

Reviewed Preprint

Published from the original preprint after peer review and assessment by eLife.

[About eLife's process](#)

Reviewed preprint posted

June 22, 2023 (this version)

Sent for peer review

May 5, 2023

Posted to bioRxiv

May 1, 2023

Molecular dissection of PI3K β synergistic activation by receptor tyrosine kinases, G β G γ , and Rho-family GTPases

Benjamin R. Duewell, Naomi E. Wilson, Gabriela M. Bailey, Sarah E. Peabody, Scott D. Hansen 

Department of Chemistry and Biochemistry, Institute of Molecular Biology, University of Oregon, Eugene, OR 97403

 (https://en.wikipedia.org/wiki/Open_access)

 (<https://creativecommons.org/licenses/by/4.0/>)

Abstract

The class 1A phosphoinositide 3-kinase (PI3K) beta (PI3K β) is functionally unique in the ability to integrate signals derived from receptor tyrosine kinases (RTKs), heterotrimeric guanine nucleotide-binding protein (G-protein)-coupled receptors (GPCRs), and Rho-family GTPases. The mechanism by which PI3K β prioritizes interactions with various membrane tethered signaling inputs, however, remains unclear. Previous experiments have not been able to elucidate whether interactions with membrane-tethered proteins primarily control PI3K β localization versus directly modulate lipid kinase activity. To address this gap in our understanding of PI3K β regulation, we established an assay to directly visualize and decipher how three binding interactions regulate PI3K β when presented to the kinase in a biologically relevant configuration on supported lipid bilayers. Using single molecule Total Internal Reflection Fluorescence (TIRF) Microscopy, we determined the mechanism controlling membrane localization of PI3K β , prioritization of signaling inputs, and lipid kinase activation. We find that auto-inhibited PI3K β must first cooperatively engage a single RTK-derived tyrosine phosphorylated (pY) peptide before it can engage either G β G γ or Rac1(GTP). Although pY peptides strongly localize PI3K β to membranes, they only modestly stimulate lipid kinase activity. In the presence of either pY/G β G γ or pY/Rac1(GTP), PI3K β activity is dramatically enhanced beyond what can be explained by the increase in membrane avidity for these complexes. Instead, PI3K β is synergistically activated by pY/G β G γ and pY/Rac1(GTP) through a mechanism of allosteric regulation.

eLife assessment

The manuscript describes the synergy among PI3Kbeta activators, providing **compelling** results concerning the mechanism of their activation. The particular strengths of the work arise to a great extent from the reconstitution system better mimicking the natural environment of the plasma membrane than previous setups have. The study will be a **landmark** contribution to the signaling field.

Introduction

Critical for cellular organization, phosphatidylinositol phosphate (PIP) lipids regulate the localization and activity of numerous proteins across intracellular membranes in eukaryotic cells (Di Paolo and De Camilli 2006). The interconversion between various PIP lipid species through the phosphorylation and dephosphorylation of inositol head groups is regulated by lipid kinases and phosphatases (Balla 2013; Burke 2018). Serving a critical role in cell signaling, the class I family of phosphoinositide 3-kinases (PI3Ks) catalyze the phosphorylation of phosphatidylinositol 4,5-bisphosphate [PI(4,5)P₂] to generate PI(3,4,5)P₃. Although a low-abundance lipid (< 0.05%) in the plasma membrane (Wenk et al. 2003; Nasuhoglu et al. 2002; Stephens, Jackson, and Hawkins 1993), PI(3,4,5)P₃ can increase 40-fold following receptor activation (Stephens, Hughes, and Irvine 1991; Parent et al. 1998; Insall and Weiner 2001). Although signal adaptation mechanisms typically restore PI(3,4,5)P₃ to the basal level following receptor activation (Funamoto et al. 2002; Yip et al. 2008; Auger et al. 1989), misregulation of the PI3K signaling pathway can result in constitutively high levels of PI(3,4,5)P₃ that are detrimental to cell health. Since PI(3,4,5)P₃ lipids serve an instructive role in driving actin based membrane protrusions (Howard and Oresajo 1985; Weiner 2002;

Graziano et al. 2017), sustained PI(3,4,5)P₃ signaling is known to drive cancer cell metastasis (Hanker et al. 2013). Elevated PI(3,4,5)P₃ levels also stimulates the AKT signaling pathway and Tec family kinases, which can drive cellular proliferation and tumorigenesis (Manning and Cantley 2007; Fruman et al. 2017). While much work has been dedicated in determining the factors that participate in the PI3K signaling pathway, how these molecules collaborate to rapidly synthesize PI(3,4,5)P₃ remains an important open question. To decipher how amplification of PI(3,4,5)P₃ arises from the relay of signals between cell surface receptors, lipids, and peripheral membrane proteins, we must understand how membrane localization and activity of PI3Ks is regulated by different signaling inputs. Determining how these biochemical reactions are orchestrated will provide new insight concerning the molecular basis of asymmetric cell division, cell migration, and tissue organization, which are critical for understanding development and tumorigenesis.

In the absence of a stimulatory input, the class IA family of PI3Ks (PI3K α , PI3K β , PI3K δ) are thought to reside in the cytoplasm as auto-inhibited heterodimeric protein complexes composed of a catalytic (p110 α , p110 β , or p110 δ) and regulatory subunit (p85 α , p85 β , p55 γ , p50 α , or p55 α) (Burke 2018; Vadas et al. 2011). The catalytic subunits of class IA PI3Ks contain an N-terminal adaptor binding domain (ABD), a Ras/Rho binding domain (RBD), a C2 domain (C2), and an adenosine triphosphate (ATP) binding pocket (Vadas et al. 2011). The inter-SH2 (iSH2) domain of the regulatory subunit tightly associates with the ABD of the catalytic subunit (Yu et al. 1998), providing structural integrity, while limiting dynamic conformational changes. The nSH2 and cSH2 domains of the regulatory subunit form additional inhibitory contacts that limit the conformational dynamics of the catalytic subunit (Zhang et al. 2011a; Mandelker et al. 2009; Burke et al. 2011; Carpenter et al. 1993; Yu et al. 1998). A clearer understanding of the how various proteins control PI3K localization and activity would help facilitate the development of drugs that perturb specific protein-protein binding interfaces that are critical for membrane targeting and lipid kinase activity. Among the class IA PI3Ks, PI3K β is uniquely capable of interacting with Rho-family GTPases (Fritsch et al. 2013a), Rab GTPases (Christoforidis et al. 1999; Heitz et al. 2019), heterotrimeric G-protein complexes (G β G γ) (Kurosu et al. 1997; Maier, Babich, and Nürnberg 1999; Guillermet-Guibert et al. 2008), and phosphorylated receptor tyrosine kinases (RTKs) (Zhang et al. 2011a; Carpenter et al. 1993). Like other class IA PI3Ks, interactions with receptor tyrosine kinase (RTK) derived phosphotyrosine peptides release nSH2 and cSH2-mediated inhibition of the catalytic subunit to stimulate PI3K β lipid kinase activity (H. A. Dbouk et al. 2012; Zhang et al. 2011b). G β G γ and Rac1(GTP) in solution have also been shown to stimulate

PI3K β lipid kinase activity (Hashem A. Dbouk et al. 2012; Fritsch et al. 2013a; Maier, Babich, and Nürnberg 1999). Similarly, activation of Rho-family GTPases (Fritsch et al. 2013a) and G-protein coupled receptors (Houslay et al. 2016) stimulate PI3K β lipid kinase activity in cells. However, it's unclear how individual interactions with G β G γ or Rac1(GTP) can bypass autoinhibition of full-length PI3K β (p110 β -p85 α / β). Studies in neutrophils and *in vitro* biochemistry suggest that PI3K β is synergistically activated through coincidence detection of RTKs and G β G γ (Houslay et al. 2016; Hashem A. Dbouk et al. 2012). Similarly, Rac1(GTP) and G β G γ have been reported to synergistically activate PI3K β in cells (Erami et al. 2017). An enhanced membrane recruitment mechanism is the most prominent model used to explain synergistic activation of PI3Ks.

There is limited kinetic data examining how PI3K β is regulated by different membrane-tethered proteins. Previous biochemical studies of PI3K β have utilized solution-based assays to measure P(3,4,5)P $_3$ production. As a result, the mechanisms that determine how PI3K β prioritizes interactions with RTKs, small GTPases, or G β G γ remains unclear. In the case of synergistic PI3K β activation, it's unclear which protein-protein interactions regulate membrane localization versus stimulate lipid kinase activity. No studies have simultaneously measured PI3K β membrane association and lipid kinase activity to decipher potential mechanisms of allosteric regulation. Previous studies concerning the synergistic activation of PI3Ks are challenging to interpret because RTK derived peptides are always presented in solution alongside membrane anchored signaling inputs. However, all the common signaling inputs for PI3K activation (i.e. RTKs, G β G γ , Rac1/Cdc42) are membrane associated proteins. Activation of class 1A PI3Ks has never been reconstituted using solely membrane tethered activators conjugated to membranes in a biologically relevant configuration. As a result, we currently lack a comprehensive description of PI3K β membrane recruitment and catalysis.

To decipher the mechanisms controlling PI3K β membrane binding and activation, we established a biochemical reconstitution using supported lipid bilayers (SLBs). We used single molecule Total Internal Reflection Fluorescence (TIRF) microscopy to quantify the relationship between PI3K β localization, lipid kinase activity, and the density of various membrane-tethered signaling inputs. This approach allowed us to measure the dwell time, binding frequency, and diffusion coefficients of single fluorescently labeled PI3K β in the presence of RTK derived peptides, Rac1(GTP), and G β G γ . Simultaneous measurements of PI3K β membrane recruitment and lipid kinase activity allowed us to define the relationship between PI3K β localization and PI(3,4,5)P $_3$ production in the presence of different regulators. Overall, we found that membrane docking of PI3K β first requires interactions with RTK-derived tyrosine phosphorylated (pY) peptides, while PI3K β localization is insensitive to membranes that contain either Rac1(GTP) or G β G γ alone. Following engagement with a pY peptide, PI3K β can associate with either G β G γ or Rac1(GTP). In the case of synergistic PI3K β localization mediated by pY/G β G γ , it's essential for the nSH2 domain to move away from the G β G γ binding site. Although both the PI3K β -pY-Rac1(GTP) and PI3K β -pY-G β G γ complexes display a ~2-fold increase in membrane localization, the corresponding increase in catalytic efficiency is much greater. Overall, our results indicate that synergistic activation of PI3K β depends on allosteric modulation of lipid kinase activity.

Results

PI3K β prioritizes interactions with pY peptides over Rac1(GTP) and G β G γ

Previous biochemical analysis of p110 β -p85 α , referred to as PI3K β , established that receptor tyrosine kinases (Zhang et al. 2011b), Rho-type GTPases (Fritsch et al. 2013a), and

heterotrimeric G-protein G β G γ (Hashem A. Dbouk et al. 2012) are capable of binding and stimulating lipid kinase activity. To decipher how PI3K β prioritizes interactions between these three membrane-tethered proteins we established a method to directly visualize PI3K β localization on supported lipid bilayers (SLBs) using Total Internal Reflection Fluorescence (TIRF) Microscopy (Figure 1A). For this assay, we covalently attached either a doubly tyrosine phosphorylated platelet derived growth factor (PDGF) peptide (pY) peptide or recombinantly purified Rac1 to supported membranes using cysteine reactive maleimide lipids. We confirmed membrane conjugation of the pY peptide and Rac1 by visualizing the localization of fluorescently labeled nSH2-Cy5 or Cy3-p67/phox (Rac1(GTP) sensor), respectively (Figure 1B). Nucleotide exchange of membrane conjugated Rac1(GDP) was achieved by the addition of a guanine nucleotide exchange factor, P-Rex1 (phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein) diluted in GTP containing buffer (Figure 1C). As previously described (Rathinaswamy et al. 2021; 2023), AF488-SNAP dye labeled farnesyl G β G γ was directly visualized following passive absorption into supported membranes (Figure 1D and Figure 1 – figure supplement 1). We confirmed that membrane bound G β G γ was functional by visualizing robust membrane recruitment of Dy647-PI3K β by TIRF-M (Figure 1E). Overall, this assay functions as a mimetic to the cellular plasma membrane and allowed us to examine how different membrane tethered signaling inputs regulate PI3K β membrane localization in vitro.

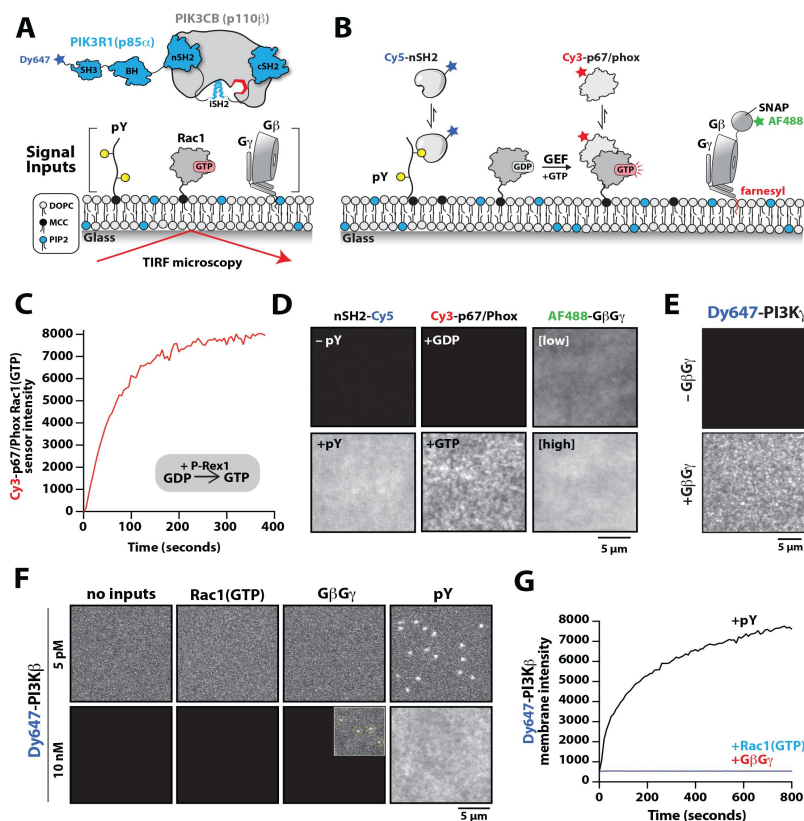


Figure 1

PI3K β prioritizes membrane interactions with RTK-derived pY peptides over Rac1(GTP) and G β G γ

(A) Cartoon schematic showing membrane tethered signaling inputs (i.e. pY, Rac1(GTP), and G β G γ) attached to a supported lipid bilayer and visualized by TIRF-M. Heterodimeric Dy647-PI3K β (p110 β -p85 α) in solution can dynamically associate with membrane bound proteins. (B) Cartoon schematic showing method for visualizing membrane tethered signaling inputs. (C) Kinetics of Rac1 nucleotide exchange measured in the presence of 20 nM Rac1(GTP) sensor (Cy3-p67/phox) and 50 nM P-Rex1. (D) Visualization of membrane conjugated RTK derived pY peptide, Rac1(GTP), and G β G γ by TIRF-M. Representative TIRF-M images showing the membrane localization of 20 nM nSH2-Cy3 in the absence and presence of membranes conjugated with a solution concentration of

10 μ M pY peptide. Representative images showing the membrane localization of 20 nM Cy3-p67/phox Rac1(GTP) sensor before (GDP) and after (GTP) the addition of the guanine nucleotide exchange factor, P-Rex1. Equilibrium localization of 50 nM (low) or 200 nM (high) farnesyl G β G γ -SNAP-AF488. (E) Representative TIRF-M images showing the equilibrium membrane localization of 10 nM Dy647-PI3K β measured in the absence and presence of membranes equilibrated with 200 nM farnesyl G β G γ . (F) Representative TIRF-M images showing the equilibrium membrane localization of 5 pM and 10 nM Dy647-PI3K β measured in the presence of membranes containing either pY, Rac1(GTP), or G β G γ . The inset image

(+GβGγ) shows low frequency single molecule binding events detected in the presence of 10 nM Dy647-PI3Kβ. **(G)** Bulk membrane absorption kinetics for 10 nM Dy647-PI3Kβ measured on membranes containing either pY, Rac1(GTP), or GβGγ. Membrane composition: 96% DOPC, 2% PI(4,5)P₂, 2% MCC-PE.

We visualized both single molecule binding events and bulk membrane localization of Dy647-PI3Kβ by TIRF-M to determine which inputs can autonomously recruit autoinhibited Dy647-PI3Kβ from solution to a supported membrane (**Figure 1F**). Comparing membrane localization of Dy647-PI3Kβ in the presence of pY, Rac1(GTP), and GβGγ revealed that only the tyrosine phosphorylated peptide (pY) could robustly localize Dy647-PI3Kβ to supported membranes (**Figure 1F-1G**). This prioritization of interactions was consistently observed across a variety of membrane lipid compositions (**Figure 1 – figure supplement 2**). Incorporation of up to 20% phosphatidylserine (PS) in supported membranes to increase the anionic charge did not facilitate complex formation between Dy647-PI3Kβ and Rac1(GTP) or GβGγ (**Figure 1 – figure supplement 2**). Although we could detect some transient Dy647-PI3Kβ membrane binding events in the presence of GβGγ alone, the binding frequency was reduced 2000-fold compared our measurements on pY membranes (**Figure 1 – figure supplement 2**). In addition, localization of wild-type Dy647-PI3Kβ phenocopied the GβGγ binding mutant, Dy647-PI3Kβ (K532D, K533D), indicating that the low frequency binding events we observed are mostly mediated by lipid interactions rather than direct binding to GβGγ (**Figure 1 – figure supplement 2**).

