cell differentiation, plasma cell, PIM2, ER stress

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19 Abstract

The differentiation of B cells into antibody-secreting plasma cells is a complex process 20 that involves extensive changes in morphology, lifespan, and cellular metabolism to 21 support the high rates of antibody production. During the final stage of differentiation, 22 B cells undergo significant expansion of their endoplasmic reticulum and mitochondria, 23 which induces cellular stress and may lead to cell death in absence of effective 24 inhibition of the apoptotic pathway. These changes are tightly regulated at 25 transcriptional and epigenetic levels, as well as at post-translational level, with protein 26 modifications playing a critical role in the process of cellular modification and 27 adaptation. 28

Our recent research has highlighted the pivotal role of the serine/threonine kinase PIM2 in B cell differentiation, from commitment stage to plasmablast and maintenance of expression in mature plasma cells. PIM2 has been shown to promote cell cycle progression during the final stage of differentiation and to inhibit Caspase 3 activation, raising the threshold for apoptosis. In this review, we examine the key molecular mechanisms controlled by PIM2 that contribute to plasma cell development and maintenance.

37 **1. Introduction**

Before becoming CD138-positive non-proliferating plasma cells, B cells first pass 38 through an immature, proliferative plasmablast stage. Plasmablasts emerge after 39 major changes in B cell morphology, epigenome-sustained expression profile and 40 changes in the proliferation/survival compared to uncommitted B cells. Using an in vitro 41 model of human naive B cell differentiation, we have shown that the transition from 42 activated B cells to plasmablasts involves an entanglement between cell division and 43 differentiation programs and a cellular machinery largely open to apoptosis ¹. Indeed, 44 the final stage of commitment, when a human B cell becomes a plasmablast, is 45 synchronized with the cell cycle and associated with a dynamic epigenetic process on 46 plasmablast fate-determining genes. 47

In the context of this extensive cell metamorphosis, it is of interest to identify the key 48 protein kinases that control the process by modifying substrate activity. Thus, signal 49 transduction pathways depend on protein phosphorylation to relay information through 50 signaling cascades or effector proteins that elicit the end result of pathway activation. 51 The cell cycle is a highly regulated process, and protein phosphorylation is a major 52 mechanism by which it is controlled. In fact, the cell cycle phosphoproteome is one of 53 the largest phosphoproteomes for any cellular process, with up to 70% of proteins 54 containing phosphorylation sites. This regulation is particularly important during 55 mitosis, where phosphorylation events play a crucial role in ensuring the proper 56 segregation of chromosomes and completion of cell division². Misregulation of protein 57 kinase signaling has been linked to several human diseases and has been the subject 58 of attention for several decades. Deciphering the cellular roles of any protein kinase 59 requires the elucidation of its downstream effector substrates. 60

In this review we will focus on some of the molecules and pathways that are involved 61 in the changes that take place during the terminal transition from a non-secreting B cell 62 to plasmablasts. We will then describe the serine/threonine kinase PIM2, its 63 involvement in modifications which, through its action on specific substrates, acts on 64 the control of the cell cycle, the adaptation of the cell to the new constraints of 65 immunoglobulin (Ig) secretion and, finally, the maintenance of plasmablast and plasma 66 cell survival. Curiously to date, this kinase has never been studied during normal and 67 terminal differentiation of the B cell until our recently published article ³. However, PIM2 68 has been extensively studied in malignant plasma cells during multiple myeloma. In 69 70 this paper, we will present the action of PIM2 in the completion of B cell differentiation 71 into plasmablasts as well as in the survival of plasma cells, thus assuming the role of the pivotal plasma cell kinase. 72

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2. Extensive molecular changes during the B cell to plasmablast transition step.

75 Transcription factors play a critical role in determining and maintaining cellular identity, and their activities are modulated by the underlying epigenetic landscape. As 76 77 differentiating cells evolve, DNA demethylation can contribute to a more permissive epigenetic state that allows for greater flexibility in gene expression and cellular 78 function. In activated B cells, plasma cell progenitors may need to adapt transcriptional 79 program to support cellular metamorphosis conducting to an eccentric nucleus and an 80 abundant cytoplasmic endoplasmic reticulum (ER) with abundant secretion of Ig 81 82 proteins.

