Regulation of the pancreatic KATP channel

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# [ch:1-intro]Introduction

## Pancreatic islets and the b-cell

Pancreatic islets are endocrine cells which are responsible for maintaining glucose homeostasis. It has been estimated that there are between 3 × 106–1.5 × 107 islets in a human pancreas, constituting 1 %–2 % of the total pancreatic mass.1 Islets consist of three principal cell types; insulin secreting b-cells, glucagon secreting a-cells and somatostatin secreting d-cells.2 Islets respond to increases in blood glucose by releasing insulin, which acts on peripheral tissues to increase glucose uptake and reduce blood glucose levels. Conversely, decreases in blood glucose leads to the release of glucagon, which acts on those tissues to stimulate glucose production and increase blood glucose.

Insulin secretion in beta cells - and indeed in all three cell types of pancreatic islets - is induced by the firing of action potentials, which leads to the influx of Ca2+ ions and the activation of secretory granule exocytosis (Figure [1.1](#ch1fig:beta_cells)).2 This electrical excitability is controlled by the ATP-sensitive (KATP) potassium channel. At rest, KATP channel activity results in a leak current of K+ ions out of the cell, hyperpolarising the membrane. Glucose metabolism in beta cells increases the ATP:ADP ratio, closing KATP channels and releasing their hyperpolarising clamp on the membrane potential.3,4 When KATP channels are closed and membrane resistance is high, even small currents are sufficient to induce large membrane potential depolarisations and action potential initiation (Figure [1.2](#ch1fig:beta_cells_firing)).

## Architecture of the pancreatic KATP channel

KATP channels are present in many tissues, where they couple the metabolic state of a cell to its electrical activity by regulating the flow of K+ across the membrane.5 KATP channels are an octameric complex, comprised of four inwardly-rectifying potassium channel subunits (Kir6.1 or Kir6.2), each of which is associated with a sulphonylurea receptor subunit (SUR1, SUR2A or SUR2B).6–9 In pancreatic b-cells, the KATP channel isoform is composed of Kir6.2 and SUR1.10 Together, Kir6.2 and SUR1 form a complex nearly a megadalton in size and over 15 nanometres across (Figure [1.8](#ch1fig:katp_cartoon), [1.9](#ch1fig:sur_topdown)).

Inwardly-rectifying potassium channels are so named because they allow K+ to flow more easily into the cell than out of it (Figure [1.3](#ch1fig:rectification)).11,12 This phenomenon is a consequence of voltage-dependent pore blockade by intracellular divalent cations (especially Mg2+) and polyamines. At depolarising membrane potentials, blockers are driven into the pore and K+ current is blocked, while at hyperpolarising potentials the blockers and cleared and K+ current can flow. Strongly rectifying Kir channels display drastically reduced conductance at potentials more positive than the K+ reversal potential. In contrast, Kir6.2 is a weak rectifier, and allows substantial current to flow at more positive potentials.

In addition to voltage, Kir6.2 is regulated by two endogenous ligands; phosphatidylinositol 4,5-bisphosphate (PIP2) and adenine nucleotides (Figure [1.4](#ch1fig:kir_struct)).13,14 The binding of adenine nucleotides to Kir6.2 leads to closure of the channel pore, while the binding of PIP2 promotes the opening of the pore (Figure [1.5](#ch1fig:shyng_trace)). Activation by PIP2 is a mechanism common to the whole Kir family, whereas inhibition by nucleotides is unique to the Kir6 subfamily.15

SUR1 is a member of the ATP-binding cassette (ABC) family of transporters. While other ABC proteins transport substrate across the membrane, SUR1 does not appear to do so; instead it acts to modulate the function of its associated ion channel.16,17 The cystic fibrosis transmembrane conductance regulator (CFTR) is another member of the ABC family, and is an ion channel in its own right, capable of conducting chloride across the membrane.18 Like other ABC proteins, SUR1 contains two sets of transmembrane domains (TMD1 and TMD2) and two cytosolic nucleotide binding domains (NBD1 and NBD2).16,19 Unique to SUR is the presence of an additional transmembrane domain (TMD0) N-terminal to the core of the protein, and this domain forms the primary contact between SUR1 and Kir6.2.20–23

The NBDs of ABC transporters are highly conserved, and consist of two subdomains: a larger RecA-like subdomain found in other P-loop ATPases, and a smaller a-helical subdomain which is unique to ABC transporters.19,24 There are three key structural motifs present in these subdomains: the RecA-like subdomain contains the Walker A (WA) and B (WB) motifs, while the a-helical subdomain contains the ABC signature motif (typically LSGGQ).

The two domains come together to form an antiparallel dimer with two nucleotide binding sites (NBS1 and NBS2) at the interface, such that NBS1 is formed from the WA and WB motifs of NBD1 and the signature motif from NBD2, whereas NBS2 is formed from the WA and WB motifs of NBD2 and the signature motif from NBD1. NBS2, also known as the consensus site as it is more similar in sequence to other ABC family members, is catalytically competent and able to hydrolyse ATP.25–27 In contrast, NBS1 is the degenerate site, with a less conserved sequence and an inability to catalyse hydrolysis of ATP.19,24

## Ligand-independent regulation of the pancreatic KATP channel

### Assembly and trafficking

Biogenesis of KATP channels occurs in the endoplasmic reticulum (ER), and is an important checkpoint in determining surface expression and channel stoichiometry.28,29 The precise nature of the events which occur between subunit translation and insertion of octameric KATP into the cell membrane are not fully mapped out, but studies have highlighted some important quality control steps in this process which regulate KATP channel expression. When Kir6.2 or SUR1 are expressed alone in heterologous systems, they are retained in the ER.28 This mechanism is achieved through the exposure of a three amino acid ER-retention motif (RKR) in the cytoplasmic domains of both Kir6.2 and SUR1. Only upon complete assembly of the channel complex are the RKR motifs masked, allowing forward trafficking of KATP to the cell surface. Deletion of the RKR motif,30 or mutation of the motif to AAA,28 results in unregulated surface expression of individual subunits and/or partially assembled channel complexes. Addition of a GFP label to the C-terminus of Kir6.2 is also sufficient to allow trafficking of subunits to the cell surface in the absence of SUR1.31

In addition to the RKR motif, there are two N-linked glycosylation sites on SUR1 (N10 and N1050) which are required for cell surface expression.32 Mutation of these sites to glutamines results in retention in the ER and drastically reduced expression of KATP on the cell surface. This mechanism is thought to be separate to that for the ER-retention motif, as mutation of RKR to AAA is not sufficient to drive surface expression of the glycosylation mutants.32

A putatitive third site of trafficking regulation is in the C-terminus of SUR1. Mutation or deletion of a dileucine motif 16 amino acids distal to the C-terminal of SUR1 results in reduced surface expression of KATP channels in COSm6 cells.33 This reduction in expression is not rescued by C-terminal truncation of Kir6.2, indicating that this result is not due to masking of the RKR retention motif. The dileucines are therefore suggested to promote forward trafficking of assembled channel complexes to the cell membrane.33 Expression of KATP channels expressed in *Xenopus* oocytes is also dramatically reduced by truncation of the C-terminal 42 amino acids of SUR1.34 However, longer deletions of the SUR1 C-terminus did not reduce surface expression of channels in HEK293 cells,35 and other modifications of the SUR1 C-terminus do not exhibit effects on surface expression.36 In fact, a splice variant of SUR1 missing the entirety of the NBD2 domain (truncated at residue 1355) was found to successfully traffic to the cell membrane of *Xenopus* oocytes.37 The precise role of the dileucine motif remains unclear, and is potentially confounded by the use of expression system29,35

Failure of the channel complex to pass these three checkpoints results in ER-associated degradation (ERAD), a common pathway shared by most membrane and secretory proteins.38,39 Both SUR1 and Kir6.2 are substrates for polyubiquitination, both when heterologously expressed and in INS-1 cells.39 Application of proteasome inhibitors both reduces the rate of degradation for Kir6.2 and SUR1, and increases the surface expression of KATP channels by increasing their biogenesis efficiency.39

The surface expression of KATP channels is therefore controlled by a variety of different quality control mechanisms to ensure that only correctly assembled octameric channel complexes reach the cell membrane. Mutations which lead to defects in assembly and trafficking are therefore a common cause of congenital hyperinsulinemia (HI) as they result in permanent membrane depolarisation and unregulated insulin secretion. These mutations are found throughout both Kir6.2 and SUR1, although they are more commonly found in SUR1.29

Interestingly, sulphonylureas are able to act as pharmacological chaperones and rescue surface expression of several mutations which would otherwise not traffic to the cell surface.40–44 Sulphonylureas bind directly to the channel during biogenesis, as mutation of residues in SUR1 which are critical for sulphonylurea binding abolished or reduced the effectiveness of expression rescue.41 Pharmacological chaperoning requires full assembly of the channel complex, as the presence of Kir6.2 was required to rescue expression of trafficking mutants even when the SUR1 RKR motif was mutated to AAA.41 In addition, reducing the temperature at which cells are cultured can rescue some trafficking defects.45

### Regulation of intrinsic gating

In the absence of nucleotides, KATP channels are spontaneously active. This can be seen at a macroscopic level in excised patches. Upon excision of a patch from a cell membrane containing KATP channels, the magnitude of current dramatically increases when voltage is applied (Figure [1.5](#ch1fig:shyng_trace)), reflecting the relief from inhibition of cytoplasmic nucleotides. While this macroscopic time course is smooth and graded, it consists of hundreds or thousands of individual channels which exhibit binary behaviour, switching between a nonconducting closed state and a conducting open state.11 The summed activity of these individual channels constitutes the large currents observed in macroscopic excised patches.

Single KATP channels exhibit bursts of brief openings, separated by long interburst closures.46–49 Thus, the open probability () of the channel is determined both by the kinetics of the burst (open and closed durations within a burst) and the duration of the long interburst closures. The intrinsic gating of KATP can therefore be separated into two separate ’gating’ processes; fast (responsible for intraburst closures) and slow (responsible for interburst closures). While it is helpful to distinguish between fast and slow gating processes to characterise channel regulation, doing so does not require the existence of separate structural gates.11,49

Gating is a property intrinsic to Kir6.2, which is able to open and close in the absence of SUR130,50 (Figure [1.12](#ch1fig:singles_sur)); albeit with very different kinetic properties as will be discussed later. The open and intraburst closed time of single channels is dependent on the electrochemical gradient across the cell membrane, otherwise called the K+ driving force.51 As the name implies, the electrochemical gradient depends on two things: the voltage across the membrane, and the K+ concentration gradient. Increasing hyperpolarisation decreases the amount of time channels remain in the open state and increases the amount of time channels remain in the closed state within bursts.52,53 This is a characteristic feature shared by other inwardly-rectifying K+ channels.52,54 In addition, altering the K+ gradient across the membrane by changing the K+ concentration in the pipette or bath solution has the same effect on fast gating kinetics.51,55 As the driving force for K+ increases, the open lifetime of the KATP channel decreases. This is in contrast to other K+ channels such as KV2.1, which exhibits the opposite relationship.56

There are a number of domains within Kir6.2 that regulate the intrinsic gating of the channel. Firstly, the P-loop is a conserved feature across K+ channels.57 In Kir channels, the P-loop connects the two transmembrane domains, and dips into the plasma membrane to form the K+ selectivity filter. While the P-loop is broadly conserved between Kir family members, there are key residues which differ. Notably, the K+ selectivity filter signature sequence (TxGYG) is identical across all other Kir subtypes (TIGYG), but in Kir6.1 and Kir6.2 the tyrosine is replaced by a phenylalanine at position 133 (TIGFG), a feature shared only by eag-like K+ channels.58 Another particularly interesting residue is V127, which is unique to Kir6.1 and Kir6.2 within the Kir family - all other Kir channels posess a threonine at this location.59

59 investigated a range of substitutions at these two residues. Mutation of V127 to the conserved threonine (V127T) dramatically increases the open time of KATP, while also increasing the intraburst closed time. There is also some suggestion of an additional open state existing in this mutant construct, evidenced by the appearance of a second peak in the open time histograms. Mutation of F133 to the conserved tyrosine (F133Y) did not produce expression of functional channels; however combining the two mutations (V127T,F133Y) resulted in functional channels with a further increase in the open time when compared to the single mutant V127T. In addition, substitutions at other residues in the P-loop of Kir6.2 leads to a range of effects on the intraburst kinetics of KATP. Crucially, none of the substitutions affected the slow gating of the channel; i.e. burst duration and interburst closed times remained similar despite the varied alterations in the intraburst kinetics.59 concluded that the P-loop is instrumental in regulating the fast gating of KATP, and suggested that the lack of correlation between perturbations of inter- and intra-burst kinetics is evidence for independence between the fast and slow gating processes.

Other domains of Kir6.2 are involved in the regulation of slow gating. The cytosolic end of the second transmembrane domain of Kir6.2 has been implicated in regulation of KATP slow gating by a number of mutational studies.53,60–62 Substitution of C166 with a more bulky or hydrophobic residue dramatically reduces the frequency of the channel entering the long, closed interburst state, and increases the open time of the channel in the bursts.53 However, no effect is seen on the length of the intraburst closed times, which is additional evidence for the independence of the fast and slow gating processes. Substitutions at N160,60 L164,63 I167,61 and T17161,64 also increase channel open time and decrease the rate of entry into the interburst closed state, further implicating this region of Kir6.2 in modulating the slow gating of KATP.

The slide-helix of Kir6.2 is the interface between the transmembrane domain and the cytoplasmic domain, and mutations in this region result in changes in the single channel kinetics and of KATP.65–69 Mutations examined at the single channel level show changes in burst duration65–67 but unaltered intraburst kinetics. Interpretation of the mechanism underlying these single channel kinetics alterations is complicated by the proximity of this region of Kir6.2 to the putative PIP2 binding site.70 Perturbations of this region could be affecting intrinsic gating directly, or indirectly by altering PIP2 regulation, both of which would lead to changes in slow gating.

While Kir6.2 is able to gate intrinsically when expressed alone, coassembly with SUR1 alters the intrinsic gating of the channel in a number of ways. Compared to the single channel kinetics of Kir6.2DC or Kir6.2-GFP alone, coexpression of Kir6.2 with SUR1 increases the open time of the channel within the bursts, and increases their duration, while the intraburst closed times are unaffected.31,53,71 This suggests that interactions of SUR1 with Kir6.2 serve to regulate the slow gating of the channel, rather than the fast gating. The mechanisms by which SUR1 regulates intrinsic gating of the KATP channel are complex and not yet fully understood. Structurally, the primary contacts between the two subunits are formed between the N-terminus and first transmembrane domain of Kir6.2 and TMD0 and L0 of SUR1 (Figure [1.6](#ch1fig:sur_struct)).22,72,73 The contributions of the interactions of these regions have been studied in a variety of ways.

47 constructed a series of SUR1/SUR2A chimeras and characterised the changes in single channel kinetics that resulted from swapping different domains between the two isoforms of SUR. They found that Kir6.2+SUR2A channels exhibited a far higher single channel than Kir6.2+SUR1 channels (0.91 and 0.64 respectively). This difference could be attributed to increased burst durations and decreased interburst periods, while fast gating is indistinguishable. They found that a chimerical construct replacing the N-terminal 291 amino acids of SUR1 with those of SUR2A was sufficient to recapitulate the single channel kinetics of full-length SUR2A, suggesting that this region is critical for specifying the intrinsic gating of KATP.

Later work established that truncations of SUR1 to TMD0 or TMD0-L0 fragments allowed expression of "mini-KATP" channels at the cell membrane.74–76 The first two studies showed that expression of Kir6.2 with TMD0 alone (residues 1-195 or 1-196 of SUR1) essentially recapitulates the intrinsic gating characteristics of Kir6.2 expressed with full-length SUR1, restoring the increased open time duration and burst duration as compared to expression of Kir6.2 alone.74,7576 later found that in their hands, mini-KATP channels formed from Kir6.2DC and SUR1-TMD0 were similar to full-length KATP but they consistently observed differences in the burst durations. This discrepancy may be, at least in part, due to differences in the heterologous expression system (COSm6 cells in,74 *Xenopus* oocytes in).76 Otherwise, the remaining difference between KATP and mini-KATP channels could either be due to differences in structural interactions due to the truncation, or could implicate a role for the ABC core domain in regulating slow gating.76

Increasing the length of the SUR1 fragment to include the first section of the L0 linker (residues 1-232 of SUR1) results in a nearly constitutively open channel, with dramatically increased open time duration and few observable interburst closures.74 The resulting of 0.93 reflects a near saturation of the slow gating process; as without changes to the fast gating there can be limited further increases in due to the flickery closure. Increasing the length of the L0 linker included in the SUR1 truncation fragment results in a progressive decrease in the open time duration, burst length and , although it never regresses to the kinetics observed in Kir6.2 expressed alone.74 These findings suggest that while the TMD0 and the initial segment of L0 help to stabilise the open state of KATP channels, sections of the L0 linker act to destabilise the open state in some fashion.74,77

One hypothesis for this destabilisation is that parts of the L0 linker interact with the N-terminus of Kir6.2 to regulate intrinsic gating of KATP channels.78–81 When Kir6.2DC is expressed alone, deletion of the first 14 amino acids of the N-terminus of Kir6.2 does not affect the single channel kinetics.80 However, in the presence of SUR1, truncations of up to the first 44 amino acids of the N-terminus reduce the frequency of transitions to the long closed state, increasing the .78–80 This effect increases with progressive truncations from DN4 to DN30, but increasing the truncation past this point does not appear to have additional effects.

82 conducted an alanine scan of positively charged residues in the N-terminus of Kir6.2. They identified two residues in the proximal 30 amino acids which reduced when substituted (R4A, K5A) and two residues which increased when substituted (R16A, R27A).

Application of a synthetic peptide which contains the first 33 amino acids of the N-terminus of Kir6.2 to full-length KATP channels decreases the frequency of transitions to the closed state, in a manner comparable to truncation of the N-terminus.81 This effect was dependent on the presence of SUR1, as with the N-terminal truncation experiments. This finding suggests that the synthetic peptide competes with the endogenous N-terminus of Kir6.2 for an interaction within the KATP channel complex.

Finally,83 investigated an in-frame deletion of five amino acids (28D32) identified in neonatal diabetes patients. This deletion resulted in KATP channels with increased only in the presence of SUR1; single Kir6.2DC and Kir6.228D32,DC channel currents were indistinguishable. The authors then made use of the 1-195 and 1-288 truncated SUR1 constructs described in reference,74 and determined that only when the L0 linker was present (i.e. SUR1 residues 1-288) was there a difference in intrinsic gating upon the 28D32 deletion.

Together, these results provide evidence for interactions between SUR1 and the N-terminus of Kir6.2 which facilitate transitions to the long closed state of the channel.74

Of course, when measuring currents from hundreds or thousands of KATP channels, it is not possible to distinguish between perturbations which alter fast gating and perturbations which alter slow gating; the current measured reflects the sum of both of these processes. At a macroscopic level, anything which increases single channel open time or burst duration, or decreases the intraburst closed time or frequency of entering the interburst state will be indistinguishable.

## Ligand dependent regulation of the pancreatic KATP channel

KATP channels are regulated by two classes of endogenous ligands (nucleotides and phosphoinositides) and a range of exogenous ligands (predominantly sulphonylureas and glinides) (Figure [[ch1fig:regulation\_diagram]](#ch1fig:regulation_diagram)). Thus far, the action of each of these ligands appears to exclusively affect the slow gating of channel.49 While the binding of adenine nucleotides to the Kir6.2 binding site leads to closure of the pore, binding of nucleotides to the NBSs of SUR1 in the presence of Mg2+ activates the channel.84,85 The interplay between the action of nucleotides at these distinct sites (Figure [1.10](#ch1fig:sur_ctd)) determines the response of the KATP channel to metabolic changes, and therefore even subtle mutations or modifications to these sites can lead to diseases of insulin secretion. Phosphoinositides present in cell membranes are also regulators of KATP function, a property which is shared amongst the Kir family of channels.5,86,87 PIP2 stimulates the opening of KATP, and excision of membrane patches results in a decline of channel activity due to the loss of PIP2 in the excised membrane over time.88 Finally, in addition to allowing activation of the channel by Mg-nucleotides, proper assembly of Kir6.2 and SUR1 allows for highly sensitive inhibition of currents by sulphonylureas and glinides.89,90

Proteins are inherently dynamic and sample a vast ensemble of accessible conformations.91 Techniques with high temporal resolution such as NMR spectroscopy have revealed the breadth of the energy landscape of macromolecules, and highlighted the ability of molecules at equilibrium to adopt a variety of conformational states.92 The KATP channel is no exception. The ability of the channel to open and close in the absence of ligand (i.e. after channel rundown due to loss of PIP2) shows that at equilbrium, the KATP channel is able to exchange between open and closed states, albeit with a much higher occupancy of closed states.88,93 One mechanism by which ligands are proposed to regulate the equilibrium of KATP channels (and macromolecules in general) is by being selective for particular conformations. For example, PIP2 will exhibit a higher binding affinity for an open state of the channel that it will for a closed state; and thus the presence of PIP2 will selectively stabilise the open state of KATP channels. This mechanism is the cornerstone of the MWC model of allostery,94–97 and its assumptions and implications will be discussed in more detail in [[ch4]](#ch4). In this framework, the link between ligand binding and channel gating, sometimes called transduction, is the factor by which a ligand preferentially stabilises a particular conformation. Figure [[ch1fig:regulation\_diagram]](#ch1fig:regulation_diagram) is a simplified diagram of how ligands interact to regulate the KATP channel. Briefly, describes the unliganded equilibrium between open and closed, while ligands which bind with affinity constants preferentially stabilise the open state by a factor or the closed state by a factor .

### Nucleotide regulation of the pancreatic KATP channel

The physiological regulation of channel activity by nucleotides is the summed contribution of activation by Mg-nucleotides binding to the NBSs of SUR1, and inhibition by nucleotides binding to Kir6.2.98 To study these contributions experimentally, most research to date has relied on electrophysiological recordings of KATP currents. Separating the contributions of the different classes of site has been achieved through a variety of methods. Firstly, activation of the channel by Mg-nucleotides can be eliminated by removing Mg2+ ions from the solutions used to perfuse excised patches by inclusion of high concentrations of chelators such as EGTA.99,100 While it may still be possible that nucleotides bind to the NBDs in the absence of Mg2+ ions and affect channel inhibition, it is widely assumed that the absence of Mg2+ ions allows for the measurement of inhibition at Kir6.2 alone. Secondly, activation of the channel by Mg-nucleotides can be isolated by introducing mutations which abolish nucleotide binding to Kir6.2.99,100

Mutation of residues which are involved in nucleotide inhibition of the KATP channel can result in one of two functional effects. In the first category are residues which, when substituted, reduce the sensitivity of the channel to nucleotide inhibition (i.e. increase the IC50 for nucleotide inhibition) while not perturbing the intrinsic gating of the channel. Mapping these residues to the cryo-EM structures of ATP-bound KATP channels reveals that the residues in this category are invariably located close to the nucleotide binding site of Kir6.2. The binding site is composed of part of the N-terminal region of one Kir6.2 subunit, and part of the C-terminal region of its neighbouring subunit. Well characterised mutations of residues in this region of the N-terminus (e.g. R50,82,101–105 and G53)66 and the C-terminus (e.g. I182,64,106,107 K185,102–104 F333,108 and G334)64,100,108,109 have no effect on the single channel kinetics in the absence of nucleotide. However, they are far less sensitive to inhibition by nucleotides. The simplest hypothesis to explain this data given the location of the residues in the structures is that mutations of these residues perturb interactions between KATP and nucleotides, reducing the direct binding affinity of nucleotides for the inhibitory binding site (i.e. a reduction of in Figure [[ch1fig:regulation\_diagram]](#ch1fig:regulation_diagram)).

Alternatively, mutations which do not affect intrinsic gating but reduce sensitivity to nucleotide inhibition may be decreasing the efficacy of nucleotides, rather than the affinity, causing nucleotide binding to no longer be as strongly coupled to the pore (i.e. approaches unity in Figure [[ch1fig:regulation\_diagram]](#ch1fig:regulation_diagram)). R201 was hypothesised to form part of the binding site as a cysteine65,110 or histidine111 substitution at this site results in reduced inhibition of KATP channels by nucleotides, without any changes in intrinsic gating . Curiously, an alanine at this position results in KATP channels which exhibit both reduced sensitivity to ATP inhibition and reduced activation by PIP2.112 Examining the cryo-EM structures suggests that this residue does not form direct contacts with bound ATP, and would therefore have to alter the nucleotide binding site allosterically - potentially by stabilising the short helix containing the critical F333 and G334 residues.24102,103 proposed that mutating R201 to an alanine instead acts by perturbing the preference of nucleotides for the closed state of the channel, increasing .

The second category of residues are those which, when mutated, increase the of the channel and also affect the sensitivity of the channel to nucleotide inhibition. This category is far larger, and these residues are found across both Kir6.2 and SUR1 structures. Within the MWC framework in Figure [[ch1fig:regulation\_diagram]](#ch1fig:regulation_diagram), mutations which increase (and therefore increase the observed ) reduce the ability of nucleotides to inhibit the channel. By increasing the stability of the open state, the selectivity of nucleotides for the closed state () results in a decreased probability of nucleotide binding, and thus reducing inhibition. Mutations within this category are difficult to fully characterise in the cell membrane environment due to the presence of phosphoinositides. An observed increase in in an excised patch may either stem from an increase in , or from an increase in or .