PI3Kβ cooperatively engages a single membrane tethered pY peptide

Previous biochemical analysis of PI3Kβ utilized pY peptides in solution to study the regulation of lipid kinase activity (Zhang et al. 2011b; Hashem A. Dbouk et al. 2012). Using membrane-tethered pY peptide, we quantitatively mapped the relationship between the pY membrane surface density and the membrane binding behavior of Dy647-PI3Kβ (**Figure 2A**). To calculate the membrane surface density of conjugated pY, we incorporated a defined concentration of Alexa488-pY (**Figure 2A**). We measured the relationship between the total solution concentration of pY peptide used for the membrane conjugation step and the corresponding final membrane surface density (pY per μm²). Over a range of pY peptide solution concentrations (0-10 μM), we observed a linear increase in the membrane conjugation efficiency based on the incorporation of fluorescent Alexa488-pY (**Figure 2B**). Bulk membrane localization of a nSH2-Cy3 sensor showed a corresponding linear increase in fluorescence as a function of pY peptide membrane density (**Figure 2C**). By quantifying the average number of Alexa488-pY particles per unit area of supported membrane we calculated the absolute density of pY per μm² (**Figure 2D**).

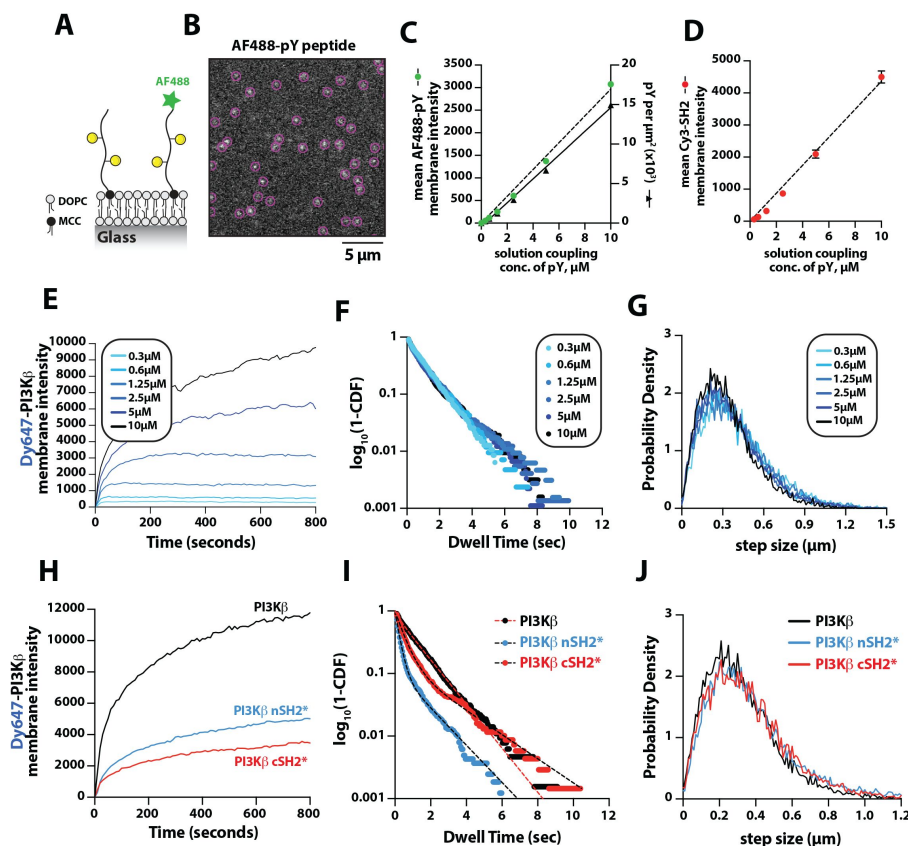


Figure 2

Density dependent membrane binding behavior of Dy647-PI3K β measured in the presence of RTK-derived pY peptides

(A) Cartoon schematic showing conjugation of pY peptides (+/- Alexa488 label) using thiol reactive maleimide lipids (MCC-PE). (B) Representative image showing the single molecule localization of Alexa488-pY. Particle detection (purple circles) was used to quantify the number of pY peptides per μm^2 . (C) Relationship between the total pY solution conjugation concentration (x-axis) used for covalent conjugation, the bulk membrane intensity of covalently attached Alexa488-pY (left y-axis), and the final surface density of pY peptides per μm^2 (right y-axis). (D) Relationship between the total

pY solution conjugation concentration and bulk membrane intensity of measured in the presence of 50 nM nSH2-Cy3. (E-G) Membrane localization dynamics of Dy647-PI3K β measured on SLBs containing a range of pY surface densities (250–15,000 pY/ μm^2 , based on Figure 1C). (E) Bulk membrane localization of 10 nM Dy647-PI3K β as a function of pY density. (F) Single molecule dwell time distributions measured in the presence of 5 pM Dy647-PI3K β . Data plotted as $\log_{10}(1-\text{CDF})$ (cumulative distribution frequency). (G) Step size distributions showing Dy647-PI3K β single molecule displacements from > 500 particles (>10,000 steps) per pY surface density. (H-J) Membrane localization dynamics of Dy647-PI3K β nSH2(R358A) and cSH2(R649A) mutants measured on SLBs containing $\sim 15,000$ pY/ μm^2 (10 μM conjugation concentration). (H) Bulk membrane absorption kinetics of 10 nM Dy647-PI3K β (WT, nSH2*, and cSH2*). (I) Single molecule dwell time distributions measured in the presence of 5 pM Dy647-PI3K β (WT, nSH2*, and cSH2*). Data plotted as $\log_{10}(1-\text{CDF})$ (cumulative distribution frequency). (J) Step size distributions showing single molecule displacements of > 500 particles (>10,000 steps) in the presence of 5 pM Dy647-PI3K β (WT, nSH2*, and cSH2*). Membrane composition: 96% DOPC, 2% PI(4,5) P_2 , 2% MCC-PE.

To determine how the membrane binding behavior of PI3K β is modulated by the membrane surface density of pY, we measured the bulk membrane absorption kinetics of Dy647-PI3K β . When Dy647-PI3K β was flowed over a membrane containing a low density of ≤ 500 pY/ μm^2 , we observed rapid equilibration kinetics consistent with a 1:1 binding stoichiometry (Figure 2E). When the membrane surface density of pY crossed a threshold density of ~ 1000 pY/ μm^2 , we observed slower equilibration kinetics consistent with Dy647-PI3K β either engaging two pY peptides or exhibiting membrane hopping. Single particle tracking of Dy647-PI3K β on membranes containing varying densities of pY peptide revealed that the dwell time was relatively insensitive to the pY peptide density (Figure 2F and Table 1). Similarly, the displacement (or step size) of pY-tethered Dy647-PI3K β was nearly identical across a range of pY membrane densities examined (Figure 2G and Table 1). Together, these results suggest

that Dy647-PI3K β engages one doubly phosphorylated peptide over a broad range of pY densities in our bilayer assay.

TABLE 1

protein visualized	pY/ μm^2	$\tau_1 \pm \text{SD}$ (sec)	$\tau_2 \pm \text{SD}$ (sec)	$\alpha \pm \text{SD}$	Ave DT (sec)	$D_1 \pm \text{SD}$ ($\mu\text{m}^2/\text{sec}$)	$D_2 \pm \text{SD}$ ($\mu\text{m}^2/\text{sec}$)	$\alpha \pm \text{SD}$	MEDIAN step (μm)
PI3K β (WT)	250	0.58 $\pm$ 0.28	1.78 $\pm$ 0.58	0.60 $\pm$ 0.37	1.00 $\pm$ 0.09	0.39 $\pm$ 0.07	1.45 $\pm$ 0.09	0.29 $\pm$ 0.08	0.37 $\pm$ 0.02
PI3K β (WT)	573	0.39 $\pm$ 0.06	1.37 $\pm$ 0.14	0.27 $\pm$ 0.02	1.12 $\pm$ 0.09	0.28 $\pm$ 0.06	1.15 $\pm$ 0.14	0.22 $\pm$ 0.04	0.35 $\pm$ 0.01
PI3K β (WT)	1226	0.36 $\pm$ 0.13	1.29 $\pm$ 0.06	0.30 $\pm$ 0.09	1.05 $\pm$ 0.11	0.20 $\pm$ 0.02	1.18 $\pm$ 0.09	0.16 $\pm$ 0.02	0.36 $\pm$ 0.02
PI3K β (WT)	2935	0.44 $\pm$ 0.11	1.53 $\pm$ 0.38	0.47 $\pm$ 0.25	1.00 $\pm$ 0.07	0.28 $\pm$ 0.09	1.09 $\pm$ 0.12	0.26 $\pm$ 0.09	0.33 $\pm$ 0.01
PI3K β (WT)	6661	0.46 $\pm$ 0.08	1.28 $\pm$ 0.16	0.61 $\pm$ 0.13	0.82 $\pm$ 0.11	0.35 $\pm$ 0.17	1.28 $\pm$ 0.34	0.35 $\pm$ 0.18	0.34 $\pm$ 0.01
PI3K β (WT)	14944	0.55 $\pm$ 0.11	1.44 $\pm$ 0.56	0.54 $\pm$ 0.22	0.91 $\pm$ 0.09	0.45 $\pm$ 0.15	1.40 $\pm$ 0.54	0.48 $\pm$ 0.06	0.33 $\pm$ 0.05
PI3K β (WT)	14944	0.49 $\pm$ 0.17	1.38 $\pm$ 0.19	0.35 $\pm$ 0.17	1.10 $\pm$ 0.04	0.32 $\pm$ 0.04	0.99 $\pm$ 0.12	0.40 $\pm$ 0.11	0.30 $\pm$ 0.02
PI3K β (nSH2*)	14944	0.23 $\pm$ 0.02	1.48 $\pm$ 0.23	0.86 $\pm$ 0.03	0.45 $\pm$ 0.06	0.38 $\pm$ 0.09	1.45 $\pm$ 0.25	0.41 $\pm$ 0.18	0.34 $\pm$ 0.01
PI3K β (cSH2*)	14944	0.38 $\pm$ 0.08	1.54 $\pm$ 0.55	0.76 $\pm$ 0.1	0.65 $\pm$ 0.08	0.34 $\pm$ 0.13	1.12 $\pm$ 0.29	0.43 $\pm$ 0.15	0.30 $\pm$ 0.04

SD = standard deviation from 3-5 technical replicates

N = 331 – 1909 total particles for each technical replicate

steps = 4277 – 39378 total particle displacements measured for each technical replicate

alpha (α) = fraction of molecules with characteristic dwell time (τ_1) or diffusion coefficient (D_1).

membrane composition: 96% DOPC, 2% PI(4,5)P₂, 2% MCC-PE.

DT = dwell time

The regulatory subunit of PI3K β (p85 α) contains two SH2 domains that form inhibitory contacts with the catalytic domain (p110 β) (Zhang et al. 2011b). The SH2 domains of class 1A PI3Ks have a conserved peptide motif, FLVR, that mediates the interaction with tyrosine phosphorylated peptides (Bradshaw, Mitaxov, and Waksman 1999; Waksman et al. 1992; Rameh, Chen, and Cantley 1995). Mutating the arginine to alanine (FLVA mutant) prevents the interaction with pY peptides for both PI3K α and PI3K β (Yu et al. 1998; Dornan et al. 2020; Nolte et al. 1996; Zhang et al. 2011b; Breeze et al. 1996). To determine how the membrane binding behavior of PI3K β is modulated by each SH2 domain, we individually mutated the FLVR amino acid sequence to FLVA. Compared to wild type Dy647-PI3K β , the nSH2(R358A) and cSH2(R649A) mutants showed a 60% and 75% reduction in membrane localization at equilibrium, respectively (Figure 2H). Single molecule dwell time analysis also showed a significant reduction in membrane affinity for Dy647-PI3K β nSH2(R358A) and cSH2(R649A) compared to wild type PI3K β (Figure 2I and Table 1). Single molecule diffusion (or mobility) of membrane bound nSH2(R358A) and cSH2(R649A) mutants, however, were nearly identical to wild type Dy647-PI3K β (Figure 2J and Table 1). Because the nSH2 and cSH2 mutants can only interact with a single phosphorylated tyrosine residue on the doubly phosphorylated pY peptide, this further supports a model in which the p85 α regulatory subunit of PI3K β cooperatively engages one doubly phosphorylated pY peptide under our experimental conditions.

G β G γ dependent enhancement in PI3K β localization requires release of the nSH2

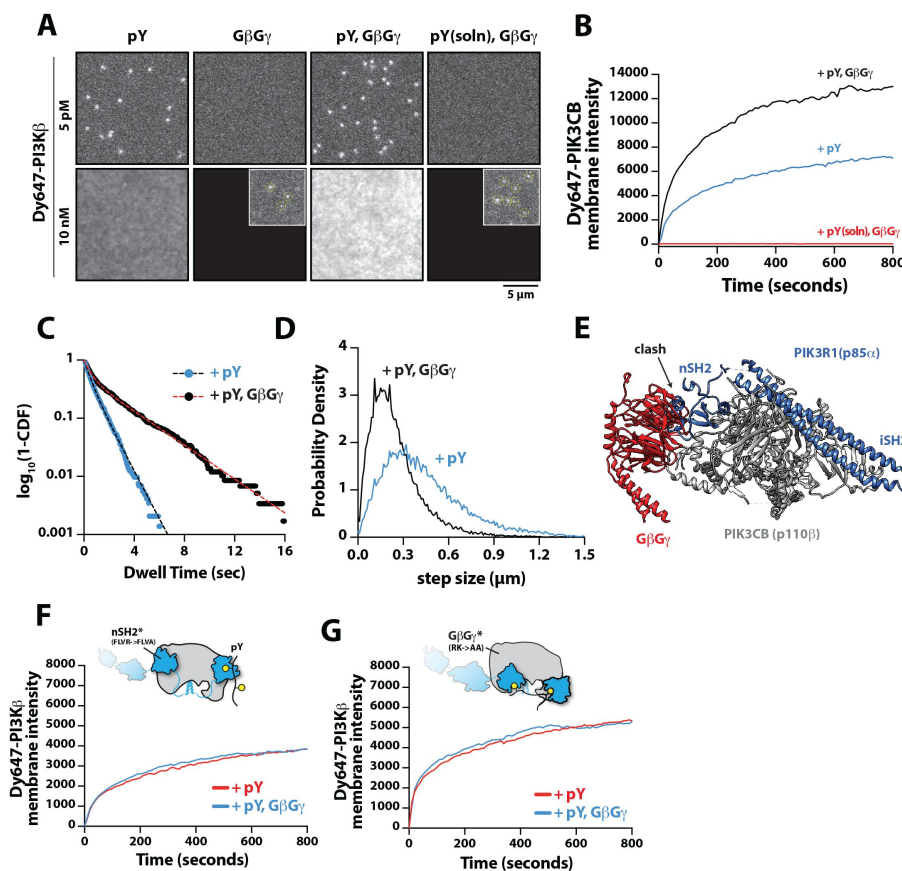
Having established that PI3K β engagement with a membrane tethered pY peptide is the critical first step for robust membrane localization, we examined the secondary role that G β G γ serves in controlling membrane localization of PI3K β bound to pY. To measure synergistic membrane localization mediated by the combination of pY and G β G γ , we covalently linked pY peptides to supported membrane at a surface density of $\sim 10,000$ pY/ μm^2 and then allowed farnesyl G β G γ to equilibrate into the membrane. Comparing the bulk membrane absorption of Dy647-PI3K β in the presence of pY alone, we observed a 2-fold increase in membrane localization due to synergistic association with pY and G β G γ (Figure

3A-3B). Single molecule imaging experiments also showed a 1.9-fold increase in the membrane dwell time of Dy647-PI3K β in the presence of both pY and G β G γ (**Figure 3C**). Consistent with Dy647-PI3K β forming a complex with pY and G β G γ , we observed a 22% reduction in the average single particle displacement and a decrease in the diffusion coefficient due to synergistic binding (**Figure 3D**).

Figure 3

Mechanism controlling synergistic Dy647-PI3K β membrane binding by pY and G β G γ

(A) Representative TIRF-M images showing the equilibrium membrane localization of 5 pM and 10 nM Dy647-PI3K β on membranes containing either pY, G β G γ , pY/G β G γ , or pY(solution)/G β G γ . The inset image (+G β G γ and +pY/G β G γ) shows low frequency single molecule binding events detected in the presence of 10 nM Dy647-PI3K β . Supported membranes were conjugated with 10 μ M pY peptide (final surface density of $\sim 15,000$ pY/ μ m²) and equilibrated with 200 nM farnesyl-G β G γ before adding Dy647-PI3K β . pY(solution) = 10 μ M. **(B)** Bulk membrane recruitment dynamics of 10 nM Dy647-PI3K β measured in the presence of either pY alone, pY/G β G γ , or pY(solu-



tion)/G β G γ . pY(solution) = 10 μ M. **(C)** Single molecule dwell time distributions measured in the presence of 5 pM Dy647-PI3K β on supported membranes containing pY alone ($\tau_1=0.55\pm0.11$ s, $\tau_2=1.44\pm0.56$ s, $\alpha=0.54$, $N=4698$ particles, $n=5$ technical replicates) or pY/G β G γ ($\tau_1=0.61\pm0.13$ s, $\tau_2=3.09\pm0.27$ s, $\alpha=0.58$, $N=3421$ particles, $n=4$ technical replicates). **(D)** Step size distributions showing single molecule displacements measured in the presence of either pY alone ($D1=0.34\pm0.04$ μ m²/sec, $D2=1.02\pm0.07$ μ m²/sec, $\alpha=0.45$) or pY/G β G γ ($D1=0.23\pm0.03$ μ m²/sec, $D2=0.88\pm0.08$ μ m²/sec, $\alpha=0.6$); $n=3-4$ technical replicates from > 3000 tracked particles with 10,000-30,000 total displacements measured. **(E)** Combined model of the putative nSH2 and G β G γ binding sites on p110 β . The p110 β -G β G γ binding site is based on an AlphaFold multimer model supported by previous HDX-MS and mutagenesis experiments. The orientation of the nSH2 is based on previous X-ray crystallographic data on PI3K α (p110 α -p85 α , nSH2, PDB:3HHM) aligned to the structure of PI3K β (p110 β -p85 α , icSH2, PDB:2Y3A). **(F)** Bulk membrane recruitment dynamics of 10 nM Dy647-PI3K β , WT and nSH2(R358A), measured on membranes containing either pY or pY/G β G γ . **(G)** Bulk membrane recruitment dynamics of 10 nM Dy647-PI3K β , WT and G β G γ binding mutant, measured on membranes containing either pY or pY/G β G γ . **(A-G)** Membrane composition: 96% DOPC, 2% PI(4,5)P₂, 2% MCC-PE.