To study the molecular events that contribute to the cellular changes during the B cell to plasmablast transition, we developed and standardized an in vitro model of human

naive B cell differentiation into plasmablasts. Starting from blood donor buffy coat we 85 purify B cells and then culture them with IL-2, CD40L, CpG and anti-IgM Fab'2 to 86 activate them via a transcriptional burst ⁴. By day 1, B cells are activated with a large 87 number of cells in S-phase and significant gene expression modifications as shown 88 previously ^{4,5}. Beyond day 4, culture conditions are modified and cells maintained only 89 with IL-2, IL-4 and IL-10 stimulation for an additional 2-3 days to complete the 90 91 plasmablast differentiation. A third step of the culture is required with addition of IL-6 92 and interferon α to obtain CD138-positive nonproliferating plasma cells after 3 days ³. 93 We have recently demonstrated that committed B cells, which differentiate into plasmablasts, exhibit an extinction of both IL-4/STAT6 signaling and CBLB ubiquitin 94 ligase expression, coinciding with IRF4 induction ⁶. As a surrogate marker of this 95 commitment, CD23 expression on the membrane surface disappears due to IL-96 4/STAT6 extinction. When B cells reach the post-proliferation stage, they undergo a 97 98 transcriptional shift that is supported by a replication-dependent passive demethylation of DNA ^{1,7} and enter the G1 phase of the cell cycle. However, beyond day 4, in the 99 absence of BCR, CpG and CD40L stimuli, and induced by IL-10 (or IL-21), a small 100 fraction of B cells belonging to the CD23-negative subpopulation enters into cell cycle 101 after promoting the G1/S transition ^{1,8}. In contrast to their CD23-positive counterparts 102 that are unable to differentiate, CD23-negative B cell progenitors morphologically 103 change from an activated-B cell phenotype to a plasmablast phenotype. This cellular 104 metamorphosis is accompanied by a dramatic reorganization of the pool of DNA-active 105 106 enhancers, as evidenced by oxidative enrichment of 5'-methyl-cytosine (5mC) due to the activity of translocation ten-eleven (TET) methylcytosine dioxygenases on selected 107 regions of the genome, including genes encoding plasma cell identity factors, which 108 were previously protected from passive replication-dependent demethylation. TET 109

activity produces stable 5-hydroxymethylcytosine (5hmC) residues along with open chromatin and specific histone methylation marks leading together to active transcription coupled to the S phase of the cell cycle ^{1,9,10}. This TET hemihydroxymethylated DNA is misrecognized by DNA methyltransferase 1 (DNMT1), allowing maintenance of DNA methylation.

While they become plasmablasts and are fully efficient in Ig secretion, the cells 115 undergo massive changes in their organelles, including membrane amplification, 116 trafficking, endoplasmic reticulum (ER) remodeling and a metabolic switch with a large 117 increase in nutrients to meet the growing need (reviewed in ^{11,12}). At the mature plasma 118 cell stage, to meet cellular needs and adapt to stress conditions, the ER dynamically 119 changes its morphology leading to its peak of protein production; a particular challenge 120 knowing that measurements of their secretion rates - although varying - indicate that 121 these cells release up to $\frac{1}{4}$ - $\frac{1}{2}$ of their total weight as secreted glycoprotein each day 122 ¹¹. Ig processing is overwhelmed into the ER lumen, resulting in an increased level of 123 unfolded and misfolded proteins with a high ER stress state, inducing the production 124 of chaperones that attempt to refold the misfolded proteins ¹³. Cells expand their ER 125 primarily through the inositol-requiring enzyme 1α (IRE1 α) pathway, the most studied 126 unfolded protein response (UPR) signals in plasma cells. IRE1 α leads to the formation 127 of spliced X-box Binding Protein (sXBP1), which in turn promotes the mitochondrial 128 and the ER expansion, both of which are significantly reduced when XBP1 is deleted 129 in B cells ^{14–16}. In addition to IRE1, UPR in mammals is regulated by two other ER 130 sensors: ATF6, a member of the ATF/CREB transcription factor family, and the R-like 131 ER kinase protein, PERK ^{17,18}. All three UPR response factors are activated after 132 release of the ATPase Ig-binding protein (BiP) (reviewed in ^{5,19}). It is noteworthy that 133 XBP1 expression increases in human activated naïve B cells without the need for 134