Activation of KATP channels by Mg-nucleotides is not quite as trivial to measure in isolation. The most common experimental paradigm used to isolate activatory effects is introducing a mutation into Kir6.2 which renders it insensitive to inhibition by nucleotides.99,100 Application of Mg-nucleotides to mutant channels such as Kir6.2-G334D then results in an increase in the burst duration and therefore the of KATP channels.100 This stimulatory effect is conferred by the NBSs of SUR1, as mutation of the Walker A motif in either NBS1 or NBS2 results in KATP channels which are no longer activated by Mg-nucleotides.98,113

In ABC transporters, the conformational changes which allow substrate movement across the membrane are driven by ATP hydrolysis.114 In addition, there is strict coupling between ATP hydrolysis and channel gating in CFTR, an ABC family member which is in itself a chloride channel.115 The NBDs of SUR are capable of hydrolysing ATP at rates comparable to that of CFTR,24,25,116 although by necessity these studies were carried out on purified channels or purified NBD fragments and may not reflect the physiological rate.117 used beryllium-fluoride and orthovanadate to stabilise the pre- and post-hydrolytic states of SUR2A respectively, and suggested that the post-hydrolytic state favoured channel opening.

However,118 analysed the microscopic reversibility of single-channel kinetics to determine whether ATP hydrolysis is coupled to channel gating. Microscopic reversibility is a property of equilibrium systems such that their dynamics are time-reversible. As ATP hydrolysis is irreversible and thus not in equilibrium, if channel gating is dependent on ATP hydrolysis it will not obey microscopic reversibility.119 Unlike for CFTR,115118 found no evidence for ATP-dependent violations of microscopic reversibility in KATP channel gating, supporting the conclusion that ATP hydrolysis by the NBDs of SUR1 is not directly coupled to conformational changes of the channel. In addition, Mg-ADP is sufficient to activate channel currents, obviating the need for ATP hydrolysis.100 It is most likely that the activatory function of Mg-nucleotides occurs in a similar manner as in inhibitory function of nucleotides; via an allosteric equilibrium effect on the channel pore ( in Figure [[ch1fig:regulation\_diagram]](#ch1fig:regulation_diagram)). It remains unclear whether Mg-ATP is capable of activating KATP channel currents upon binding to SUR1, or whether it first needs to be hydrolysed to Mg-ADP.

### PIP2 regulation of the pancreatic KATP channel

A conserved feature of Kir channels is that they are regulated by phosphoinositides, in particular PIP2, and Kir6.2 is no exception.13,14,86,87 Studying the nature of the regulation of KATP by PIP2 is difficult experimentally due to the lack of control over PIP2 concentrations, and our inability to precisely measure them. Firstly, while the contaminating effects of intracellular nucleotides are removed by excision of a patch, the same is not true for PIP2. The rundown of channel currents is largely attributable to dissociation and/or degradation of PIP2 from the membrane patch, but rundown is a complex phenomenon and the relative amounts of PIP2 in the membrane varies between patches and experimental conditions.88 The hydrophobicity of PIP2 means that perfusing a membrane patch results in accumulation of lipid in the membrane; it is impossible to reach an equilibrium with a known concentration. An alternative is using analogs of PIP2 with increased solubility due to shortening of the acyl chain length, such as dioctanoyl (diC8) PIP2.120 While more soluble analogs are easier to work with and an experimenter can reach a quasi-equilibrium, we do not know how the concentration of diC8 PIP2 applied to a membrane equates to the concentration achieved in the membrane. Another alternative is using polyamines such as neomycin as negative charge chelators; screening the negatively-charged phospholipid head groups present in the membrane away from their normal binding sites.86,121 This approach runs into the problems of both methods previously outlined; we do not know the precise correlation between the concentration of neomycin applied and the concentration of active, un-chelated PIP2 in the membrane; and due to rundown it is impossible to reach a true equilibrium.

Despite all these complexities, there is still a great deal of research exploring how PIP2 regulates KATP channel gating. PIP2 stimulates KATP channel currents by increasing channel open time and burst duration, and reduces the sensitivity of KATP channel currents to inhibition by nucleotides.13,14,122,122,123 The stimulatory effect occurs in the absence of SUR1, as the of Kir6.2DC or Kir6.2-cGFP expressed alone is still enhanced by perfusion of PIP2.122,123 However, the presence of SUR1 appears to enhance the ability of PIP2 to stimulate channel currents.13,14,122,123 This enhancement has been proposed to occur through the interaction between the N-terminus of Kir6.2 and TMD0 of SUR1, and may account (at least in part) for the increase in ’intrinisc’ observed when Kir6.2 and SUR1 are coexpressed.124124 introduced a mutation (E128K) into the TMD0 region of SUR1 and found that KATP channels formed either with full-length mutant SUR1 or mutant TMD0 exhibited drastically reduced when compared to their wild-type counterparts. In addition, the E128K mutation reduced the activation of channel currents by PIP2, and exposure to PIP2 did not reduce the sensitivity of E128K channels to nucleotide inhibition. These findings highlight the complexity of the regulatory role of SUR1, and also the difficulty in separating effects on intrinsic channel gating from effects on PIP2 regulation, given the difficulty in measuring and controlling the latter.

The second functional aspect of PIP2 modulation is its effects on the sensitivity of KATP channels to nucleotide inhibition. Application of PIP2 reduces the ability of nucleotides to inhibit KATP channels, and reduction of PIP2 activity from rundown or application of neomycin increases the ability of nucleotides to inhibit KATP channels.13,14,122,123 In addition, photoaffinity labelling of Kir6.2 by ATP analogs is reduced in the presence of phosphoinositides.125 This phenomenon can be explained by the allosteric effects of increasing channel , which would result in a corresponding decrease in nucleotide binding and inhibition due to the energetic coupling of the nucleotide binding site and the channel pore ( in Figure [[ch1fig:regulation\_diagram]](#ch1fig:regulation_diagram)).49 However, it has also been hypothesised that there is an additional interaction between nucleotides and PIP2 which is not mediated through energetic coupling to the channel pore ( in Figure [[ch1fig:regulation\_diagram]](#ch1fig:regulation_diagram)).49,122,126,127 This interaction could be due to direct competition between PIP2 and nucleotides for the same site, or by local allosteric interactions which energetically disfavour binding of one ligand when the other is already bound.

While the cryo-EM structures of KATP were not able to capture a PIP2-bound state, there is a crystal structure of Kir2.2 complexed with PIP2 which suggests that the Kir6.2 PIP2 binding site is not the same as the nucleotide binding site.128 This is supported by mutagenic electrophysiological studies, which show that substitutions at residues which alter nucleotide sensitivity but not also do not affect activation of channel currents by PIP2 (with the notable exception of R201, which is discussed previously).86,112,121,127 This does not rule out the possibility of separate but overlapping sites for nucleotide and PIP2 binding, and whether nucleotides and PIP2 are able to simultaneously bind to the same subunit remains an open question.49,129

## Fluorescence applications for ion channels

Electrophysiological studies of ion channels allow recordings with high temporal resolution and exquistive sensitivity to protein energetics. However, while current recordings give detailed functional information even at a single protein level, it is difficult to reconcile function with structural "snapshots" obtained with X-ray crystallography or cryo-EM. Fluorescence techniques offer a window into the structural dynamics of ion channels in their native environments which can be correlated with functional data.12 The simultaneous measurements of current and fluorescence are often referred to as voltage-clamp fluorometry (VCF, when the electrophysiological configuration is two-electrode voltage clamp or cut-open oocyte clamp) or patch-clamp fluorometry (PCF, when the electrophysiological configuration is patch-clamp).

There are a two main features of fluorophores which make them attractive for dynamic structural studies. Firstly, some fluorophores are sensitive to their local environments and can be used to detect movements of protein domains. For example,130 labelled residues in the S4 helix of Shaker K+ channels with a variety of fluorophores to investigate the structural dynamics of the voltage-sensing domain (VSD) during channel gating. They labelled two residues (M356C and A359C) with tetramethylrhodamine (TMRM) and captured the fluorescence spectra of the labelled Shaker channel in cut-open oocytes at a series of different membrane potentials. TMRM exhibits a characteristic shift in the peak of its emission spectra according to the hydrophobicity of its environment, with a decrease in wavelength of 7 nm from solvation in methanol to solvation in isopropanol.130 Thus, when130 observed a constant peak in the emission spectrum over a range of voltages, they were able to conclude that it was unlikely that the labelled residues move from a buried, purely hydrophobic environment to an external aqueous environment as the voltage changes.

The second feature is that fluorescence can be quenched, which occurs when the excited state of the fluorophore is dissipated through interaction with a different molecule.12 Quenching can be static, with the fluorophore and quencher forming a non-fluorescent pair, or quenching can be collisional, with the fluorophore transferring energy to the quencher upon the pair colliding with each other. In the above study,130 introduced potassium iodide (KI) into the extracellular solution as a collisional quencher to determine the accessibility of the labelled residues. Consistent with their spectral observations, the proportion of fluorescence quenched by KI did not change on depolarisation of the membrane, indicating that the residues were equally exposed to the iodide in the external solution at different voltages.

More commonly, quenchers are residues in the surrounding protein, with tryptophan being the strongest quencher followed by tyrosine.131,132 Relative movements of fluorophore and quencher which result in overlap of the van der Waals radii of the pair result in quenching, the efficiency of which depends on the species of quencher and the nature of the fluorophore. Bimane and its derivatives are particularly sensitive to quenching by tryptophans,133 but are otherwise remarkably environmentally insensitive.134135 used the positively charged bimane derivative monobromo(trimethylammonio)bimane (qBBr) to replace arginine residues in the S4 helix of Shaker K+ channels. By substituting a cysteine for a native gating charge and then covalently attaching qBBr to this site, the authors produced a fluorescent analogue of a discrete charge in the voltage sensor of the channel. Voltage induced conformational changes of the fluorescent gating charge could then be detected by quenching from either a native tryptophan, or site-specific insertions of tryptophan.

### Labelling techniques

The examples described above both used thiol-reactive fluorophores which can be covalently linked to cysteine residues in the protein of interest. Cysteine resides are relatively scarce in the extracellular domains of most transmembrane proteins, which enables the insertion of cysteines into extracellular loops of ion channels for labelling.130,136–138 However, the relative abundance of cysteine residues on the intracellular side of proteins and the inacessability of many residues in transmembrane domains to solution restricts the wider applicability of this method. In addition, the presence of cysteines in other membrane proteins make it difficult to eliminate background fluorescence from fluorphore conjugation to off-target proteins.

Genetically encoded fluorescent labels are an alternative to chemical conjugation which avoid the problems of off-target labelling. Initial fluorescence studies of ion channels used fluorescent proteins such as GFP,139 which are typically used to label the N- or C-termini of proteins (although there are exceptions).140,141 While fluorescent proteins are bright and photostable, their large size (Figure [[ch1fig:fluorophore\_sizes]](#ch1fig:fluorophore_sizes)) results in limited utility for investigating subtle conformational dynamics.

An alternative to fluorescent proteins are fluorescent unnatural amino acids (UAAs). UAAs expand the available palette beyond the 20 naturally occuring amino acids and enable the site-specific insertion of more exotic side chains to explore protein function.12,137,138,142,143 One particularly hard-working fluorescent UAA is L-3-(6-acetylnaphthalen-2-ylamino)-2-aminopropionic acid (ANAP), which was developed in the Schultz laboratory.144,145146 were the first to realise the potential of ANAP for the study of ion channels, incorporating ANAP into a number of strategically chosen locations in the Shaker K+ channel to investigate its conformational dynamics. This work built on the previously described work of130 by labelling previously inaccessible residues in the lower part of the S4 helix and the intracellular loops of the channel. Since then, 32 primary research articles published (or pre-printed) as of March 2021 include the use of ANAP, and 21 of those are ion channel studies.143

Finally, ligands and toxins can be fluorescently labelled to investigate the ion channels they regulate.12,138 A good illustration of this approach is the use of a fluorescent analogue of cAMP (fcAMP) to study hyperpolarisation-activated cyclic nucleotide-modulated (HCN) pacemaker channels, which are regulated by membrane voltage and the endogenous ligand cAMP. Binding of fcAMP to HCN channels in membrane patches leads to increased fluorescence at the membrane and activation of channel current, which can be measured simultaneously to correlate ligand binding to channel gating.147–149 The authors measured the increase in fluorescence and channel current in response to step changes in fcAMP to discriminate between possible models of HCN channel function, and found that their measurements were most consistent with asymmetric contributions of the four subunits of the channel.148 Curiously, conformational states of the channel appeared to be most stable with zero, two or four ligands bound.

While this series of studies illustrates the power of patch-clamp fluorometry, measuring the fluorescence intensity is not without its pitfalls. Firstly, the correlation between fluorescence intensity and ligand binding is not perfect. A necessary assumption is that at saturating fluorescence intensities, the binding sites are fully occupied. Secondly, careful controls are required to ensure that fluorescence increases are specific to ligand binding to the channel of interest.147 achieved this as described in a previous study,150 by including free fluorescent dye (DY647) in the bath solution, which allowed the authors to separate the specific bound fraction. Finally, this method is unsuitable for channels with more than one class of binding site for the fluorescent ligand, as it is not possible to assign an increase in fluorescence to ligand binding to one site over another.

# [ch:2-methods]Methods

## Molecular biology.

Human Kir6.2 and SUR1 were subcloned into pcDNA4/TO and pCGFP\_EU vectors for expression of wild-type and GFP-tagged constructs, respectively. pcDNA4/TO and pANAP were obtained from Addgene. peRF1-E55D and pCGFP\_EU were kind gifts from the Chin Laboratory (MRC Laboratory of Molecular Biology, Cambridge, UK) and the Gouaux Laboratory (Vollum Institute, Oregon, USA) respectively. Amber stop codons and point mutations were introduced using the QuikChange XL system (Stratagene; San Diego, CA). All constructs were confirmed by DNA sequencing (DNA Sequencing and Services, University of Dundee, Scotland).

## Cell culture and channel expression

HEK-293T cells were obtained from and verified/tested for mycoplasma by LGC standards (ATTC CRL-3216, Middlesex, UK). Our working stock tested negative for mycoplasma contamination using the MycoAlert Mycoplasma Detection Kit (Lonza Bioscience; Burton on Trent, UK). Cells were plated onto either poly-L-lysine coated borosilicate glass coverslips (VWR International; Radnor, PA) or poly-D-lysine coated glass-bottomed FluoroDishes (FD35-PDL-100, World Precision Instruments). ANAP-tagged Kir6.2 constructs were labelled using amber stop codon suppression as described in reference.145 Transfections were carried out 24 hours after plating using TransIT-LT1 (Mirus Bio LLC; Madison, WI) at a ratio of 3 μl per μg of DNA. Unless specified otherwise, all transfections included a Kir6.2 construct with an amber stop codon (TAG) at position 311 (Kir6.2-W311TAG), SUR1, pANAP and eRF1-E55D in the ratio 0.5:1.5:1:1. Transfected cells cultured in Dulbecco’s Modified Eagle Medium (Sigma; St. Louis, MO) + 10% foetal bovine serum, 100 /ml penicillin and 100 μg/ml streptomycin (Thermo Fisher Scientific; Waltham, MA) supplemented with 20 m ANAP (free acid, AsisChem; Waltham, MA). Cells were incubated at 33 °C and in the presence of 300 μ tolbutamide to enhance protein expression and channel trafficking to the plasma membrane.29,40 eRF1-E55D was included to increase efficiency of ANAP incorporation. Experiments were carried out 2-4 days after transfection. We also expressed constructs labelled with ANAP at positions I182, F183, F198, and I210. Kir6.2-F183\*, Kir6.2-F198\*, and Kir6.2-I210\* co-expressed with SUR1 did not produce sufficient currents for subsequent experimentation. Mutations at I182 are known to produce profound effects on nucleotide inhibition of KATP. Thus, we did not consider this site for further experimentation.

## Western blots

Transfected HEK-293T cells grown in 6-well plates were harvested in cold PBS (Life Technologies Limited; Paisley, UK), pelleted at 0.2 x g for 2.5 minutes and resuspended in lysis buffer containing 0.5 % Triton X-100, 100 m potassium acetate, and a cOmplete protease inhibitor tablet (1 tablet/50 ml, Roche; Basel, Switzerland), buffered to pH 7.4. After a 30-minute benzonase (Sigma) treatment at room temperature, samples were mixed with a DTT containing reducing agent and loading buffer (NuPAGE, Invitrogen; Carlsbad, CA) and run on a precast Bis-Tris 4 %–12 % poly-acrylamide gel at 200 V for 40 minutes. Proteins were wet transferred overnight onto polyvinylidene difluoride (PVDF) membranes (Immobilon P, Merck Millipore; Burlington, VT) in 25 m Tris, 192 m glycine, 20 % methanol, and 0.1 % SDS at 10 V on ice. Membranes were blocked with 5 % milk in TBS-Tw (150 m NaCl, 0.05 % Tween 20, 25 m Tris, pH 7.2) before staining for 30 minutes with a 1:1000 dilution of rat anti-HA monoclonal antibody in TBS-Tw (clone 3F10, Roche). After washing with TBS-Tw, membranes were incubated for 30 minutes with a 1:20,000 dilution of HRP-conjugated goat anti-rat polyclonal antibodies in TBS-Tw (Jackson ImmunoResearch; Ely, UK). Detection was performed using the SuperSignal West Pico Chemiluminescent Substrate (Thermo Fisher) and a C-DiGit Blot Scanner (Licor Biosciences; Lincoln, NE). Analysis was performed using custom code written in Python.

To confirm our ability to express full-length W311\*-GFP, we performed western blots for HA-tagged Kir6.2 constructs in detergent-solubilized HEK-293T cells (Figure [3.10](#ch3fig:western_1)). The HA tag plus a short linker (YAYMEKGITDLAYPYDVPDY) was inserted in the extracellular region following helix M1 of Kir6.2 between L100 and A101. Transfection of wild-type Kir6.2-HA or Kir6.2-HA-GFP resulted in two bands on the western blots. The upper bands were close to the expected sizes for full-length Kir6.2-HA and Kir6.2-HA-GFP (46 kDa and 77 kDa, respectively).

We consistently observed a lower molecular weight band as well. This band must correspond to an N-terminally truncated Kir6.2 product, as the apparent molecular weight shifted with addition of the C-terminal GFP tag. Based on the molecular weight, we predict that the truncated protein product initiated from a start codon in the first transmembrane domain. Therefore, we believe it is unlikely that this protein would form functional channels or traffic to the plasma membrane. When Kir6.2-W311TAG-HA or Kir6.2-W311TAG-HA-GFP were co-transfected with SUR1, pANAP, and eRF1-E55D, and cells were cultured in the presence of ANAP, the western blots were similar to wild-type Kir6.2-HA or Kir6.2-HA-GFP. Over 90 % full-length W311\*-HA-GFP was produced under these conditions. We were unable to quantify the percentage of full-length W311\*-HA produced as the C-terminally truncated band resulting from termination at the TAG codon was very similar in size to the N-terminally truncated band. Co-expression with SUR1 increased the percentage of full-length W311\*-HA-GFP produced. In the absence of ANAP, we did not observe any full-length Kir6.2, indicating that there was no read-through of the amber (TAG) stop codon.

## Confocal microscopy

Confocal imaging was performed using a spinning-disk system (Ultra-VIEW VoX, PerkinElmer; Waltham, MA) mounted on an IX81 microscope (Olympus; Southend-on-Sea, UK) with a Plan Apo 60x oil immersion objective (NA = 1.4), provided by the Micron Advanced Bioimaging Unit, Oxford. Transfected HEK-293T cells were incubated for 15 minutes with 1 n CellMask Deep Red (Thermo Fisher) to stain plasma membranes before washing with PBS and imaging. ANAP was excited with a solid-state laser at 405 n. GFP and CellMask were excited with an argon laser at 488 n and 633 n respectively. Images were captured on an EMCCD camera (ImagEM; Hamamatsu Photonics; Welwyn Garden City, UK) binned at 2 x 2 pixels and analysed using Python. A median filter with a box size of 32 x 32 pixels was applied to improve the signal-to-noise ratio by reducing background fluorescence.

We examined the surface expression of our ANAP-labelled constructs using confocal microscopy. When Kir6.2-W311TAG-GFP was co-transfected with SUR1 along with pANAP and eRF1-E55D in the presence of ANAP, the ANAP and GFP fluorescence were co-localized at the plasma membrane. When wild-type Kir6.2-GFP was transfected under the same conditions, only GFP fluorescence was observed at the plasma membrane. ANAP fluorescence was diffuse and confined to the cytoplasm or intracellular structures. Thus, the plasma-membrane ANAP signal was specific for W311\*-GFP.

## Surface expression assays

We measured surface expression of HA-tagged Kir6.2 subunits using an approach outlined by Zerangue et al. Cells were plated on 19 mm coverslips coated with poly-L-lysine and transfected as described above. Following incubation, cells were rinsed with PBS before fixation with 10 % formalin for 30 minutes at room temperature. After washing again, cells were blocked with 1 % BSA in PBS for 30 minutes at 4 °C before a 1-hour incubation at 4 °C with a 1:1000 dilution (in PBS) of rat anti-HA monoclonal antibodies. Cells were then washed 5 times on ice with 1 % BSA in PBS followed by a 30-minute incubation at 4 °C with a 1:2000 dilution of HRP-conjugated goat anti-rat polyclonal antibodies. Cells were washed 5 times in PBS + 1 % BSA and 4 times in PBS. Coverslips were removed from the culture dishes and placed in clean, untreated dishes for measurement. 300 μl of SuperSignal ELISA Femto Maximum Sensitivity Substrate (Thermo Fisher) was added to each sample and the luminescence was measured using a Glomax 20/20 Luminometer (Promega; Madison, WI) after a 10 second incubation.

HEK-293T cells were transfected with Kir6.2 constructs with or without a TAG stop codon corresponding to position 311. Cells were co-transfected with pANAP and eRF1-E55D in the presence or absence of SUR1 and cultured with or without ANAP. Wild-type Kir6.2-HA and Kir6.2-HA-GFP in the presence of SUR1 were included as positive controls. Kir6.2 constructs with no HA tag served as negative controls. In the presence of ANAP, we observed strong trafficking of W311\*-HA-GFP to the plasma membrane, but much less trafficking of W311\*-HA (Figure 1—Figure supplement 1E). When cells were cultured in the absence of ANAP, we observed little to no Kir6.2 surface expression from cells that were transfected with Kir6.2-W311TAG-HA or Kir6.2-W311TAG-HA-GFP, suggesting that prematurely truncated constructs did not traffic to the plasma membrane. In the absence of SUR1, surface expression was weak for both wild-type and tagged constructs, despite the reported ability of Kir6.2-GFP to traffic to the plasma membrane in the absence of SUR1.

## Epifluorescence imaging and spectroscopy

Epifluorescence imaging and spectroscopy were performed using a Nikon Eclipse TE2000-U microscope with a 60x water immersion objective (Plan Apo VC, NA = 1.2, Nikon; Kingston upon Thames, UK) or a 100x oil immersion objective (Nikon, Apo TIRF, NA = 1.49). Imaging of ANAP was performed using a 385 nm LED source (ThorLabs; Newton, NJ) with a 390/18 nm band-pass excitation filter, an MD416 dichroic and a 479/40 nm band-pass emission filter (all from ThorLabs). GFP was imaged using a 490 nm LED source (ThorLabs) with a 480/40 nm band-pass excitation filter, a DM505 dichroic, and a 510 nm long-pass emission filter (all from Chroma; Bellows Falls, VT). Fluorescence spectra were collected by exciting ANAP as above but using a 400 nm long-pass emission filter (ThorLabs), then passing emitted light through an IsoPlane 160 Spectrometer (Princeton Instruments; Trenton, NJ) with a 300 g/mm grating. Images were collected with 1 s exposures on a Pixis 400BR\_eXcelon CCD (Princeton Instruments).

## Electrophysiology.

Patch pipettes were pulled from thick-walled borosilicate glass capillaries (GC150F-15, Harvard Apparatus; Holliston, MA) to a resistance of 1.5 MΩ–2.5 MΩ when filled with pipette solution. Currents were recorded at −60 mV from excised inside-out patches using an Axopatch 200B amplifier equipped with a Digidata 1322A digitizer and using pClamp 10 software (Molecular Devices; San Jose, CA). Currents were low-pass filtered at 5 kHz and digitized at 20 kHz. The bath solution (intracellular) contained 140 m KCl, 10 m HEPES, 1 m EDTA and 1 m EGTA (pH 7.3 with KOH). The pipette solution (extracellular) contained 140 m KCl, 10 m HEPES and 1 m EDTA (pH 7.4 with KOH). All experiments were carried out in Mg2+-free conditions. Currents were leak corrected using the current remaining in bath solution containing 5 m barium chloride at 60 mV, assuming a linear leak with a reversal potential of 0 mV. Inhibition was calculated and corrected for rundown by alternating test concentrations of nucleotide solution with nucleotide-free solution, then expressing the test currents as a fraction of the average of the control currents before and after the test solution.