Parallel to our experiments using membrane conjugated pY, we tested whether solution pY could promote Dy647-PI3K β localization to G β G γ -containing membranes. Based on the bulk membrane recruitment, solution pY did not strongly enhance membrane binding of Dy647-

PI3K β on G β G γ -containing membranes (**Figure 3B**). Single molecule dwell analysis revealed few transient Dy647-PI3K β membrane interactions (inset **Figure 3A**) with a mean dwell time of 116 ms in the presence of G β G γ alone (**Figure 3 – figure supplement 1A**). The presence of 10 μ M solution pY modestly increased the mean dwell time of Dy647-PI3K β to 136 ms on G β G γ containing membranes (**Figure 3 – figure supplement 1B**). This suggests that the affinity between PI3K β and G β G γ is relatively weak, which is consistent with previous structural biochemistry studies (Hashem A. Dbouk et al. 2012).

For PI3K β to engage G β G γ , it is hypothesized that the nSH2 domain must move out of the way from sterically occluding the G β G γ binding site. This model is supported by previous hydrogen deuterium exchange mass spectrometry (HDX-MS) experiments that only detected interactions between G β G γ and PI3K β (p110 β) when the nSH2 domain was either absent or disengaged by activation using a soluble RTK pY peptide (H. A. Dbouk et al. 2012). We examined the putative interface of G β G γ bound to the p110 β catalytic domain using AlphaFold multimer (Jumper et al. 2021; Evans et al. 2022; Varadi et al. 2022) which defined α 1 in the helical domain as the binding site. This result was consistent with previous mutagenesis and HDX-MS analysis of G β G γ binding to p110 β (Hashem A. Dbouk et al. 2012). Comparing our model to previous X-ray crystallographic data of SH2 binding to either p110 α and p110 β (Zhang et al. 2011a; Mandelker et al. 2009) suggested that the nSH2 domain sterically obstructs the G β G γ binding interface (**Figure 3E** and **Figure 3 – figure supplement 2**), with G β G γ activation only possible when the p110 β -nSH2 interface is disrupted. To test this hypothesis, we measured the membrane binding dynamics of Dy647-PI3K β nSH2(R358A) on membranes containing pY and G β G γ . Comparing the bulk membrane recruitment of these constructs revealed that the inability of the Dy647-PI3K β nSH2 domain to bind to pY peptides, made the kinase insensitive to synergistic membrane recruitment mediated by pY and G β G γ (**Figure 3F**). Similarly, the membrane association dynamics of Dy647-PI3K β nSH2(R358A), phenocopied a PI3K β (K532D, K533D) mutant that lacks the ability to engage G β G γ (**Figure 3G**).

Rac1(GTP) and pY synergistically enhance PI3K β membrane localization

PI3K β is the only class IA PI3K that has been shown to interact with Rho-family GTPases, Rac1 and Cdc42 (Fritsch et al. 2013b). Our membrane localization studies indicate however that Dy647-PI3K β does not strongly localize to membranes containing Rac1(GTP) alone (**Figure 1C-1D** and **Figure 1 – figure supplement 2B**). To determine whether membrane anchored pY peptides can facilitate interactions with Rac1(GTP), we visualized the localization of Dy647-PI3K β on membranes containing pY-Rac1(GDP) or pY-Rac1(GTP). Our experiments were designed to have the same pY surface density across conditions. By incorporating a small fraction of Cy3-Rac1 and

Alexa488-pY into our Rac1-pY membrane coupling reaction we were able to visualize single membrane anchored proteins and calculate the membrane surface density of $\sim 4,000$ Rac1/ μ m² and $\sim 5,000$ pY/ μ m² (**Figure 4A-4B**). Bulk localization to membranes containing either pY-Rac1(GDP) or pY-Rac1(GTP), revealed that active Rac1 could enhance Dy647-PI3K β localization by 1.4-fold (**Figure 4C-4D**). Similarly, single molecule analysis revealed a 1.5-fold increase in the mean dwell time of Dy647-PI3K β in the presence of pY-Rac1(GTP) (**Figure 4E**). The average displacement of Dy647-PI3K β per frame (i.e. 52 ms) also decreased by 28% in the presence of pY and Rac1(GTP) (**Figure 4F**), consistent with the formation of a membrane bound PI3K β -pY-Rac1(GTP) complex.

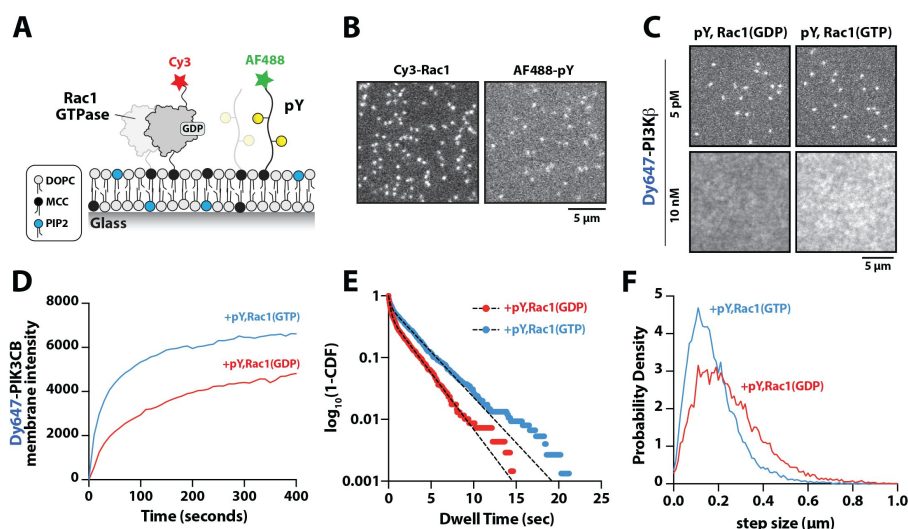


Figure 4

Membrane anchored pY peptides synergistically enhance Dy647-PI3K β membrane binding in the presence of Rac1(GTP)

(A) Cartoon schematic showing membrane conjugation of Cy3-Rac1 and AF488-pY on membranes containing unlabeled Rac1 and pY. (B) Representative TIRF-M images showing localization of Cy3-Rac1 (1:10,000 dilution) and AF488-pY (1:30,000 dilution) after membrane conjugation in the presence of 30 μ M Rac1 and 10 μ M pY. Membrane surface density equals $\sim$ 4,000 Rac1/ μ m² and $\sim$ 5,000 pY/ μ m². (C) Representative TIRF-M images showing the equilibrium membrane localization of 5 pM and 10 nM Dy647-PI3K β measured in the presence of membranes containing either pY/Rac1(GDP) or pY/Rac1(GTP). (D) Bulk membrane recruitment dynamics of 10 nM Dy647-PI3K β measured in the presence of pY/Rac1(GDP) or pY/Rac1(GTP). (E) Single molecule dwell time distributions measured in the presence of 5 pM Dy647-PI3K β on supported membranes containing pY/Rac1(GDP) or pY/Rac1(GTP). (F) Step size distributions showing single molecule displacements from > 500 Dy647-PI3K β particles (>10,000 steps) in the presence of either pY/Rac1(GDP) or pY/Rac1(GTP). Membrane composition: 96% DOPC, 2% PI(4,5)P₂, 2% MCC-PE.

Rac1(GTP) and G β G γ stimulate PI3K β activity beyond enhancing membrane localization

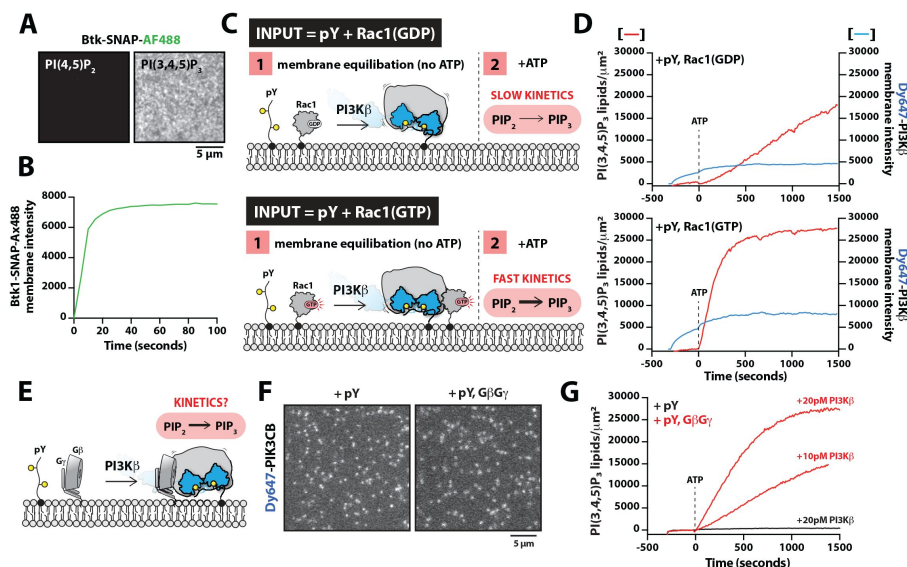
Previous *in vitro* measurements of PI3K β activity have shown that solution pY stimulates lipid kinase activity (Zhang et al. 2011b; Hashem A. Dbouk et al. 2012). Similar mechanisms of activation have been reported for other class IA kinases, including PI3K α and PI3K δ (Buckles et al. 2017; Burke et al. 2011; Dornan et al. 2017). Functioning in concert with pY peptides, G β G γ (Hashem A. Dbouk et al. 2012) or Rho-family GTPase (Fritsch et al. 2013b) synergistically enhance PI3K β activity by a mechanism that remains unclear. Similarly, RTK derived peptides and H-Ras(GTP) have been shown to synergistically activate PI3K α (Buckles et al. 2017; Siempelkamp et al. 2017; Yang et al. 2012). In the case of PI3K β , previous experiments have not determined whether synergistic activation by multiple signaling inputs results from an increase in membrane affinity (K_D) or direct modulation of lipid

kinase activity (k_{cat}) through an allosteric mechanism. To determine how PI3K β lipid kinase activity is synergistically modulated by either G β G γ or Rho-family GTPases, in the presence of membrane tethered pY peptides, we used TIRF-M to simultaneously visualize Dy647-PI3K β membrane binding and monitor the production of PI(3,4,5)P $_3$ lipids. To measure the kinetics of PI(3,4,5)P $_3$ formation, we purified and fluorescently labeled the pleckstrin homology and Tec homology (PH-TH) domain derived from Bruton's tyrosine kinase (Btk). We used a form of Btk containing a mutation that disrupts the peripheral PI(3,4,5)P $_3$ lipid binding domain (Wang et al. 2015). This Btk mutant was previously shown to associate with a single PI(3,4,5)P $_3$ head group and exhibits rapid membrane equilibration kinetics *in vitro* (Chung et al. 2019). Consistent with previous observations, Btk fused to SNAP-AF488 displayed high specificity and rapid membrane equilibration kinetics on SLBs containing PI(3,4,5)P $_3$ (Figure 5A–5B). Compared to the PI(3,4,5)P $_3$ lipid sensor derived from the Cytohesin/ Grp1 PH domain (He et al. 2008; J. D. Knight et al. 2010), the Btk mutant sensor had a faster association rate constant (k_{ON}) and a more transient dwell time ($1/k_{OFF}$) making it ideal for kinetic analysis of PI3K β lipid kinase activity (Figure 5 – figure supplement 1). Using Btk-SNAP-AF488, we measured the production of PI(3,4,5)P $_3$ lipids on SLBs by quantifying the time dependent recruitment in the presence of PI3K β . The change in Btk-SNAP-AF488 membrane fluorescence could be converted to the absolute number of PI(3,4,5)P $_3$ lipids produced per μm^2 to determine the catalytic efficiency per membrane bound Dy647-PI3K β . While our findings provide a mechanism for enhanced PI3K β membrane localization in the presence of either pY-Rac1(GTP) or pY-G β G γ , these results did not reveal the mechanism controlling synergistic activation of lipid kinase activity. To probe if synergistic activation results from enhanced membrane localization or allosteric modulation of PI3K β , we first examined how well the pY peptide stimulates PI3K β lipid kinase activity on SLBs. In the absence of pY peptides, PI3K β did not catalyze the production of PI(3,4,5)P $_3$ lipids, while the addition of 10 μM pY in solution resulted in a subtle but detectable increase in PI3K β lipid kinase activity (Figure 5 – figure supplement 2). By contrast, covalent conjugation of pY peptides to supported lipid bilayers increased the rate of PI(3,4,5)P $_3$ production by 207-fold (Figure 5 – figure supplement 2). The observed difference in kinetics were consistent with robust membrane recruitment of Dy647-PI3K β requiring membrane tethered pY peptides.

Figure 5

G β G γ and Rac1(GTP) stimulate PI3K β activity beyond enhancing localization on pY membranes

(A) Representative TIRF-M images showing localization of 20nM Btk-SNAP-AF488 on SLBs containing either 2% PI(4,5)P $_2$ or 2% PI(3,4,5)P $_3$, plus 98% DOPC. (B) Bulk membrane recruitment kinetics of 50nM Btk-SNAP-AF488 on a SLB containing 98% DOPC, 2% PI(3,4,5)P $_3$. (C) Cartoon schematic illustrating method for



measuring Dy647-PI3K β activity in the presence of either pY/Rac1(GDP) or pY/ Rac1(GTP). Phase 1 of the reconstitution involves membrane equilibration of Dy647-PI3K β in the absence of ATP. During phase 2, 1 mM ATP is added to stimulate lipid kinase activity of Dy647-PI3K β . (D) Dual color TIRF-M imaging showing 2 nM Dy647-PI3K β localization and catalysis

measured in the presence of 20nM Btk-SNAP-AF488. Dashed line represents the addition of 1 mM ATP to the reaction chamber. **(E)** Cartoon schematic showing experimental design for measuring synergistic binding and activation of Dy647-PI3K β in the presence of pY and G β Gy. **(F)** Representative single molecule TIRF-M images showing the localization of 20 pM Dy647-PI3K β in (G). **(G)** Kinetics of PI(3,4,5)P₃ production monitored in the presence of 20nM Btk-SNAP-AF488 and 20 pM Dy647-PI3K β . Membrane contained either pY or pY/G β Gy. **(D,F,G)** Membrane composition: 96% DOPC, 2% PI(4,5)P₂, 2% MCC-PE.

Next, we sought to assess if the combination of pY and Rac1(GTP) could synergistically stimulate PI3K β activity beyond the expected increase due to the enhanced membrane localization of the PI3K β -pY-Rac1(GTP) complex. To decipher the mechanism of synergistic activation, we performed two-phase experiments that accounted for both the total amount of membrane localized Dy647-PI3K β and the corresponding kinetics of PI(3,4,5)P₃ generation. In phase 1 of our experiments, Dy647-PI3K β was flowed over SLBs and allowed to equilibrate with either pY-Rac1(GDP) or pY-Rac1(GTP) in the absence of ATP (**Figure 5C-5D**). This resulted in a 1.8-fold increase in Dy647-PI3K β localization mediated by Rac1(GTP) on pY containing membranes. Following membrane equilibration of Dy647-PI3K β , phase 2 was initiated by adding 1 mM ATP to the reaction chamber to stimulate lipid kinase activity. We found that the addition of ATP did not alter the bulk localization of Dy647-PI3K β , though the kinase was in dynamic equilibrium between the solution and membrane. Conducting experiments in this manner allowed us to measure activation by inputs while removing uncertainty from differential Dy647-PI3K β association with various signaling inputs. After accounting for the 1.8-fold difference in Dy647-PI3K β membrane localization comparing pY-Rac1(GDP) and pY-Rac1(GTP) membranes, we calculated a 4.3-fold increase in PI3K β activity that was Rac1(GTP) dependent.

We next examined how pY and G β Gy synergistically activate PI3K β using the two-phase kinase assay described above (**Figure 5E**). In our pilot experiments, we immediately observed more robust PI3K β activation in the presence of pY-G β Gy, compared to pY-Rac1(GTP). To accurately measure the rapid kinetics of PI(3,4,5)P₃ generation on SLBs we had to use a 100-fold lower concentration of Dy647-PI3K β . Under these conditions, single membrane bound Dy647-PI3K β molecules could be spatially resolved, which allowed us to measure the catalytic efficiency per PI3K β (**Figure 5F**). Comparing the activity of Dy647-PI3K β on membranes with either pY or pY-G β Gy, we observed a 22-fold increase in catalytic efficiency comparing the PI3K β -pY and PI3K β -pY-G β Gy complexes (**Figure 5G**). Based on membrane bound density of ~ 0.2 Dy647-PI3K β per μm^2 , we calculate a k_{cat} of 57 PI(3,4,5)P₃ lipids/sec•PI3K β on pY-G β Gy containing membranes. By contrast, the Dy647-PI3K β -pY complex had a k_{cat} of ~ 3 PI(3,4,5)P₃ lipids/sec•PI3K β .