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6

BLIMP1 induction ²⁰, which is consistent with mouse activated follicular B cells where 135 the serine/threonine kinase mTORC1 plays a role before Blimp induction and promotes 136 the transcription of various UPR target genes. Thus, during B cell terminal 137 differentiation, mTORC1 expression establishes the secretory program, which 138 gradually transitions to the amplified and sustained Blimp1-IRE1/Xbp1 program ^{21,22}. 139 Nevertheless, BLIMP1 is intimately involved in the UPR, directly regulating IRE1 and 140 ATF6, as well as 38% of the downstream genes of the UPR, which are largely 141 independent of those regulated by XBP1 and are part of the BLIMP1-driven 142 differentiation process ^{23,24}. Finally, plasma cells use autophagy to limit ER expansion 143 144 and antibody production, and to provide nutrients through the degradation of cellular components (reviewed in ²⁴). It is worth noting that mTORC1 downregulates 145 autophagy, indicating that plasma cells maintain a balance between autophagy and 146 mTORC1 activity to optimize their antibody secretion rates without compromising their 147 survival²⁵. 148

Unlike IRE1 and ATF6, PERK is a member of the eukaryotic initiation factor 2 (eIF- 2α) 149 kinase and functions to inhibit most cap-dependent protein synthesis at the onset of 150 the UPR. However, paradoxically, it allows ATF4 transcription factors to be translated 151 ^{26,27}. In contrast to other secretory cells such as pancreatic beta cells (Fest lab, 152 unpublished), the PERK/ATF4 arm of the UPR is selectively inactivated in plasma cells. 153 This has been demonstrated in Perk-/- B cells, which can differentiate and produce Ig 154 synthesis and antibody secretion upon stimulation with LPS ²⁸. Moreover, in our in vitro 155 model of naïve B cell differentiation, PERK and its target genes are immediately 156 downregulated after B cell activation, without an increase in generated plasmablasts ⁵. 157

3. Plasma cell biology depends of the integrated stress response (ISR).

Chronic ER stress is linked to apoptosis, making it important to understand how plasma 159 cells manage prolonged UPR activation without triggering the terminal proapoptotic 160 aspects of the UPR. Transcriptomic analysis of B cell commitment to plasma cell output 161 revealed that the first enriched gene list was related to cell death and survival. Notably, 162 the proapoptotic BCL2L11 (encoding BIM) and CASP3 (encoding Caspase 3) genes 163 were significantly upregulated, alongside the pro-survival genes BCL2L1 (encoding 164 BCLXL), MCL1, and XIAP genes ^{1,3,6}. New generated plasmablasts die within days of 165 their generation, and short-lived plasma cells are much more prevalent than long-lived 166 ones (reviewed in ¹²). This suggests that plasma cell longevity is only marginally related 167 168 to reasons intrinsic to the cells themselves - such as an antigen-specific humoral response, as proposed by Amanna et Slifka with their "imprinted lifespan" model of 169 plasma cell longevity ²⁹ - but rather depends on their environment. Indeed, individual 170 plasma cells localize among a set of cells that provide localization and survival cues 171 and belong to specialized survival niches ^{30 31}. Differentiation and maintenance of 172 plasma cells require an attenuation of the stress response coupled to UPR. The 173 integrated stress response (ISR), a central and evolutionary conserved signaling 174 network, responds to a broad variety of stress conditions and operates by 175 reprogramming translation with reduction of general initiation translation rates and the 176 increase in translation of specific messengers RNAs. Both of these processes 177 reprogram translation towards damage mitigation and recovery by maintaining 178 functional balance of cells throughout their lifespan, allowing them to adapt. ISR does 179 not act like an on-off switch but rather as a molecular rheostat controlling fast and slow 180 changes to support complex cell-wide changes and also local protein synthesis as in 181 the brain at dendrites during memory consolidation and long-term memory formation 182 ^{32–34}. Pharmacogenetic activation of ISR in rodents impairs long-term memory. Based 183