## FRET calculations

We calculated the expected FRET efficiency between ANAP incorporated at amino acid position 311 and a docked TNP-ATP molecule. The efficiency of energy transfer is exquisitely distance-dependent, and can be calculated with the following formula:

where is the distance between donor and acceptor fluorophores and is a characteristic distance at which 50 % of the energy is transferred. We calculated the R0 of the ANAP:TNP-ATP FRET pair using the following equations from:151

where (in //cmnm4) is the normalised spectral overlap of the donor emission () and acceptor extinction (), is the quantum efficiency of the donor measured in the absence of the acceptor, is the refractive index for the medium the experiment is performed in, and is a geometric factor related to the relative orientation of the two transition dipoles of donor and acceptor that can take values between 0 and 4.

For our purposes, we measured the overlap between donor emission measured from the averaged spectra from multiple unroofed membranes containing W311\* without the C-terminal GFP tag, and acceptor extinction spectra measured from TNP-ATP in solution using a Beckman Coulter DU800 spectrophotometer (Pasadena, CA). We did not measure the of ANAP ourselves, instead using the quantum yield of 0.22 measured by.152 As our experiments were performed in a water-based medium, we used the refractive index of water (). We used a value of , which is the case when the orientation of dipoles of donor and acceptor are able to rotate freely within the excited state donor lifetime.

The equivalency between FRET efficiency (measured as ANAP quenching) and nucleotide binding is based on two main assumptions. Firstly, we assume that the observed quenching from a bound nucleotide does not differ dramatically between open and closed states of the channel. As there is no open-state structure of KATP, we do not know exactly how much relative movement would occur between a bound TNP-ATP and Kir6.2-W311. However, based on cryo-EM structures of apo and nucleotide-bound Kir6.2 we do not expect to see a change in the distance between these two positions. Secondly, we assume that the orientation of the ANAP and TNP-ATP dipoles can be well described by a value of . This assumption is commonly made in FRET assays, and reference153 shows that uncertainty introduced by this assumption is relatively small (typically less than 20 %). Empirically, our results showing FRET occurs to a similar extent as predicted by formula [[eq:forster\_fret]](#eq:forster_fret) supports this assumption as reasonable.

## Unroofed binding measurements.

Unroofed membranes were prepared as follows. A coverslip plated with transfected HEK-293T cells was removed from the culture media and rinsed with PBS. The coverslip was then briefly sonicated using a probe sonicator (Vibra-cell; Newtown, CT) leaving behind adherent plasma membrane fragments. Cells cultured on FluoroDishes were rinsed and sonicated directly in the dish. Unroofed membrane fragments were nearly invisible in bright-field images and identified by the presence of GFP and ANAP fluorescence. Fluorescent TNP-nucleotides (Jena Bioscience; Jena, Germany) were diluted in bath solution and perfused onto unroofed membranes using a valve controlled microvolume superfusion system (μFlow, ALA Scientific Instruments; Farmingdale, NY).

Fluorescence spectra were collected as described above. A region of interest corresponding to the membrane fragment was manually selected and line-averaged for each wavelength. A similarly sized region of background was selected and averaged, then subtracted from the spectrum of interest. After subtraction, ANAP intensity was calculated by averaging the fluorescence intensity measured between 469.5 nm and 474.5 nm. Bleaching was corrected by fitting the normalised ANAP intensity of exposures taken during perfusion with nucleotide-free solution to a single exponential decay of the form

then using the fit to correct the intensity of exposures taken during perfusion with test nucleotide solutions.

Some experiments were excluded from further analysis due to obvious cross-contamination between different solutions within the μFlow superfusion system. These were identified by noticeable colour changes in the solution in the delivery tubes.

## Patch-clamp fluorometry.

The tip of the patch pipette was centred on the slit of the spectrometer immediately after patch excision. Currents were measured as described above. Fluorescence emission spectra from the excised patch were acquired concurrently with current measurements, both during test solution application as well as nucleotide-free solution. Background subtraction was slightly imperfect due to the exclusion of TNP-ATP from volume of the glass of the pipette, resulting in spectra that have negative intensities at the TNP-ATP peak at high nucleotide concentrations. However, this over-subtraction does not affect the size of the ANAP peak, which we used to quantify nucleotide binding.

Some experiments were excluded from further analysis due to low fluorescence intensity, as we were concerned about a low signal to noise ratio influencing our results.

## Concentration response processing and presentation

Raw spectrographic images and current traces were pre-processed in Python and Clampfit (Axon) before analysis with R. Where applicable, all experimental data points are displayed in each figure. To help visualise uncertainty and prevent some data points being hidden, they are arranged with a small amount of horizontal jitter; vertical position remains unaffected.

We fit our fluorescence quenching data with the following equation:

where represents corrected fluorescence intensity, and are values, and is the remaining variance. For the fluorescence quenching data, was fixed to the value obtained from W311\*-GFP+SUR1 unroofed experiments (0.1) as explained in more detail in chapter [[ch4]](#ch4). Current inhibition data were fit to the same equation but with representing normalised current magnitude, instead of , and instead of .

We used the brms package in R to perform a non-linear fit to equation [[eq:hill]](#eq:hill) reformulated as a multilevel (or hierarchical) model. The parameters in the equation were supplied as:

Multilevel models seek to describe datasets which consist of clusters or groups of measurements that may differ from one another.154,**andrew\_gelman\_bayesian\_2014?** In this case, each cluster of measurements is the set of current inhibition or fluorescence quenching values obtained from a single excised patch or unroofed membrane. As opposed to fitting each cluster individually, the multilevel model laid out in equation [[eq:drc\_priors]](#eq:drc_priors) allows for ’pooling’ of information between clusters, so that the parameters for each experiment are influenced by all other experiments on the same construct. This pooling tends to improve estimates about each cluster.

Essentially, the (or ) parameter for each concentration-response experiment can be described as the combination of a population parameter that is an estimate of the construct-specific value (b), and an additional ’random’ component that varies between experiments on the same construct (dexperiment).

## MWC model equations and fitting

The concerted MWC-type model fitted to the patch-clamp fluorometry data was formulated as follows:

When no ligand is present (i.e. when ), equation [[eq:mwc\_gating]](#eq:mwc_gating) becomes:

We can use this to normalise the predicted changes in the open fraction to an observed change in current:

We used the brms package in R to fit a multilevel model to equations [[eq:mwc\_binding]](#eq:mwc_binding) and [[eq:normalised\_po]](#eq:normalised_po). First, we normalised the fluorescence quenching data by the determined from W311\*-GFP+SUR1 unroofed experiments (0.1). We then corrected it by transforming each data point as as described in more detail in Chapter [[ch3]](#ch3).

The parameters in the equation were supplied as:

Each of the three parameters was modelled as a combination of a population parameter and an additional random component . Each combined set of current inhibition and nucleotide binding measurements from one excised patch was grouped as one experiment. The remaining variance was allowed to vary between fluorescence and current data.

The alternate single-binding model was formulated as follows:

The extra length of these formulas when compared to equations [[eq:mwc\_binding]](#eq:mwc_binding) and [[eq:normalised\_po]](#eq:normalised_po) do not represent any additional complexity; just an unfortunate consequence of the lack of exponents of which make it impossible to simplify further. Parameters were supplied and fitted as in equation [[eq:mwc\_priors]](#eq:mwc_priors).

## Computational docking.

Computational docking of TNP-ATP into the nucleotide binding site of Kir6.2 was performed using AutoDock-Vina and Pymol (Schrödinger, LLC; New York, NY). 11 TNP-ATP structures from the Protein Data Bank (PDB accession #s 1I5D, 3AR7, 5NCQ, 5SVQ, 5XW6, 2GVD, 5A3S, 2PMK, and 3B5J) were used as starting poses and a 15x11.25x15 Å box was centred on the ATP bound to Kir6.2 in PDB accession #6BAA. Protonation states for each residue were assigned using PDB2PQR and PROPKA 3.0. The modal highest-scoring pose from the docking run was selected (PDB accession #5XW6) and distances were measured from a pseudo atom at the centre of the fluorescent moiety. TNP-ATP (PDB #3AR7) was positioned into the first nucleotide binding site of SUR1 (PDB #6PZI) using the alignment tool in Pymol.

## Chemicals and stock solutions.

Unless otherwise noted, all chemicals were obtained from Sigma. TNP-ATP was obtained as a 10 m aqueous stock from Jena Bioscience and stored at −20 °C. 1 m aqueous stocks of ANAP-TFA were prepared by dissolving the free acid in 30 m NaOH, and were stored at −20 °C. Tolbutamide stocks (50 m) were prepared in 100 m KOH and stored at −20 °C.

# [ch:3]Measuring nucleotide binding to KATP

## Designing a nucleotide binding assay

### Criteria for a useful assay for nucleotide binding to Kir6.2

Previous approaches to measuring nucleotide binding directly to the different binding sites of KATP have relied on isolating binding to individual classes of site by disrupting protein function; either by introducing mutations which abolish binding to a particular site, by measuring binding to Kir6.2 or SUR1 alone, or by measuring binding to fragments of the two subunits.

Two key studies have attempted to measure nucleotide binding to the inhibitory site on Kir6.2 directly. The first relied on photoaffinity labelling of Kir6.2 by the radionucleotide 8-azido-[g-32P]-ATP.155 In these experiments, Kir6.2 with an N-terminal FLAG-tag was expressed in COS-7 cells, and membranes were separated by centrifugation. After incubating the membrane fractions with 8-azido-[g-32P]-ATP, application of UV light results in a covalent linkage between the bound 8-azido-[g-32P]-ATP and Kir6.2. After separation of the membrane fraction proteins on a gel, the quantity of bound radionucleotide can then by quantified by counting the radioactivity of the band corresponding to Kir6.2. These experiments were able to definitively establish that the inhibitory nucleotide binding site of KATP was on Kir6.2, and suggested that the Kir6.2 binding site possessed a lower affinity toward the radionucleotide than the SUR1 binding sites.

The second made use of a fluorescent congener for ATP, trinitrophenyl (TNP)-ATP. TNP-ATP had previously been used in binding measurements of purified proteins due to it’s increased quantum yield (and thus increase in observed fluorescence) upon binding (need a ref). TNP-ATP is most commonly used as an antogonist of P2X receptors, which are also sensitive to endogenous ATP. The authors measured binding of TNP-ATP to the purified carboxyl terminal of Kir6.2 (residues 169 to 354) solubilised by linking it to mannose binding protein (MBP).156 The increased fluoresence of TNP-ATP when bound to the Kir6.2-MBP construct could be measured in a spectrometer, and allowed for equlibrium measurements of nucleotide binding. These experiments were able to establish an initial estimate for the binding affinity of the Kir6.2 site for TNP-ATP at 5 μ. These findings were replicated in a similar study, which used fusion proteins constructed from residues 170 to 390 of Kir6.2 fused to glutathione-S-transferase (GST) and estimated a binding affinity of 5 μ.157

These studies were hampered by the need to isolate the Kir6.2 binding site from the two SUR1 binding sites, which leads to unphysiological experimental conditions. To improve on these methods, an ideal assay measuring nucleotide binding to the KATP channel neeeds to fulfill a number of criteria.

1. We need sufficient spatial sensitivity to distinguish between different classes of binding site; i.e. the assay should be capable of distingushing binding to Kir6.2 from binding to NBS1 or NBS2.
2. We should be able to measure binding to a channel which we know is functional, so our experimental conditions cannot be drastically different from those used to measure channel function.
3. There should be minimal perturbation of the channel in order for binding measurements to be physiologically relevant.
4. For accurate measures of affinity, binding should be at equilibrium so we cannot use covalent interactions or other forms of non-equilibrium labelling.
5. We should be able to achieve a higher temporal resolution.

TO fulfill these criteria, we used an approach involving a fluorescent unnatural amino acid, ANAP. ANAP has been used increasing widely in the study of ion channel structure and function due to several desirable qualities.

1. It is smaller than traditional fluorescent labels such as fluorescent proteins or rhodamine derivatives. Therefore, it should be less perturbing to the function of the protein it labels.
2. As it is an amino acid, it can be site-specifically inserted into any protein. This avoids the issues of other small chemical dyes which are targeted to a site via post-translational covalent modifications, typically by reacting with a cysteine residue. While this can be avoided in some proteins by mutating each cysteine residue to an alternative residue to avoid off-target labelling, there are functionally important cysteines in the KATP channel which cannot be mutated. In addition, this does not solve the problem of off-target labelling of other membrane proteins
3. ANAP is environmentally sensitive, which has been used to great effect in other studies. Notably, the peak emission ranges from ~450nm to ~490nm depending on the hydrophobicity of the surrounding environment.

Initially, we hoped that the environmental sensitivity of ANAP fluorescence might be sufficient for the peak of the emission spectrum of an ANAP residue inserted into an ATP binding site to measureably change when ATP was bound. Unfortunately, when we introduced ANAP directly into the Kir6.2 binding site in place of residues I182 or F183 we were not able to observe any functional KATP channels at the cell membrane.

Instead, we turned to FRET as a reporter for ATP binding. As ATP itself is not fluorescent, and has no intrinsic fluorescence quenching, we turned to TNP-ATP (Figure [3.1](#ch3fig:chemical_structures)). TNP-ATP is an excellent FRET partner of ANAP, as evidenced by the good overlap in the TNP emission spectra and the ANAP extinction spectra (Figure [3.2](#ch3fig:spectral_overlap)). This leads to a theoretical distance-dependency of FRET which is most sensitive between 20 Å–60 Å (Figure [3.3](#ch3fig:fret_efficiency)) with a calculated R0 of 38.4 Å.

### Choosing a site to incorporate ANAP

THe theoretical R0 of 38.4 Å for FRET between ANAP and TNP-ATP allowed for flexibility when choosing a site to incorporate ANAP. Ideally, a residue should be chosen to maximise the following aims:

1. The incorporated ANAP needs to be close enough to the nucleotide binding site of interest to report a quantifiable change in FRET when TNP-ATP is bound. This would not have to be close enough for 100 % FRET to occur, but the greater the efficiency achieved the higher the signal-to-noise ratio would be for measuring binding.
2. It also needs to be far enough from each other class of nucleotide binding site to avoid quenching by TNP-ATP bound to other sites.
3. In addition to avoiding interference from other classes of binding site, we also need to avoid cross-talk between nucleotide binding sites of the same class on different subunits, as this would lead to difficulty interpreting the measured quenching. The ideal theoretical solution would be labelling only one nucleotide binding site per ion channel, but without using a concatemer this is not so easy in practise.
4. More practically, incorporation of ANAP should not lead to drastic changes in nucleotide binding or channel gating properties, and the complete KATP channel needs to be expressed on the membrane.

To narrow down which residues could be candidates for ANAP incorporation to measure binding at Kir6.2, we took three cryo-EM structures of KATP with ATP bound and computationally docked TNP-ATP into the nucleotide binding pocket (Figure [[ch3fig:docking]](#ch3fig:docking)). To assess the validity of computationally docking a ligand to each structure, we first attempted to dock ATP into the inhibitory binding pocket of Kir6.2 to check that the highest-scoring binding poses were similar to those observed in the cryo-EM structures. Docking ATP to both #6C3P and #6C3O yielded binding poses which were very similar to the pose found in the cryo-EM structures (Figures [3.5](#ch3fig:6c3p_docking), [3.6](#ch3fig:6c3o_docking)). However, docking ATP to #6BAA resulted in binding poses which were in a flipped orientation relative to the pose found in the cryo-EM structure (Figure [3.4](#ch3fig:6baa_docking)).

We then took TNP-nucleotide structures from eleven different X-ray diffraction and cryo-EM structures published on RCSB to dock to the Kir6.2 binding site of KATP. For both #6BAA and #6C3P we observed that the three highest scoring binding poses for TNP-nucleotides closely resemble those of the ATP solved in complex with the channel (Figures [3.4](#ch3fig:6baa_docking), [3.5](#ch3fig:6c3p_docking)). It is not so clear for #6C3O, for which the highest scoring poses are not in agreement with each other or the solved structure of ATP.

Based on the predicted TNP-ATP poses for #6BAA and #6C3P, we could narrow down potential ANAP incorporation sites to within 25 Å of the centre of the TNP-moiety, at which distance we would expect to see over 90 % FRET efficiency when TNP-ATP is bound to Kir6.2. In addition, we excluded residues which fell within 45 Å of NBS1 or NBS2, as this restricts the potential FRET between TNP-ATP bound at these sites and our chosen residue to roughly 25 % or less. While we can exclude residues which fall too close to the NBS’s of SUR1, the close proximity of the Kir6.2 nucleotide binding sites to each other means that we cannot exclude intersubunit FRET occuring; i.e. TNP-ATP binding to a neighbouring subunit will also be able to quench ANAP to a certain extent. However, this occurs in a predictable way that we can measure and account for.

We ended up with one residue which fulfilled these criteria and for which membrane expression of the ANAP-incorporated channel could be detected: W311. It is a bulky hydrophobic residue similar to ANAP, and no mutations at this residue have been previously identified to alter KATP function.

## Incorporating ANAP into the Kir6.2 binding site

### Amber stop codon expression system

ANAP can be introduced into a protein of interest by essentially expanding the genetic code to incorporate a noncanconical amino acid.158 The amber stop codon (TAG) is the least frequently occuring stop codon in eukaryotic cells,159 and can be repurposed to encode ANAP. This requires the introduction of a transfer RNA (tRNA) which recognises the TAG codon, and an aminoacyl-tRNA synthetase (aaRS) which selectively aminoacylates the tRNA with ANAP into the heterologous expression system, without crossreacting with the existing translational machinery.144,145

144 used directed evolution to develop a tRNA/aaRS pair to encode ANAP in *Saccharomyces cerevisiae*.144 Briefly, they altered the specificity of *Escherichia coli* leucyl-tRNA synthetase so that it was able to aminoacylate the leucyl-tRNA with ANAP, and not endogenous amino acids. The coevolved tRNA/aaRS pair were built into an expression plasmid pANAP (Figure [3.9](#ch3fig:amber_codon)) which is capable of driving expression in mammalian cells.145 HEK293 cells transfected with pANAP and a plasmid encoding GFP with an amber stop codon at residue position 40 (40TAG) exhibited green fluorescence only when incubated in the presence of ANAP in the culture media,145 demonstrating that ANAP can be selectively incorporated into proteins in mammalian cells.

As far as we are aware, only two other studies have incorporated unnatural amino acids into Kir6.2.160,161160 incorporated three unnatural tryptophan variants at position W68 to highlight the necessity of a planar amino acid side-chain at this location to maintain physiological KATP channel function.160 However, in this study *Xenopus* oocytes were the heterologous expression system, so rather than transfecting a combination of plasmids, the authors injected a combination of transcribed mRNAs.

161 incorporated azidophenylalanine (AzF) at three different positions on the N-terminus of Kir6.2 (residue numbers 12, 18 and 52).161 AzF is photocross-linkable upon exposure to UV light, and the authors used this phenomenon to investigate the extent of physical interactions between the N-terminus of Kir6.2 and SUR1, and how these interactions are mediated by pharmacological chaperones. In this study, COSm6 cells were the heterologous expression system, and expression of AzF containing constructs was found to be dramatically reduced when compared to wild-type channels.

### ANAP incorporation into amber stop codon containing constructs

The nature of the amber stop codon suppression system requires a number of careful controls to ensure the following:

1. Stop codon recognition is not perfect, and there is a chance of read-through. Instead of incorporating ANAP, it is possible that the translation machinery can insert endogenous amino acids instead, leading to production of full length,unlabelled Kir6.2. However, we found that cells transfected with W311TAG constructs and pANAP which were not cultured in the presence of ANAP did not produce full length Kir6.2 (Figure [3.10](#ch3fig:western_1), [3.11](#ch3fig:western_2)), suggesting there is minimal read-through of the stop codon in our experiments.
2. Introducing a stop codon creates a risk that truncated Kir6.2 will be produced instead of ANAP labelled Kir6.2. This risk can be reduced by transfecting a dominant negative engineered version of eukaryotic translation termination factor 1(eRF1-E55D), which does not efficiently terminate protein synthesis in response to the amber stop codon (but leaves opal and ochre stop codons nearly unaffected) and thus increases the incorporation of ANAP.162 We found that transfection of W311TAG constructs with a C-terminal GFP tag produced minimal truncated Kir6.2 (less than 10 % of the total density observed in Figure [3.11](#ch3fig:western_2)).
3. Despite being the least frequent eukaryotic stop codon, the amber stop codon is still present in a significant number of proetin sequences. We must be careful that ANAP is not incorporated into a protein which localises to the plasma membrane to an extent which would affect our ability to assign ANAP fluorescence to Kir6.2. We found that in cells transfected with GFP-tagged Kir6.2 without an amber stop codon, there was no increase in ANAP fluorescence at the cell membrane (Figure [3.12](#ch3fig:wt_confocal), [3.13](#ch3fig:wt_confocal_profiles)). By contrast, when W311TAG-GFP was transfected, we saw a clear increase in ANAP fluorescence at the cell membrane (Figure [3.14](#ch3fig:w311_confocal), [3.15](#ch3fig:w311_confocal_profiles)), suggesting that any observed ANAP fluorescence at the cell membrane originates from our labelled Kir6.2 construct.

## Testing for functional membrane expression

### Surface expression of HA-epitope labelled Kir6.2 constructs

To assess the ability of ANAP-incorporating constructs to traffic to the plasma membrane, we used a luminence-based surface expression assay. This assay relies on the recognition of an HA-epitope introduced into an extracellular region of the protein of interest (in this case, the N-terminal region of Kir6.2) by an anti-HA primary antibody followed by an HRP-conjugated secondary antibody. The luminescence after applying HRP substrate is then proportional to the amount of protein at the plasma membrane of the cells.

We assessed the membrane expression of N-terminally HA-tagged Kir6.2 (nHA-Kir6.2) in the presence or absence of ANAP in the culture media and in the presence or absence of cotransfected SUR1. We also measured how the addition of a C-terminal GFP tag affected membrane expression under these conditions. We used untagged Kir6.2 as a control for nonspecific luminesence.

We find that for wild-type Kir6.2 (WT) there is roughly a 20-fold increase in observed luminescence when coexpressed with SUR1 over background, and roughly a 100-fold increase for the C-terminally GFP tagged Kir6.2 (WT-GFP, Figure [3.16](#ch3fig:surface_expression_1), [3.18](#ch3fig:surface_expression_3)). There is no difference in surface expression of these constructs when ANAP is present in the culture medium (Figure [3.16](#ch3fig:surface_expression_1), [3.19](#ch3fig:surface_expression_4)). When ANAP is incorporated at either residue 183 or 311 (F183\* and W311\* respectively) we see an increase in luminescence over background when coexpressed with SUR1 and with ANAP present in the culture medium (Figure [3.16](#ch3fig:surface_expression_1), [3.18](#ch3fig:surface_expression_3)). The presence of the C-terminal GFP tag increases luminescence further for both constructs, dramatically so for W311\*. However, when F183\* is transfected and ANAP is not present in the culture media we still see a similar increase in fluorescence over background when compared to the luminescence when ANAP is present (Figure [3.16](#ch3fig:surface_expression_1), [3.19](#ch3fig:surface_expression_4)), suggesting that a large proportion of the protein reaching the membrane does not have ANAP incorporated. In contrast, when W311\*-GFP is transfected with SUR1 in the presence of ANAP, we see a 10-fold increase in luminescence compared to when ANAP is not present, consitent with the majority of surface expressed protein incorporating ANAP. We also see a consistent increase in luminescence for all constructs aside from W311\* due to cotransfection with SUR1 (Figure [3.17](#ch3fig:surface_expression_2)), suggesting that the incorporation of ANAP and the addition of a C-terminal GFP tag do not affect the role of SUR1 in forming the full KATP complex and trafficking to the membrane.

### Electrophysiology of Kir6.2 constructs

To establish whether W311\*-GFP formed KATP channels with similar function to wild-type, we excised patches from cells transfected with either WT-GFP or W311\*-GFP cotransfected with SUR1. Excision was performed in Mg2+-free solution to reduce rundown and to prevent activation of the channel by nucleotides. We observed similar magnitudes of current for both WT-GFP and W311\*-GFP, and currents ran own at similar rates.

We fit our inhibition data with equation [[eq:hill]](#eq:hill) (Figure [3.20](#ch3fig:atp_inhibition_1)) as described in the methods. Briefly, our fitting procedure assumes that there is a population parameter for , and , and an additional ’random’ effect on that can differ between experiments (shown in Figure [3.22](#ch3fig:atp_inhibition_2)). Our fits result in posterior probability distributions for the population parameter shown in blue in Figure [3.24](#ch3fig:ec50_fits_1). These distributions reflect our confidence in the population parameter for the , marginalising over the random effect of different experiments. For all and values fitted this way, in the text we will report the 95 % intervals of the posterior probability distribution for the fitted population parameter.