Discussion

Prioritization of signaling inputs

The exact mechanisms that regulate how PI3K β prioritizes interactions with signaling input, such as pY, Rac1(GTP), and G β Gy remains unclear. To fill this gap in knowledge, we directly visualized the membrane association and dissociation dynamics of fluorescently labeled PI3K β on supported lipid bilayers using single molecule TIRF microscopy. This is the first study to reconstitute membrane localization and activation of a class 1A PI3K using multiple signaling inputs that are all membrane tethered in a physiologically relevant configuration. Previous experiments have relied exclusively on phosphotyrosine peptides (pY) in solution to activate PI3K α , PI3K β , or PI3K δ (Zhang et al. 2011a; Dornan et al. 2017; Hashem A. Dbouk

et al. 2012). However, pY peptides are derived from the cytoplasmic domain of transmembrane receptors, such as receptor tyrosine kinases (RTKs), which reside in the plasma membrane (Lemmon and Schlessinger 2010). Although pY peptides in solution can disrupt the inhibitory contacts between the regulatory and catalytic subunits of class 1A PI3Ks (Zhang et al. 2011a; Yu et al. 1998), they do not robustly localize PI3Ks to membranes. When conjugated to a SLB we find that pY peptides strongly localize auto-inhibited PI3K β , while membranes containing only Rac1(GTP) or G β G γ are unable to localize PI3K β . We observed this prioritization of signaling input interactions over a range of membrane compositions that contained physiologically relevant densities of anionic lipids, such as phosphatidylserine and PI(4,5)P₂. Although a small fraction of PI3K β may transiently adopt a conformation that is compatible with direct Rac1(GTP) or G β G γ association in the absence of pY, these events are rare and do not represent a probable path for initial membrane docking of PI3K β .

Based on our single molecule dwell time and diffusion analysis, Dy647-PI3K β can cooperatively bind to one doubly phosphorylated peptide derived from the PDGF receptor. Supporting this model, Dy647-PI3K β with a mutated nSH2 or cSH2 domain that eliminates pY binding, still displayed membrane diffusivity indistinguishable from wild-type PI3K β . The diffusion coefficient of membrane bound pY-PI3K β complexes also did not significantly change over a broad range of pY membrane surface densities that span 3 orders of magnitude. Given that diffusivity of peripheral membrane binding proteins is strongly correlated with the valency of membrane interactions (Ziemba and Falke 2013; Hansen et al. 2022), we expected to observe a decrease in Dy647-PI3K β diffusion with increasing membrane surface densities of pY. Instead, our data suggests that the vast majority of PI3K β molecules engage a single pY peptide, rather than binding one tyrosine phosphorylated residue on two separate pY peptides. While no structural studies have shown how exactly the tandem SH2 domains of PI3K (p85 α) simultaneously bind to a doubly phosphorylated pY peptide, the interactions likely resemble the mechanism reported for ZAP-70 (β -chain of T-cell Receptor Associated Protein Kinase 70). The tandem SH2 domains of ZAP-70 can bind to a doubly phosphorylated β -chain derived from the TCR with only 11 amino acids spacing between the two tyrosine phosphorylation sites (Hatada et al. 1995). In the case of our PDGFR derived pY peptide that binds p85 α , 10 amino acids separate the two tyrosine phosphorylated residues.

Following the engagement of a pY peptide, we find that PI3K β can then associate with membrane anchored Rac1(GTP) or G β G γ . We detected the formation of PI3K β -pY-Rac1(GTP) and PI3K β -pY-G β G γ complexes based on the following criteria: (1) increase in Dy647-PI3K β bulk membrane recruitment, (2) increase in single molecule dwell time, and (3) a decrease in membrane diffusivity. Consistent with Dy647-PI3K β having a weak affinity for G β G γ , pY peptides in solution were unable to strongly localize Dy647-PI3K β to SLBs containing membrane anchored G β G γ . This is in agreement with HDX-MS data showing that the p110 β -G β G γ interaction can only be detected using a G β G γ -p85 α (icSH2) chimeric fusion or pre-activating PI3K β with solution pY (Hashem A. Dbouk et al. 2012). Using AlphaFold Multimer (Evans et al. 2022; Jumper et al. 2021), we created a model that illustrates how the p85 α (nSH2) domain is predicted to sterically block G β G γ binding to p110 β . This model was validated by comparing the AlphaFold Multimer model to previous reported HDX-MS (H. A. Dbouk et al. 2010) and X-ray crystallography data (Zhang et al. 2011a). Further supporting this model, we found that the Dy647-PI3K β nSH2(R358A) mutant tethered to membrane conjugated pY peptide was unable to engage membrane anchored G β G γ . Membrane targeting of PI3K β by pY was required to relieve nSH2 mediated autoinhibition and expose the G β G γ binding site. Recruitment by membrane tethered pY also reduces the translational and rotational entropy of PI3K β , which facilitates PI3K β -pY-G β G γ complex formation. We observed a similar mechanism of synergistic PI3K β localization on SLBs containing pY and Rac1(GTP). However, we did not determine the role p85 α inhibition serves in regulating the

association between PI3K β and Rac1(GTP). In the case of PI3K α , interactions with Ras(GTP) on vesicles or in solution have previously been shown to require pY peptide to relieve autoinhibition.

Mechanism of synergistic activation

Previous characterization of PI3K β lipid kinase activity has utilized solution-based assays to measure P(3,4,5) P₃ production. These solution-based measurements lack spatial information concerning the mechanism of PI3K β membrane recruitment and activation. Our ability to simultaneously visualize PI3K β membrane localization and P(3,4,5)P₃ production is critical for determining which regulatory factors directly modulate the catalytic efficiency of PI3K β . In the case of PI3K α , the enhanced membrane recruitment model has been used to explain the synergistic activation mediated by pY and Ras(GTP) (Buckles et al. 2017). In other words, the PI3K α -pY-Ras complex is more robustly localized to membranes compared to the PI3K α -pY and PI3K α -Ras complexes, which results in a larger total catalytic output for the system. Although the Ras binding domain (RBD) of PI3K α and PI3K β are conserved, these kinases interact with distinct Ras superfamily GTPases (Fritsch et al. 2013b). Therefore, it's possible that PI3K α and PI3K β display different mechanisms of synergistic activation, which could explain their non-overlapping roles in cell signaling.

Studies of PI3K β mouse knock-in mutations in primary macrophages and neutrophils have shown that robust PI3K β activation requires coincident activation through the RTK and GPCR signaling pathways (Houslay et al. 2016). This response most strongly depends on the ability of PI3K β to bind G β Gy and to a lesser extent Rac1/Cdc42 (Houslay et al. 2016). Although these mutational studies have nicely demonstrated the modes of synergistic PI3K β activation in cells, signaling network crosstalk and redundancy limits our mechanistic understanding of how PI3K β prioritizes signaling inputs and the exact mechanism for driving PI(3,4,5)P₃ production. Based on our single molecule membrane binding experiments, auto-inhibited PI3K β is unable to bind directly to either Rac1(GTP) or G β Gy in the absence of pY peptides. We found that PI3K β kinase activity is also relatively insensitive to either Rac1(GTP) or G β Gy alone. This is in contrast to previous reports that showed Rho-GTPases (Fritsch et al. 2013a) and G β Gy (Katada et al. 1999; Hashem A. Dbouk et al. 2012; Maier, Babich, and Nürnberg 1999) can activate PI3K β , albeit modest, compared to synergistic activation with pY peptides plus Rac1(GTP) or G β Gy.

In our single molecule TIRF experiments, we find that the pY peptide is the only factor that robustly localizes PI3K β to supported membranes in an autonomous manner. However, the pY-PI3K β complex displays weak lipid kinase activity ($k_{cat} = \sim 3$ PI(3,4,5) P₃ lipids/sec•PI3K β). This is consistent with cellular measurements showing that RTK activation by insulin (Z. A. Knight et al. 2006), PDGF (Guillermet-Guibert et al. 2008), or EGF (Ciraolo et al. 2008) show little PI3K β dependence for PI(3,4,5)P₃ production. Although the dominant role of PI3K α in controlling PI(3,4,5)P₃ production downstream of RTKs can mask the contribution from PI3K β in some cell types, these results highlight the need for PI3K β to be synergistically activated. When we measured the kinetics of lipid phosphorylation for PI3K β -pY-Rac1(GTP) and PI3K β -pY-G β Gy complexes we observed synergistic activation beyond simply enhancing PI3K β membrane localization. After accounting for the ~ 1.8 -fold increase in membrane localization between PI3K β -pY-Rac1(GTP) and PI3K β -pY-Rac1(GDP), we calculated a 4.3-fold increase in k_{cat} that was dependent on engaging Rac1(GTP). Comparing the kinase activity of PI3K β -pY and PI3K β -pY-G β Gy complexes that are present at the same membrane surface density (~ 0.2 PI3K β /μm²) revealed a 22-fold increase in k_{cat} mediated by the G β Gy interaction. Together, these results indicate that PI3K β -pY complex association with either Rac1(GTP) or G β Gy allosterically modulates PI3K β , making it more catalytically efficient.

Mechanisms controlling cellular activation of PI3K β

Studies of PI3K activation by pY peptides have mostly been performed using peptides derived from the IRS-1 (Insulin Receptor Substrate 1) and the EGFR/PDGF receptors (Backer et al. 1992; Fantl, Martin, and Turck 1992). As a result, we still have not defined the broad specificity p85 α has for tyrosine phosphorylated peptides. Biochemistry studies indicate that the nSH2 and cSH2 domains of p85 α robustly bind pY residues with a methionine in the +3 position (pYXXM) (Breeze et al. 1996; Nolte et al. 1996; Backer et al. 1992; Fantl, Martin, and Turck 1992). The p85 α subunit is also predicted to interact with the broad repertoire of receptors that contain immunoreceptor tyrosine-based activation motifs (ITAMs) bearing the pYXX(L/I) motif (Reth 1989; Osman et al. 1996; Zenner et al. 1996; Love and Hayes 2010). Based on RNA seq data, human neutrophils express at least six different Fc receptors (FcRs) that all contain phosphorylated ITAMs that can potentially facilitate membrane localization of class 1A PI3Ks (Rincón, Rocha-Gregg, and Collins 2018).

A variety of human diseases result from the overexpression of RTKs, especially the epithelial growth factor receptor (EGFR) (Sauter et al. 1996). When the cellular plasma membrane contains densities of EGFR greater than 2000 receptors/ μm^2 , trans-autophosphorylation and activation can occur in a EGF-independent manner (Endres et al. 2013). Receptor membrane surface densities above the threshold needed for spontaneous receptor trans-autophosphorylation have been observed in many cancer cells (Haigler et al. 1978). In these disease states, PI3K is expected to localize to the plasma membrane in the absence of ligand induced RTK or GPCR signaling. The slow rate of PI(3,4,5)P₃ production we measured for the membrane tethered pY-PI3K β complex suggests that PI(3,4,5)P₃ levels are not likely to rise above the global inhibition imposed by lipid phosphatases until synergistic activation of PI3K β by RTKs and GPCRs. However, loss of PTEN in some cancers (Jia et al. 2008) could produce an elevated level of PI(3,4,5)P₃ due to PI3K β being constitutively membrane localized via ligand independent trans-autophosphorylation of RTKs.

Acknowledgements

We thank John Burke (University of Victoria) for assistance generating the AlphaFold2 Multimer model of PI3K β bound to G β G γ . We thank Grace Waddell for preliminary characterization of PI3K β . We thank Colin Hawkinson for assistance with protein purification. We thank Jean Chung (Colorado State, Fort Collins) and Orion Weiner (University of California at San Francisco) for plasmids encoding Btk and P-Rex1 plasmids, respectively.

Author contributions

Resources: B.R.D, G.M.B, S.E.P, S.D.H.

Experiments and investigation: B.R.D, N.E.W., G.M.B, S.E.P, S.D.H.

Data Analysis: B.R.D, N.E.W., S.E.P., S.D.H.

Conceptualization: B.R.D, N.E.W., S.D.H.

Interpretation: B.R.D, N.E.W., S.D.H.

Data curation: B.R.D, N.E.W., S.D.H.

Writing – Review and editing: B.R.D, N.E.W., G.M.B, S.E.P, S.D.H.

Writing – Original draft: S.D.H.

Supervision: S.D.H.

Project administration: S.D.H.

Funding acquisition: S.D.H.

Funding

Research was supported by the University of Oregon Start-up funds (S.D.H.), National Science Foundation CAREER Award (S.D.H., MCB-2048060), Molecular Biology and Biophysics Training Program (B.R.D, N.E.W., NIH T32 GM007759), and the Summer Program for Undergraduate Research (SPUR) at the University of Oregon (G.M.B.). The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Science Foundation.

Data availability

All the information needed for interpretation of the data is presented in the manuscript or the supplemental material. Plasmids related to this work are available upon request.

Conflict of interest

The authors declare that they have no conflicts of interest with the contents of this article.

Materials methods

Molecular Biology

The following genes were used as templates for PCR to clone plasmids used for recombinant protein expression: *PIK3CB* (human 1-1070aa; Uniprot Accession #P42338), *PIK3R1* (human 1-724aa; Uniprot Accession #P27986), *PIK3CG* (mouse 1-1102aa; Uniprot Accession #Q9JHG7), *PIK3R5* (mouse 1-871aa; Uniprot Accession #Q5SW28), *RAC1* (human 1-192aa; Uniprot Accession #P63000), *CYTH3/Grp1* (human 1-400aa; Uniprot Accession #O43739), *BTB* (bovine 1-659aa; Uniprot Accession #Q3ZC95), neutrophil cytosol factor 2 (*NCF2*, human 1-526aa; Uniprot Accession #P19878, referred to as p67/phox), *PREX1* (human 1-1659aa; Uniprot Accession #Q8TCU6), *GNB1/GBB1* ($G\beta_1$, bovine 1-340aa; Uniprot Accession #P62871), *GNG2/GBG2* ($G\gamma_2$, bovine 1-71aa; Uniprot Accession #P63212). The following plasmids were purchased as cDNA clones from Horizon (PerkinElmer), formerly known as Open Biosystems and Dharmacon: mouse *PIK3CG* (clone #BC051246, cat #MMM1013-202770664) and mouse *PIK3R5* (clone #BC128076, cat #MMM1013-211693360), human *PIK3R1* (clone #30528412, cat #MHS6278-202806334), human *CYTH3/Grp1* (clone #4811560, cat #MHS6278-202806616). Genes encoding bovine $G\beta_1$ and $G\gamma_2$ were derived from the following plasmids: YFP- $G\beta_1$

(Addgene plasmid # 36397) and YFP-Gy₂ (Addgene plasmid # 36102). These Gβ₁ and Gy₂ containing plasmids were kindly provided to Addgene by Narasimhan Gautam (Saini et al. 2007). In this study, we used a previously described mutant form of Btk with mutations in the peripheral PI(3,4,5)P₃ binding site (R49S/K52S) (Chung et al. 2019; Wang et al. 2015). The Btk peripheral site mutant was PCR amplified using a plasmid provided by Jean Chung (Colorado State, Fort Collins) that contained the following coding sequence: his6-SUMO-Btk(PH-TH, R49S/K52S)-EGFP. The nSH2 biosensor was derived from human *PIK3R1*. The gene encoding human *PREX1* was provided by Orion Weiner (University of California San Francisco). Refer to supplemental text to see exact peptide sequence of every protein purified in this study. The following mutations were introduced into either the *PIK3CB* (p110β) or *PIK3R1* (p85α) genes using site-directed mutagenesis: p85α nSH2 (R358A, FLVR->FLVA), p85α cSH2 (R649A, FLVR->FLVA), p110β GβG mutant (K532D/K533D). For cloning, genes were PCR amplified using AccuPrime Pfx master mix (ThermoFisher, Cat#12344040) and combined with a restriction digested plasmids using Gibson assembly (Gibson et al. 2009). Refer to supplemental text for a complete list of plasmids used in this study. Information about the specific peptide sequences for recombinantly expressed and purified proteins is organized in the supplemental information document. The complete open reading frame of all vectors used in this study were sequenced to ensure the plasmids lacked deleterious mutations.

BACMID and baculovirus production

We generated BACMID DNA as previously described (Hansen et al. 2019). FASTBac1 plasmids containing our gene of interest were transformed into DH10 Bac cells and plated on LB agar media containing 50 µg/mL kanamycin, 10 µg/mL tetracycline, 7 µg/mL gentamycin, 40 µg/mL X-GAL, and 40 µg/mL IPTG. Plated cells were incubated for 2-3 days at 37°C before positive clones were isolated based on blue-white colony selection. White colonies were inoculated into 5mL of TPM containing 50 µg/mL kanamycin, 10 µg/mL tetracycline, 7 µg/mL gentamycin and grown overnight at 37°C. To purify the BACMID DNA, we first pelleted the cultures via centrifugation, then re-suspended the pellet in 300 µL of buffer containing 50 mM Tris [pH 8.0], 10 mM EDTA, 100 µg/mL RNase A. We lysed bacteria via addition of 300 µL of buffer containing 200 mM NaOH, 1% SDS before neutralization with 300 µL of 4.2 M Guanidine HCl, 0.9 M KOAc [pH 4.8]. We then centrifuged the sample at 23°C for 10 minutes at 14,000 x g. Supernatant containing the BACMID DNA was combined with 700 µL 100% isopropanol and spun for 10-minute at 14,000 x g. The DNA pellets were washed twice with 70% ethanol (200 µL and 50 µL) and centrifuged. The ethanol was removed by vacuum aspiration and the final DNA pellet was dried in a biosafety hood. Finally, we solubilized the BACMID DNA in 50-100 µL of sterile filtered MilliQ water. A Nanodrop was used to quantify the total DNA concentration. BACMID DNA was stored at -20°C or used immediately for higher transfection efficiency. Baculovirus was generated as previously described. In brief, we incubated 5-7 µg of BACMID DNA with 4 µL Fugene (Thermo Fisher, Cat# 10362100) in 250 µL of Opti-MEM serum free media for 30 minutes at 23°C. The DNA-Fugene mixture was then added to a Corning 6-well plastic dish (Cat# 07-200-80) containing 1 × 10⁶ *Spodoptera frugiperda* (Sf9) insect cells in 2 mL of ESF 921 Serum-Free Insect Cell Culture media (Expression Systems, Cat# 96-001, Davis, CA.). 4-5 days following the initial transfection, we harvested and centrifuged the viral supernatant (called “P0”). P0 was used to generate a P1 titer by infecting 7 × 10⁶ Sf9 cells plated in a 10 cm tissue culture grade petri dish containing 10 mL of ESF 921 media and 2% Fetal Bovine serum (Seradigm, Cat# 1500-500, Lot# 176B14). We harvested and centrifuged the P1 titer after 4 days of transfection. The P1 titer was expanded at a concentration of 1% vol/vol of P1 titer into a 100 mL Sf9 cell culture grown to a density of 1.25-1.5 × 10⁶ cells/mL in a sterile 250 mL polycarbonate Erlenmeyer flask with vented cap (Corning, #431144). The P2 titer (viral supernatant) was harvested, centrifuged, and 0.22 µm filtered in 150 mL filter-top bottle (Corning, polyethersulfone (PES),

Cat#431153). We used this P2 titer for protein expression in High 5 cells grown in ESF 921 Serum-Free Insect Cell Culture media (0% FBS) at a final baculovirus concentration of ~2% vol/vol. All our media contained 1x concentration of Antibiotic-Antimycotic (Gibco/Invitrogen, Cat#15240-062).