on these considerations it is tempting to speculate that in plasma cells the ISR may 184 play a role in the process leading to becoming a long-lived cell ^{33,35}. Cellular stress is 185 sensed by four specialized kinases (GCN2, HRI, PKR and PERK as well) that converge 186 on phosphorylation of a single serine on the eukaryotic translation initiation factor eIF2, 187 resulting in blockage of the nucleotide exchange factor eIF2B (reviewed in ³⁶). In 188 plasma cells, as terminal B cell differentiation takes place independently of PERK ²⁸ 189 and, GCN2 and HRI respond to nutrient deprivation and heme deficiency, respectively, 190 PKR may be the kinase responsible for ISR-mediated translation regulation in 191 managing ER stress ³⁶. PKR contains a double-stranded RNA binding domain (dsRNA) 192 193 that binds to dsRNA which induces dimerization of PKR which triggers an activating autophosphorylation of the kinase. Thus activated, PKR phosphorylates eIF2a leading 194 to the inhibition of cellular and viral mRNA translation which represents an efficient way 195 to inhibit viral replication ^{37,38}. However, PKR activation may be detected in absence of 196 dsRNA by a wide range of different cell stresses through the recruitment of PACT 197 (PKR-associated activator) and binding to PKR ³⁹ consistent with several diverse 198 cellular functions where PKR has been implicated such as growth regulation, apoptosis 199 signaling pathway and differentiation (reviewed in ³⁸). For example, in mouse 200 201 fibroblasts, PKR has been shown to be an important signal in controlling growth arrest and subsequent differentiation to adipocytes ^{40,41}. Interestingly, accumulating evidence 202 suggests that dsRNAs are not limited to virally infected cells, but can be produced from 203 endogenous sources and activate the same receptors that have evolved to detect 204 "danger" signals that alert dysregulated cellular processes leading to an innate immune 205 response ^{42,43}. Interestingly, mitochondrial RNAs, which exist as intermolecular 206 dsRNAs, interact strongly with PKR and regulate downstream activation, especially 207 under stress conditions ⁴⁴. This dsRNA-induced response is consistent with the role of 208

209 mitochondrial UPR in cytosolic ISR activation ^{42,45}. Taken collectively these data 210 represent a good starting point for further exploration of the PKR-dependent ISR 211 response during terminal B cell differentiation and its possible role in plasma cell 212 survival.

4. PIM2 is strongly induced in B cells engaged in differentiation into
 plasmablasts.

CD23-negative preplasmablasts compared to uncommitted CD23-positive B cells 215 exhibit strong expression of PIM2 - ahead of the PRDM1 gene in our single-cell RNA 216 dataset and detection of the protein by western blotting - which occurs after release of 217 BACH2 repression ³. This upregulation of PIM2 is driven by STAT3 and induced by the 218 cytokines IL-21/IL-10 and IL-6 in plasma cells. Thus, BACH2 repression can be viewed 219 as a gateway to the ultimate commitment of antibody-secreting cells, mediated by an 220 IL2/ERK/ELK1 signaling pathway^{8,46} and responsible for the release of both PIM2 and 221 222 BLIMP1 expression, with PIM2 upregulation preceding BLIMP1 expression (Fest lab, unpublished). These findings suggest that PIM2, independent of BLIMP1, plays a 223 critical role in the differentiation of B cells into plasma cells. 224

The kinase domain of PIM2 shares unique structural features with PIM1 and PIM3, 225 making them constitutively active. Characterized by a short half-life, PIM2 expression 226 is tightly regulated and establishes a growth factor-induced, kinase-dependent 227 pathway that promotes cell-autonomous survival ^{47,48}. As previously mentioned, the 228 final commitment of B cells to plasmablasts requires cell cycle entry with the 229 development of an active gene-specific DNA demethylation process targeting plasma 230 cell identity genes, as well as cell survival and proliferation genes¹. This process may 231 involve an altered balance between DNMT1 and TET enzyme activities. There is some 232 evidence for a relationship between PIM kinases and DNMT1. DNMT1 methylates 233