Perfusion of ATP resulted in current inhibition with an IC50 of 24 μ–45 μ for WT-GFP+SUR1 and 75 μ–124 μ for W311\*-GFP+SUR1. Thus, despite the distance from the ATP binding site, the incorporation of ANAP at W311 clearly affects some aspect of nucleotide inhibition. However, we assume that insights into the function of the ANAP-incorporating channel will still be applicable to wild-type channels despite the change in nucleotide inhibition.

Next, we established that TNP-ATP inhibits KATP (Figure [3.21](#ch3fig:tnpatp_inhibition_1), [3.23](#ch3fig:tnpatp_inhibition_2)). We observed current inhibition with an IC50 of 0.7 μ–1.8 μ for WT-GFP+SUR1 and 2.9 μ–10 μ for W311\*-GFP+SUR1. KATP thus appears to be more sensitive to inhibition by TNP-ATP than by ATP. This could potentially be due to extra contacts made by the TNP moiety with Kir6.2, seen in our computational docking (Figure [[ch3fig:docking]](#ch3fig:docking)).

### Unroofed membrane binding assay of Kir6.2 constructs

We then directly measured nucleotide binding to W311\*-GFP in unroofed membranes. Briefly sonicating transfected cells adhered to coverslips results in the lower membrane of the cell remaining stuck to the coverslip while the rest of the cell contents is disrupted and perfused away. This leaves the cytoplasmic domains of expressed KATP channels open to perfusion of TNP-ATP. These patches of membrane are barely visible under brightfield illumination, but due to the presence of the C-terminal GFP tag and the incorporated ANAP, we can see patches of membrane expressing KATP channels light up when we excite either fluorophore (Figure [3.25](#ch3fig:unroofed_images)). By measuring the fluorescence spectra of patches of unroofed membrane, we can separate the fluorescence emission peaks of the C-terminal GFP tag and the incorporated ANAP (Figure [3.26](#ch3fig:unroofed_spectral_images)). The peak at 472 nm corresponds to ANAP emission, while the peak at 508 nm corresponds to GFP emission. We observed no change in the locations of those peaks in the presence of ATP or TNP-ATP.

Perfusing TNP-ATP results in a decrease in the peak corresponding to ANAP fluorescence, and a concomittant increase in a fluorescence peak which corresponds to the TNP-ATP (Figure [3.27](#ch3fig:unroofed_spectral_traces)). This phenomenon is the fresult of FRET between TNP-ATP bound to the channel at the Kir6.2 binding site. The decrease in ANAP fluorescence is almost directly correlated to an increase in bound nucleotide. We chose to measure the decrease in ANAP fluorescence rather than the increase in TNP-ATP fluorescence or the change in the ratio of ANAP:TNP-ATP fluorescence as we know that the ANAP fluorescence is specific to the Kir6.2 binding site. Increases in TNP-ATP fluorescence could in part be due to direct excitation of TNP-ATP bound to other membrane proteins. We can plot the quenching of ANAP fluorescence as a concentration-response curve as in Figure [3.28](#ch3fig:unroofed_intensities).

Before analysis, ANAP bleaching was corrected as shown in Figure [3.29](#ch3fig:bleaching_plots_2). ANAP intensities of spectra imaged during bath perfusion in between applications of TNP-ATP were fit with Equation [[eq:bleaching]](#eq:bleaching). We found that all unroofed experiments showed bleaching well described by the single exponential fit to equation [[eq:bleaching]](#eq:bleaching). In each experiment, there was a mean proportion of 49 % ANAP fluorescence remaining by the last exposure (Figure [3.31](#ch3fig:bleaching_terms_4)), maintaining a good signal-to-noise ratio for each spectra imaged.

While our measurements of ANAP quenching are proportional to nucleotide binding to KATP, the raw observations are not directly equivalent to the unbound fraction of Kir6.2 subunits. This non-equivalence is due to two factors. Firstly, there is the potential for crosstalk between ANAP incorporated in one subunit and TNP-ATP bound to the adjacent subunits. To determine the extent to which this crosstalk would affect the measured FRET efficiency when ANAP is incorporated at position 311, we adapted a program described by163 which uses a numerical method to model FRET in complex geometries. We implemented a simple version of this program in Python which uses a Monte Carlo simulation scheme to approximate the observed FRET efficiency for a given set of donor and acceptor fluorophores and coordinates. An overview of the program is shown in Figure [3.32](#ch3fig:exifret_program). We did not measure the fluorescence lifetimes and quantum yields of ANAP and TNP-ATP directly, instead using previously determined values.164–166 The fluorescence lifetime of TNP-ATP differs when it is bound to proteins; we ran simulations using the fluorescence lifetime of TNP-ATP in solution and the fluorescence lifetime of bound TNP-ATP and saw no difference in the FRET efficiency.

We simulated the expected FRET for a single KATP channel bound to 0-4 molecules of TNP-ATP in two different scenarios. In the idealised scenario, each ANAP molecule is only able to FRET with the TNP-ATP molecule bound at the closest inhibitory binding site (Figure [3.33](#ch3fig:exifret_coords)). In the actual scenario, which resembles the experimental paradigm, each ANAP molecule is able to FRET with any bound TNP-ATP molecule in a probabilistic manner dependent on the inter-fluorophore distance. We can observe that there is a systematic deviation in the FRET efficiency between these two scenarios (Figure [3.34](#ch3fig:exifret_out)), which we can correct by transforming the actual values () into adjusted values ().

Secondly, we need to correct for incomplete FRET due to the distance between the donor and acceptor. Based on the results of the computational docking, we predict a maximal FRET efficiency of 91 % when every Kir6.2 subunit is bound by TNP-ATP. Fitting our adjusted data to a Hill equation results in a maximum observed FRET efficiency () of 90 %, agreeing well with our prediction. We can then constrain our Hill fits so that is equal to this maximum FRET efficiency, so that the parameter we obtain is equivalent to the of TNP-ATP binding.

Overall, these two corrections do not dramatically alter our results (Figure [3.35](#ch3fig:tnpatp_quenching_1)). We observed quenching of ANAP fluorescence over a concentration range of TNP-ATP similar to the range in which we observed inhibition of current in W311\*-GFP (Figure [3.36](#ch3fig:ec50_fits_3), [3.37](#ch3fig:tnpatp_quenching_2)). When fit to a Hill equation, quenching () was fit with an EC50 of 21 μ–31 μ, while the corrected binding data (adjusted ) gave an EC50 of 30 μ–45 μ.

### Patch-clamp fluorometry of Kir6.2 constructs

To ensure that the ANAP fluorescence we observe in the unroofed membranes is emitted by functional channels, we measured fluorescence quenching and current inhibition from the same excised patches (Figure [3.41](#ch3fig:atp_tnpatp_trace), [3.42](#ch3fig:atp_tnpatp_spectra_1), [3.43](#ch3fig:atp_tnpatp_spectra_2)).

This experimental paradigm leads to two complications compared to performing the measurements separately. Firstly, the number of channels in an excised patch are far smaller than the number of channels in an unroofed membrane patch. This results in a much dimmer fluorescence readout, and a lower signal-to-noise ratio. Secondly, the presence of the pipette glass in the images results in some abnormalities in the background subtraction procedure. This is not due to the glass itself, but results from the occlusion of TNP-ATP from the image surrounding the patch. This leads to oversubtraction of the background TNP-ATP spectra, leading to an apparent negative peak in our corrected images. However, we find that there is no overlap of this peak and the ANAP peak, so our fluorescence quenching measurements are unaffected by this phenomenon. We were able to correct for ANAP bleaching in the same manner as we did for unroofed membranes (Figure [[ch3fig:pcf\_bleaching]](#ch3fig:pcf_bleaching)).

Our fluoresence measurements from excised patches are right-shifted when compared to our measurements for unroofed membranes (Figure [3.44](#ch3fig:pcf_1)), with an value of 76 μ–144 μ. Our finding that the EC50 for TNP-ATP binding is right-shifted compared to the IC50 for TNP-ATP inhibition is consistent between each experimental paradigm (Figure [3.45](#ch3fig:ec50_fits_4)). This finding has implications for how exactly the binding of nucleotides to Kir6.2 leads to closure of the KATP channel pore.

## Discussion

We have demonstrated that we can measure nucleotide binding to the inhibitory nucleotide binding site of Kir6.2 in intact, functional KATP channels in their native membrane environment. Measuring binding directly in either unroofed membrane patches or in excised patches simultaneously with current recordings reveals that nucleotide binding is right-shifted compared to nucleotide inhibition; i.e. KATP channels begin to close at nucleotide concentrations where there is very little binding. This observation rules out certain models of ion channel function, which will be explored further in chapter [[ch:4]](#ch:4).

These findings come with some important caveats. Firstly, the introduction of ANAP into Kir6.2 at residue 311 clearly impacts nucleotide inhibition of the channel, increasing the observed values for ATP. Our analysis of nucleotide binding and inhibition is therefore predicated on this decrease in sensitivity to ATP inhibition not reflecting a disruption of the normal physiological mechanism of ATP inhibition. As all of our binding experiments are performed in the W311\* background by necessity, we hope that measurements of relative changes in binding and inhibition will still be meaningfuly interpretable as they will mirror similar relative changes in inhibition observed in the WT background.

Secondly, KATP channels are more sensitive to inhibition by TNP-ATP than by ATP. Again, this means that any conclusions we draw from experiments measuring relative changes in binding and inhibition rely on those relative changes affecting ATP binding and inhibition to a similar extent. To try and ameliorate these caveats as best as we can, where possible we have performed control experiments in the WT background with ATP to ensure that introduced mutations result in similar relative effects on nucleotide inhibition despite the background of the construct or the identitity of the nucleotide. As control experiments of this sort are not possible in unroofed membranes, where it is impossible to measure current inhibition, we have focused on patch-clamp fluorometry for constructs where expression is good enough to measure sufficient fluorescence.

This methodology should be readily adaptable to the study of other nucleotide-regulated channels, such as the P2X receptor family or CFTR.

# [ch:4]MWC modelling

## Modelling nucleotide regulation of the KATP channel

The complex regulation of KATP channel activity by nucleotides and phosphoinositides has led to a wide range of scientists seeking to unify the constellation of structural and functional studies into one mechanistic framework, which is capable of explaining each aspect of channel regulation. The importance of KATP channels in regulating insulin secretion, responding to cardiac stress, and protecting against seizures is one driving force behind the search for a model.49 Another aim is more holistic; hoping that increasing our understanding of how the KATP channel is regulated by the interplay of its ligands may shed light on other ion channels or proteins.**garfinkel\_modeling\_2017?** In any case, the primary goal of constructing a mathematical model of the KATP channel is to explain as much of the diversity of channel function as possible, while keeping the model as simple and biologically relevant as possible; a balancing act between completeness and complexity.

Previous attempts at modelling KATP channel regulation have primarily focused on nucleotide inhibition,93,123,167–174 due to the relative ease of isolating the effects of nucleotide inhibition. There have been fewer attempts at incorporating activation by Mg-nucleotides.85,93,100 The difficulty in quantifying phosphinositide regulation of the KATP channel means that in most cases where it is considered, it is implicitly included as a component of the intrinisc gating of the channel, rather than explicitly described,13,122,123 although there are some exceptions.93,169,175

What does a model of ion channel function look like? Broadly, a model attempts to categorise discrete conformational states of the channel, and describe the transitions between those states. In the simplest case, an ion channel can be described as fluctuating between an open state and a closed state (Figure [[ch4fig:simple\_model\_diagram]](#ch4fig:simple_model_diagram)). As these states exist in equilibrium, they can be described by an equilbrium constant () which is composed of the rate constant for the opening transition () divided by the rate constant for the closing transition ().

To relate this to empirical measurements of ion channel function, is equivalent to the of this two-state channel. Alternatively, in this simple two-state channel, and can be calculated directly by measuring the lifetimes of the closed and open states respectively from single-channel recordings.176,177 Of course, real ion channels are more complicated and two states are not sufficient to describe the complexity of the ligand regulation of KATP channels, which visit a multitude of conformational states. As our understanding of the channel grows, the more complex a model needs to be to fully account for all observed aspects of function.

One shortcoming of KATP channel functional models to date is that there are limited data directly measuring binding of nucleotides to the channel, and as such the nucleotide-bound conformational states and transitions of the channel have had to be inferred from electrophysiologcal measurements. Here, we hope to apply our correlated measurements of nucleotide binding and channel inhibition to reconcile the predictions of existing models of KATP channel inhibition by nucleotides.

### Restricting the subset of possible models

The two classes of models which have been proposed to describe KATP channel inhibition can be categorised into two groups; models in which each Kir6.2 subunit is able to change between open and closed conformations independently, and models in which opening and closing take place via a concerted mechanism of all four subunits.49,50,76,85,170,174,178,179 The independent class of models are often referred to as Hodgkin and Huxley (HH)-like models, after the original model proposed to describe voltage-gated ion channels.180 The concerted class of models are often referred to as Monod-Wyman-Changeaux (MWC)-like models, after the allosteric model formulated by Monod, Wyman and Changeaux to describe hemoglobin.181

Conceptually, an MWC-like model is easier to reconcile with the structure of KATP given that each inhibitory nucleotide binding site is composed of domains from two adjacent subunits; it is hard to imagine how nucleotide binding could lead to an indepedent conformational change in one subunit alone.174 Empirically, the two types of model make testable predictions about channel behaviour and nucleotide binding. In a concerted model, each nucleotide binding event contributes the same amount of energy towards closure of the pore, such that each subunit binding a nucleotide will have an additive effect on the probability of the channel closing. In an independent model, as each subunit is free to change its conformation independently, the stochiometry of nucleotide binding is less clear. Most formulations of an independent model have suggested that KATP channel behaviour is most consistent with a single nucleotide binding event being sufficient to drive closure of the channel.48,167,168,182

A number of studies have examined the kinetics of single KATP channels to determine which model best describes nucleotide inhibition.170,174,179,182170 examined single channel currents in patches excised from *Xenopus* oocytes injected with a mixture of Kir6.2DC and Kir6.2DC-N160D,T171A subunits. The T171A mutation appears to eliminate the interburst closures of the Kir6.2DC by dramatically slowing the rate at which the ATP-sensitive inhibition gate closes. The authors classified the single channel stoichiometry by assessing the sensitivity of currents to inhibition by spermine, which is provided to a subunit by the N160D mutation. An exponential relationship between the mean burst time of the channel and the number of mutant subunits incorporated into it fit the predictions made by a concerted model of inhibition.

179 and174 constructed tetrameric concatemers of Kir6.2 subunits to precisely control the stochiometry of the resulting channels. The authors introduced mutations which affected either nucleotide binding (K185E)174,179 or mutations which altered intrinsic gating (C166S, T171Y)179 into a fixed proportion of Kir6.2 subunits in the concatemerised channels. This selective disruption of individual subunits resulted in changes in ATP-dependent inhibition which could only be explained by a concerted model of KATP channel inhibition. However, as these experiments relied on introducing an additional physical linker between Kir6.2 subunits, the observed concerted gating behaviour may in part be due to the concatemerisation.

## Implementing an MWC model

### A simple case

The simplest case of an allosteric MWC model for an ion channel is shown as Scheme I in Figure [4.3](#ch4fig:mwc_model_diagrams). This simple case assumes a channel composed of a single monomer with a single binding site for ligand . The channel is restricted to two functional states, open and closed. These two states exist in an equilibrium described by L, which is equivalent to . Ligand binds to the protein with a microscopic affinity constant . The ligand differentially stabilises the open and closed states by a constant . When is unity, the ligand binds equally to both states and so does not influence the conformational changes of the channel. When , the ligand preferentially stabilises the open state, while when the ligand instead preferentially stabilises the closed state. therefore represents *transduction* of nucleotide binding to channel gating, and vice versa.

For KATP inhibition, each monomer in Scheme I represents a subunit of Kir6.2, and in our case the ligand is TNP-ATP. Expansion of Scheme I to account for four identical subunits is shown in [[ch2-methods]](#ch2-methods). Importantly, in an MWC model, cooperativity between subunits is not due to the incorporation of an additional paramater, but a phenomenon which arises naturally due to the energetic coupling between ligand binding and channel gating described by the transduction paramater .

### The role of PIP2

Of course, nucleotide inhibition is not the only ligand regulation of KATP channels. If we assume that activation of KATP currents by Mg-nucleotides binding at the NBDs of SUR1 or by PIP2 binding to Kir6.2 are independent processes, the effects of these ligands on nucleotide inhibition can be incorporated implicitly through their effects on . Mg-nucleotide activation of KATP channel currents is well described by assuming independence from nucleotide inhibition; i.e. there is no evidence to suggest that there is a direct interaction between binding of Mg-nucleotides to SUR1 and the ability of nucleotides to bind to Kir6.2.85,100 However, there is some evidence to suggest that there is a direct interaction between the nucleotide and PIP2 binding sites.49,122,126,127 The existence of a direct interaction, either by competition for an overlapping binding site or through allosteric rearrangements of the two binding sites, may make it difficult to incorporate regulation by PIP2 implicitly as an effect on . We investigated how the existence of direct interaction between the two ligand binding sites may manifest in our observations by simulating data from three progressively expanded MWC-like schemes (Figure [4.3](#ch4fig:mwc_model_diagrams)).

If we consider introducing a second ligand which binds to a distinct site on the same monomer and does not directly interact with ligand , we introduce the states shown in Scheme II of Figure [4.3](#ch4fig:mwc_model_diagrams). Each ligand has its own microscopic association constant ( or ) and its transduction factor ( or ). Importantly, there is no interaction term between ligand and ligand ; the only way the binding of the ligands can impact each other is through effects on . Scheme II is therefore a restricted form of scheme III, which explicity introduces a term for direct interaction () between binding sites for ligands and on the same monomer. When is unity, Scheme III becomes Scheme II. When , binding of one ligand reduces the ability of the other ligand to bind on the same monomer. When , binding of one ligand enhances the ability of the other ligand to bind on the same monomer.

Under Scheme II, in which there is no direct interaction between ligands, changes in the parameters describing ligand (perturbations of PIP2 regulation) should manifest in the data in the same way as if there was a change in in Scheme I.95 It is unclear whether under Scheme III, with the introduction of the direct interaction , the same assumption is true - and if not, how much it would affect channel behaviour. To determine whether this approximation is appropriate, we generated data using each of the three schemes in Figure [4.3](#ch4fig:mwc_model_diagrams) as the underlying model of channel function and then fit the generated observations to Scheme I (Figure [4.4](#ch4fig:mwc_scheme_1_fits), [4.5](#ch4fig:mwc_scheme_2_fits), [4.6](#ch4fig:mwc_scheme_3_fits)). Ten individual sets of observations were generated using the inputs shown above each figure panel as the centre of a lognormal distribution with a standard deviation of 0.25. These observations were then fit to Scheme I and the values of the three free parameters (, and ) were estimated (Figure [4.7](#ch4fig:mwc_params_1)).

We can show that when Scheme II or Scheme III are the underlying data generating model, with ligand representing PIP2, we are still able to extract the true values of and by fitting the generated data to Scheme I (Figure [[ch4fig:mwc\_models]](#ch4fig:mwc_models)). Parameter choices for Scheme II and III are such that the open probability of the channel at 0 [ATP] is still 50%, equivalent to in Scheme I.

We can also show that when Scheme I is the underlying data generating model, changes in any of the three parameters are easily identified and retrieved by fitting the observed data to Scheme I (Figure [[ch4fig:scheme\_1\_shifts]](#ch4fig:scheme_1_shifts)). This suggests that introducing mutations or perturbing nucleotide inhibition in any other way which directly affects any of the three parameters of this model would be easily identifiable if Scheme I was the true underlying model.

What if Scheme II or III were the underlying model? We would still expect changes in the three parameters which exist in Scheme I to be identifiable (, and ), although would not represent the true unliganded open/closed equilibrium as we would be estimating an modified by the resting PIP2 concentration, , and - in this case, the estimated parameter in fact represents the ATP-unbound open/closed equilibrium.

However, it is unclear how changes in parameters which are not explicitly modelled in Scheme I will affect the generated data and the parameter estimates obtained by fitting the data to Scheme I. Figure [[ch4fig:scheme\_2\_3\_shifts]](#ch4fig:scheme_2_3_shifts) shows the results of increasing by tenfold on data generated from Scheme II (Figure [4.12](#ch4fig:scheme_2_kb_shift)) or Scheme III (Figure [4.13](#ch4fig:scheme_3_kb_shift)). The first observation of note is that the generated data closely resemble those generated from Scheme I when is increased (Figure [4.10](#ch4fig:scheme_1_l_shift)), and indeed when the parameter estimates for a tenfold shift in in Scheme II/III and tenfold shift in for Scheme I are compared (Figure [4.14](#ch4fig:mwc_params_3), right panel) are compared they appear to be similar. So far so good, as an observed increase in when fit with Scheme I would lead us to draw the correct inferences about changes in the underlying model (i.e. the open probability of the channel has indeed increased).

However, changes in under Scheme III are not perfectly captured by changes in when fit to scheme I. Notably, if a direct interaction exists between the nucleotide and PIP2 binding site - if Scheme III is the true underlying model - then fitting the observed data to Scheme I would lead us to estimate an incorrect value for (Figure [4.12](#ch4fig:scheme_2_kb_shift)). Thus, if there is a direct interaction between the sites, then a mutation which induces an increase in the binding affinity for PIP2 would not just increase our estimate of (which would lead to a correct inference) but it would also decrease our estimate of by a not-insignificant amount. This could lead to the incorrect inference that a mutation is causing a direct change in nucleotide binding when it is in fact causing a direct change in PIP2 binding, which is influencing our estimates of through a direct interaction with the inhibitory nucleotide binding site.

### Determining open probability

As represents the fraction of channels in the open state, it is directly measurable by determining the channel open probability. Ideally then, to fit an MWC model to our data we would like to establish the open proability of the channels in our experiments. Measuring the open probability of an ion channel is most accurately accomplished by single-channel electrophysiological recordings, which allows direct measurement of the time a channel spends in an open state. Measuring open probability directly is not possible in macroscopic patches, which consist of hundreds or thousands of individual channels. Thus it would not be possible to determine single channel open probability simultaneously with nucleotide binding, as the fluorescence signal from a small number of channels would be impossible to resolve.

Another approach is noise analysis of currents from large populations of channels.183,184 The ’noise’ in noise analysis refers to current fluctuations which occur when recording from a population of ion channels due to the stochastic channel gating of individual channels. If there are a constant number of channels () which are gated independently from each other and share a homogenous open probability () and a single open conductance level (), the observed macroscopic current level can be described by equation [[eq:inpo]](#eq:inpo):

and the observed variance of the macroscopic current can be described by the variance of the binomial distribution, equation [[eq:bin\_1]](#eq:bin_1):

where the single channel current is essentially a scaling factor. If we assume that in a given recording and remain constant, and it is which changes in response to any given stimuli, then we can combine equations [[eq:inpo]](#eq:inpo) and [[eq:bin\_1]](#eq:bin_1) to yield equation [[eq:bin\_2]](#eq:bin_2):

This equation yields a parabola from to . Intuitively, there can be no variance when is exactly 0 or 1, as there will be no opening or closing events which can give rise to current fluctuations. Once and have been determined for a given experiment, the observed current magnitude can be converted into the for the population of channels by rearranging equation [[eq:inpo]](#eq:inpo) as follows:

Equation [[eq:bin\_2]](#eq:bin_2) can be fit to experimental data by calculating the variance of observed current at different current magnitudes. This calculation is not exactly trivial, and has been accomplished a number of different ways for different purposes. For channels with fast inactivation such as the NaV family, non-stationary noise analysis involves repeating a stimulus multiple times and measuring variance as the squared sum of deviations from the mean of the current magnitude calculated at the same time point across multiple stimuli, referred to in the literature as an ’isochrone’.185 For channels which do not inactivate, stationary noise analysis is possible, and variance can be measured as the squared sum of deviations from the mean current magnitude over a period of time for which is ’stationary’(Figure [4.15](#ch4fig:noise_example_1), [4.16](#ch4fig:noise_example_2), [4.17](#ch4fig:noise_example_3)).

Stationary noise analysis has been performed for KATP channels before by a number of different researchers.60,81,82,100,186–188 Unfortunately, in most of the published research the exact procedure for extracting the parameters in equation [[eq:bin\_1]](#eq:bin_1) is described in the methods section, but the quality of the fits and the value of the fitted parameters besides the final calculated is not discussed. A notable exception to this rule is in reference,186 in which two findings are discussed. Firstly, fitting equation [[eq:bin\_2]](#eq:bin_2) to the mean and variance of 200 ms sections of macroscopic currents from wild-type Kir6.2+SUR2A resulted in a systematic underestimation of the single channel current . From single channel experiments, the single channel current was determined to be 4 pA, while the value obtained from fitting macroscopic currents was only 2 pA. In the case of WT-GFP+SUR1, we see a similar understimation of single channel current (Figure [4.18](#ch4fig:noise_example_fits_1), [4.19](#ch4fig:noise_example_fits_2), [4.20](#ch4fig:noise_example_fits_3)), with fits yielding estimates of 1.66 pA–2.64 pA, while measured single channel currents are at least 4 pA at a holding potential of −60 mV.59,60 This underestimate of is most likely due to a reduction in observed channel current variance when compared to the predictions of equation [[eq:bin\_2]](#eq:bin_2).