Protein purification

PI3K β and PI3K γ

Genes encoding human his6-TEV-PIK3CB (1-1070aa) and ybbr-PIK3R1 (1-724aa) were cloned into a modified FastBac1 dual expression vector containing tandem polyhedrin (pH) promoters. Genes encoding mouse his6-TEV-PIK3CG (1-1102aa) and mouse his6-TEV-ybbr-PIK3R5 (1-871aa) were expressed from separate FastBac1 vectors under the polyhedrin (pH) promoters. For protein expression, high titer baculovirus was generated by transfecting 1×10^6 *Spodoptera frugiperda* (Sf9) with 0.75-1 μ g of BACMID DNA as previously described (Hansen et al. 2019). After two rounds of baculovirus amplification and protein test expression, 2×10^6 cells/mL High 5 cells were infected with 2% vol/vol PI3K β (PIK3CB/PIK3R1) or 2% vol/vol PI3K γ (PIK3CG/PIK3R5) baculovirus and grown at 27°C in ESF 921 Serum-Free Insect Cell Culture media (Expression Systems, Cat# 96-001) for 48 hours. High 5 cells were harvested by centrifugation and washed with 1x PBS [pH 7.2] and centrifuged again. Final cell pellets were resuspending in an equal volume of 1x PBS [pH 7.2] buffer containing 10% glycerol and 2x protease inhibitor cocktail (Sigma, Cat# P5726) before being stored in the -80°C freezer. For protein purification, frozen cell pellets from 4 liters of cell culture were lysed by Dounce homogenization into buffer containing 50 mM Na₂HPO₄ [pH 8.0], 10 mM imidazole, 400 mM NaCl, 5% glycerol, 2 mM PMSF, 5 mM BME, 100 μ g/mL DNase, 1x protease inhibitor cocktail (Sigma, Cat# P5726). Lysate was centrifuged at 35,000 rpm (140,000 x g) for 60 minutes under vacuum in a Beckman centrifuge using a Ti-45 rotor at 4°C. Lysate was batch bound to 5 mL of Ni-NTA Agarose (Qiagen, Cat# 30230) resin for 90 minutes stirring in a beaker at 4°C. Resin was washed with buffer containing 50 mM Na₂HPO₄ [pH 8.0], 30 mM imidazole, 400 mM NaCl, and 5 mM BME. Protein was eluted from NiNTA resin with wash buffer containing 500 mM imidazole. The his6-TEV-PIK3CB/ybbr-PIK3R1 complex was then desalted on a G25 Sephadex column in buffer containing 20 mM Tris [pH 8.0], 100 mM NaCl, 1 mM DTT. Peak fractions were pooled and loaded onto a Heparin anion exchange column equilibrated in 20 mM Tris [pH 8.0], 100 mM NaCl, 1 mM DTT buffer. Proteins were resolved over a 10-100% linear gradient (0.1-1 M NaCl) at 2 mL/min flow rate over 20 minutes. Peak fractions were pooled and supplemented with 10% glycerol, 0.05% CHAPS, and 200 μ g/mL his6-TEV(S291V) protease. The his6-TEV-PIK3CB/ybbr-PIK3R1 complex was incubated overnight at 4°C with TEV protease to remove the affinity tag. The TEV protease cleaved PIK3CB/ybbr-PIK3R1 complex was separated on a Superdex 200 size exclusion column (GE Healthcare, Cat# 17-5174-01) equilibrated with 20 mM Tris [pH 8.0], 150 mM NaCl, 10% glycerol, 1 mM TCEP, 0.05% CHAPS. Peak fractions were concentrated in a 50 kDa MWCO Amicon centrifuge tube and snap frozen at a final concentration of 10 μ M using liquid nitrogen. This protein is referred to as PI3K β throughout the manuscript. The same protocol was followed to purify mouse PI3K γ (PIK3CG/ybbr-PIK3R5) and the various PI3K β mutants reported in this study.

Rac1

The gene encoding human Rac1 were expressed in BL21 (DE3) bacteria as his10-SUMO3-(Gly)₅ fusion proteins. Bacteria were grown at 37°C in 4L of Terrific Broth for two hours or until OD₆₀₀ = 0.8. Cultures were shifted to 18°C for 1 hour then induced with 0.1 mM IPTG. Expression was allowed to continue for 20 hours before harvesting. Cells were lysed into 50 mM Na₂HPO₄ [pH 8.0], 400 mM NaCl, 0.4 mM BME, 1 mM PMSF, 100 μ g/mL DNase using a

microfluidizer. Lysate was centrifuged at 16,000 rpm (35000 x g) for 60 minutes in a Beckman JA-20 rotor at 4°C. Lysate was circulated over 5 mL HiTrap Chelating column (GE Healthcare, Cat# 17-0409-01) loaded with CoCl_2 . Bound protein was eluted at a flow rate of 4mL/min into 50 mM Na_2HPO_4 [pH 8.0], 400 mM NaCl, 500mM imidazole. Peak fractions were pooled and combined with SUMO protease (SenP2) at a final concentration of 50 $\mu\text{g}/\text{mL}$ and dialyzed against 4 liters of buffer containing 20 mM Tris [pH 8.0], 250 mM NaCl, 10% Glycerol, 1 mM MgCl_2 , 0.4mM BME. Dialysate containing SUMO cleaved protein was recirculated for 2 hours over a 5 mL HiTrap Chelating column. Flowthrough containing (Gly)₅-Rac1 was concentrated in a 5 MWCO Vivaspin 20 before being loaded on a 124 mL Superdex 75 column equilibrated in 20 mM Tris [pH 8.0], 150 mM NaCl, 10% Glycerol, 1 mM TCEP, 1 mM MgCl_2 . Peak fractions containing (Gly)₅-Rac1 were pooled and concentrated to a concentration of 400-500 μM (~10 mg/mL) and snap frozen with liquid nitrogen and stored at -80°C.

Grp1 and nSH2

The gene encoding the Grp1 PH domain derived from human CYTH3 was expressed in BL21 (DE3) bacteria as a his6-MBP-N10-TEV-GGGG-Grp1-Cys fusion protein. The gene encoding the N-terminal SH2 (nSH2, 322-440aa) domain derived from the *PIK3R1* gene was cloned and expressed as a his6-GST-TEV-nSH2 fusion protein. A single cysteine was added to the C-terminus of the nSH2 domain to allow for chemical labeling with maleimide dyes. For both recombinant proteins, bacteria were grown at 37°C in 4 L of Terrific Broth for two hours or until $\text{OD}_{600} = 0.8$ and then shifted to 18°C for 1 hour. Cells were then induced to express either the Grp1 or nSH2 fusion by adding 0.1 mM IPTG. Cells were harvested 20 hours post-induction. We lysed bacteria into 50 mM Na_2HPO_4 [pH 8.0], 400 mM NaCl, 0.4 mM BME, 1 mM PMSF, 100 $\mu\text{g}/\text{mL}$ DNase using a microfluidizer. Next, lysate was centrifuged at 16,000 rpm (35000 x g) for 60 minutes in a Beckman JA-20 rotor at 4°C. Supernatant was circulated over 5 mL HiTrap chelating column (GE Healthcare, Cat# 17-0409-01) that was pre-incubated with 100 mM CoCl_2 for 10 minutes, wash with MilliQ water, and equilibrated into lysis buffer lacking PMSF and DNase. Clarified cell lysate containing his6-MBP-N10-TEV-GGGG-Grp1-Cys was circulated over the HiTrap column and washed with 20 column volumes of 50 mM Na_2HPO_4 [pH 8.0], 300 mM NaCl, 0.4 mM BME containing buffer. Protein was eluted with buffer containing 50 mM Na_2HPO_4 [pH 8.0], 300 mM NaCl, and 500 mM imidazole at a flow rate of 4mL/min. Peak HiTrap elutant fractions were combined with 750 μL of 2 mg/mL TEV protease and dialyzed overnight against 4L of buffer containing 20 mM Tris [pH 8.0], 200 mM NaCl, and 0.4 mM BME. The next day, we recirculated cleaved proteins over two HiTrap (Co^{+2}) columns (2×5 mL) that were equilibrated in 50 mM Na_2HPO_4 [pH 8.0], 300 mM NaCl, and 0.4 mM BME containing buffer for 1 hour. We concentrated the proteins via 10 kDa MWCO Vivaspin 20 to a volume of 5mL. The concentrated Grp1 protein was then loaded on a 124 mL Superdex 75 column equilibrated in 20 mM Tris [pH 8], 200 mM NaCl, 10% glycerol, and 1 mM TCEP. Protein was eluted at a flow rate of 1mL/min. Peak fractions containing Grp1 were pooled and concentrated to 500-600 μM (~8mg/mL). Peak fractions containing nSH2 were pooled and concentrated to 200-250 μM (~3mg/mL). Proteins were frozen with liquid nitrogen and stored at -80°C.

P-Rex1 (DH-PH) domain

The DH-PH domain of human P-Rex1 was expressed as a fusion protein, his6-MBP-N10-TEV-PRex1(40-405aa), in BL21(DE3) Star bacteria. Bacteria were grown at 37°C in 2L of Terrific Broth for two hours or until $\text{OD}_{600} = 0.8$. Cultures were shifted to 18°C for 1 hour then induced with 0.1 mM IPTG. Expression was allowed to continue for 20 hours before harvesting. Cells were lysed into buffer containing 50 mM NaHPO_4 [pH 8.0], 400 mM NaCl, 5% glycerol, 1 mM PMSF, 0.4 mM BME, 100 $\mu\text{g}/\text{mL}$ DNase using microtip sonication. Cell

lysate was clarified by centrifugation at 16,000 rpm (35000 $\times$ g) for 60 minutes in a Beckman JA-20 rotor at 4°C. To capture his₆-tagged P-Rex1, cell lysate was circulated over a 5 mL HiTrap Chelating column (GE Healthcare, Cat# 17-0409-01) charged CoCl₂. The column was washed with 100 mL of 50 mM NaHPO₄ [pH 8.0], 400 mM NaCl, 5% glycerol, 0.4 mM BME buffer. Protein was eluted into 15 mL with buffer containing 50 mM NaHPO₄ [pH 8.0], 400 mM NaCl, 500 mM imidazole, 5% glycerol, 0.4 mM BME. Peak fractions were pooled and combined with his6-TEV protease and dialyzed against 4 liters of buffer containing 50 mM NaHPO₄ [pH 8.0], 400 mM NaCl, 5% glycerol, 0.4 mM BME. The next day, dialysate containing TEV protease cleaved protein was recirculated for 2 hours over a 5 mL HiTrap chelating column. Flowthrough containing P-Rex1 (40-405aa) was desalted into 20 mM Tris [pH 8.0], 50 mM NaCl, 1 mM DTT using a G25 Sephadex column. Note that some of the protein precipitated during the desalting step. Desalted protein was clarified using centrifugation followed by a 0.22 μ m syringe filter. P-Rex1(40-405aa, pI = 8.68) was further purified by cation exchange chromatography (i.e. MonoS) using a 20 mM Tris [pH 8.0], 0 – 1000 mM NaCl, 1 mM DTT. P-Rex1(40-405aa) bound eluted broadly in the presence of 100-260 mM NaCl. Pure fractions as determined by SDS-PAGE were pooled, concentration, and loaded onto a 120 mL Superdex 75 column equilibrated in 20 mM Tris [pH 8], 150 mM NaCl, 10% glycerol, 1 mM TCEP. Peak fractions containing P-Rex1(40-405aa) were pooled and concentrated to a concentration of 114 μ M, aliquoted, frozen with liquid nitrogen, and stored at -80°C.

Btk

The mutant Btk PI(3,4,5)P₃ fluorescent biosensor was recombinantly expressed in BL21 Star *E. coli* as a his6-SUMO-Btk(1-171aa PH-TH domain; R49S/K52S)-SNAP fusion. Bacteria were grown at 37°C in Terrific Broth to an OD₆₀₀ of 0.8. These cultures were then shifted to 18°C for 1 hr, induced with 0.1 mM IPTG, and allowed to express protein for 20 hr at 18°C before being harvested. Cells were lysed into 50 mM NaPO₄ (pH 8.0), 400 mM NaCl, 0.5 mM BME, 10 mM Imidazole, and 5% glycerol. Lysate was then centrifuged at 16,000 rpm (35,172 $\times$ g) for 60 min in a Beckman JA-20 rotor chilled to 4°C. Lysate was circulated over 5 mL HiTrap Chelating column (GE Healthcare, Cat# 17-0409-01) charged with 100 mM CoCl₂ for 2 hrs. Bound protein was then eluted with a linear gradient of imidazole (0–500 mM, 8 CV, 40 mL total, 2 mL/min flow rate). Peak fractions were pooled, combined with SUMO protease Ulp1 (50 μ g/mL final concentration), and dialyzed against 4 L of buffer containing 20 mM Tris [pH 8.0], 200 mM NaCl, and 0.5 mM BME for 16–18 hr at 4°C. SUMO protease cleaved Btk was recirculated for 1 hr over a 5 mL HiTrap Chelating column. Flow-through containing Btk-SNAP was then concentrated in a 5 kDa MWCO Vivaspin 20 before being loaded on a Superdex 75 size-exclusion column equilibrated in 20 mM Tris [pH 8.0], 200 mM NaCl, 10% glycerol, 1 mM TCEP. Peak fractions containing Btk-SNAP were pooled and concentrated to a concentration of 30 μ M before snap-freezing with liquid nitrogen and storage at -80°C. For labeling, Btk-SNAP was combined with a 1.5x molar excess of SNAP-Surface Alexa488 dye (NEB, Cat# S9129S) and incubated overnight at 4°C. The next day, Btk-SNAP-AF488 was desalted into buffer containing 20 mM Tris [pH 8.0], 200 mM NaCl, 10% glycerol, 1 mM TCEP using a PD10 column. The protein was then spin concentrated using a Amicon filter and loaded onto a Superdex 75 column to isolate dye free monodispersed Btk-SNAP-AF488. The peak elution was pooled, concentrated, aliquoted, and flash frozen with liquid nitrogen.

p67/phox

Genes encoding the Rac1(GTP) biosensor, p67/phox, were cloned into a his10-TEV-SUMO plasmid and expressed in Rosetta2 (DE3) pLysS bacteria. We grew bacteria in 3L of Terrific Broth 37°C for two hours or until OD₆₀₀ = 0.8 before shifting temperature to 18°C for 1 hour. We induced protein expression in cells via addition of 50 μ M IPTG. Cells expressed overnight for 20 hours at 18°C before harvesting. We lysed cells into buffer containing 50 mM

Na₂HPO₄ [pH 8.0], 400 mM NaCl, 0.4 mM BME, 1 mM PMSF, and 100 µg/mL DNase using a microfluidizer. The lysate was centrifuged at 16,000 rpm (35000 x g) for 60 minutes in a Beckman JA-20 rotor at 4°C. Supernatant was then circulated over 5 mL HiTrap Chelating column (GE Healthcare, Cat# 17-0409-01) that was inoculated with 100mM CoCl₂ for ten minutes. The HiTrap column was washed with 20 column volumes (100mL) of 50 mM Na₂HPO₄ [pH 8.0], 400 mM NaCl, 10 mM imidazole, and 0.4 mM BME containing buffer. Bound protein was eluted at a flow rate of 4mL/min with 15-20 mL of 50 mM Na₂HPO₄ [pH 8.0], 400 mM NaCl, and 500 mM imidazole containing buffer. Peak fractions were pooled and combined with his6-SenP2 (SUMO protease) at a final concentration of 50 µg/mL and dialyzed against 4 liters of buffer containing 25 mM Tris [pH 8.0], 400 mM NaCl, and 0.4 mM BME. Dialysate containing SUMO cleaved protein was recirculated for 2 hours over two 5 mL HiTrap Chelating (Co²⁺) columns that were equilibrated in buffer containing 25 mM Tris [pH 8.0], 400 mM NaCl, and 0.4 mM BME. Recirculated protein was concentrated to a volume of 5 mL using a 5 kDa MWCO Vivaspinn 20 before loading on a 124 mL Superdex 75 column at a flow rate of 1mL/min. The column was equilibrated in buffer containing 20 mM HEPES [pH 7], 200 mM NaCl, 10% glycerol, and 1 mM TCEP. Peak fractions off the Superdex 75 column were concentrated in a 5 kDa MWCO Vivaspinn 20 to a concentration between 200-500 µM (5-12mg/mL). Protein was frozen with liquid nitrogen and stored at -80°C.