10

newly synthesized DNA during S phase with the help of UHRF1 for proper loading 234 within the replication fork ⁴⁹. Several studies have described human DNMT1 235 phosphorylation at multiple serine/threonine sites, including the phosphorylation by 236 Akt/PKC which disrupts the DNMT1/UHRF1/PCNA complex ⁵⁰. On the other hand, 237 PIM1 kinase expression has been implicated in cell senescence through 238 downregulation of DNMT1 via a PIM1-HBP1 axis ⁵¹ and through phosphorylation at 239 Ser³¹¹ of UHRF1, leading to its degradation ⁵². Finally, TET2 is a substrate of AMP-240 activated kinase (AMPK), which phosphorylates TET2 at serine 99, thereby stabilizing 241 its activity and the production of 5hmC DNA ⁵³. Notably, PIM2 can regulate AMPK 242 activity through a direct Thr467 phosphorylation and/or by suppressing the tumor 243 suppressor LKB1, which activates AMPK after Thr183 phosphorylation ^{54,55}. The 244 information presented in our previous work highlights the role of PIM2 in the G1/S 245 246 transition of B cells to plasmablasts by activating CDC25A and exporting p27Kip1 out of the nucleus ³. Given this, it is plausible to speculate that the increased cytoplasmic 247 expression of PIM2 may play a role in regulating the balance of TET2 and DNMT1 248 activity, leading to the production of 5hmC prior to complete demethylation beyond S 249 phase. This process may occur on previously protected regions of the genome during 250 251 B cell maturation, thus contributing to the epigenetic landscape that governs cellular identity¹. 252

In murine B cells, Pim2 was shown to work in parallel with the Akt/mTOR pathway to promote the survival and resistance to atrophy of resting cells stimulated with the obligate B cell survival factor BLyS ⁵⁶. BLyS-mediated B cell survival in the presence of rapamycin, an Akt/mTOR inhibitor, was dependent on Pim2. When Pim-deficient B cells were cultured with rapamycin, the addition of BLyS did not improve survival, whereas Pim-sufficient B cells were able to utilize BLyS to improve survival. Signaling

11

events downstream of Pim2 facilitated the production of the anti-apoptotic protein Mcl-259 1 as a mechanism for enhanced survival ⁵⁶. Given the level of PIM2 expression in 260 human plasma cells, it can be estimated that this kinase greatly exceeds the average 261 of 14 substrates per kinase as proposed by human kinome analysis ⁵⁷. Newly 262 generated plasmablasts experience an increase in the expression of BIM and Caspase 263 3 as a result of UPR. PIM2 plays a role in inhibiting apoptosis by promoting the 264 265 phosphorylation of BAD, which leads to its cytoplasmic sequestration. Additionally, PIM2 prevents the activation of Caspase 3 by promoting the phosphorylation of 266 p21Cip1, which then binds to and inactivates Caspase 3. Furthermore, PIM2 inhibits 267 268 mitochondrial depolarization, which indirectly contributes to the stabilization of the antiapoptotic protein XIAP that binds to Caspase 3 and prevents its activation ^{3,6,58}. Finally, 269 short-lived plasma cells retain the requirement of mTORC1 signaling, which is no 270 longer required in long-lived plasma cells ⁵⁹. PIM2 may participate in the maintenance 271 of mTORC1 signaling in nascent plasma cells by downregulating TSC2, a repressor of 272 mTORC1⁶⁰. 273

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5. PIM2 in mature plasma cells

Long-lived plasma cells can persist to the end of host's life in the absence of repeated 275 antigen stimulation. Thus, it is critical to understand the maintenance of mature plasma 276 cells and how they overcome pro-apoptotic forces due to ER stress. CD138-positive 277 human plasma cells generated in vitro showed maintenance of high levels of 278 cytoplasmic PIM2 expression as well as expression of p-BAD, which drives BAD 279 inactivation and thus stabilizes mitochondrial membrane polarization³. In guiescent 280 cells, p21Cip1 is usually nuclear and participates in cell cycle arrest. In mature 281 nonproliferative plasma cells as well as in bone marrow plasma cells, p21Cip1 remains 282 cytoplasmic and maintains binding to Caspase 3, thereby inhibiting Caspase 3 283