There are two possible explanations for this reduction. Firstly, the process of filtering and digitising channel currents can lead to underestimates of variance depending on the relationship between the open time of the measured channel and the cut-off frequency of the filter used. It is unlikely that this phenomenon is responsible for our findings, as the KATP mean open time duration is close to 1 ms and therefore filtering at 5 kHz would lead to less than a 5 % underestimation of . Even if the mean open time of WT-GFP+SUR1 was closer to 0.1 ms, we would expect a 20 % reduction rather than the 50 % we actually observe. Empirically, we can use the frequency power spectrum of our measured current fluctuations to determine whether there may be high frequency channel openings we are missing (Figure [4.21](#ch4fig:spectra_converge)). For WT-GFP+SUR1, we observe that at frequencies approaching our filter cut-off at 5 kHz there is very little observed amplitude in active channels when compared to fully inhibited channels, suggesting we are not missing high frequency current fluctuations.

Secondly, an underestimation of could occur due to violations in the underlying assumptions of the binomial distribution. The first two assumptions are that and are constant throughout a recording. We know that is unaffected by nucleotide inhibition of KATP channels, nor is it affected by PIP2 or channel rundown. Given that we are recording from excised patches, it is unlikely that there will be any change in the number of channels present in the membrane () during the short time course of a recording. The third assumption in using equation [[eq:bin\_2]](#eq:bin_2) is that the channels in a patch share a homogenous , which can be perturbed to a similar extent by a stimulus (in our case, application of nucleotide). This assumption is far harder to justify for our experimental condition, in which channel rundown due to loss of PIP2 results in a complicated mixture of channel populations with different s, which respond differently to nucleotide inhibition.

An extreme case in which channels transition between two states, one where and one where can be approximated by equation [[eq:bin\_1]](#eq:bin_1), with a channel transitioning to the state essentially considered to be no longer available to open, reducing . Thus, fitting the observed current-variance data with [[eq:bin\_1]](#eq:bin_1) would yield a straight line where the slope of the line is equal to . This formulation of equation [[eq:bin\_1]](#eq:bin_1) has been used successfully in the analysis of currents from CRAC channels,189 VSOA channels,190,191 and in the analysis of a specific cardiac KATP channel mutation.186 Unfortunately, in our case channel rundown does not render the KATP channel completely unable to open, with fully rundown channels still displaying openings. Instead of each current measurement being a draw from a single binomial distribution, we are instead drawing from a mixture of binomial distributions with different . We can demonstrate how this could lead to an underestimation of by simulating a simple case where there are two populations of channels, and , with a shared single channel conductance but one with a tenfold lower than the other:

where population consists of channels with an open probability , and population consists of channels with an open probability .

Comparing the mean current/variance relationship of simulated currents from a single binomial (Figure [4.22](#ch4fig:simulated_noise_1), [4.23](#ch4fig:simulated_noise_2)) to that of simulated currents from the mixture of binomials in equation [[eq:bibi\_sim]](#eq:bibi_sim) (Figure [4.24](#ch4fig:simulated_noise_3)) reveals that equation [[eq:bin\_1]](#eq:bin_1) is no longer able to retrieve the true values of and when the data generating process is not a single binomial distribution. In fact, the underestimation of from fitting to data simulated in this way is very similar to the underestimation of we see when fitting to our measure data (Figure [[ch4fig:noise\_manual]](#ch4fig:noise_manual)).

We considered whether the underestimation of and the poor fits to equation [[eq:bin\_2]](#eq:bin_2) when was fixed to 4.32 pA (Figure [[ch4fig:noise\_manual]](#ch4fig:noise_manual)) may be due to the low number of data points when selecting segments of current manually. We took our full current records from each excised patch from cells expressing WT-GFP+SUR1 or W311\*-GFP+SUR1, divided them into 1 second segments, and plotted the mean current/variance relationship for each segment (Figure [4.25](#ch4fig:noise_fits_1)). We fit the data to equation [[eq:bin\_2]](#eq:bin_2) either with allowed to vary freely, or with fixed to 4.32 pA. Our estimates for when it was allowed to vary freely were similar to our estimates from Figure [[ch4fig:noise\_manual]](#ch4fig:noise_manual), with no patch yielding a value above 3 pA (Figure [4.26](#ch4fig:noise_fits_2)). The fits with fixed to 4.32 pA clearly fit the data less well, and the resulting estimate for the open probability on patch excision exceeded 1 for nearly every patch, which is of course not possible.

Given these results, we chose not to use noise analysis to calculate the directly for each patch. In addition,82 compared the calculated from noise analysis and the calculated by application of saturating concentrations of PIP2 of a variety of KATP channel mutants, and found only a weak correlation between the two methods.82

### Comparing models

We expanded Scheme I from Figure [4.3](#ch4fig:mwc_model_diagrams) to account for the four inhibitory nucleotide binding sites of KATP (Figure [4.27](#ch4fig:model_expansion_1)). In addition, we considered an alternate model in which only the first nucleotide binding event contributes towards closure of the channel, and thus there is no cooperativity between subunits (Figure [4.28](#ch4fig:model_expansion_2)). We then fit our observed TNP-ATP binding and current inhibition data from excised patches expressing W311\*-GFP+SUR1 to equations [[eq:mwc\_binding]](#eq:mwc_binding) and [[eq:normalised\_po]](#eq:normalised_po) respectively.

Both models fit our data reasonably well (Figure [[ch4fig:w311\_model\_comparison]](#ch4fig:w311_model_comparison)), although the posterior distributions of the fits to the MWC model (Figure [4.29](#ch4fig:w311_mwc_fit_1), [4.30](#ch4fig:w311_mwc_fit_2)) are narrower than those for the single binding model (Figure [4.31](#ch4fig:w311_single_fit_1), [4.32](#ch4fig:w311_single_fit_2)). Examining the posterior distributions for the three parameters, both models yield similar estimates, with much narrow distributions for than for and (Figure [4.33](#ch4fig:w311_mwc_fit_3)). The cross-correlation plots for the parameter estimates indicate that the model is identifiable given the data, with well bounded ellipses clearly visible (Figure [8.1](#apxfig:inhib_cc_1)). We compared the ability of the two models to explain the data with two complimentary methods. First, we used bridge sampling to calculate a Bayes factor of 1.1 × 104 in favor of the MWC model over the single binding model.192 The Bayes factor can be interpreted as the weight of evidence in favour of one model over another.193 Specifically, the observed data are 1.1 × 104 more likely to have occured under the MWC model than they are under the single binding model. In addition, we performed leave-one-out cross-validation (LOO-CV), which approximates the out-of-sample predictive accuracy of each of the fitted models.194 The MWC model fit has a higher expected predictive accuracy than the single binding model (elpd difference of 27.3 (63)). Together, the Bayes factor and LOO-CV scores favour a concerted MWC binding model.

The 95 % intervals for are 9 × 103 /–1.7 × 104 / for the MWC model, corresponding to a of 56 μ–110 μ. The 95 % intervals for are .007–.254, which is equivalent to an unliganded of <0.01–0.2. This is a broad range of predicted , which may reflect the variability of PIP2 concentrations in the excised patches. The 95 % intervals for are .002–.096. This low range for indicates very strong coupling between TNP-ATP binding to Kir6.2 and KATP channel closure. Based on the fits to the data, we can illustrate how these models couple nucleotide binding to the functional state of the channel by predicting the occupancy of the different states of the KATP channel defined in Figure [[ch4fig:model\_compare]](#ch4fig:model_compare). Figure [[ch4fig:w311\_model\_comparison]](#ch4fig:w311_model_comparison) shows the weighted occupancy of each of the ten states across a range of TNP-ATP concentrations as predicted by our fits to an MWC or single binding model. Qualitatively, the models make similar predictions; as nucleotide binding is so tightly coupled to pore closure, there is a vanishingly small proportion of KATP channels which exist in the open state with two or more TNP-ATP molecules bound to Kir6.2 subunits under the MWC model. Crucially however, for the single binding model to explain the data in Figure [[ch4fig:model\_compare]](#ch4fig:model_compare), it predicts that even at saturating nucleotide concentrations a reasonable fraction of KATP channels (up to 1 %) will be open even with all four Kir6.2 subunits bound to nucleotide.

### Discussion

Measuring binding of TNP-ATP to KATP channels concurrently with measuring inhibition of channel currents has allowed us to test the predictions of prior studies about the stochiometry of nucleotide binding, and the suitability of an MWC model to describe inhibition of the channel. We have established that a simple MWC model is capable of describing both inhibition of KATP channel currents as well as the binding of nucleotides to the Kir6.2 subunit. There has been some debate over the stochiometry of nucleotide inhibition of the KATP channel, with some research indicating that a single Kir6.2 subunit binding to ATP is sufficient to close the channel, while other studies have suggested that further subunit binding events contribute additively to pore closure. Our data suggest that these findings can be reconciled with the observation that even within the framework of a concerted MWC model, where each nucleotide binding event is energetically coupled to the pore, the proportion of KATP channels which are in the open state with more than Kir6.2 subunit bound by TNP-ATP is essentially nil. This is of course caveated by our assumption that TNP-ATP, while exhibiting a higher affinity for the channel than by ATP, does not alter transduction of binding to inhibition.

However, a model capable of describing KATP channel function should also be able to explain how mutations or other perturbations disrupt the regulation of channel function by nucleotide inhibition. In the following chapters, we will explore whether this method and model are capable of discerning between alterations of nucleotide binding, KATP channel gating, and transduction of nucleotide binding to the pore. In addition, these experiments should allow us to test the ability of a simple MWC model to explain the variety of functional changes we observe.

# [ch:5]Nucleotide regulation of Kir6.2

## Introduction

There are variety of ways in which mutations in Kir6.2 can lead to altered KATP channel function, and often lead to diseases of insulin secretion.2,195–200 These can be divided into two broad categories; mutations which have a ligand-independent effect, and those which affect the ligand-dependent regulation of the channel, covered in more detail in Chapter [[ch1-intro]](#ch1-intro). Nucleotide inhibition of the KATP channel can be altered by mutations through three separate mechanistic routes. A mutation which reduces sensitivity of the channel to nucleotide inhibition may act by either reducing the affinity of binding of nucleotides to Kir6.2, increasing the open probability of the channel, reducing the transduction of nucleotide binding to channel closure, or a combinatuon of all three.

Interrogation of residues in this second category is very difficult using electrophysiological measures alone, as without measuring binding of nucleotides directly it is hard to truly separate effects on open probability from effects on binding and transduction.201 In this chapter, we aim to clarify the role of several residues implicated in regulating the inhibitory effect of nucleotides on KATP channel function by measuring TNP-ATP binding directly to the inhibitory nucleotide binding site on Kir6.2, where possible in conjunction with simultaneous current measurements.

## Nucleotide binding

### G334D abolishes nucleotide binding

Residue G334 of Kir6.2 is located in the C-terminal region (Figure [5.1](#ch5fig:g334d_loc)) and has been hypothesised to form part of the ATP binding site since electrophysiological studies demonstrated a dramatic reduction in nucleotide sensitivity upon mutation of the residue.48,64,172 In addition, mutation of this residue to aspartic acid (G334D) results in severe permanent neonatal diabetes mellitus.109 This hypothesis was confirmed by the solving of cryo-EM structures of KATP in the presence of ATP, which revealed the close proximity of residue G334 to the bound ATP.20,72,77,202 Mutating G334 to a total of 13 different amino acid substitutions led to a increase in the IC50 for ATP by over an order of magnitude in excised patches.172 However, only two of those substitutions (R and K) resulted in any changes in nucleotide-independent channel gating when examined at the single-channel level, with unliganded remaining constant. It has therefore been suggested that while G334 forms part of the ATP binding site of Kir6.2, it does not participate in channel gating or transduction of ligand binding to the channel pore.

We sought to test this directly by measuring the binding of TNP-ATP in unroofed membranes to W311\*,G334D-GFP+SUR1. Fluorescence spectra captured from unroofed membrane patches expressing W311\*,G334D-GFP+SUR1 were indistinguishable from those expressing W311\*-GFP+SUR1. The location of the ANAP peak and the bleaching characteristics were also identical. We found that ANAP fluorescence from W311\*,G334D-GFP+SUR1 was barely quenched by even 1 m TNP-ATP (Figure [5.2](#ch5fig:g334d_popfits), [5.3](#ch5fig:g334d_indfits)), reducing the apparant binding EC50 from 30 μ–45 μ to at least 2.8 m (Figure [5.4](#ch5fig:g334d_params)). We cannot be sure of the upper bound of the apparent binding EC50 given how little quenching we were able to achieve even with 1 m TNP-ATP. Unfortunately, we were unable to resolve macroscopic currents from W311\*,G334D-GFP+SUR1 in excised patches despite seeing fluorescence in unroofed membranes. Thus, we were unable to measure nucleotide inhibition of this construct ourselves. In electrophysiological experiments on KATP channels containing the G334D mutation, other studies have found that currents are insensitive to inhibition by ATP even up to 10.64,109 In the framework of our MWC model, the only explanation for a dramatic decrease in both nucleotide binding and inhibition is a decrease in , the microscopic binding affinity. However, as we were unable to measure TNP-ATP inhibition ourselves, we were unable to determine whether the G334D substitution affected transduction in addition to this binding effect.

## Channel gating

### C166S alters inhibition without affecting binding

Residue C166 of Kir6.2 is located at the cytosolic end of the second transmembrane domain (Figure [5.5](#ch5fig:c166s_loc),),20,72,77,202 and has been suggested to play a role in regulating the intrinsic gating of the channel.62,123,167,203–205 Mutations at this residue lead to dramatically increased unliganded in single-channel experiments,123,167,204 and a reduction in sensitivity to nucleotide inhibition at both single-channel and the macroscopic level.68,123,167,204,205 In addition, two substitutions at this residue (F and Y) have been found to cause severe neonatal diabetes.203 Electrophysiological measurements alone are not sufficient to distinguish between the reduction in sensitivity to nucleotide inhibition being caused by the increase in intrinsic alone, or whether there is an additional disregulation of transduction.

We measured TNP-ATP binding to W311\*,C166S-GFP+SUR1 in unroofed membranes to determine the how mutations at C166 reduce sensitivity to nucleotide inhibition (Figure [[ch5fig:c166s\_unroofed]](#ch5fig:c166s_unroofed)). We observed no real change in binding of TNP-ATP to the channel, with an EC50 of 44 μ–74 μ. If the C166S mutation solely increases the of the channel, we would expect an increase in the apparent EC50 of nucleotide binding due to the preference of nucleotides for the closed state of the channel. This finding therefore suggests a role for C166 in the transduction of nucleotide binding to the channel pore.

To investigate this further, we excised patches expressing W311\*,C166S-GFP+SUR1 and measured current inhibition and fluorescence quenching by TNP-ATP simultaneously (Figure [5.9](#ch5fig:c166s_traces)). We found that the apprent affinity for nucleotide binding was indistinguishable from that for W311\*-GFP+SUR1, and similar to our observations in unroofed membranes (Figure [5.10](#ch5fig:c166s_popfits_2), EC50 of 26 μ–218 μ). Consistent with the literature, we did observe a large reduction in the apparent sensitivity of W311\*,C166S-GFP+SUR1 currents to inhibition by TNP-ATP (Figure [5.11](#ch5fig:c166s_popfits_3), IC50 of at least 155 μ). Intuitively, a change in nucleotide-dependent channel gating which is not accompanied by a change in nucleotide binding must be due (at least in part) to a change in the transduction of nucleotide binding to channel gating.

Fitting our data to the MWC-type model described previously (Figure [5.14](#ch5fig:c166s_mwc_fit_1), [5.15](#ch5fig:c166s_mwc_fit_2)), we found that in addition to the effects of the C166S mutation on the intrinsic open probability of KATP, there is a striking shift in (Figure [5.16](#ch5fig:c166s_mwc_params_1)). This shift to a value much closer to unity indicates that binding of TNP-ATP to W311\*,C166S-GFP+SUR1 favours the closed state far less than binding of TNP-ATP to W311\*-GFP+SUR1. Equivalently, binding of TNP-ATP to the mutant channel is less able to induce closure of the pore. Thus, even at millimolar concentrations of TNP-ATP when all of the Kir6.2 subunits are predicted to be bound by nucleotide, the mutant KATP channels are still able to open.

Notably, the MWC fit to the current inhibition data has wide 95 % posterior probability intervals (Figure [5.15](#ch5fig:c166s_mwc_fit_2)). Unfortunately, we were not able to use higher concentrations of TNP-ATP due to its purification as a TEA+ salt. High m concentrations of TEA+ inhibit KATP channels, and we determined that for W311\*-GFP+SUR1 and W311\*,C166S-GFP+SUR1 concentrations of above 1 m TEA+ began to inhibit currents to an extent that would interfere with our measurements (Figure [5.17](#ch5fig:tea_trace), [5.18](#ch5fig:tea_drc)). The precise ratio of TEA+ to TNP-ATP in our solutions is unknown, but is assumed to be between 1:1 and 3:1. Any additional inhibition observed at TNP-ATP concentrations greater than 1 m for W311\*,C166S-GFP+SUR1 will therefore be (at least in part) due to the presence of TEA+. However, we do see that even at concentrations of 10 m ATP, W311\*,C166S-GFP+SUR1 is not fully inhibited (Figure [5.15](#ch5fig:c166s_mwc_fit_2), open circle).

Curiously, despite the wide posterior probability intervals for the MWC fit to the observed current inhibiton data in Figure [5.15](#ch5fig:c166s_mwc_fit_2), the probability distributions for the underlying parameter values for W311\*,C166S-GFP+SUR1 are not much wider than those observed for W311\*-GFP+SUR1 (Figure [5.16](#ch5fig:c166s_mwc_params_1)). Thus, the variability of current inhibition observed for 1 m TNP-ATP is not due to increased uncertainty in our MWC parameter estimates. Instead, the variability may reflect that the C166S substitution alters the nucleotide regulation of the KATP channel such that small changes in the energetics of the underlying gating mechanism result in large changes in the observed current. This may help to explain the differences in inhibition of KATP channels with substitutions at C166 by high nucleotide concentrations observed across multiple electrophysiological studies.169,173,205,206

### Mutations at E179 alter both inhibition and binding

Residue E179 of Kir6.2 is located in the C-terminal region of Kir6.2 between the inhibitory nucleotide binding site and the proposed PIP2 binding site. In one early predicted structures of Kir6.2, it was theorised that E179 would form part of the nucleotide binding pocket directly, potentially coordinating the adenine ring of ATP directly through hydrogen bonding.110 In another, it was hypothesised to form part of the PIP2 binding pocket instead.127 Electrophysiological experiments painted a confusing picture of the residues role.110 Mutation to an amino acid capable of forming hydrogen bonds (Q) resulted in no change in the IC50 for nucleotide inhibition (although a separate study found that Q increased the IC50),101 while only one of two amino acids incapable of forming hydrogen bonds tested (M and L) resulted in an increased IC50. In addition, mutation of the residue to asparagine (which is not capable of forming hydrogen bonds) not only dramatically increased the nucleotide IC50, but increased the intrinsic open probability of the channel.110

The cryo-EM structures of KATP in complex with ATP revealed that bound ATP adopted a radically different conformation to that proposed in early models, and the E179 side chain actually lies over 8 Å away from bound ATP20,72,77,202 (FIgure [5.19](#ch5fig:e179_loc). Unfortunately, no structure has been resolved in the presence of PIP2 to date. However, coarse-grained molecular dynamics simulations using the cryo-EM structures as a starting point indicate that E179 may form part of the PIP2 binding pocket.70 In addition, mutation to E179K results in reduced inhibition of the channel by the sequestering agent neomycin - potentially due to an increased affinity of the mutated residue for PIP2.70

To attempt to resolve the precise role of E179 in nucleotide binding and inhibition, we first determined how ATP and TNP-ATP inhibiton of KATP channels was affected by mutation of E179 to A or K (Figure [5.20](#ch5fig:e179_atp_popfits), [5.21](#ch5fig:e179_tnpatp_popfits_1). For E179A-GFP+SUR1 and E179K-GFP+SUR1, we observed an increase in IC50 for both ATP and TNP-ATP inhibition (Figure [5.23](#ch5fig:e179_ec50_fits)). ATP inhibition did not seem to be influenced by the identity of the replacement amino acid (49 μ–145 μ and 43 μ–138 μ respectively), while TNP-ATP inhibition was less reduced by mutation to an A than a K (6.5 μ–21 μ and 16 μ–87 μ respectively). Introducing the mutations into the ANAP-labelled construct did not affect the relative changes in inhibition by either nucleotide, with ATP inhibition occurring at similar IC50s for A and K (162 μ–562 μ and 191 μ–479 μ respectively) and with A increasing the IC50 for TNP-ATP less than K (14 μ–44 μ and 42 μ–224 μ respectively). Measurements of TNP-ATP binding mirrored our observations for current inhibition by TNP-ATP, with mutation to both A and K resulting in an increased apparant binding EC50, with A having less of an effect than K (166 μ–417 μ and 347 μ–813 μ respectively). Fitting the combined data to the MWC-type model, we found that both mutations resulted in a decreased estimate, with no apparent change in . In addition, mutation to a K led to a value closer to unity than for E or the wild-type A (Figure [[ch5fig:e179\_2]](#ch5fig:e179_2)).

### Mutations at K39 alter both inhibition and binding

Residue K39 of Kir6.2 is located in the N-terminal region of Kir6.2, and is positioned between the inhibitory nucleotide binding site and the proposed PIP2 binding site (Figure [5.26](#ch5fig:k39_loc)). In previous studies, the mutation K39A has shown a small reduction in open probability,82 and a small reduction in sensitivity to nucleotide inhibition.61,82 These effects are somewhat contradictory, as mutations which reduce open probability tend also to increase sensitivity to nucleotide inhibition. In each of the cryo-EM structures of KATP, the K39 side chain appears to coordinate the bound ATP molecule.20,72,77,202 These structures are presumed to represent the closed state of the channel, and no PIP2 bound structure of the channel has yet been solved. However, molecular dynamics simulations using the ATP-bound structure as a starting point and introducing PIP2 suggest that the K39 residue is able to contact both ligands (in press). This suggests a potential role for K39 in the binding sites of both ATP and PIP2, which may explain the contradictory findings of open probability and nucleotide inhibition changes when the residue is mutated.

We tested three mutations at K39 (K39A, K39E, K39R) to examine the effects of changing the side chain characteristics on nucleotide binding and inhibition. Mutation to E (opposite charge) or R (same charge) results in an increase in IC50 for ATP inhibition for both WT and W311\* backgrounds (Figure [5.27](#ch5fig:k39_atp_popfits), [5.30](#ch5fig:k39_ec50_fits)). We did not see an increase in the IC50 for ATP inhibition when K39 was mutated to A (neutral) in either background (Figure [5.27](#ch5fig:k39_atp_popfits), [5.30](#ch5fig:k39_ec50_fits)). Inhibition by TNP-ATP displayed a different profile depending on the mutant residue (Figure [5.28](#ch5fig:k39_tnpatp_popfits_1)). In both WT and W311\* backgrounds, inhibition by TNP-ATP exhibited higher IC50 values for K39A and K39E than we observed for K39R, which was not really distinguishable from K39 ([5.30](#ch5fig:k39_ec50_fits)). Our docked conformation for TNP-ATP suggests that the TNP-moiety of the nucleotide may result in extra contacts with K39 compared to ATP, which may be the cause of the different sensitivity to inhibition between the two nucleotides when this residue is mutated. Measurements of TNP-ATP binding showed increases in the EC50 estimates for each of the three mutations (Figure [5.29](#ch5fig:k39_tnpatp_popfits_2), [5.30](#ch5fig:k39_ec50_fits)).

Fits of the combined data to the MWC model gave parameter estimates for that decreased from K>R>E>A (Figure [[ch5fig:k39\_2]](#ch5fig:k39_2)). In addition, mutation to an E or an A resulted in values closer to unity. Interpretation of these parameters for the R and A mutations is frustrated by the differences in inhibition between TNP-ATP and ATP; we cannot be sure that these differences in binding and inhibition are due to the identity of the nucleotide rather than the identity of the residue. However, the K39E mutation displayed similar inhibition for both TNP-ATP and ATP. The increase in our estimate for when K39 is mutated to an A or an E, but not for R, may indicate a positive charge at the sidechain of this residue being important for transduction of nucleotide binding to the channel pore.

## Discussion

Fitting a concerted MWC model to the combined datasets obtained by measuring TNP-ATP binding to Kir6.2 in combination with current inhibition allows us to distinguish between mutations which affect nucleotide binding, ligand-independent channel gating, and transduction of nucleotide binding to channel gating. This is best demonstrated by our results for W311\*,C166S-GFP+SUR1, which we propose not only increases the unliganded of the KATP channel as described many times previously (illustrated in this experiment by the increase in from the MWC fit), but also reduces the ability of TNP-ATP to induce channel closure ( approaches unity). Substitutions of C166 must therefore alter the structure of the channel such that in addition to the unliganded open state being more energetically favourable than in wild-type channels, nucleotides are no longer able to stabilise the closed state to the same extent as in wild type channels.