Farnesylated Gβ₁/Gγ₂ and SNAP-Gβ₁/Gγ₂

The native eukaryotic farnesyl Gβ₁/Gγ₂ and SNAP-Gβ₁/Gγ₂ complexes were expressed and purified from insect cells as previously described (Rathinaswamy et al. 2021; Kozasa and Gilman 1995; Hashem A. bouk et al. 2012). The Gβ₁ and Gγ₂ genes were cloned into dual expression vectors containing tandem polyhedron promoters. A single baculovirus expressing either Gβ₁/his₆-TEV-Gγ₂ or SNAP-Gβ₁/his₆-TEV-Gγ₂ were used to infect 2-4 liters of High Five cells (2 × 10⁶ cells/mL) with 2% vol/vol of baculovirus. Cultures were then grown in shaker flasks (120 rpm) for 48 hours at 27°C before harvesting cells by centrifugation. Insect cells pellets were stored as 10 g pellets in the -80°C before purification. To isolate farnesylated Gβ₁/his₆-TEV-Gγ₂ or SNAP-Gβ₁/his₆-TEV-Gγ₂ complexes, insect cells were lysed by Dounce homogenization into 50 mM HEPES-NaOH [pH 8], 100 mM NaCl, 3 mM MgCl₂, 0.1 mM EDTA, 10 µM GDP, 10 mM BME, Sigma PI tablets (Cat #P5726), 1 mM PMSF, DNase (GoldBio, Cat# D-303-1). We centrifuged homogenized lysate for 10 minutes at 800 x g to remove nuclei and large cell debris. We then centrifuged remaining lysate using a Beckman Ti45 rotor 100,000 x g for 30 minutes at 4 °C. The post-centrifugation pellet containing plasma membranes was the resuspended in a buffer containing 50 mM HEPES-NaOH [pH 8], 50 mM NaCl, 3 mM MgCl₂, 1% sodium deoxycholate (wt/vol, Sigma D6750), 10µM GDP (Sigma, cat# G7127), 10 mM BME, and a Sigma Protease Inhibitor tablet (Cat #P5726) to a concentration of 5 mg/mL total protein. We Dounce homogenized the sample to break apart membranes and then allowed the homogenized solution to stir for 1 hour at 4°C. We centrifuged the solubilized extracted membrane solution in a Beckman Ti45 rotor 100,000 x g for 45 minutes at 4°C. We diluted the supernatant containing solubilized Gβ₁/his₆-TEV-Gγ₂ or SNAP-Gβ₁/his₆-TEV-Gγ₂ in buffer composed of 20 mM HEPES-NaOH [pH 7.7], 100 mM NaCl, 0.1 % C₁₂E₁₀ (Polyoxyethylene (10) lauryl ether; Sigma, P9769), 25 mM imidazole, and 2 mM BME.

We affinity purified the soluble membrane extracted Gβ₁/his₆-TEV-Gγ₂ or SNAP-Gβ₁/his₆-TEV-Gγ₂ using Qiagen NiNTA resin. After adding NiNTA resin to the diluted solubilized extracted membrane solution, we allowed the resin to incubate and stir in a beaker at 4°C for 2 hours. We packed our protein-bound resin beads into a gravity flow column and washed with 20 column volumes of buffer containing 20 mM HEPES-NaOH [pH 7.7], 100 mM NaCl, 0.1 % C₁₂E₁₀, 20 mM imidazole, and 2 mM BME. We eluted and discarded the G alpha subunit of the heterotrimeric G-protein complex by washing with warm buffer (30°C)

containing 20 mM HEPES-NaOH [pH 7.7], 100 mM NaCl, 0.1 % C₁₂E₁₀, 20 mM imidazole, 2 mM BME, 50 mM MgCl₂, 10 μM GDP, 30 μM AlCl₃ (J.T. Baker 5-0660), and 10 mM NaF. We eluted Gβ₁/his₆-TEV-Gγ₂ or SNAP-Gβ₁/his₆-TEV-Gγ₂ from the NiNTA resin using buffer containing 20 mM Tris-HCl (pH 8.0), 25 mM NaCl, 0.1 % C₁₂E₁₀, 200 mM imidazole, and 2 mM BME. The eluted protein was incubated overnight at 4°C with TEV protease to cleave off the his₆ affinity tag.

The next day, the cleaved protein was desalted on a G25 Sephadex column into buffer containing 20 mM Tris-HCl [pH 8.0], 25 mM NaCl, 8 mM CHAPS, and 2 mM TCEP. Next, we performed anion exchange chromatography using a MonoQ column equilibrated with the desalting column buffer. We eluted Gβ₁/Gγ₂ or SNAP-Gβ₁/Gγ₂ from the MonoQ column in the presence of 175-200 mM NaCl. Peak-containing fractions were combined and concentrated using a Millipore Amicon Ultra-4 (10 kDa MWCO) centrifuge filter. Concentrated samples of Gβ₁/Gγ₂ or SNAP-Gβ₁/Gγ₂, respectively, were loaded on either Superdex 75 or Superdex 200 gel filtration columns equilibrated 20 mM Tris [pH 8.0], 100 mM NaCl, 8 mM CHAPS, and 2 mM TCEP. Peak fractions were combined and concentrated in a Millipore Amicon Ultra-4 (10 kDa MWCO) centrifuge tube. Finally, we aliquoted the concentrated Gβ₁/Gγ₂ or SNAP-Gβ₁/Gγ₂ and flash frozen with liquid nitrogen before storing at -80°C.

Fluorescent labeling of SNAP-Gβ₁/Gγ₂

To fluorescently label SNAP-Gβ₁/Gγ₂, protein was combined with 1.5x molar excess of SNAP-Surface Alexa488 dye (NEB, Cat# S9129S). SNAP dye labeling was performed in buffer containing 20 mM Tris [pH 8.0], 100 mM NaCl, 8 mM CHAPS, and 2 mM TCEP overnight at 4°C. Labeled protein was then separated from free Alexa488-SNAP surface dye using a 10 kDa MWCO Amicon spin concentrator followed by size exclusion chromatography (Superdex 75 10/300 GL) in buffer containing 20 mM Tris [pH 8.0], 100 mM NaCl, 8 mM CHAPS, 1 mM TCEP. Peak SEC fractions containing Alexa488-SNAP-Gβ₁/Gγ₂ were pooled and centrifuged in a 10 kDa MWCO Amicon spin concentrator to reach a final concentration of 15-20 μM before snap freezing in liquid nitrogen and storing in the -80°C. To calculate the SNAP dye labeling efficiency, we determined that Alexa488 contributes 11% of the peak A₄₉₄ signal to the measured A₂₈₀. Note that Alexa488 non-intuitively has a peak absorbance at 494 nm. We calculate the final concentration of Alexa488-SNAP-Gβ₁/Gγ₂ using an adjusted A₂₈₀ (i.e. $A_{280(\text{protein})} = A_{280(\text{observed})} - A_{494(\text{dye})} \cdot 0.11$) and the following extinction coefficients: $\epsilon_{280(\text{SNAP-G}\beta_1/\text{G}\gamma_2)} = 78380 \text{ M}^{-1} \cdot \text{cm}^{-1}$, $\epsilon_{494(\text{Alexa488})} = 71,000 \text{ M}^{-1} \cdot \text{cm}^{-1}$.

Fluorescent labeling of PI3K using Sfp transferase

As previously described (Rathinaswamy et al. 2021), we generated a Dyomics647-CoA derivative by incubating a mixture of 15 mM Dyomics647 maleimide (Dyomics, Cat #647P1-03) in DMSO with 10 mM CoA (Sigma, #C3019, MW = 785.33 g/mole) overnight at 23°C. To quench excess unreacted Dyomics647 maleimide, we added 5 mM DTT. We thawed purified PIK3CB/ybbr-PIK3R1 (referred to as PI3Kβ or p110β-p85α in manuscript) and chemically labeled with Dyomics647-CoA using Sfp-his₆. The ybbrR13 motif fused to PIK3R1 contained the following peptide sequence: DSLEFIASKLA (Yin et al. 2006). In a total reaction volume of 2 mL we combined 5 μM PI3Kβ, 4 μM Sfp-his₆, and 10 μM DY647-CoA in buffer containing 20 mM Tris [pH 8], 150 mM NaCl, 10 mM MgCl₂, 10% Glycerol, 1 mM TCEP, and 0.05% CHAPS. The ybbr labeling reaction was allowed to proceed for 4 hours on ice. Excess Dyomics647-CoA was removed via a using a gravity flow PD-10 column. We concentrated labeled Dy647-PI3Kβ in a 50 kDa MWCO Amicon centrifuge tube before loading on a Superdex 200 gel filtration column equilibrated in 20 mM Tris [pH 8], 150 mM NaCl, 10% glycerol, 1 mM TCEP, and 0.05% CHAPS (GoldBio, Cat# C-080-100). We pooled and concentrated peak fractions to 5-

10 μ M before we aliquoted and flash froze with liquid nitrogen. Labeled protein was stored at -80°C.

Preparation of supported lipid bilayers

We generated small unilamellar vesicles (SUVs) for this study using the following lipids: 1,2-dioleoyl-sn-glycero-3-phosphocholine (18:1 DOPC, Avanti # 850375C) and 1,2-dioleoyl-sn-glycero-3-phospho-L-serine (18:1 DOPS, Avanti # 840035C), L- α -phosphatidylinositol-4,5-bisphosphate (Brain PI(4,5)P₂, Avanti # 840046X), synthetic phosphatidylinositol 4,5-bisphosphate 18:0/20:4 (PI(4,5)P₂, Echelon, P-4524), and 1,2-dioleoyl-sn-glycero-3-phosphoethanolamine-N-[4-(p-maleimidomethyl)cyclohexane-carboxamide] (18:1 MCC-PE, Avanti # 780201C). We report lipid mixtures as percentages equivalent to molar fractions. We dried a total of 2 μ moles lipids were combined with 2 mL of chloroform in a 35 mL glass round bottom flask containing. This mixture was dried to a thin film via rotary evaporation where the glass round-bottom flask was kept in a 42°C water bath. Following evaporation, we either flushed the lipid-containing flask with nitrogen gas or placed in it a vacuum desiccator for a minimum of 30 minutes. We obtained a concentration of 1 mM of lipids by resuspending the dried film in 2 mL of 1x PBS [pH 7.2]. We generated 30-50 nm SUVs from this 1 mM total lipid mixture via extrusion of the resuspended lipid mixture through 0.03 μ m pore size 19 mm polycarbonate membrane (Avanti #610002) with filter supports (Avanti #610014) on both sides of the PC membrane. We prepared coverglass (25×75 mm, IBIDI, cat #10812) for depositing of SUV's by first cleaning with heated (60-70°C) 2% Hellmanex III (Fisher, Cat#14-385-864) in a glass coplin jar. We incubated hot Hellmanex III and coverglass for at least 30 minutes before rinsing with MilliQ water. The cleaned glass was then etched with Piranha solution (1:3, hydrogen peroxide:sulfuric acid) for 5-10 minutes. We rinsed and stored the etched coverglass in MilliQ. We rapidly dried our MilliQ-rinsed etched coverglass slides with nitrogen gas before adhering to a 6-well sticky-side chamber (IBIDI, Cat# 80608). We created SLBs by flowing 100-150 μ L of SUVs with a total lipid concentration of 0.25 mM in 1x PBS [pH 7.2] into the IBIDI chamber. Following 30 minutes of incubation, supported membranes were washed with 4 mL of 1x PBS [pH 7.2] to remove non-absorbed SUVs. To block membrane defects, we prepared 1 mg/mL beta casein (Thermo FisherSci, Cat# 37528) by clarifying with a centrifugation step at 4°C for 30 minutes at 21370 x g before passing through 0.22 μ m syringe filtration unit (0.22 μ m PES syringe filter (Foxy Life Sciences, Cat#381-2116-OEM). We then blocked membrane defects with 1 mg/mL beta casein (Thermo FisherSci, Cat# 37528) for 5-10 minutes.

Protein conjugation of maleimide lipid

After blocking SLBs with beta casein, membranes were washed with 2 mL of 1x PBS and stored at room temperature for up to 2 hours before mounting on the TIRF microscope. Prior to single molecule imaging experiments, supported membranes were washed into TIRF imaging buffer. Supported membrane containing with MCC-PE lipids were used to covalently couple either H-Ras(GDP) or phosphotyrosine peptide (pY). For the pY peptide experiments we used a doubly phosphorylated peptide derived from the mouse platelet derived growth factor receptor (PDGFR) with the following sequence: CSDGG(pY)MDMSKDESID(pY)VPMLDMKGDIKYADIE (33aa). The Alexa488-pY contained the same sequence with the dye conjugated to the C-terminus of the peptide. For these SLBs, 100 μ L of 30 μ M H-Ras diluted in a 1x PBS [pH 7.2] and 0.1 mM TCEP buffer was added to the IBIDI chamber and incubated for 2 hours at 23°C. Importantly, the addition of 0.1 mM TCEP significantly increases the coupling efficiency. SLBs with MCC-PE lipids were then washed with 2 mL of 1x PBS [pH 7.2] containing 5 mM beta-mercaptoethanol (BME) and incubated for 15 minutes to neutralize the unreacted maleimide headgroups. SLBs were washed with 1 mL of 1x PBS, followed by 1 mL of kinase buffer before starting smTIRF-M experiments.

Nucleotide exchange of Rac1

Membrane conjugated Rac1(GDP) was converted to Rac1(GTP) using either chemical activation (i.e. EDTA/ GTP/MgCl₂) or the guanine nucleotide exchange factor (GEF), P-Rex1. Chemical activation was accomplished by washing supported membranes containing maleimide linked Rac1(GDP) with 1x PBS [pH 7.2] containing 1 mM EDTA and 1 mM GTP. Following a 15-minute incubation to exchange GDP for GTP, chambers were washed 1x PBS [pH 7.2] containing 1 mM MgCl₂ and 50 μM GTP. A complementary approach that utilizes GEF-mediated activation of Rac1 was achieved by flowing 50 nM P-Rex1 DH-PH domain over Rac1(GDP) conjugated membranes (**Figure 1C**). Nucleotide exchange was carried out in buffer containing 1x PBS, 1 mM MgCl₂, 50 μM GTP. Both methods of activation yielded the same density of Rac1(GTP). Nucleotide exchange of membrane tethered Rac1 was assessed by visualizing the localization of the Cy3-p67/phox Rac1(GTP) sensor using TIRF-M.

Single molecule TIRF microscopy

We preformed all supported membrane TIRF-M experiments in buffer containing 20 mM HEPES [pH 7.0], 150 mM NaCl, 1 mM ATP, 5 mM MgCl₂, 0.5 mM EGTA, 20 mM glucose, 200 μg/mL beta casein (ThermoScientific, Cat# 37528), 20 mM BME, 320 μg/mL glucose oxidase (Biophoretics, Cat #B01357.02 *Aspergillus niger*), 50 μg/mL catalase (Sigma, #C40-100MG Bovine Liver), and 2 mM Trolox (Cayman Chemicals, Cat# 10011659). Perishable reagents (i.e. glucose oxidase, catalase, and Trolox) were added 5-10 minutes before starting image acquisition.

Microscope hardware and imaging acquisition

Single molecule imaging experiments were performed at room temperature (23°C) using an inverted Nikon Ti2 microscope using a 100x oil immersion Nikon TIRF objective (1.49 NA). We controlled the x-axis and y-axis position using a Nikon motorized stage, joystick, and Nikon's NIS element software. We also controlled microscope hardware using Nikon NIS elements. Fluorescently labelled proteins were excited with one of three diode lasers: a 488 nm, a 561nm, or 637 nm (OBIS laser diode, Coherent Inc. Santa Clara, CA). The lasers were controlled with a Vortran laser launch and acousto-optic tuneable filters (AOTF) control. Excitation and emission light was transmitted through a multi-bandpass quad filter cube (C-TIRF ULTRA HI S/N QUAD 405/488/561/638; Semrock) containing a dichroic mirror. The laser power measured through the objective for single particle visualized was 1-3 mW. Fluorescence emission was captured on an iXion Life 897 EMCCD camera (Andor Technology Ltd., UK) after passing through one of the following 25 mm a Nikon Ti2 emission filters mounted in a Nikon emission filter wheel: ET525/50M, ET600/50M, and ET700/75M (Semrock).

Kinetics measurements of PI(3,4,5)P₃ lipid production

The phosphorylation of PI(3,4,5)P₃ was measured on SLB's formed in IBIDI chambers visualized via TIRF microscopy. We monitored the production of PI(3,4,5)P₃ by solution-based PI3K at membrane surfaces using solution concentrations of 50 nM Btk-SNAP-AF488. Reaction buffer for experiments contained 20mM HEPES (pH 7.0), 150 mM NaCl, 5 mM MgCl₂, 1 mM ATP, 0.1mM GTP, 0.5 mM EGTA, 20 mM glucose, 200 μg/mL beta-casein (Thermo Scientific, Cat# 37528), 20 mM BME, 320 μg/mL glucose oxidase (Serva, #22780.01 *Aspergillus niger*), 50 μg/mL catalase (Sigma, #C40-100MG Bovine Liver), and 2 mM Trolox (Cayman Chemicals, Cat# 10011659). In experiments where inactive GTPases were coupled to membranes, no ATP was present in the reaction buffer and the 0.1 mM of GTP was replaced

with 0.1 mM of GDP. 5-10 minutes before image acquisition, chemicals and enzymes needed the oxygen scavenging system were added to the TIRF imaging buffer.

Surface density calibration

The density of membrane-tethered proteins attached to supported lipid bilayers was determined by coupling a defined ratio of either fluorescently labeled Cy3-Rac1 (e.g. 1:10,000) or Alexa488-pY (1:30,000) in the presence of either 10 μ M pY or 30 μ M Rac1. Single spatially resolved fluorescent proteins were visualized by TIRF microscopy. We calculated the density of fluorescent particles using ImageJ/Fiji Trackmate Plugin. The total surface density was calculated based on the dilution factor.

AlphaFold2 Multimer modelling

We utilized the AlphaFold2 using Mmseqs2 notebook of ColabFold at colab.research.google.com/github/sokrypton/ColabFold/blob/main/AlphaFold2.ipynb to make structural predictions of PI3K β (p110 β /p85 α) bound to G β γ . The pLDDT confidence values consistently scored above 90% for all models, with the predicted aligned error and pLDDT scores for all models are shown in [Figure 3 – figure Supplement 1](#).