12

activation (³ and Fest lab, unpublished data). It is plausible to hypothesize that the ISR 284 must be tightly regulated to ensure proper functioning and production of a wide range 285 of immunoglobulins. In this context, PIM2 may play a central role in controlling ISR. 286 Our preliminary experiments suggest that PIM2 regulates the activation of PERK and 287 PKR (Fest lab, unpublished data). By modulating the activity of these proteins, PIM2 288 may regulate the threshold at which cells undergo ISR, ensuring a balance between 289 290 the stress response and efficient Ig production. Further studies are needed to fully understand the regulatory mechanisms involved in this process. 291

Recently, in humans, we found that in addition to high PIM2 expression, bone marrow plasma cells increase PIM1 expression. The latter is essentially nuclear, while PIM2 remains present in the cytoplasm (Fest lab, unpublished data). As previous work has shown that PIM1 is essential for the surface expression of CXCR4 and for the migration of cells towards a CXCL12 gradient ⁶¹, we therefore hypothesize that PIMs could be functionally involved in the structuration of a favourable microenvironment in the bone marrow for plasma cell localization and survival.

299 (Insert Figure here)

300 6. PIM2 and malignant plasma cells

Although the involvement of PIM2 in multiple myeloma (MM) has been recognized for more than a decade, we have further investigated the status of PIM2 in malignant PCs. Data from the DepMap Project (<u>https://depmap.org/portal/</u>) involving up to 800 different cancer cell lines, showed that PIM2 (but not PIM1) mRNA expression was particularly high in MM cells compared with other tumor cells. CRISPR and shRNA screening revealed a specific high PIM2 dependency score for malignant plasma cells ³. The control of mitochondrial depolarization by PIM2 is similar in normal and malignant

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plasma cells (Fest lab, unpublished). The anti-apoptotic effects of PIM2, mediated through BAD phosphorylation, may complement those of MCL1, as BAD only antagonizes BCLXL and BCL2 ⁶². Therefore, dual inhibition of PIM2 and MCL1 may provide a synergistic effect and offer new treatment options. Additionally, reducing the dose of anti-MCL1 inhibitors, which bind to MCL1 with subnanomolar affinity and can cause cardiotoxicity in some patients, is a potential benefit of this approach ⁶³.

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7. Conclusions and perspective

In recent years, new factors have emerged that contribute to a better understanding of 315 B cell differentiation into plasmablasts, including specific transcription factors and 316 regulators of genome organization and epigenetic landscape. Protein phosphorylation, 317 a post-translational modification that regulates many biological processes, is of broad 318 interest for identifying therapeutic targets through high specificity drugs. In vitro human 319 B cell differentiation models have identified the serine/threonine kinase PIM2 as 320 specifically linked to the late stage of differentiation by supporting cell cycle entry and 321 322 inhibiting apoptosis. While several substrates have been studied, the high level of cytoplasmic PIM2 expression in plasma cells suggests that it may act on a broad range 323 of proteins. Immunoprecipitation experiments in MM cell lines and human primary 324 plasmablasts obtained from in vitro culture of B cells revealed an enrichment of various 325 proteins, including several factors acting on the same transcriptional machinery, 326 epigenome, or ISR, indicating that PIM2 binds to protein complexes (Fest lab, 327 unpublished). This link to protein complexes provides a level of regulation through 328 phosphorylation of Ser/Thr residues on a particular peptide motif, out of a total of 38 329 identified motifs, that respond more specifically to PIM2 ⁶⁴. 330

Future directions for the study of PIM2 in plasma cells may involve rodent models.
However, in mouse plasma cells it appears that the expression of Pim1 and Pim2 are

at comparable levels, which is not the case in humans (Fest Lab, unpublished). A 333 comparative analysis of these two kinases in the plasma cell seems therefore important 334 possibility of redundancy of functions, differential cell by assessing the 335 compartmentalization and their respective capacity to bind to protein complexes. A 336 second aspect of exploration involves the exact role of PIM2 in the organization of a 337 supportive niche for the long survival of plasma cells including a study of interactions 338 with the microenvironment. IL-6 signals through the STAT3 pathway and is essential 339 for rapid induction of PIM2³. In the bone marrow, apart from stromal cells, other cells 340 such as megakaryocytes produce IL-6 which could correspond to different sites for 341 342 plasma cell localization with different functional capacities. If PIM2 allows cell cycle entry at plasmablast differentiation, in the long-lived plasma cell it is likely that PIM2 343 participates in the quiescence through factors or functions that need to be identified. 344 Finally, quantitative phosphoproteomics that explore changes in phosphorylation 345 levels of proteins in response to stimuli is a powerful tool for understanding signaling 346 pathways and identifying potential targets. However, it is important to ensure that 347 experimental conditions are reproducible in order to obtain reliable results. This 348 includes carefully preparing the cells and samples, controlling for variability in 349 350 experimental conditions, and using appropriate statistical methods to analyze the data. In addition, it is important to validate any findings from phosphoproteomic studies using 351 complementary techniques, such as western blotting or functional assays, to confirm 352 the biological relevance of the observed changes in protein phosphorylation ⁶⁵. 353