We can quantify this difference by calculating the energy contribution of nucleotide binding to the closed state of the two constructs at saturating concentrations of TNP-ATP, given by the formula where is the gas constant and is the absolute temperature (assumed to be 296 K). The free energy TNP-ATP binding contributes to the closed state of W311\*-GFP+SUR1 is 23.0 kJ/–63.4 kJ/, while the free energy TNP-ATP binding contributes to the closed state of W311\*,C166S-GFP+SUR1 is only 20.4 kJ/–−3.05 kJ/. However, as the transduction of binding is a combination of both the channel and the ligand, it is possible that TNP-ATP stabilises the closed state of the channel to a different extent than ATP.

Interpretation of our findings for substitutions at E179 and K39 of Kir6.2 are not as straightforward. Mutations at these residues lead to a complex mixture of changes to both the microscopic binding affinity for TNP-ATP () and the transduction of nucleotide binding (). Given that E179 is predicted to form part of the PIP2 binding site,70,127 we might expect mutations at this location to alter the of channels in excised patches due to changes in the PIP2 binding affinity.110 found that mutation to asparagine increased the of KATP channels in excised patches, while70 observed that mutation to a lysine caused a reduction in the IC50 for neomycin inhibition of the channel. Here, mutation to alanine or lysine did not result in a change in our estimate for , which we would expect to see if there was a change in the of the channel resulting from altered OIP2 affinity. Instead, we observed changes in our estimates for , the microscopic binding affinity for TNP-ATP, and , the transduction of nucleotide binding to channel gating.

We believe there are two possible ways to interpret these findings. The first is to accept the shift in at face value - a decrease in the apparent TNP-ATP binding affinity would suggest a role for residue E179 in forming the nucleotide binding pocket, and this function is abrogated by our mutations. Despite the distance of the residue from the bound ATP, there could be interactions between E179 and the sidechains of residues which do form the pocket (e.g. R54), such that mutation of E179 leads to alterations in the binding pocket which reduce nucleotide binding affinity and therefore our estimate of . The additional effect on caused by mutating the residue to K suggests a dysregulation of the transduction of nucleotide binding to the channel pore, making nucleotides less selective for the closed state.

The second interpretation is possible due to the simplification of the role of PIP2 in our MWC model as discussed in chapter [[ch:4]](#ch:4). Briefly, if there is an additional allosteric interaction between nucleotide and PIP2 binding to Kir6.2 which is separate to the channels open/closed state, then changes in may reflect alterations in the affinity for PIP2 binding in addition to or instead of alterations in the affinity for nucleotide binding. Thus, the decrease in upon mutation of E179 may reflect an increase in PIP2 affinity and demonstrate the presence of local allostery between nucleotide and lipid.

Distinguishing between these two interpretations is difficult given our current evidence, and essentially depends on the weight you place on the assumptions of each, but should be possible with one or two further experiments. Firstly, an increase in PIP2 affinity should lead to an increase in channel open probability on excision (barring an effect on the relative preference of PIP2 for the open state). Our inability to accurately determine the open probability of the macroscopic experiments described so far could be supplemented by single channel analysis of the mutants to test this directly. In addition, we could measure the affinity of PIP2 directly in macroscopic patches. Finally, to definitively test the existence of local allostery between the nucleotide and PIP2 binding sites, we could introduce PIP2 binding mutants into the C166S background. C166S channels exhibit almost no nucleotide-dependent gating; i.e. nucleotide binding is uncoupled from gating of the channel pore. Thus, any changes observed in nucleotide binding in the C166S background when PIP2 affinity is changed would have to be due to a local allosteric interaction which does not involve the pore.

K39 is a residue which may be involved in both nucleotide and PIP2 binding to Kir6.2, which may explain how mutation to an alanine at this residue appears to reduce both and sensitivity to nucleotide inhibiton.61,82 We aimed to elucidate whether K39 was directly involved in nucleotide binding by making three different substitutions with different sidechain charges - alanine, lysine, or glutamic acid - and directly measuring TNP-ATP binding. Unfortunately, we observed differences in the relative changes in inhibition by ATP and TNP-ATP in the three different constructs, such that the substitution which had the largest effect on ATP inhibition (K39R) had the smallest effect on TNP-ATP inhibition. On examination of the cryo-EM structure of KATP, K39 is in close proximity to the ribose ring of bound ATP (Figure [5.33](#ch5fig:k39_clash_atp)). The computational docking of TNP-ATP predicts that the TNP moiety will therefore be in close proximity of K39 (Figure [5.34](#ch5fig:k39_clash_tnpatp)). Given this proximity, it is possible that there are extra contacts made between TNP-ATP and the K39 residue, which may go some way towards explaining the incresed sensitivity of inhibition of KATP to TNP-ATP. It may also explain why we do not observe consistent relative changes in inhibition by ATP and TNP-ATP for different mutations of the residue.

However, given that substitutions of K39 decrease the sensitivity of KATP channels to ATP inhibition, and decrease both the sensitivity to TNP-ATP inhibition and the apparent TNP-ATP binding affinity, we can still conclude that K39 is involved in nucleotide binding to Kir6.2. For TNP-ATP, this involvement manifests mostly as a reduction in the microscopic binding affinity (), although substitution with a glutamic acid which has an oppositely-charged side chain also reduces the transduction of TNP-ATP binding to channel closure (). Despite the previously observed reduction in open probability for the K39A mutation,61,82 we did not observe any large changes in our estimates for for any of the mutations tested (Figure [5.32](#ch5fig:mwc_k39_2)). There is some evidence to suggest that the identity of the amino acid at position 39 affects , with K39A exhibiting an estimated range of 0.005–0.15 compared to 0.017–0.51 for K39E (Figure [5.32](#ch5fig:mwc_k39_2)); but given the uncertainty inherent in our data due to patch-to-patch differences in PIP2 concentrations, run-down over the course of experiments, and having to normalise our data, we cannot confidently suggest there is an effect.

# [ch:6]Regulation of Kir6.2 by SUR1

## Introduction

The SUR1 subunit exerts a number of different regulatory effects on the KATP channel. Firstly, it dramatically enhances trafficking of Kir6.2 to the cell membrane by masking the endoplasmic retention motif in Kir6.2 (RKR). Without coexpression with SUR1, Kir6.2 is confined to the endoplasmic reticulum. Truncating the C-terminal by deleting the last 26 (Kir6.2-DC26) or 36 (Kir6.2-DC36) amino acids,30 mutation of the RKR motif to AAA,207 or addition of a C-terminal GFP tag208 are sufficient to allow expression of Kir6.2 at the membrane alone without the presence of SUR1. Comparing the function of these modified Kir6.2 subunits alone to the function of octameric KATP channels makes it possible to discern the multifaceted roles of SUR1. Crucially, these C-terminal modifications do not appear to alter KATP function when they are coexpressed with SUR130,204,208 and the cryo-EM structure solved for C-terminally GFP labelled Kir6.2202 was highly similar to those solved without the GFP label.21,73

Coexpression of SUR1 has two effects on KATP channel function. Firstly, SUR1 increases the of the channel.30,71,208 Expressing the TMD0 region of SUR1 (residues 1 - 195) alone is sufficient to recapitulate the increase in observed when full-length SUR1 is coexpressed71,209. When TMD0 is coexpressed with Kir6.2, there is additionally a decrease in the sensitivity of Kir6.2 to nucleotide inhibition - allosterically, an increase in would result in a decrease in apparent ATP affinity due to the reduction in stability of the closed state. However, when full length SUR1 is coexpressed with Kir6.2, there is a marked increase in sensitivity to ATP inhibition.30,71,204,208 This increase in sensitivity has been suggested to be not due to the L0 linker, the other domain of SUR1 postulated to make contacts with Kir6.2. Expression of TMD0-L0 (residues 1 - 232) with Kir6.2 increases the to nearly saturating, and reduces ATP inhibition even further.209 Increasing the fraction of L0 (up to residue number 256 or 288) attenuates this increase in , but there is not the dramatic increase in ATP sensitivity observed from expression of full-length SUR1, implicating a role for the core region of SUR1 in regulating nuclelotide binding and inhibition.24

In this chapter, we aim to clarify the role of SUR1 in regulating the inhibitory effect of nucleotides on KATP channel function.

## Intrinsic effects of SUR1

### SUR1 dramatically alters nucleotide inhibition, but only subtly effects nucleotide binding

Expressing WT-GFP alone without SUR1 results in smaller, noisier currents than when coexpressed with SUR1. Currents are less sensitive to ATP and TNP-ATP by an order of magnitude (Figure [6.1](#ch6fig:nosur_atp), [6.2](#ch6fig:nosur_tnpatp). Our surface expression assay suggested that while WT-GFP was able to reach the membrane in the absence of SUR1, W311\*-GFP was not, and when we excised patches from cells expressing W311\*-GFP alone, we were not able to resolve any currents (Figure [3.17](#ch3fig:surface_expression_2)). We were still able to resolved fluorescence in unroofed membranes expressing W311\*-GFP alone, and so we measured binding of TNP-ATP to W311\*-GFP alone in unroofed membranes. We observed very minimal differences in the EC50 for binding. However, given that we did not observe currents under these experimental conditions, we cannot determine the functional state of these channels and so this finding may not be representative for KATP channels physiologically.

Given that we were able to observe currents in the absence of SUR1, we confirmed that when SUR1 was cotransfected with our constructs we were measuring currents and fluorescence from correctly assembled KATP channels. Firstly, we used tolbutamide to inhibit excised patches from cells expressing either WT-GFP alone, WT-GFP+SUR1 or W311\*-GFP+SUR1. Tolbutamide inhibition occurs at two sites on the KATP channel; a high affinity site on SUR1 and a low affinity site on Kir6.2.210,211 Inhibition occurring at these two sites can be well separated, with the high affinity site saturating at 100 μ tolbutamide at 50 % fractional inhibition. Tolbutamide inhibition of Kir6.2 expressed alone does not display inhibition until concentrations of over 100 μ. When we expressed WT-GFP alone, we saw no inhibition of currents by 100 μ, whereas when we expressed WT-GFP+SUR1 or W311\*-GFP+SUR1, we observed roughly a 50 % fractional inhibition of current as expected for proper associated of Kir6.2 and SUR1.

While tolbutamide inhibition provides evidence for SUR1 association with our Kir6.2 constructs in excised patches, we cannot perform the same experiment to test for association in unroofed membranes. Instead, we labelled the C-terminus of SUR1 with the fluorophore mOrange (SUR1-mO), and measured FRET between the GFP attached to WT-GFP or W311\*-GFP and the mOrange attached to SUR1. The cryo-EM structures suggest a distance between the C-termini of Kir6.2 and SUR1 of roughly 60 Å, while the GFP-mOrange FRET pair has a theoretical R0 of 54 Å. We would therefore expect to see FRET between GFP and mOrange if our Kir6.2 and SUR1 contructs are coassembling.

To measure FRET, we used an approach outlined by212 and151 whereby FRET is measured as an increase in the emission of the acceptor fluorophore (mOrange) on excitation of the donor fluorophore (GFP) (Figure [[sur\_assays]](#sur_assays)). We can directly excite both GFP and mOrange with 490 nm light. When WT-GFP is expressed alone we can measure the resulting emission spectrum as the donor fluorescence alone, and when SUR1-mO is expressed alone we can measure the resulting emission spectrum as the acceptor fluorescence alone (Figure [6.6](#ch6fig:gfp_mo_spectra_1)). In addition, we can excite mOrange directly with 565 nm light and avoid excitation of GFP. However, in the experimental condition with both WT/W311\*-GFP and SUR1-mO, excitation with 490 nm light results in an emission spectrum which is a mixture of three components: the emission from the donor fluorophore GFP, emission from the acceptor fluorophore mOrange due to direct excitation, and emission from the acceptor fluorophore mOrange due to energy transfer from the donor GFP (Figure [6.7](#ch6fig:wt_gfp_mo_spectra_1), [6.9](#ch6fig:w311_gfp_mo_spectra_1)). To extract the component we are interested in (emission due to energy transfer), we can first remove the contribution of the donor fluorescence to the emission spectrum by subtracting an idealised WT/W311\*-GFP spectrum averaged from multiple cells expressing it alone (Figure [6.8](#ch6fig:wt_gfp_mo_spectra_2), [6.10](#ch6fig:w311_gfp_mo_spectra_2)). We can then take the ratio of the fluorescence intensity of the acceptor mOrange after excitation by 490 nm light (which contains both direct excitation of the acceptor and FRET) to the fluorescence intensity of the acceptor mOrange after excitation by 565 nm light (which contains only direct excitation of the acceptor). Any increase in this ratio over that observed in cells expressing the acceptor alone is evidence for FRET between the fluorophores.

We captured spectra from the membranes of whole cells to improve our signal-to-noise ratio. We observed an increase in the emission ratio when we coexpressed WT-GFP and SUR1-mO, consistent with the two subunits being in close proximity (Figure [[gfp\_ofp\_contrasts\_1]](#gfp_ofp_contrasts_1). While we still observed an increase in the emission ratio when we coexpressed W311\*-GFP and SUR1-mO, there is less strong evidence in this case; i.e. the posterior probability distribution for the emission ratio is not as different to one. This could result from three underlying mechanisms. Firstly, W311\*-GFP and SUR1-mO may assemble differently to WT-GFP and SUR1-mO and the difference in FRET reflects a different distance between the C-termini of the two subunits. We consider this improbable. Secondly, we may be measuring fluorescence from a heterogenous population of channels; some with W311\*-GFP and SUR1-mO coassembled, and some with W311\*-GFP alone. This mixture would result in an intermediate value of FRET when measured from the total population. Finally, this method of calculating FRET is sensitive to the ratio of donor and acceptor fluorophores. If the acceptor fluorophore is present in excess (which we believe to be true as we transfect a molar excess of SUR1 constructs in all our experiments), a decrease in the amount of donor fluorophore present will decrease the proportion of acceptor fluorescence which comes from FRET, and will reduce the measure emission ratio. As our surface expression experiments suggest that W311\*-GFP is present at the membrane in lower quantities than WT-GFP (Figure [3.18](#ch3fig:surface_expression_3)), this is our preferred hypothesis. However, as we cannot discount the possibility that there may be some W311\*-GFP present alone in unroofed membranes even when we coexpress SUR1, our interpretations of binding data acquired from unroofed membranes must be more cautious.

### Presence of SUR1-TMD0 alone does not dramatically alter nucleotide binding

We sought to clarify the role of the TMD0 and L0 regions of SUR1 in binding to the inhibitory nucleotide binding site of Kir6.2. We used two SUR1 truncation constructs; TMD0 consisting of the N-terminal 1-195 residues of SUR1, and TMD0-L0 consisting of the N-terminal 1-232 residues of SUR1. Firstly, we established whether these constructs were capable of supporting trafficking and expression at the cell membrane as previously reported [[babenko\_sur\_2003-1, chan\_n-terminal\_2003-1]](#Xa9fe899d868eba85555b86f51e9db157a3d5067). In our luminesence based cell-surface expression assay, we found that TMD0 and TMD0-L0 increased the expression of WT-GFP approximately 3-fold over the expression of WT-GFP alone (Figure [6.12](#ch6fig:tmd0s_surface_expression_1), [6.14](#ch6fig:tmd0s_surface_expression_2)). This level of expression is somewhat less than observed for full-length SUR1. However, when we coexpressed either TMD0 or TMD0-L0 with W311\*-GFP, we found less evidence to suggest an increase of surface expression when compared to expression of W311\*-GFP alone (Figure [6.12](#ch6fig:tmd0s_surface_expression_1), [[ch6fig:tmd0s\_surface\_expression\_3]](#ch6fig:tmd0s_surface_expression_3)); i.e., our posterior probability distributions for the fold increase in expression overlapped 1. Indeed, when we attempted to excise patches coexpressing W311\*-GFP and either TMD0 or TMD0-L0, we were unable to detect channel currents, while we were able to measure nA currents from WT-GFP coexpressed with TMD0 or TMD0-L0.

Despite being unable to detect channel currents, as with W311\*-GFP expressed alone, we were able to detect ANAP and GFP fluorescence from unroofed membrane patches coexpressing W311\*-GFP with either TMD0 or TMD0-L0. To determine whether this fluorescence was emitted from W311\*-GFP correctly coassembled with the truncated SUR1 constructs, we measured the emission ratio of TMD0-L0 labelled at the C-terminus with mOrange (TMD0-L0-mO) as described previously. We coexpressed either WT-GFP or W311\*-GFP with TMD0-L0-mO and measured the emission ratio of directly excited mOrange to indirectly excited mOrange in whole cells (Figure [6.15](#ch6fig:gfp_ofp_contrasts_2)). For WT-GFP+TMD0-L0-mO, we observed an increase in emission ratio over TMD0-L0-mO of a similar magnitude for the increase observed for WT-GFP+SUR1-mO (Figure [6.11](#ch6fig:gfp_ofp_contrasts_1)). This is consistent with TMD0-L0-mO coassembling with WT-GFP in unroofed membanes, as an increase in emission ratio requires the two fluorophores to be in close proximity. However, coexpression of W311\*-GFP and TMD0-L0-mO resulted in an emission ratio with a posterior probability distribution which overlaps 1; i.e. there is little evidence to suggest there is an increase in the emission ratio. Again, this may be due to decreased expression of W311\*-GFP compared to WT-GFP, but we cannot discount the possibility that we are measuring from a heterogenous population of W311\*-GFP channels and W311\*-GFP+TMD0-L0 channels.

We coexpressed either TMD0 or TMD0-L0 in combination with W311\*-GFP and measured TNP-ATP binding in unroofed membranes (Figure [6.16](#ch6fig:tmd0s_unroofed_1)). We found that the data were not particularly distinguishable from that collected from TNP-ATP binding to W311\*-GFP expressed alone; although this may be due to measuring from a mixed population of channels. To confirm that we could replicate the functional effects of TMD0-L0 on Kir6.2, we measured currents frome excised patches expressing WT-GFP+TMD0-L0 and measured inhibition by ATP (Figure [6.17](#ch6fig:tmd0_atp_trace)). Similarly to209 and,71 we observed a decrease in sensitivity to nucleotide inhibition in channels formed from WT-GFP and TMD0-L0 to channels formed from WT-GFP alone (Figure [6.18](#ch6fig:tmd0_atp_1)).

## SUR1 and nucleotide regulation

### Mutations at SUR-K205 alter nucleotide binding and inhibition

Residue K205 of SUR1 is located in the L0 region which links TMD0 and TMD1. While expression of Kir6.2 and TMD0-L0 have shown that the region is important in modulating the of KATP channels,71,74,124 it does not confer the high sensitivity to ATP inhibition seen in Kir6.2+SUR1 channels. It has therefore been suggested that the elements of SUR1 which contribute to the higher sensitivity of KATP channels to ATP inhibition lie outside of this region.74,188 However, the cryo-EM structures of KATP suggest a close proximity between L0 and the ATP binding pocket21,73,202 and mutations in this region reduce the sensitivity of KATP to nucleotide inhibition.188,213,214 Mutation of K205 to A213 or E215 have resulted in marked reduction of KATP channel sensitivity to nucleotide inhibition.

We excised patches expressing W311\*-GFP+SUR1-K205A or W311\*-GFP+SUR1-K205E and measured current inhibition and fluorescence quenching by TNP-ATP simultaneously. We found that both substitutions resulted in an increased IC50 for TNP-ATP inhibition and an increased EC50 for TNP-ATP binding, with K205E exhibiting a more pronounced effect than K205A. Fitting the data to our MWC model gave parameter estimates for which were reduced when compared to wild-type SUR1; with the neutral mutation K205A not affecting quite as much as the charge reversal mutation K205E. In addition, both mutations led to similar increases in . Thus, the reduced sensitivity to nucleotide inhibition is due to a combination of reduced apparent binding affinity in addition to reduced stabilisation of the closed state of the channel by nucleotides.

## Discussion

Expression of W311\*-GFP in the absence of SUR1 reduces the apparent nucleotide binding affinity by only a small amount in unroofed membranes; approxiamtely 2-fold. This is in contrast to the dramatic 10-fold reduction in sensitivity to inhibition by ATP observed when WT-GFP is expressed in the absence of SUR1. We also found that coexpression of W311\*-GFP with TMD0 or TMD0-L0 did not result in an increase in apparent nucleotide binding affinity, although this finding is caveated by the possible mixture of correctly complexed mini-KATP channels and W311\*-GFP subunits alone in the unroofed membranes.

Despite these somewhat inconclusive findings, we saw a clear effect of mutating residue K205 in the L0 loop of SUR1. Similar to the findings of,213 we observed a marked reduction in sensitivity to TNP-ATP inhibition when the residue was mutated to an alanine, and a further reduction when it was mutated to glutamic acid. Fitting the data to the MWC model reveals that the reduction in sensitivity is due to both a reduction in the microscopic binding affinity for TNP-ATP, and a decrease in the transduction of nucleotide binding to channel closure.

The structure of K205 resolved by213 suggested that the long, positively charged side chain directly coordinates the b- and g-phosphates of bound ATP.213 Our results are consistent with the hypothesis that mutation to an alanine, thus removing the positive charge, directly disrupts nucleotide binding. We also observe a further reduction in the microscopic binding affinity upon substitution by glutamic acid, which has a long and negatively charged side chain. Again, this is consistent with the idea that K205 directly coordinates the negatively charged phosphates of ATP, and explains the reduction in sensitivity to ATP inhibition observed by215 when they made the same mutation.

Our MWC fits also suggest that mutation of K205 reduces the ability of nucleotides to close the channel. As we calculated for the C166S mutation in Kir6.2, we can express this reduction in terms of the free energy contributed to the conformational change of closure. For the SUR1-K205A construct, the free energy is 5.6 kJ/–18.3 kJ/,and for the SUR1-K205E construct, the free energy is 3.3 kJ/–13.9 kJ/, much reduced from that of wild-type SUR1 which is 23.0 kJ/–63.4 kJ/. This suggests that the positive charge K205 contributes to the inhibitory binding site is important for transduction of nucleotide binding to channel closure.

This finding does not explain why TMD0-L0 expression alone is not enough to restore full-length SUR1 like nucleotide inhibition. Coexpression of TMD0-L0 with WT-GFP exhibits decreased sensitivity to nucleotide inhibition when compared to full length SUR1, as seen in previous studies.71,74,124 Our findings are consistent with the hypothesis that the elements of the L0 linker which enhance the binding affinity of nucleotides for Kir6.2 and which increase the intrinsic open probability of the KATP channel are separate; and also suggest that the linker plays an active role in transducing binding to closure.

# [ch:7]Discussion

## Summary of findings

David Colquhoun wrote the following in 1998: "Distinguishing between effects on binding and effects on conformation change is arguably the fundamental problem of modern molecular studies of receptors. It is not an easy distinction to make, but unless it can be solved, the interpretation of structure‐function studies is quite likely to be nonsense".201 A few months earlier, the first crystal structure of an ion channel (the K+ channel from *Streptomyces lividans*, KcsA) was published by a team from Roderick MacKinnon’s group.216 While Colquhoun acknowledged that such structures would resolve many questions about the location of ligand binding sites, he emphasised that knowledge of structure does not preclude the search for mechanisms and dynamics: "Structures are static but receptors are not".201

It took nearly two decades after solving KcsA for structures of the KATP channel to be resolved through cryo-EM.20–23 Impressively, many of the predictions made from detailed electrophysiological experiments and molecular modelling about the inhibitory nucleotide binding site of Kir6.2 were validated by the structures.61,64,82,104,107,110,127,172,217 As the structures were solved in complex with ATP and in the absence of lipids, we can assume that they resemble the physiological closed state of the KATP channel. The difficulty of obtaining open states of ion channels means that relating the captured structures to the function of KATP is not trivial, and many open questions remain.24

In this thesis, I have aimed to show four things:

* We can directly measure nucleotide binding to Kir6.2 by site-specifically inserting ANAP at position W311 and measuring its quenching by TNP-ATP.
* Measuring binding in combination with KATP channel current inhibition allows us to confirm that an MWC model is able to describe KATP inhibition by nucleotides.
* Effects on nucleotide binding and effects on conformational change can be well distinguished by fitting combined binding and inhibition data to an MWC model.
* SUR1 directly contributes to nucleotide binding to Kir6.2.

In doing so, I have built directly on the work of numerous studies using a variety of electrophysiological approaches to provide answers to the above questions. Where this work differs, and - I believe - adds value, is in two aspects of the approach. Firstly, while the use of fluorescence to study ligand binding to ion channels is far from novel, the site-specific nature of ANAP incorporation is a development which crucially allows for the separation of nucleotide binding to Kir6.2 from binding to the NBDs of SUR1. In addition, measuring the quenching of ANAP fluorescence rather than an increase in ligand fluorescence allows us to directly translate our observations into the bound fraction of Kir6.2 subunits, without having to assume that at saturation each subunit is bound.

Secondly, formulating the MWC model in a Bayesian fashion allows us to determine whether the parameters in the models we fit are practically identifiable. In other words, are the parameters we estimate uniquely constrained by the data we can collect? The problem of parameter identifiability has been discussed in much greater detail elsewhere.218–221 Briefly, even seemingly simple binding or inhibition curves may often be fit arbitrarily well by many combinations of parameter values. This is further complicated by the inescapable noise present in experimental data.