Single particle tracking

Single fluorescent Dy647-PI3K β complexes bound to supported lipid bilayers were identified and tracked using the ImageJ/Fiji TrackMate plugin (Jaqaman et al. 2008). Data was loaded into ImageJ/Fiji as .nd2 files. We used the LoG detector to identify particles based on their size (~6 pixel diameter), brightness, and signal-to-noise ratio. We then used the LAP tracker to generate trajectories that followed particle displacement as a function of time. Particle trajectories were then filtered based on Track Start (remove particles at start of movie), Track End (remove particles at end of movie), Duration (particles track ≥ 2 frames), Track displacement, and X - Y location (removed particles near the edge of the movie). The output files from TrackMate were then analyzed using Prism 9 graphing software to calculate the dwell times. To calculate the dwell times of membrane bound proteins we generated cumulative distribution frequency (CDF) plots with the bin size set to image acquisition frame interval (e.g. 52 ms). The $\log_{10}(1-\text{CDF})$ was plotted as a function dwell time and fit to a single or double exponential curve. For the double exponential curve fits, the alpha value is the percentage of the fast-dissociating molecules characterized by the time constant, τ_1 . A typical data set contained dwell times measured for $n \geq 1000$ trajectories repeated as $n = 3$ technical replicates.

Single exponential curve fit:

$$f(x) = e^{(-x/\tau)}$$

Two exponential curve fit:

$$f(x) = \alpha * e^{(-x/\tau_1)} + (1 - \alpha) * e^{(-x/\tau_2)}$$

To calculate the diffusion coefficient ($\mu\text{m}^2/\text{sec}$), we plotted probability density (i.e. frequency divided by bin size of 0.01 μm) versus step size (μm). The step size distribution was fit to the following models:

Single species model:

$$f(r) = \frac{r}{2D\tau} e^{-\left(\frac{r^2}{4D\tau}\right)}$$

Two species model:

$$f(r) = \alpha \frac{r}{2D_1\tau} e^{-\left(\frac{r^2}{4D_1\tau}\right)} + (1 - \alpha) \frac{r}{2D_2\tau} e^{-\left(\frac{r^2}{4D_2\tau}\right)}$$

Image processing, statistics, and data analysis

Image analysis was performed on ImageJ/Fiji and MatLab. Curve fitting was performed using Prism 9 GraphPad. The X-fold change in dwell time we report in the main text was calculated by comparing the mean single particle dwell time for different experimental conditions (e.g. [Figure 3C](#)). Note that this is different from directly comparing the calculated dwell time (or exponential decay time constant, τ_1). The X% reduction in diffusion or mobility (e.g. [Figure 3D](#)) we report in the main text was calculated by comparing the mean single particle displacement (or step size) measured under different experimental conditions.

References

Auger Kurt R. , Serunian Leslie A. , Soltoff Stephen P. , Libby Peter , Cantley Lewis C. (1989) **PDGF-Dependent Tyrosine Phosphorylation Stimulates Production of Novel Polyphosphoinositides in Intact Cells** *Cell* **57**:167–75
[https://doi.org/10.1016/0092-8674\(89\)90182-7](https://doi.org/10.1016/0092-8674(89)90182-7)

Backer J M , Myers M G , Shoelson S E , Chin D J , Sun X J , Miralpeix M , Hu P , Margolis B , Skolnik E Y , Schlessinger J (1992) **Phosphatidylinositol 3'-Kinase Is Activated by Association with IRS-1 during Insulin Stimulation** *The EMBO Journal* **11**:3469–79

Balla Tamas (2013) **Phosphoinositides: Tiny Lipids with Giant Impact on Cell Regulation** *Physiological Reviews* **93**:1019–1137
<https://doi.org/10.1152/physrev.00028.2012>

Bradshaw J. Michael , Mitaxov Vesselin , Waksman Gabriel (1999) **Investigation of Phosphotyrosine Recognition by the SH2 Domain of the Src Kinase** Edited by P. E. Wright *Journal of Molecular Biology* **293**:971–85
<https://doi.org/10.1006/jmbi.1999.3190>

Breeze A. L. , Kara B. V. , Barratt D. G. , Anderson M. , Smith J. C. , Luke R. W. , Best J. R. , Cartledge S. A. (1996) **Structure of a Specific Peptide Complex of the Carboxy-Terminal SH2 Domain from the P85 Alpha Subunit of Phosphatidylinositol 3-Kinase** *The EMBO Journal* **15**:3579–89
<https://doi.org/10.1002/j.1460-2075.1996.tb00727.x>

Buckles Thomas C. , Ziemba Brian P. , Masson Glenn R. , Williams Roger L. , Falke Joseph J. (2017) **Single-Molecule Study Reveals How Receptor and Ras Synergistically Activate PI3K α and PIP3 Signaling** *Biophysical Journal* **113**:2396–2405
<https://doi.org/10.1016/j.bpj.2017.09.018>

Burke John E. (2018) **Structural Basis for Regulation of Phosphoinositide Kinases and Their Involvement in Human Disease** *Molecular Cell* **71**:653–73
<https://doi.org/10.1016/j.molcel.2018.08.005>

Burke John E. , Vadas Oscar , Berndt Alex , Finegan Tara , Perisic Olga , Williams Roger L. (2011) **Dynamics of the Phosphoinositide 3-Kinase P110 δ Interaction with P85 α and Membranes Reveals Aspects of Regulation Distinct from P110 α** *Structure* **19**:1127–37
<https://doi.org/10.1016/j.str.2011.06.003>

Carpenter Christopher L , AugerII Kurt R , ChanudhuriI Manas , Yoakim IMonique , Schaffhausen Brian , ShoelsonII Steven , Cantley Lewis C (1993) **Carpenter, Christopher L, Kurt R AugerII, Manas ChanudhuriI, IMonique Yoakim, Brian Schaffhausen, Steven ShoelsonII, and Lewis C Cantley. 1993. "Phosphoinositide 3-Kinase Is Activated by Phosphopeptides That Bind to the SH2 Domains Ofthe 85-KDa Subunit," 6.** *"Phosphoinositide 3-Kinase Is Activated by Phosphopeptides That Bind to the SH2 Domains Ofthe 85-KDa Subunit," 6*

Christoforidis Savvas , Miaczynska Marta , Ashman Keith , Wilm Matthias , Zhao Liyun , Yip Shu-Chin , Waterfield Michael D. , Backer Jonathan M. , Zerial Marino (1999) **Phosphatidylinositol-3-OH Kinases Are Rab5 Effectors** *Nature Cell Biology* **1**:249–52
<https://doi.org/10.1038/12075>

Chung Jean K. , Nocka Laura M. , Decker Aubrianna , Wang Qi , Kadlecsek Theresa A. , Weiss Arthur , Kuriyan John , Groves Jay T. (2019) **Switch-like Activation of Bruton's Tyrosine Kinase by Membrane-Mediated Dimerization** *Proceedings of the National Academy of Sciences* **116**:10798–803
<https://doi.org/10.1073/pnas.1819309116>

Ciraolo Elisa , Iezzi Manuela , Marone Romina , Marengo Stefano , Curcio Claudia , Costa Carlotta , Azzolino Ornella , et al. (2008) **Phosphoinositide 3-Kinase P110 β Activity: Key Role in Metabolism and Mammary Gland Cancer but Not Development** *Science Signaling* **1**
<https://doi.org/10.1126/scisignal.1161577>

Dbouk H. A. , Pang H. , Fiser A. , Backer J. M. (2010) **A Biochemical Mechanism for the Oncogenic Potential of the P110 Catalytic Subunit of Phosphoinositide 3-Kinase** *Proceedings of the National Academy of Sciences* **107**:19897–902
<https://doi.org/10.1073/pnas.1008739107>

Dbouk H. A. , Vadas O. , Shymanets A. , Burke J. E. , Salamon R. S. , Khalil B. D. , Barrett M. O. , et al. (2012) **G Protein-Coupled Receptor-Mediated Activation of P110 by G Is Required for Cellular Transformation and Invasiveness** *Science Signaling* **5**:ra89–ra89
<https://doi.org/10.1126/scisignal.2003264>

Dbouk Hashem A. , Vadas Oscar , Shymanets Aliaksei , Burke John E. , Salamon Rachel S. , Khalil Bassem D. , Barrett Mathew O. , et al. (2012) **G Protein- Coupled Receptor-Mediated Activation of P110 β by G β Is Required for Cellular Transformation and Invasiveness** *Science Signaling* **5**
<https://doi.org/10.1126/scisignal.2003264>

Di Paolo Gilbert , De Camilli Pietro (2006) **Phosphoinositides in Cell Regulation and Membrane Dynamics** *Nature* **443**:651–57
<https://doi.org/10.1038/nature05185>

Dornan Gillian L. , Siempelkamp Braden D. , Jenkins Meredith L. , Vadas Oscar , Lucas Carrie L. , Burke John E. (2017) **Conformational Disruption of PI3K δ Regulation by Immunodeficiency Mutations in PIK3CD and PIK3R1** *Proceedings of the National Academy of Sciences* **114**:1982–87
<https://doi.org/10.1073/pnas.1617244114>

Dornan Gillian L. , Stariha Jordan T. B. , Rathinaswamy Manoj K. , Powell Cameron J. , Boulanger Martin J. , Burke John E. (2020) **Defining How Oncogenic and Developmental Mutations of PIK3R1 Alter the Regulation of Class IA Phosphoinositide 3-Kinases** *Structure* **28**:145–156
<https://doi.org/10.1016/j.str.2019.11.013>

Endres Nicholas F. , Das Rahul , Smith Adam W. , Arkhipov Anton , Kovacs Erika , Huang Yongjian , Pelton Jeffrey G. , et al. (2013) **Conformational Coupling across the Plasma Membrane in Activation of the EGF Receptor** *Cell* **152**:543–56
<https://doi.org/10.1016/j.cell.2012.12.032>

Erami Zahra , Khalil Bassem D. , Salloum Gilbert , Yao Yanhua , LoPiccolo Jaclyn , Shymanets Aliaksei , Nürnberg Bernd , Bresnick Anne R. , Backer Jonathan M. (2017) **Rac1-Stimulated Macropinocytosis Enhances G β Activation of PI3K β** *Biochemical Journal* **474**:3903–14
<https://doi.org/10.1042/BCJ20170279>

Evans Richard , O'Neill Michael , Pritzel Alexander , Antropova Natasha , Senior Andrew , Green Tim , Židek Augustin , et al. (2022) **Protein Complex Prediction with AlphaFold-Multimer**
<https://doi.org/10.1101/2021.10.04.463034>

Fantl J , Martin A , Turck W (1992) **“Distinct Phosphotyrosines on a Growth Factor Receptor Bind to Specific Molecuks That Mediate Different Signaling Pathways,”**

Fritsch Ralph , de Krijger Inge , Fritsch Kornelia , George Roger , Reason Beth , Kumar Madhu S. , Diefenbacher Markus , Stamp Gordon , Downward Julian (2013) **RAS and RHO Families of GTPases Directly Regulate Distinct Phosphoinositide 3-Kinase Isoforms** *Cell* **153**:1050–63
<https://doi.org/10.1016/j.cell.2013.04.031>

Fruman David A. , Chiu Honyin , Hopkins Benjamin D. , Bagrodia Shubha , Cantley Lewis C. , Abraham Robert T. (2017) **The PI3K Pathway in Human Disease** *Cell* **170**:605–35
<https://doi.org/10.1016/j.cell.2017.07.029>

Funamoto Satoru , Meili Ruedi , Lee Susan , Parry Lisa , Firtel Richard A. (2002) **Spatial and Temporal Regulation of 3-Phosphoinositides by PI 3-Kinase and PTEN Mediates Chemotaxis** *Cell* **109**:611–23
[https://doi.org/10.1016/S0092-8674\(02\)00755-9](https://doi.org/10.1016/S0092-8674(02)00755-9)

Gibson Daniel G , Young Lei , Chuang Ray-Yuan , Venter J Craig , Hutchison Clyde A , Smith Hamilton O (2009) **Enzymatic Assembly of DNA Molecules up to Several Hundred Kilobases** *Nature Methods* **6**:343–45
<https://doi.org/10.1038/nmeth.1318>

Graziano Brian R. , Gong Delquin , Anderson Karen E. , Pipathsouk Anne , Goldberg Anna R. , Weiner Orion D. (2017) **A Module for Rac Temporal Signal Integration Revealed with Optogenetics** *Journal of Cell Biology* **216**:2515–31
<https://doi.org/10.1083/jcb.201604113>

Guillemet-Guibert J. , Bjorklof K. , Salpekar A. , Gonella C. , Ramadani F. , Bilancio A. , Meek S. , Smith A. J. H. , Okkenhaug K. , Vanhaesebroeck B. (2008) **The P110 Isoform of Phosphoinositide 3-Kinase Signals Downstream of G Protein-Coupled Receptors and Is Functionally Redundant with P110** *Proceedings of the National Academy of Sciences* **105**:8292–97
<https://doi.org/10.1073/pnas.0707761105>

Haigler H. , Ash J. F. , Singer S. J. , Cohen S. (1978) **Visualization by Fluorescence of the Binding and Internalization of Epidermal Growth Factor in Human Carcinoma Cells A-431** *Proceedings of the National Academy of Sciences of the United States of America* **75**:3317–21
<https://doi.org/10.1073/pnas.75.7.3317>

Hanker Ariella B. , Pfefferle Adam D. , Balko Justin M. , Kuba María Gabriela , Young Christian D. , Sánchez Violeta , Sutton Cammie R. , et al. (2013) **Mutant PIK3CA Accelerates HER2-Driven Transgenic Mammary Tumors and Induces Resistance to Combinations of Anti-HER2 Therapies** *Proceedings of the National Academy of Sciences of the United States of America* **110**:14372–77
<https://doi.org/10.1073/pnas.1303204110>

Hansen Scott D. , Huang William Y. C. , Lee Young Kwang , Bieling Peter , Christensen Sune M. , Groves Jay T. (2019) **Stochastic Geometry Sensing and Polarization in a Lipid Kinase-Phosphatase Competitive Reaction** *Proceedings of the National Academy of Sciences* **116**:15013–22
<https://doi.org/10.1073/pnas.1901744116>

Hansen Scott D , Lee Albert A , Duewell Benjamin R , Groves Jay T (2022) **Membrane-Mediated Dimerization Potentiates PIP5K Lipid Kinase Activity** *ELife* **11**
<https://doi.org/10.7554/eLife.73747>

Hatada Marcos H. , Lu Xiaode , Laird Ellen R. , Green Jeremy , Morgenstern Jay P. , Lou Meizhen , Marr Chris S. , et al. (1995) **Molecular Basis for Interaction of the Protein Tyrosine Kinase ZAP-70 with the T-Cell Receptor** *Nature* **377**:32–38
<https://doi.org/10.1038/377032a0>

- He Ju , Haney Rachel M. , Vora Mohsin , Verkhusha Vladislav V. , Stahelin Robert V. , Kutateladze Tatiana G. (2008) **Molecular Mechanism of Membrane Targeting by the GRP1 PH Domain*** *Journal of Lipid Research* **49**:1807–15
<https://doi.org/10.1194/jlr.M800150-JLR200>
- Heitz Samantha D. , Hamelin David J. , Hoffmann Reece M. , Greenberg Nili , Salloum Gilbert , Erami Zahra , Khalil Bassem D. , et al. (2019) **A Single Discrete Rab5-Binding Site in Phosphoinositide 3-Kinase β Is Required for Tumor Cell Invasion** *Journal of Biological Chemistry* **294**:4621–33
<https://doi.org/10.1074/jbc.RA118.006032>
- Houslay Daniel M. , Anderson Karen E. , Chessa Tamara , Kulkarni Suhasini , Fritsch Ralph , Downward Julian , Backer Jonathan M. , Stephens Len R. , Hawkins Phillip T. (2016) **Coincident Signals from GPCRs and Receptor Tyrosine Kinases Are Uniquely Transduced by PI3K β in Myeloid Cells** *Science Signaling* **9**:ra82–ra82
<https://doi.org/10.1126/scisignal.aae0453>
- Howard T H , Oresajo C O (1985) **The Kinetics of Chemotactic Peptide-Induced Change in F-Actin Content, F-Actin Distribution, and the Shape of Neutrophils** *Journal of Cell Biology* **101**:1078–85
<https://doi.org/10.1083/jcb.101.3.1078>
- Insall Robert H. , Weiner Orion D. (2001) **PIP3, PIP2, and Cell Movement—Similar Messages, Different Meanings?** *Developmental Cell* **1**:743–47
[https://doi.org/10.1016/S1534-5807\(01\)00086-7](https://doi.org/10.1016/S1534-5807(01)00086-7)
- Jaqaman Khuloud , Loerke Dinah , Mettlen Marcel , Kuwata Hirotaka , Grinstein Sergio , Schmid Sandra L , Danuser Gaudenz (2008) **Robust Single-Particle Tracking in Live-Cell Time-Lapse Sequences** *Nature Methods* **5**:695–702
<https://doi.org/10.1038/nmeth.1237>
- Jia Shidong , Liu Zhenning , Zhang Sen , Liu Pixu , Zhang Lei , Lee Sang Hyun , Zhang Jing , et al. (2008) **Essential Roles of PI(3)K-P110 β in Cell Growth, Metabolism and Tumorigenesis** *Nature* **454**:776–79
<https://doi.org/10.1038/nature07091>
- Jumper John , Evans Richard , Pritzel Alexander , Green Tim , Figurnov Michael , Ronneberger Olaf , Tunyasuvunakool Kathryn , et al. (2021) **Highly Accurate Protein Structure Prediction with AlphaFold** *Nature* **596**:583–89
<https://doi.org/10.1038/s41586-021-03819-2>
- Katada Toshiaki , Kurosu Hiroshi , Okada Taro , Suzuki Takahiro , Tsujimoto Noriko , Takasuga Shunsuke , Kontani Kenji , Hazeki Osamu , Ui Michio (1999) **Synergistic Activation of a Family of Phosphoinositide 3-Kinase via G-Protein Coupled and Tyrosine Kinase-Related Receptors** *Chemistry and Physics of Lipids* **98**:79–86
[https://doi.org/10.1016/S0009-3084\(99\)00020-1](https://doi.org/10.1016/S0009-3084(99)00020-1)