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355 AUTHOR CONTRIBUTIONS

356 MH and TF performed the literature search, wrote the manuscript.

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358 CONFLICT OF INTEREST

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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363 **FUNDING INFORMATION**

This study was funded by Programmes labellisés (PGA) 2022 ARC N° ARCPGA2021120004244_4856, Ligue Régionale GO, 2020, and an internal grant from the Hematology Laboratory, CHU de Rennes. M. Haas has received a doctoral

367 fellowship from FHU CAMIn, Ligue Contre le Cancer/Comité d'Ile et Vilaine.

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525 Figure Legend:

526 An overview of the demonstrated and few potential effects of PIM2 kinase during 527 *in vitro* differentiation of human naive B cells.

To undergo plasma cell differentiation, B cells must respond to various stimuli. Naive 528 B cells (NBC) are initially activated and subsequently selected to commit to the 529 differentiation process. Activated cells are initially screened based on their 530 responsiveness to the cytokine IL-4, which triggers the expression of the CD23 marker 531 through STAT6 activation. Only cells that downregulate the IL-4 receptor expression. 532 and consequently become CD23 negative, can progress in the differentiation process 533 (Pignarre et al., Blood 2021). In vitro experiments have shown that minimal IL-2 534 stimulation experienced by recently activated NBCs initiates plasma cell differentiation. 535 Notably, BACH2 has been identified as an early regulator of B cell fate decision, and 536 its timely repression by IL-2-mediated ERK/ELK1 signaling facilitates plasma cell 537 commitment (Hipp et al., Nat Comms 2017). Upon release of BACH2 and in response 538 to the cytokine IL-21, which activates the STAT3 pathway, PIM2 expression is induced. 539 This leads to robust serine/threonine kinase activity, associated with early plasma cell 540 541 commitment. In fact, the initial high expression of PIM2 enables cell cycle entry by degrading p27Kip1 and activating CDC25A, both of which facilitate the G1/S transition 542 543 (Haas et al., Blood 2022). Commitment is also accompanied by transcriptional reprogramming of B cells, partially mediated by epigenetic modifications. TET2 activity, 544 but not DNMT1 activity, allows hydroxymethylation of 5-methyl-cytosine residues at 545 the promoters of genes responsible for plasma cell identity, including PRDM1 (Caron 546 et al., Cell Report 2015). Preliminary findings suggest that PIM2 kinase may play a role 547 in attenuating DNMT1 protein expression. This terminal stage of B cell differentiation 548 gives rise to antibody-secreting plasmablasts, which serve as precursors to plasma 549 cells. These differentiated cells exhibit high levels of PIM2, which plays a crucial role 550 in protecting cells from apoptosis. The kinase accomplishes this by preventing 551 mitochondrial depolarization through phosphorylation of BAD and by stabilizing 552 cytoplasmic p21Cip1 protein, both of which hinder caspase 3 activation (Haas et al., 553 Blood 2022). Finally, the differentiation process is accompanied by a physical 554 transformation of the cells, characterized by the development of an extensive protein 555 synthesis machinery involving a highly expanded endoplasmic reticulum for 556 immunoglobulin synthesis. This heightened activity induces significant cellular stress, 557 which is counteracted by activating the unfolded protein response (UPR) pathways. 558

- 559 Additionally, the Integrated Stress Response (ISR) pathway is potentially inhibited by
- PIM2, which could inactivate certain ISR kinases, such as PKR and PERK, therebypreventing cell death mediated by the ISR pathway.



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