Here, we address this issue in two ways. Firstly, collecting simultaneous binding and inhibition data allows us to constrain the parameters of a more complex model than would be possible based on either alone. Secondly, the Bayesian MCMC fitting procedure allows us to visualise the full posterior probability distribution of parameter estimates for fits to a given model. It is then trivial to determine whether parameter estimates are unique by visually inspecting the cross-correlation plots of paired parameters,219 which for all the constructs tested yield well bounded ellipses (Figure [[apxfig:inhibition\_crosscorr]](#apxfig:inhibition_crosscorr)).

Applying this approach to a series of residue substitutions in Kir6.2 shows that we are able to discriminate not only between effects on binding and effects on conformational change, but that we can further distinguish between effects on intrinsic and ligand-dependent regulation of conformational change. We have demonstrated this for a number of different substitutions at residues on Kir6.2; C166, E179 and K39. In addition, while our attempts to measure TNP-ATP binding to Kir6.2 in the absence of SUR1 (or in the presence of truncated forms of SUR1) were limited in their success, we were able to identify K205 as a residue in L0 which directly contributes to binding of nucleotides to Kir6.2, and plays a role in the transduction of binding to channel closure.

## Inhibition in the context of KATP regulation

Nucleotide inhibition of the KATP channel does not occur in isolation in the physiological context, and must be considered in the context of regulation by nucleotide stimulation at SUR1 and PIP2 (Figure [[ch7fig:regulation\_diagram]](#ch7fig:regulation_diagram), duplicated from Figure [[ch1fig:regulation\_diagram]](#ch1fig:regulation_diagram) for ease of reference).

How does inhibitory nucleotide binding to Kir6.2 interplay with the stimulatory nucleotide binding to the NBDs of SUR1? In parallel work published in,222 we established a similar experimental paradigm to measure MgTNP-ADP binding to NBS2 of SUR1 in unroofed membranes. While we were unable to measure current activation and nucleotide binding simultaneously, we collected data separately for the two processes. Here we refit that data in combination with the inhibition data presented in Figure [3.44](#ch3fig:pcf_1)to an MWC model which comprises both inhibition at Kir6.2 by TNP-ATP and activation at SUR1 by MgTNP-ADP with a shared open probability (Figure [[ch7fig:activation\_fits]](#ch7fig:activation_fits)). Comparison of the binding association constants for TNP-nucleotides at Kir6.2 and NBS2 shows that MgTNP-ADP binds more readily to NBS2 than TNP-ATP binds to Kir6.2 (Figure [7.2](#ch7fig:activation_params_1)). In contrast, the transduction of binding is far stronger for TNP-ATP bound to Kir6.2 than for MgTNP-ADP bound to NBS2. In terms of free energy, binding to Kir6.2 contributes 32.7 kJ/–68.0 kJ/ to the closed state of the channel(slightly higher than the 23.0 kJ/–63.4 kJ/ estimated from fitting the inhibition data alone), whereas binding to NBS2 contributes 0.6 kJ/–33.9 kJ/ to the open state of the channel.

Assuming that the excitatory and inhibitory processes are independent, inhibition would be expected to dominate under conditions at which all the nucleotide binding sites of KATP are occupied. This is consistent with published measurements of wild-type KATP in the presence of Mg2+.223 The ability of MgADP to increase KATP currents in the presence of ATP99 and the bell-shaped MgADP concentration response curve for KATP85,223 can then be explained by the higher binding affinity of NBS2 resulting in an increase in current at low nucleotide concentrations, followed by inhibition at higher concentrations due to stronger transduction from nucleotides binding to Kir6.2.

Of course, this interpretation relies on data which has been obtained from different constructs and under different conditions. Ideally, we would explore this further by carrying out patch-clamp fluorometry experiments under conditions where all three nucleotide binding sites simultaneously affect channel gating (in the presence of Mg2+). Our initial attempts to do so were limited by the rapid rate of rundown of KATP currents in the presence of divalent ions, which made it difficult to collect useable data with simultaneous current and fluorescence recordings. Introducing mutations which slow the rate of rundown may be one method to ameliorate this problem and synthesise a more complete model of KATP function.

How does inhibitory nucleotide binding to Kir6.2 interplay with PIP2 regulation of the KATP channel? As descibed in Chapter [[ch:1-intro]](#ch:1-intro), directly measuring or varying the PIP2 concentration in the membrane is challenging, and in the experiments presented here we have tried as far as possible to keep PIP2 constant. Our simplifying assumption which assumes PIP2 acts solely on the open probability of the channel and does not vary significantly in our recordings seem sufficient to explain the variety of effects we see from the mutations studied in Kir6.2 and SUR1.

However, it remains an open question is whether PIP2 binding to Kir6.2 only affects the channel through increasing the open probability (Figure [[ch7fig:regulation\_diagram]](#ch7fig:regulation_diagram), ) or whether there is a mechanism which directly couples the PIP2 binding site to the inhibitory nucleotide binding site (Figure [[ch7fig:regulation\_diagram]](#ch7fig:regulation_diagram), ). Our experiments with substitutions at E179 on Kir6.2, predicted to be in the PIP2 binding pocket, do not rule out the existence of a direct coupling. However, the observed reduction in the binding affinity for TNP-ATP is only circumstantial evidence as it may also be explained by the two substitutions examined (E179A and E179K) altering the nucleotide binding pocket instead. Experiments to directly test for the existence of direct coupling would need to involve manipulation and measurement of PIP2 levels, which as described in Chapter [[ch:1-intro]](#ch:1-intro) is difficult to achieve.

# [ch:8-appendix]Appendices

1. Da Silva Xavier, G. The Cells of the Islets of Langerhans. *Journal of Clinical Medicine* **7**, (2018).

2. Ashcroft, F. M. & Rorsman, P. K(ATP) channels and islet hormone secretion: New insights and controversies. *Nat Rev Endocrinol* **9**, 660–9 (2013).

3. Ashcroft, F. M., Harrison, D. E. & Ashcroft, S. J. H. Glucose induces closure of single potassium channels in isolated rat pancreatic beta -cells. *Nature* **312**, 446–448 (1984).

4. Rorsman, P. & Trube, G. Glucose dependent K+-channels in pancreaticbeta-cells are regulated by intracellular ATP. *Pflügers Archiv* **405**, 305–309 (1985).

5. Nichols, C. G. K ATP channels as molecular sensors of cellular metabolism. *Nature* **440**, 470–476 (2006).

6. Inagaki, N. *et al.* A Family of Sulfonylurea Receptors Determines the Pharmacological Properties of ATP-Sensitive K+ Channels. *Neuron* **16**, 1011–1017 (1996).

7. Yamada, M. *et al.* Sulphonylurea receptor 2B and Kir6.1 form a sulphonylurea-sensitive but ATP-insensitive K+ channel. *The Journal of Physiology* **499**, 715–720 (1997).

8. Shyng, S.-L. & Nichols, C. G. Octameric Stoichiometry of the KATP Channel Complex. *Journal of General Physiology* **110**, 655–664 (1997).

9. Clement, J. P. *et al.* Association and Stoichiometry of KATP Channel Subunits. *Neuron* **18**, 827–838 (1997).

10. Inagaki, N. *et al.* Reconstitution of IKATP: An Inward Rectifier Subunit Plus the Sulfonylurea Receptor. *Science* **270**, 1166–1170 (1995).

11. Hille, B. *Ion Channels of Excitable Membranes*. (Sinauer Associates, 2001).

12. Zheng, J. & Trudeau, M. C. *Handbook of Ion Channels*. (Taylor; Francis, 2015).

13. Baukrowitz, T. *et al.* PIP2 and PIP as Determinants for ATP Inhibition of KATP Channels. *Science* **282**, 1141–1144 (1998).

14. Shyng, S.-L. & Nichols, C. G. Membrane Phospholipid Control of Nucleotide Sensitivity of KATP Channels. *Science* **282**, 1138–1141 (1998).

15. Enkvetchakul, D., Jeliazkova, I. & Nichols, C. G. Direct Modulation of Kir Channel Gating by Membrane Phosphatidylinositol 4,5-Bisphosphate\*♦. *Journal of Biological Chemistry* **280**, 35785–35788 (2005).

16. Aguilar-Bryan, L. *et al.* Cloning of the beta cell high-affinity sulfonylurea receptor: A regulator of insulin secretion. *Science* **268**, 423–426 (1995).

17. Tusnády, G. E., Bakos, É., Váradi, A. & Sarkadi, B. Membrane topology distinguishes a subfamily of the ATP-binding cassette (ABC) transporters. *FEBS Letters* **402**, 1–3 (1997).

18. Vergani, P., Lockless, S. W., Nairn, A. C. & Gadsby, D. C. CFTR channel opening by ATP-driven tight dimerization of its nucleotide-binding domains. *Nature* **433**, 876–880 (2005).

19. Beek, J. ter, Guskov, A. & Slotboom, D. J. Structural diversity of ABC transporters. *Journal of General Physiology* **143**, 419–435 (2014).

20. Lee, K. P. K., Chen, J. & MacKinnon, R. Molecular structure of human KATP in complex with ATP and ADP. *Elife* **6**, (2017).

21. Martin, G. M., Kandasamy, B., DiMaio, F., Yoshioka, C. & Shyng, S.-L. Anti-diabetic drug binding site in a mammalian KATP channel revealed by Cryo-EM. *eLife* **6**, e31054 (2017).

22. Li, N. *et al.* Structure of a Pancreatic ATP-Sensitive Potassium Channel. *Cell* **168**, 101–110.e10 (2017).

23. Martin, G. M. *et al.* Mechanism of pharmacochaperoning in a mammalian KATP channel revealed by cryo-EM. *eLife* **8**, e46417 (2019).

24. Puljung, M. C. Cryo-electron microscopy structures and progress toward a dynamic understanding of KATP channels. *Journal of General Physiology* **150**, 653–669 (2018).

25. Matsuo, M., Kioka, N., Amachi, T. & Ueda, K. ATP Binding Properties of the Nucleotide-binding Folds of SUR1 \*. *Journal of Biological Chemistry* **274**, 37479–37482 (1999).

26. Zingman, L. V. *et al.* Signaling in Channel/Enzyme Multimers: ATPase Transitions in SUR Module Gate ATP-Sensitive K+ Conductance. *Neuron* **31**, 233–245 (2001).

27. Wet, H. de *et al.* Studies of the ATPase activity of the ABC protein SUR1. *FEBS J* **274**, 3532–44 (2007).

28. Zerangue, N., Schwappach, B., Jan, Y. N. & Jan, L. Y. A New ER Trafficking Signal Regulates the Subunit Stoichiometry of Plasma Membrane KATP Channels. *Neuron* **22**, 537–548 (1999).

29. Martin, G. M., Chen, P.-C., Devaraneni, P. & Shyng, S.-L. Pharmacological rescue of trafficking-impaired ATP-sensitive potassium channels. *Frontiers in Physiology* **4**, (2013).

30. Tucker, S. J., Gribble, F. M., Zhao, C., Trapp, S. & Ashcroft, F. M. Truncation of Kir6.2 produces ATP-sensitive K + channels in the absence of the sulphonylurea receptor. *Nature* **387**, 179–183 (1997).

31. John, S. A., Monck, J. R., Weiss, J. N. & Ribalet, B. The sulphonylurea receptor SUR1 regulates ATP-sensitive mouse Kir6.2 K+ channels linked to the green fluorescent protein in human embryonic kidney cells (HEK 293). *The Journal of Physiology* **510**, 333–345 (1998).

32. Conti, L. R., Radeke, C. M. & Vandenberg, C. A. Membrane Targeting of ATP-sensitive Potassium Channel: EFFECTS OF GLYCOSYLATION ON SURFACE EXPRESSION\*. *Journal of Biological Chemistry* **277**, 25416–25422 (2002).

33. Sharma, N. *et al.* The C Terminus of SUR1 Is Required for Trafficking of KATP Channels \*. *Journal of Biological Chemistry* **274**, 20628–20632 (1999).

34. Vedovato, N., Rorsman, O., Hennis, K., Ashcroft, F. M. & Proks, P. Role of the C-terminus of SUR in the differential regulation of beta-cell and cardiac KATP channels by MgADP and metabolism. *The Journal of Physiology* **596**, 6205–6217 (2018).

35. Giblin, J. P., Quinn, K. & Tinker, A. The cytoplasmic C-terminus of the sulfonylurea receptor is important for KATP channel function but is not key for complex assembly or trafficking. *European Journal of Biochemistry* **269**, 5303–5313 (2002).

36. Schwappach, B., Zerangue, N., Jan, Y. N. & Jan, L. Y. Molecular Basis for KATP Assembly: Transmembrane Interactions Mediate Association of a K+ Channel with an ABC Transporter. *Neuron* **26**, 155–167 (2000).

37. Sakura, H., Trapp, S., Liss, B. & Ashcroft, F. M. Altered functional properties of KATP channel conferred by a novel splice variant of SUR1. *The Journal of Physiology* **521**, 337–350 (1999).

38. Bonifacino, J. S. & Weissman, A. M. Ubiquitin and the Control of Protein Fate in the Secretory and Endocytic Pathways. *Annual Review of Cell and Developmental Biology* **14**, 19–57 (1998).

39. Yan, F.-F., Lin, C.-W., Cartier, E. A. & Shyng, S.-L. Role of ubiquitin-proteasome degradation pathway in biogenesis efficiency of beta-cell ATP-sensitive potassium channels. *American Journal of Physiology-Cell Physiology* **289**, C1351–C1359 (2005).

40. Yan, F. *et al.* Sulfonylureas Correct Trafficking Defects of ATP-sensitive Potassium Channels Caused by Mutations in the Sulfonylurea Receptor\*. *Journal of Biological Chemistry* **279**, 11096–11105 (2004).

41. Yan, F.-F., Casey, J. & Shyng, S.-L. Sulfonylureas Correct Trafficking Defects of Disease-causing ATP-sensitive Potassium Channels by Binding to the Channel Complex\*. *Journal of Biological Chemistry* **281**, 33403–33413 (2006).

42. Yan, F. F. *et al.* Congenital hyperinsulinism associated ABCC8 mutations that cause defective trafficking of ATP-sensitive K+ channels: Identification and rescue. *Diabetes* **56**, 2339–48 (2007).

43. Yan, F.-F. *et al.* Congenital Hyperinsulinism–Associated ABCC8 Mutations That Cause Defective Trafficking of ATP-Sensitive K+ Channels: Identification and Rescue. *Diabetes* **56**, 2339–2348 (2007).

44. Martin, G. M. *et al.* Pharmacological Correction of Trafficking Defects in ATP-sensitive Potassium Channels Caused by Sulfonylurea Receptor 1 Mutations\* \*This work was supported by National Institutes of Health Grants R01DK066485 (to S.-L. S.), F31DK105800 (to G. M. M.), R01DK098517 (to D. D. D. L.), And R37DK056268 (to C. A. S.) And a grant from the Goldsmith Foundation (to D. D. D. L. And C. A. S.). The authors declare that they have no conflicts of interest with the contents of this article. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health. *Journal of Biological Chemistry* **291**, 21971–21983 (2016).

45. Yang, K., Fang, K., Fromondi, L. & Chan, K. W. Low temperature completely rescues the function of two misfolded KATP channel disease-mutants. *FEBS Letters* **579**, 4113–4118 (2005).

46. Alekseev, A. E., Brady, P. A. & Terzic, A. Ligand-insensitive State of Cardiac ATP-sensitive K+ Channels : Basis for Channel Opening. *Journal of General Physiology* **111**, 381–394 (1998).

47. Babenko, A. P., Gonzalez, G. & Bryan, J. Two Regions of Sulfonylurea Receptor Specify the Spontaneous Bursting and ATP Inhibition of KATP Channel Isoforms\*. *Journal of Biological Chemistry* **274**, 11587–11592 (1999).

48. Li, L., Geng, X. & Drain, P. Open State Destabilization by Atp Occupancy Is Mechanism Speeding Burst Exit Underlying KATP Channel Inhibition by Atp. *Journal of General Physiology* **119**, 105–116 (2002).

49. Proks, P. & Ashcroft, F. M. Modeling KATP channel gating and its regulation. *Progress in Biophysics and Molecular Biology* **99**, 7–19 (2009).

50. Enkvetchakul, D., Loussouarn, G., Makhina, E., Shyng, S. L. & Nichols, C. G. The Kinetic and Physical Basis of KATP Channel Gating: Toward a Unified Molecular Understanding. *Biophysical Journal* **78**, 2334–2348 (2000).

51. Benz, I., Haverkampf, K. & Kohlhardt, M. Characterization of the Driving Force as a Modulator of Gating in Cardiac ATP-sensitive K+ Channels — Evidence for Specific Elementary Properties. *The Journal of Membrane Biology* **165**, 45–52 (1998).

52. Alekseev, A. E., Kennedy, M. E., Navarro, B. & Terzic, A. Burst Kinetics of Co-expressed Kir6.2/SUR1 Clones: Comparison of Recombinant with Native ATP-sensitive K+ Channel Behavior. *The Journal of Membrane Biology* **159**, 161–168 (1997).

53. Trapp, S., Proks, P., Tucker, S. J. & Ashcroft, F. M. Molecular Analysis of ATP-sensitive K Channel Gating and Implications for Channel Inhibition by ATP. *Journal of General Physiology* **112**, 333–349 (1998).

54. Sakmann, B. & Trube, G. Voltage-dependent inactivation of inward-rectifying single-channel currents in the guinea-pig heart cell membrane. *The Journal of Physiology* **347**, 659–683 (1984).

55. Zilberter, Yu., Burnashev, N., Papin, A., Portnov, V. & Khodorov, B. Gating kinetics of ATP-sensitive single potassium channels in myocardial cells depends on electromotive force. *Pflügers Archiv* **411**, 584–589 (1988).

56. Chapman, M. L., Blanke, M. L., Krovetz, H. S. & VanDongen, A. M. J. Allosteric effects of external K+ ions mediated by the aspartate of the GYGD signature sequence in the Kv2.1 K+ channel. *Pflügers Archiv* **451**, 776–792 (2006).

57. Kuang, Q., Purhonen, P. & Hebert, H. Structure of potassium channels. *Cellular and Molecular Life Sciences* **72**, 3677–3693 (2015).

58. Heginbotham, L., Lu, Z., Abramson, T. & MacKinnon, R. Mutations in the K+ channel signature sequence. *Biophysical Journal* **66**, 1061–1067 (1994).

59. Proks, P., Capener, C. E., Jones, P. & Ashcroft, F. M. Mutations within the P-Loop of Kir6.2 Modulate the Intraburst Kinetics of the Atp-Sensitive Potassium Channel. *Journal of General Physiology* **118**, 341–353 (2001).

60. Shyng, S.-L., Ferrigni, T. & Nichols, C. G. Control of Rectification and Gating of Cloned KATP Channels by the Kir6.2 Subunit. *Journal of General Physiology* **110**, 141–153 (1997).

61. Tucker, S. J. *et al.* Molecular determinants of KATP channel inhibition by ATP. *The EMBO Journal* **17**, 3290–3296 (1998).

62. Loussouarn, G., Makhina, E. N., Rose, T. & Nichols, C. G. Structure and Dynamics of the Pore of Inwardly Rectifying KATP Channels\*. *Journal of Biological Chemistry* **275**, 1137–1144 (2000).

63. Tammaro, P. *et al.* A Kir6.2 mutation causing severe functional effects in vitro produces neonatal diabetes without the expected neurological complications. *Diabetologia* **51**, 802–810 (2008).

64. Drain, P., Li, L. & Wang, J. KATP channel inhibition by ATP requires distinct functional domains of the cytoplasmic C terminus of the pore-forming subunit. *Proceedings of the National Academy of Sciences* **95**, 13953–13958 (1998).

65. Proks, P. *et al.* Molecular basis of Kir6.2 mutations associated with neonatal diabetes or neonatal diabetes plus neurological features. *Proceedings of the National Academy of Sciences* **101**, 17539–17544 (2004).

66. Koster, J. C., Kurata, H. T., Enkvetchakul, D. & Nichols, C. G. DEND Mutation in Kir6.2 (KCNJ11) Reveals a Flexible N-Terminal Region Critical for ATP-Sensing of the KATP Channel. *Biophysical Journal* **95**, 4689–4697 (2008).

67. Männikkö, R. *et al.* Interaction between mutations in the slide helix of Kir6.2 associated with neonatal diabetes and neurological symptoms. *Human Molecular Genetics* **19**, 963–972 (2010).

68. Li, J. B. W. *et al.* Decomposition of Slide Helix Contributions to ATP-dependent Inhibition of Kir6.2 Channels\*. *Journal of Biological Chemistry* **288**, 23038–23049 (2013).

69. Cooper, P. E., McClenaghan, C., Chen, X., Stary-Weinzinger, A. & Nichols, C. G. Conserved functional consequences of disease-associated mutations in the slide helix of Kir6.1 and Kir6.2 subunits of the ATP-sensitive potassium channel. *Journal of Biological Chemistry* **292**, 17387–17398 (2017).

70. Pipatpolkai, T., Corey, R. A., Proks, P., Ashcroft, F. M. & Stansfeld, P. J. Evaluating inositol phospholipid interactions with inward rectifier potassium channels and characterising their role in disease. *Communications Chemistry* **3**, 1–10 (2020).

71. Chan, K. W., Zhang, H. & Logothetis, D. E. N-terminal transmembrane domain of the SUR controls trafficking and gating of Kir6 channel subunits. *The EMBO Journal* **22**, 3833–3843 (2003).

72. Martin, G. M., Kandasamy, B., DiMaio, F., Yoshioka, C. & Shyng, S. L. Anti-diabetic drug binding site in a mammalian KATP channel revealed by Cryo-EM. *Elife* **6**, (2017).

73. Lee, K. P. K., Chen, J. & MacKinnon, R. Molecular structure of human KATP in complex with ATP and ADP. *eLife* **6**, e32481 (2017).

74. Babenko, A. P. & Bryan, J. Sur domains that associate with and gate KATP pores define a novel gatekeeper. *J Biol Chem* **278**, 41577–80 (2003).

75. Chan, K. W., Zhang, H. & Logothetis, D. E. N-terminal transmembrane domain of the SUR controls trafficking and gating of Kir6 channel subunits. *EMBO J* **22**, 3833–43 (2003).

76. Fang, K., Csanady, L. & Chan, K. W. The N-terminal transmembrane domain (TMD0) and a cytosolic linker (L0) of sulphonylurea receptor define the unique intrinsic gating of KATP channels. *J Physiol* **576**, 379–89 (2006).

77. Puljung, M. C. Cryo-electron microscopy structures and progress toward a dynamic understanding of KATP channels. *J Gen Physiol* **150**, 653–669 (2018).

78. Koster, J. C., Sha, Q., Shyng, S.-L. & Nichols, C. G. ATP inhibition of KATP channels: Control of nucleotide sensitivity by the N-terminal domain of the Kir6.2 subunit. *The Journal of Physiology* **515**, 19–30 (1999).

79. Babenko, A. P., Gonzalez, G. & Bryan, J. The N-Terminus of KIR6.2 Limits Spontaneous Bursting and Modulates the ATP-Inhibition of KATPChannels. *Biochemical and Biophysical Research Communications* **255**, 231–238 (1999).

80. Reimann, F., Tucker, S. J., Proks, P. & Ashcroft, F. M. Involvement of the N-terminus of Kir6.2 in coupling to the sulphonylurea receptor. *The Journal of Physiology* **518**, 325–336 (1999).

81. Babenko, A. P. & Bryan, J. SUR-dependent Modulation of KATP Channels by an N-terminal KIR6.2 Peptide: DEFINING INTERSUBUNIT GATING INTERACTIONS\*. *Journal of Biological Chemistry* **277**, 43997–44004 (2002).

82. Cukras, C. A., Jeliazkova, I. & Nichols, C. G. The Role of NH2-terminal Positive Charges in the Activity of Inward Rectifier KATP Channels. *Journal of General Physiology* **120**, 437–446 (2002).

83. Craig, T. J. *et al.* An In-Frame Deletion in Kir6.2 (KCNJ11) Causing Neonatal Diabetes Reveals a Site of Interaction between Kir6.2 and SUR1. *The Journal of Clinical Endocrinology & Metabolism* **94**, 2551–2557 (2009).

84. Nichols, C. G. *et al.* Adenosine Diphosphate as an Intracellular Regulator of Insulin Secretion. *Science* **272**, 1785–1787 (1996).

85. Vedovato, N., Ashcroft, F. M. & Puljung, M. C. The Nucleotide-Binding Sites of SUR1: A Mechanistic Model. *Biophysical Journal* **109**, 2452–2460 (2015).

86. Fan, Z. & Makielski, J. C. Anionic Phospholipids Activate ATP-sensitive Potassium Channels\*. *Journal of Biological Chemistry* **272**, 5388–5395 (1997).

87. Hibino, H. *et al.* Inwardly Rectifying Potassium Channels: Their Structure, Function, and Physiological Roles. *Physiological Reviews* **90**, 291–366 (2010).

88. Proks, P. *et al.* Running out of time: The decline of channel activity and nucleotide activation in adenosine triphosphate-sensitive K-channels. *Philosophical Transactions of the Royal Society B: Biological Sciences* **371**, 20150426 (2016).