Knight Jefferson D. , Lerner Michael G. , Marcano-Velázquez Joan G. , Pastor Richard W. , Falke Joseph J. (2010) **Single Molecule Diffusion of Membrane-Bound Proteins: Window into Lipid Contacts and Bilayer Dynamics** *Biophysical Journal* **99**:2879–87
<https://doi.org/10.1016/j.bpj.2010.08.046>

Knight Zachary A. , Gonzalez Beatriz , Feldman Morri E. , Zunder Eli R. , Goldenberg David D. , Williams Olusegun , Loewith Robbie , et al. (2006) **A Pharmacological Map of the PI3-K Family Defines a Role for P110 α in Insulin Signaling** *Cell* **125**:733–47
<https://doi.org/10.1016/j.cell.2006.03.035>

Kozasa T. , Gilman A. G. (1995) **Purification of Recombinant G Proteins from Sf9 Cells by Hexahistidine Tagging of Associated Subunits. Characterization of Alpha 12 and Inhibition of Adenylyl Cyclase by Alpha z** *The Journal of Biological Chemistry* **270**:1734–41
<https://doi.org/10.1074/jbc.270.4.1734>

Kurosu H. , Maehama T. , Okada T. , Yamamoto T. , Hoshino S. , Fukui Y. , Ui M. , Hazeki O. , Katada T. (1997) **Heterodimeric Phosphoinositide 3-Kinase Consisting of P85 and P110 β Is Synergistically Activated by the Betagamma Subunits of G Proteins and Phosphotyrosyl Peptide** *The Journal of Biological Chemistry* **272**:24252–56
<https://doi.org/10.1074/jbc.272.39.24252>

Lemmon Mark A. , Schlessinger Joseph (2010) **Cell Signaling by Receptor Tyrosine Kinases** *Cell* **141**:1117–34
<https://doi.org/10.1016/j.cell.2010.06.011>

Love Paul E. , Hayes Sandra M. (2010) **ITAM-Mediated Signaling by the T-Cell Antigen Receptor** *Cold Spring Harbor Perspectives in Biology* **2**
<https://doi.org/10.1101/cshperspect.a002485>

Maier U. , Babich A. , Nürnberg B. (1999) **Roles of Non-Catalytic Subunits in Gbetagamma-Induced Activation of Class I Phosphoinositide 3-Kinase Isoforms Beta and Gamma** *The Journal of Biological Chemistry* **274**:29311–17
<https://doi.org/10.1074/jbc.274.41.29311>

Mandelker D. , Gabelli S. B. , Schmidt-Kittler O. , Zhu J. , Cheong I. , Huang C.-H. , Kinzler K. W. , Vogelstein B. , Amzel L. M. (2009) **A Frequent Kinase Domain Mutation That Changes the Interaction between PI3K and the Membrane** *Proceedings of the National Academy of Sciences* **106**:16996–1
<https://doi.org/10.1073/pnas.0908444106>

Manning Brendan D. , Cantley Lewis C. (2007) **AKT/PKB Signaling: Navigating Downstream** *Cell* **129**:1261–74
<https://doi.org/10.1016/j.cell.2007>

Nasuhoglu Cem , Feng Siyi , Mao Janping , Yamamoto Masaya , Yin Helen L. , Earnest Svetlana , Barylko Barbara , Albanesi Joseph P. , Hilgemann Donald W. (2002) **Nonradioactive Analysis of Phosphatidylinositides and Other Anionic Phospholipids by Anion-Exchange High-Performance Liquid Chromatography with Suppressed Conductivity Detection** *Analytical Biochemistry* **301**:243–54
<https://doi.org/10.1006/abio.2001.5489>

Nolte R. T. , Eck M. J. , Schlessinger J. , Shoelson S. E. , Harrison S. C. (1996) **Crystal Structure of the PI 3-Kinase P85 Amino-Terminal SH2 Domain and Its Phosphopeptide Complexes** *Nature Structural Biology* **3**:364–74
<https://doi.org/10.1038/nsb0496-364>

Osman Narin , Turner Helen , Lucas Susan , Reif Karin , Cantrell Doreen A. (1996) **The Protein Interactions of the Immunoglobulin Receptor Family Tyrosine-Based Activation Motifs Present in the T Cell Receptor ζ Subunits and the CD3 γ , δ and ϵ Chains** *European Journal of Immunology* **26**:1063–68
<https://doi.org/10.1002/eji.1830260516>

Parent Carole A. , Blacklock Brenda J. , Froehlich Wendy M. , Murphy Douglas B. , Devreotes Peter N. (1998) **G Protein Signaling Events Are Activated at the Leading Edge of Chemotactic Cells** *Cell* **95**:81–91
[https://doi.org/10.1016/S0092-8674\(00\)81784-5](https://doi.org/10.1016/S0092-8674(00)81784-5)

Rameh Lucia E. , Chen Ching-Shih , Cantley Lewis C. (1995) **Phosphatidylinositol (3,4,5)P3 Interacts with SH2 Domains and Modulates PI 3-Kinase Association with Tyrosine-Phosphorylated Proteins** *Cell* **83**:821–30
[https://doi.org/10.1016/0092-8674\(95\)90195-7](https://doi.org/10.1016/0092-8674(95)90195-7)

Rathinaswamy Manoj K. , Dalwadi Udit , Fleming Kaelin D. , Adams Carson , Stariha Jordan T. B. , Pardon Els , Baek Minkyung , et al. (2021) **Structure of the Phosphoinositide 3-Kinase (PI3K) P110 γ -P101 Complex Reveals Molecular Mechanism of GPCR Activation** *Science Advances* **7**
<https://doi.org/10.1126/sciadv.abj4282>

Rathinaswamy Manoj K. , Jenkins Meredith L. , Duewell Benjamin R. , Zhang Xuxiao , Harris Noah J. , Evans John T. , Stariha Jordan T. B. , et al. (2023) **Molecular Basis for Differential Activation of P101 and P84 Complexes of PI3K γ by Ras and GPCRs** *Cell Reports* **42**
<https://doi.org/10.1016/j.celrep.2023.112172>

Reth Michael (1989) **Antigen Receptor Tail Clue** *Nature* **338**:383–84
<https://doi.org/10.1038/338383b0>

Rincón Esther , Rocha-Gregg Briana L. , Collins Sean R. (2018) **A Map of Gene Expression in Neutrophil-like Cell Lines** *BMC Genomics* **19**
<https://doi.org/10.1186/s12864-018-4957-6>

Saini Deepak Kumar , Kalyanaraman Vani , Chisari Mariangela , Gautam Narasimhan (2007) **A Family of G Protein By Subunits Translocate Reversibly from the Plasma Membrane to Endomembranes on Receptor Activation** *The Journal of Biological Chemistry* **282**:24099–108
<https://doi.org/10.1074/jbc.M701191200>

Sauter G. , Maeda T. , Waldman F. M. , Davis R. L. , Feuerstein B. G. (1996) **Patterns of Epidermal Growth Factor Receptor Amplification in Malignant Gliomas** *The American Journal of Pathology* **148**:1047–53

Siempelkamp Braden D. , Rathinaswamy Manoj K. , Jenkins Meredith L. , Burke John E. (2017) **Molecular Mechanism of Activation of Class IA Phosphoinositide 3-Kinases (PI3Ks) by Membrane-Localized HRas** *Journal of Biological Chemistry* **292**:12256–66
<https://doi.org/10.1074/jbc.M117.789263>

Stephens L. R. , Hughes K. T. , Irvine R. F. (1991) **Pathway of Phosphatidylinositol(3,4,5)-Trisphosphate Synthesis in Activated Neutrophils** *Nature* **351**:33–39
<https://doi.org/10.1038/351033a0>

Stephens L. R. , Jackson T. R. , Hawkins P. T. (1993) **Agonist-Stimulated Synthesis of Phosphatidylinositol(3,4,5)-Trisphosphate: A New Intracellular Signalling System?** *Biochimica et Biophysica Acta (BBA) - Molecular Cell Research* **1179**:27–75
[https://doi.org/10.1016/0167-4889\(93\)90072-W](https://doi.org/10.1016/0167-4889(93)90072-W)

Vadas Oscar , Burke John E. , Zhang Xuxiao , Berndt Alex , Williams Roger L. (2011) **Structural Basis for Activation and Inhibition of Class I Phosphoinositide 3-Kinases** *Science Signaling* **4**:re2–re2
<https://doi.org/10.1126/scisignal.2002165>

Varadi Mihaly , Anyango Stephen , Deshpande Mandar , Nair Sreenath , Natassia Cindy , Yordanova Galabina , Yuan David , et al. (2022) **AlphaFold Protein Structure Database: Massively Expanding the Structural Coverage of Protein-Sequence Space with High-Accuracy Models** *Nucleic Acids Research* **50**:D439–44
<https://doi.org/10.1093/nar/gkab1061>

Waksman Gabriel , Kominos Dorothea , Robertson Scott C. , Pant Nalin , Baltimore David , Birge Raymond B. , Cowburn David , et al. (1992) **Crystal Structure of the Phosphotyrosine Recognition Domain SH2 of V-Src Complexed with Tyrosine-Phosphorylated Peptides** *Nature* **358**:646–53
<https://doi.org/10.1038/358646a0>

Wang Qi , Vogan Erik M , Nocka Laura M , Rosen Connor E , Zorn Julie A , Harrison Stephen C , Kuriyan John (2015) **Autoinhibition of Bruton's Tyrosine Kinase (Btk) and Activation by Soluble Inositol Hexakisphosphate** *ELife* **4**
<https://doi.org/10.7554/eLife.06074>

Weiner Orion D. (2002) **Rac Activation: P-Rex1 — A Convergence Point for PIP3 and Gβγ?** *Current Biology* **12**:R429–31
[https://doi.org/10.1016/S0960-9822\(02\)00917-X](https://doi.org/10.1016/S0960-9822(02)00917-X)

Wenk Markus R. , Lucast Louise , Di Paolo Gilbert , Romanelli Anthony J. , Suchy Sharon F. , Nussbaum Robert L. , Cline Gary W. , Shulman Gerald I. , McMurray Walter , De Camilli Pietro (2003) **Phosphoinositide Profiling in Complex Lipid Mixtures Using Electrospray Ionization Mass Spectrometry** *Nature Biotechnology* **21**:813–17
<https://doi.org/10.1038/nbt837>

Yang Hee Won , Shin Min-Gyoung , Lee Sangkyu , Kim Jeong-Rae , Park Wei Sun , Cho Kwang-Hyun , Meyer Tobias , Heo Won Do (2012) **Cooperative Activation of PI3K by Ras and Rho Family Small GTPases** *Molecular Cell* **47**:281–90
<https://doi.org/10.1016/j.molcel.2012.05.007>

Yin Jun , Lin Alison J , Golan David E , Walsh Christopher T (2006) **Site-Specific Protein Labeling by Sfp Phosphopantetheinyl Transferase** *Nature Protocols* **1**:280–85
<https://doi.org/10.1038/nprot.2006.43>

Yip Shu-Chin , Eddy Robert J. , Branch Angie M. , Pang Huan , Wu Haiyan , Yan Ying , Drees Beth E. , Neilsen Paul O. , Condeelis John , Backer Jonathan M. (2008) **QUANTITATION OF PI[3,4,5]P3 DYNAMICS IN EGF-STIMULATED CARCINOMA CELLS: A Comparison of PH Domain-Mediated versus Immunological Methods** *The Biochemical Journal* **411**:441–48
<https://doi.org/10.1042/BJ20071179>

Yu Jinghua , Zhang Yitao , Mcilroy James , Rordorf-Nikolic Tamara , Orr George A , Backer Jonathan M (1998) **Regulation of the P85/P110 Phosphatidylinositol 3J-Kinase: Stabilization and Inhibition of the P110y Catalytic Subunit by the P85 Regulatory Subunit** *MOL. CELL. BIOL.* **18**

Zenner G. , Vorherr T. , Mustelin T. , Burn P. (1996) **Differential and Multiple Binding of Signal Transducing Molecules to the ITAMs of the TCR-Zeta Chain** *Journal of Cellular Biochemistry* **63**:94–103
[https://doi.org/10.1002/\(sici\)1097-4644\(199610\)63:1<94::aid-jcb8>3.0.co;2-v](https://doi.org/10.1002/(sici)1097-4644(199610)63:1<94::aid-jcb8>3.0.co;2-v)

Zhang Xuxiao , Vadas Oscar , Perisic Olga , Anderson Karen E. , Clark Jonathan , Hawkins Phillip T. , Stephens Len R. , Williams Roger L. (2011) **Structure of Lipid Kinase P110β/P85β Elucidates an Unusual SH2-Domain-Mediated Inhibitory Mechanism** *Molecular Cell* **41**:567–78
<https://doi.org/10.1016/j.molcel.2011.01.026>

Ziemba Brian P. , Falke Joseph J. (2013) **Lateral Diffusion of Peripheral Membrane Proteins on Supported Lipid Bilayers Is Controlled by the Additive Frictional Drags of (1) Bound Lipids and (2) Protein Domains Penetrating into the Bilayer Hydrocarbon Core** *Chemistry and Physics of Lipids* **172**:67–77
<https://doi.org/10.1016/j.chemphyslip.2013.04.005>

Author information

Benjamin R. Duewell

Department of Chemistry and Biochemistry, Institute of Molecular Biology, University of Oregon, Eugene, OR 97403

Naomi E. Wilson

Department of Chemistry and Biochemistry, Institute of Molecular Biology, University of Oregon, Eugene, OR 97403

Gabriela M. Bailey

Department of Chemistry and Biochemistry, Institute of Molecular Biology, University of Oregon, Eugene, OR 97403

Sarah E. Peabody

Department of Chemistry and Biochemistry, Institute of Molecular Biology, University of Oregon, Eugene, OR 97403

Scott D. Hansen

Department of Chemistry and Biochemistry, Institute of Molecular Biology, University of Oregon, Eugene, OR 97403

For correspondence: shansen5@uoregon.edu

ORCID iD: [0000-0001-7005-6200](https://orcid.org/0000-0001-7005-6200)

Editors

Reviewing Editor

Volker Dötsch

Goethe University, Germany

Senior Editor

Volker Dötsch

Goethe University, Germany

Reviewer #1 (Public Review):

The manuscript aims to provide mechanistic insight into the activation of PI3K β by its known regulators tyrosine phosphorylated peptides, GTP-loaded Rac1 and G-protein β -gamma subunits. To achieve this the authors have used supported lipid bilayers, engineered recombinant peptides and proteins (often tagged with fluorophores) and TIRF microscopy to enable bulk (averages of many molecules) and single molecule quantitation. The great strength of this approach is the precision and clarity of mechanistic insight. Although the study does not use "in transfecto" or in vivo models the experiments are performed using "physiologically-based" conditions and provide a powerful insight into core regulatory principles that will be relevant in vivo.

The results are beautiful, high quality, well controlled and internally consistent (and with other published work that overlaps on some points) and as a result are compelling. The primary conclusion is that the primary regulator of PI3K β are tyrosine phosphorylated peptides (and by inference tyrosine phosphorylated receptors/adaptors) and that the other activators can synergise with that input but have relatively weak impacts on their own.

Although the methodology is not easily imported, for reasons of both cost and the experience needed to execute them well, the results have broad importance for the field and reverse an impression that had built in large parts of the broader signalling and PI3K communities that all of the inputs to PI3K β were relatively equivalent, however, these conclusions were based on "in cell" or in vivo studies that were very difficult to interpret clearly.

Reviewer #2 (Public Review):

The manuscript of Duewell et al has made critical observations that help to understand the mechanisms of activation of the class IA PI3Ks. By using single-molecule kinetic measurements, the authors have made outstanding progress toward understanding how PI3K β is uniquely activated by phosphorylated tyrosine kinase receptors, G β /gamma heterodimers and the small G protein Rac1. While previous studies have defined these as activators of PI3K β , the current manuscript makes clear the quantitative limitations of these previous observations. Most previous quantitative in vitro studies of PI3K β activation have used soluble peptides derived from bis-phosphorylated receptors to

stimulate the enzyme. These soluble peptides stimulate the enzyme, and even stimulate membrane interaction. Although these previous studies showed that the release of p85-mediated autoinhibition unmasks an intrinsic affinity of the enzyme for lipid membranes, they ignored what would be the consequence of these peptide sequences being present in the context of intrinsic membrane proteins. The current manuscript shows that the effect of membrane-conjugated peptides on the enzyme activity is profound, in terms of recruiting the enzyme to membranes. In this context, the authors show that G proteins associated with the membranes have an important contribution to membrane recruitment, but they also have a profound allosteric effect on the activity on the membrane. These are observations that would not have been possible with bulk measurements, and they do not simply recapitulate observations that were made for other class IA PI3Ks.

An important observation that the authors have made is that G β /G γ heterodimers and RAC1 alone have almost no ability to recruit PI3K β to the membranes that they are using, and this is central to one of the most profoundly novel activation mechanisms offered by the manuscript. The authors propose that the nSH2- and G β /G γ binding sites partially overlap, so that G β /G γ can only bind once the nSH2 domain releases the p110 β subunit. This mechanism would mean that once the nSH2 is engaged by membrane-conjugated pY, the Gbg heterodimer can bind and increase the association of the enzyme with membranes. Indeed, this increased membrane association is observed by the authors. However, the authors also show that this increased recruitment to membranes accounts for relatively little increase in activity, and that the far greater component of activation is due to an allosteric effect of the membrane association on the activity of the enzyme. The proposal for competition between Gbg binding and the nSH2 is consistent with the behavior of an nSH2 mutant that cannot bind to pY and which, consequently, does not vacate the Gbg-binding site. In addition to the outstanding contribution to understanding the kinetics of activation of PI3K β , the authors have offered the first structural interpretation for the kinetics of Gbg activation in synergy with pY activation. The proposal for an overlapping nSH2/Gbg binding site is supported by predictions made by John Burke, using alphafold multimer. Although there is no experimental structure to support this structural model, it is consistent with HDX-MS analyses that were published previously.