89. Gribble, F. M., Tucker, S. J. & Ashcroft, F. M. The Interaction of nucleotides with the tolbutamide block of cloned atp-sensitive k+ channel currents expressed in xenopus oocytes: A reinterpretation. *The Journal of Physiology* **504**, 35–45 (1997).

90. Ashcroft, F. M. New Uses for Old Drugs: Neonatal Diabetes and Sulphonylureas. *Cell Metabolism* **11**, 179–181 (2010).

91. Boehr, D. D., Nussinov, R. & Wright, P. E. The role of dynamic conformational ensembles in biomolecular recognition. *Nature Chemical Biology* **5**, 789–796 (2009).

92. Mittermaier, A. & Kay, L. E. New Tools Provide New Insights in NMR Studies of Protein Dynamics. *Science* **312**, 224–228 (2006).

93. Ribalet, B., John, S. A. & Weiss, J. N. Regulation of Cloned Atp–Sensitive K Channels by Phosphorylation, Mgadp, and Phosphatidylinositol Bisphosphate (Pip2): A Study of Channel Rundown and Reactivation. *Journal of General Physiology* **116**, 391–410 (2000).

94. Monod, J., Wyman, J. & Changeux, J.-P. On the nature of allosteric transitions: A plausible model. *Journal of Molecular Biology* **12**, 88–118 (1965).

95. Rubin, M. M. & Changeux, J.-P. On the nature of allosteric transitions: Implications of non-exclusive ligand binding. *Journal of Molecular Biology* **21**, 265–274 (1966).

96. Garcia, H. G., Kondev, J., Orme, N., Theriot, J. A. & Phillips, R. Chapter Two - Thermodynamics of Biological Processes. in *Methods in Enzymology* (eds. Johnson, M. L., Holt, J. M. & Ackers, G. K.) vol. 492 27–59 (Academic Press, 2011).

97. Marzen, S., Garcia, H. G. & Phillips, R. Statistical Mechanics of Monod–Wyman–Changeux (MWC) Models. *Journal of Molecular Biology* **425**, 1433–1460 (2013).

98. Nichols, C. G. *et al.* Adenosine Diphosphate as an Intracellular Regulator of Insulin Secretion. *Science* **272**, 1785–1787 (1996).

99. Gribble, F. M., Tucker, S. J., Haug, T. & Ashcroft, F. M. MgATP activates the beta cell KATP channel by interaction with its SUR1 subunit. *Proceedings of the National Academy of Sciences* **95**, 7185–7190 (1998).

100. Proks, P., Wet, H. de & Ashcroft, F. M. Activation of the KATP channel by Mg-nucleotide interaction with SUR1. *Journal of General Physiology* **136**, 389–405 (2010).

101. Proks, P., Gribble, F. M., Adhikari, R., Tucker, S. J. & Ashcroft, F. M. Involvement of the N-terminus of Kir6.2 in the inhibition of the KATP channel by ATP. *The Journal of Physiology* **514**, 19–25 (1999).

102. John, S. A., Weiss, J. N., Xie, L.-H. & Ribalet, B. Molecular Mechanism for ATP-Dependent Closure of the K+ Channel Kir6.2. *The Journal of Physiology* **552**, 23–34 (2003).

103. Ribalet, B., John, S. A. & Weiss, J. N. Molecular Basis for Kir6.2 Channel Inhibition by Adenine Nucleotides. *Biophysical Journal* **84**, 266–276 (2003).

104. Trapp, S., Haider, S., Jones, P., Sansom, M. S. P. & Ashcroft, F. M. Identification of residues contributing to the ATP binding site of Kir6.2. *The EMBO Journal* **22**, 2903–2912 (2003).

105. Shimomura, K. *et al.* Mutations at the Same Residue (R50) of Kir6.2 (KCNJ11) That Cause Neonatal Diabetes Produce Different Functional Effects. *Diabetes* **55**, 1705–1712 (2006).

106. Koster, J. C., Remedi, M. S., Dao, C. & Nichols, C. G. ATP and Sulfonylurea Sensitivity of Mutant ATP-Sensitive K+ Channels in Neonatal Diabetes: Implications for Pharmacogenomic Therapy. *Diabetes* **54**, 2645–2654 (2005).

107. Li, L., Wang, J. & Drain, P. The I182 region of k(ir)6.2 is closely associated with ligand binding in K(ATP) channel inhibition by ATP. *Biophys J* **79**, 841–52 (2000).

108. Tammaro, P., Girard, C., Molnes, J., Njolstad, P. R. & Ashcroft, F. M. Kir6.2 mutations causing neonatal diabetes provide new insights into Kir6.2-SUR1 interactions. *EMBO J* **24**, 2318–30 (2005).

109. Masia, R. *et al.* An ATP-Binding Mutation (G334D) in KCNJ11 Is Associated With a Sulfonylurea-Insensitive Form of Developmental Delay, Epilepsy, and Neonatal Diabetes. *Diabetes* **56**, 328–336 (2007).

110. Antcliff, J. F., Haider, S., Proks, P., Sansom, M. S. & Ashcroft, F. M. Functional analysis of a structural model of the ATP-binding site of the KATP channel Kir6.2 subunit. *The EMBO Journal* **24**, 229–239 (2005).

111. Tammaro, P., Proks, P. & Ashcroft, F. M. Functional effects of naturally occurring KCNJ11 mutations causing neonatal diabetes on cloned cardiac KATP channels. *The Journal of Physiology* **571**, 3–14 (2006).

112. Shyng, S.-L., Cukras, C. A., Harwood, J. & Nichols, C. G. Structural Determinants of Pip2 Regulation of Inward Rectifier KATP Channels. *Journal of General Physiology* **116**, 599–608 (2000).

113. Gribble, F. M., Tucker, S. J. & Ashcroft, F. M. The essential role of the Walker A motifs of SUR1 in K-ATP channel activation by Mg-ADP and diazoxide. *EMBO J* **16**, 1145–52 (1997).

114. Rees, D. C., Johnson, E. & Lewinson, O. ABC transporters: The power to change. *Nature Reviews Molecular Cell Biology* **10**, 218–227 (2009).

115. Csanády, L., Vergani, P. & Gadsby, D. C. Strict coupling between CFTR’s catalytic cycle and gating of its Cl− ion pore revealed by distributions of open channel burst durations. *Proceedings of the National Academy of Sciences* **107**, 1241–1246 (2010).

116. Wet, H. de *et al.* Studies of the ATPase activity of the ABC protein SUR1. *The FEBS Journal* **274**, 3532–3544 (2007).

117. Zingman, L. V. *et al.* Signaling in Channel/Enzyme Multimers: ATPase Transitions in SUR Module Gate ATP-Sensitive K+ Conductance. *Neuron* **31**, 233–245 (2001).

118. Choi, K.-H., Tantama, M. & Licht, S. Testing for Violations of Microscopic Reversibility in ATP-Sensitive Potassium Channel Gating. *The Journal of Physical Chemistry B* **112**, 10314–10321 (2008).

119. Rothberg, B. S. & Magleby, K. L. Testing for detailed balance (microscopic reversibility in ion channel gating. *Biophysical Journal* **80**, 3025–3026 (2001).

120. Rohács, T. *et al.* Specificity of activation by phosphoinositides determines lipid regulation of Kir channels. *Proceedings of the National Academy of Sciences* **100**, 745–750 (2003).

121. Schulze, D., Krauter, T., Fritzenschaft, H., Soom, M. & Baukrowitz, T. Phosphatidylinositol 4,5-Bisphosphate (PIP2) Modulation of ATP and pH Sensitivity in Kir Channels: A TALE OF AN ACTIVE AND A SILENT PIP2 SITE IN THE N TERMINUS\*. *Journal of Biological Chemistry* **278**, 10500–10505 (2003).

122. Fan, Z. & Makielski, J. C. Phosphoinositides Decrease Atp Sensitivity of the Cardiac Atp-Sensitive K+ Channel : A Molecular Probe for the Mechanism of Atp-Sensitive Inhibition. *Journal of General Physiology* **114**, 251–270 (1999).

123. Enkvetchakul, D., Loussouarn, G., Makhina, E., Shyng, S. L. & Nichols, C. G. The kinetic and physical basis of K(ATP) channel gating: Toward a unified molecular understanding. *Biophys J* **78**, 2334–48 (2000).

124. Pratt, E. B., Tewson, P., Bruederle, C. E., Skach, W. R. & Shyng, S.-L. N-terminal transmembrane domain of SUR1 controls gating of Kir6.2 by modulating channel sensitivity to PIP2. *Journal of General Physiology* **137**, 299–314 (2011).

125. Wang, C., Wang, K., Wang, W., Cui, Y. & Fan, Z. Compromised ATP binding as a mechanism of phosphoinositide modulation of ATP-sensitive K+ channels. *FEBS Letters* **532**, 177–182 (2002).

126. MacGregor, G. G. *et al.* Nucleotides and phospholipids compete for binding to the C terminus of KATP channels. *Proceedings of the National Academy of Sciences* **99**, 2726–2731 (2002).

127. Haider, S., Tarasov, A. I., Craig, T. J., Sansom, M. S. & Ashcroft, F. M. Identification of the PIP2-binding site on Kir6.2 by molecular modelling and functional analysis. *The EMBO Journal* **26**, 3749–3759 (2007).

128. Hansen, S. B., Tao, X. & MacKinnon, R. Structural basis of PIP 2 activation of the classical inward rectifier K + channel Kir2.2. *Nature* **477**, 495–498 (2011).

129. Enkvetchakul, D. & Nichols, C. G. Gating Mechanism of KATP Channels : Function Fits Form. *Journal of General Physiology* **122**, 471–480 (2003).

130. Cha, A. & Bezanilla, F. Characterizing Voltage-Dependent Conformational Changes in the ShakerK+ Channel with Fluorescence. *Neuron* **19**, 1127–1140 (1997).

131. Marmé, N., Knemeyer, J.-P., Sauer, M. & Wolfrum, J. Inter- and Intramolecular Fluorescence Quenching of Organic Dyes by Tryptophan. *Bioconjugate Chemistry* **14**, 1133–1139 (2003).

132. Lakowicz, J. R. *Principles of fluorescence spectroscopy*. (Springer, 2006).

133. Mansoor, S. E., DeWitt, M. A. & Farrens, D. L. Distance Mapping in Proteins Using Fluorescence Spectroscopy: The Tryptophan-Induced Quenching (TrIQ) Method. *Biochemistry* **49**, 9722–9731 (2010).

134. Mansoor, S. E., Mchaourab, H. S. & Farrens, D. L. Determination of Protein Secondary Structure and Solvent Accessibility Using Site-Directed Fluorescence Labeling. Studies of T4 Lysozyme Using the Fluorescent Probe Monobromobimane. *Biochemistry* **38**, 16383–16393 (1999).

135. Priest, M. F., Lee, E. E. L. & Bezanilla, F. *The trajectory of discrete gating charges in a voltage-gated potassium channel*. <http://biorxiv.org/lookup/doi/10.1101/2020.04.23.058818> (2020) doi:[10.1101/2020.04.23.058818](https://doi.org/10.1101/2020.04.23.058818).

136. Mannuzzu, L. M., Moronne, M. M. & Isacoff, E. Y. Direct Physical Measure of Conformational Rearrangement Underlying Potassium Channel Gating. *Science* **271**, 213–216 (1996).

137. Cowgill, J. & Chanda, B. The contribution of voltage clamp fluorometry to the understanding of channel and transporter mechanisms. *Journal of General Physiology* **151**, 1163–1172 (2019).

138. Braun, N., Sheikh, Z. P. & Pless, S. A. The current chemical biology tool box for studying ion channels. *The Journal of Physiology* **598**, 4455–4471 (2020).

139. Siegel, M. S. & Isacoff, E. Y. A Genetically Encoded Optical Probe of Membrane Voltage. *Neuron* **19**, 735–741 (1997).

140. Giraldez, T., Hughes, T. E. & Sigworth, F. J. Generation of Functional Fluorescent BK Channels by Random Insertion of GFP Variants. *The Journal of General Physiology* **126**, 429–438 (2005).

141. Miranda, P. *et al.* State-dependent FRET reports calcium- and voltage-dependent gating-ring motions in BK channels. *Proceedings of the National Academy of Sciences* **110**, 5217–5222 (2013).

142. Pless, S. A. & Ahern, C. A. Unnatural Amino Acids as Probes of Ligand-Receptor Interactions and Their Conformational Consequences. *Annual Review of Pharmacology and Toxicology* **53**, 211–229 (2013).

143. Puljung, M. C. ANAP: A versatile, fluorescent probe of ion channel gating and regulation. in *Methods in Enzymology* (Academic Press, 2021). doi:[10.1016/bs.mie.2021.01.048](https://doi.org/10.1016/bs.mie.2021.01.048).

144. Lee, H. S., Guo, J., Lemke, E. A., Dimla, R. D. & Schultz, P. G. Genetic Incorporation of a Small, Environmentally Sensitive, Fluorescent Probe into Proteins in Saccharomyces cerevisiae. *Journal of the American Chemical Society* **131**, 12921–12923 (2009).

145. Chatterjee, A., Guo, J., Lee, H. S. & Schultz, P. G. A genetically encoded fluorescent probe in mammalian cells. *J Am Chem Soc* **135**, 12540–3 (2013).

146. Kalstrup, T. & Blunck, R. Dynamics of internal pore opening in KV channels probed by a fluorescent unnatural amino acid. *Proceedings of the National Academy of Sciences* **110**, 8272–8277 (2013).

147. Kusch, J. *et al.* Interdependence of receptor activation and ligand binding in HCN2 pacemaker channels. *Neuron* **67**, 75–85 (2010).

148. Kusch, J. *et al.* How subunits cooperate in cAMP-induced activation of homotetrameric HCN2 channels. *Nature Chemical Biology* **8**, 162–169 (2012).

149. Thon, S., Schulz, E., Kusch, J. & Benndorf, K. Conformational Flip of Nonactivated HCN2 Channel Subunits Evoked by Cyclic Nucleotides. *Biophysical Journal* **109**, 2268–2276 (2015).

150. Biskup, C. *et al.* Relating ligand binding to activation gating in CNGA2 channels. *Nature* **446**, 440–443 (2007).

151. Selvin, P. R. [13] Fluorescence resonance energy transfer. in *Methods in Enzymology* vol. 246 300–334 (Academic Press, 1995).

152. Zagotta, W. N., Gordon, M. T., Senning, E. N., Munari, M. A. & Gordon, S. E. Measuring distances between TRPV1 and the plasma membrane using a noncanonical amino acid and transition metal ion FRET. *J Gen Physiol* **147**, 201–16 (2016).

153. Stryer, L. Fluorescence Energy Transfer as a Spectroscopic Ruler. *Annual Review of Biochemistry* **47**, 819–846 (1978).

154. McElreath, R. *Statistical Rethinking: A Bayesian Course with Examples in R and STAN (draft)*. (2020).

155. Tanabe, K. *et al.* Direct Photoaffinity Labeling of the Kir6.2 Subunit of the ATP-sensitive K+ Channel by 8-Azido-ATP\*. *Journal of Biological Chemistry* **274**, 3931–3933 (1999).

156. Vanoye, C. G. *et al.* The carboxyl termini of K(ATP) channels bind nucleotides. *J Biol Chem* **277**, 23260–70 (2002).

157. Wang, X.-L., Lu, T., Cao, S., Shah, V. H. & Lee, H.-C. Inhibition of ATP binding to the carboxyl terminus of Kir6.2 by epoxyeicosatrienoic acids. *Biochimica et Biophysica Acta (BBA) - Molecular and Cell Biology of Lipids* **1761**, 1041–1049 (2006).

158. Chin, J. W. Expanding and reprogramming the genetic code. *Nature* **550**, 53–60 (2017).

159. Cridge, A. G., Crowe-McAuliffe, C., Mathew, S. F. & Tate, W. P. Eukaryotic translational termination efficiency is influenced by the 3′ nucleotides within the ribosomal mRNA channel. *Nucleic Acids Research* **46**, 1927–1944 (2018).

160. Zhang, R. S. *et al.* A Conserved Residue Cluster That Governs Kinetics of ATP-dependent Gating of Kir6.2 Potassium Channels\*. *Journal of Biological Chemistry* **290**, 15450–15461 (2015).

161. Devaraneni, P. K., Martin, G. M., Olson, E. M., Zhou, Q. & Shyng, S.-L. Structurally Distinct Ligands Rescue Biogenesis Defects of the KATP Channel Complex via a Converging Mechanism\*. *Journal of Biological Chemistry* **290**, 7980–7991 (2015).

162. Schmied, W. H., Elsasser, S. J., Uttamapinant, C. & Chin, J. W. Efficient multisite unnatural amino acid incorporation in mammalian cells via optimized pyrrolysyl tRNA synthetase/tRNA expression and engineered eRF1. *J Am Chem Soc* **136**, 15577–83 (2014).

163. Deplazes, E., Jayatilaka, D. & Corry, B. ExiFRET: Flexible tool for understanding FRET in complex geometries. *Journal of Biomedical Optics* **17**, 011005 (2012).

164. Zagotta, W. N., Gordon, M. T., Senning, E. N., Munari, M. A. & Gordon, S. E. Measuring distances between TRPV1 and the plasma membrane using a noncanonical amino acid and transition metal ion FRET. *The Journal of General Physiology* **147**, 201–216 (2016).

165. Ye, J. Y., Yamauchi, M., Yogi, O. & Ishikawa, M. Spectroscopic Properties of 2‘-(or-3‘)-O-(2,4,6-Trinitrophenyl) Adenosine 5‘-Triphosphate Revealed by Time-Resolved Fluorescence Spectroscopy. *The Journal of Physical Chemistry B* **103**, 2812–2817 (1999).

166. Ishikawa, M., Maruyama, Y., Ye, J. Y. & Futamata, M. Single-molecule imaging and spectroscopy of adenine and an analog of adenine using surface-enhanced Raman scattering and fluorescence. *Journal of Luminescence* **98**, 81–89 (2002).

167. Trapp, S., Proks, P., Tucker, S. J. & Ashcroft, F. M. Molecular analysis of ATP-sensitive K channel gating and implications for channel inhibition by ATP. *J Gen Physiol* **112**, 333–49 (1998).

168. Markworth, E., Schwanstecher, C. & Schwanstecher, M. ATP4- mediates closure of pancreatic beta-cell ATP-sensitive potassium channels by interaction with 1 of 4 identical sites. *Diabetes* **49**, 1413–1418 (2000).

169. Enkvetchakul, D., Loussouarn, G., Makhina, E. & Nichols, C. G. ATP Interaction with the Open State of the KATP Channel. *Biophysical Journal* **80**, 719–728 (2001).

170. Drain, P., Geng, X. & Li, L. Concerted gating mechanism underlying KATP channel inhibition by ATP. *Biophys J* **86**, 2101–12 (2004).

171. Proks, P. *et al.* A gating mutation at the internal mouth of the Kir6.2 pore is associated with DEND syndrome. *EMBO reports* **6**, 470–475 (2005).

172. Li, L. *et al.* Ligand-dependent Linkage of the ATP Site to Inhibition Gate Closure in the KATP Channel. *Journal of General Physiology* **126**, 285–299 (2005).

173. Ribalet, B., John, S. A., Xie, L.-H. & Weiss, J. N. ATP-sensitive K+ channels: Regulation of bursting by the sulphonylurea receptor, PIP2 and regions of Kir6.2. *The Journal of Physiology* **571**, 303–317 (2006).

174. Craig, T. J., Ashcroft, F. M. & Proks, P. How ATP Inhibits the Open KATP Channel. *The Journal of General Physiology* **132**, 131–144 (2008).

175. Enkvetchakul, D. & Nichols, C. G. Gating mechanism of KATP channels: Function fits form. *J Gen Physiol* **122**, 471–80 (2003).

176. Reinhold Penner (auth.), E. N. (eds. )., Bert Sakmann. *Single-Channel Recording*. (Springer US, 1995).

177. Sivilotti, L. & Colquhoun, D. In praise of single channel kinetics. *Journal of General Physiology* **148**, 79–88 (2016).

178. Enkvetchakul, D., Loussouarn, G., Makhina, E. & Nichols, C. G. ATP Interaction with the Open State of the KATP Channel. *Biophysical Journal* **80**, 719–728 (2001).

179. Wang, R. *et al.* Subunit-Stoichiometric Evidence for Kir6.2 Channel Gating, ATP Binding, and Binding-Gating Coupling. *Molecular Pharmacology* **71**, 1646–1656 (2007).

180. Hodgkin, A. L. & Huxley, A. F. A quantitative description of membrane current and its application to conduction and excitation in nerve. *The Journal of Physiology* **117**, 500–544 (1952).

181. Monod, J., Wyman, J. & Changeux, J.-P. On the nature of allosteric transitions: A plausible model. *Journal of Molecular Biology* **12**, 88–118 (1965).

182. Fang, K., Csanády, L. & Chan, K. W. The N-terminal transmembrane domain (TMD0) and a cytosolic linker (L0) of sulphonylurea receptor define the unique intrinsic gating of KATP channels. *The Journal of Physiology* **576**, 379–389 (2006).

183. Heinemann, S. H. & Conti, F. [7] Nonstationary noise analysis and application to patch clamp recordings. in *Methods in Enzymology* vol. 207 131–148 (Academic Press, 1992).

184. Alvarez, O., Gonzalez, C. & Latorre, R. Counting channels: A tutorial guide on ion channel fluctuation analysis. *Advances in Physiology Education* **26**, 327–341 (2002).

185. Sigworth, F. J. The variance of sodium current fluctuations at the node of Ranvier. *The Journal of Physiology* **307**, 97–129 (1980).

186. Tammaro, P. & Ashcroft, F. M. A mutation in the ATP-binding site of the Kir6.2 subunit of the KATP channel alters coupling with the SUR2A subunit. *The Journal of Physiology* **584**, 743–753 (2007).

187. Pratt, E. B., Yan, F.-F., Gay, J. W., Stanley, C. A. & Shyng, S.-L. Sulfonylurea Receptor 1 Mutations That Cause Opposite Insulin Secretion Defects with Chemical Chaperone Exposure\*. *Journal of Biological Chemistry* **284**, 7951–7959 (2009).

188. Pratt, E. B., Zhou, Q., Gay, J. W. & Shyng, S.-L. Engineered interaction between SUR1 and Kir6.2 that enhances ATP sensitivity in KATP channels. *Journal of General Physiology* **140**, 175–187 (2012).

189. Prakriya, M. & Lewis, R. S. Regulation of CRAC Channel Activity by Recruitment of Silent Channels to a High Open-probability Gating Mode. *Journal of General Physiology* **128**, 373–386 (2006).

190. Jackson, P. S. & Strange, K. Single-channel properties of a volume-sensitive anion conductance. Current activation occurs by abrupt switching of closed channels to an open state. *Journal of General Physiology* **105**, 643–660 (1995).

191. Jackson, P. S. & Strange, K. Single channel properties of a volume sensitive anion channel: Lessons from noise analysis. *Kidney International* **49**, 1695–1699 (1996).

192. Gronau, Q. F., Singmann, H. & Wagenmakers, E.-J. Bridgesampling: An R Package for Estimating Normalizing Constants. *Journal of Statistical Software* **92**, 1–29 (2020).

193. Wagenmakers, E.-J. A practical solution to the pervasive problems ofp values. *Psychonomic Bulletin & Review* **14**, 779–804 (2007).

194. Vehtari, A., Gelman, A. & Gabry, J. Practical Bayesian model evaluation using leave-one-out cross-validation and WAIC. *Statistics and Computing* **27**, 1413–1432 (2017).

195. Aguilar-Bryan, L. & Bryan, J. Neonatal Diabetes Mellitus. *Endocrine Reviews* **29**, 265–291 (2008).

196. Hattersley, A. T. & Ashcroft, F. M. Activating Mutations in Kir6.2 and Neonatal Diabetes: New Clinical Syndromes, New Scientific Insights, and New Therapy. *Diabetes* **54**, 2503–2513 (2005).

197. Ashcroft, F. M., Puljung, M. C. & Vedovato, N. Neonatal Diabetes and the KATP Channel: From Mutation to Therapy. *Trends in Endocrinology & Metabolism* **28**, 377–387 (2017).

198. Flanagan, S. E. *et al.* Update of mutations in the genes encoding the pancreatic beta-cell KATP channel subunits Kir6.2 (KCNJ11) and sulfonylurea receptor 1 (ABCC8) in diabetes mellitus and hyperinsulinism. *Human Mutation* **30**, 170–180 (2009).

199. Ashcroft, F. M. & Rorsman, P. Diabetes Mellitus and the beta Cell: The Last Ten Years. *Cell* **148**, 1160–1171 (2012).

200. Pipatpolkai, T., Usher, S., Stansfeld, P. J. & Ashcroft, F. M. New insights into K ATP channel gene mutations and neonatal diabetes mellitus. *Nature Reviews Endocrinology* **16**, 378–393 (2020).

201. Colquhoun, D. Binding, gating, affinity and efficacy: The interpretation of structure-activity relationships for agonists and of the effects of mutating receptors. *British Journal of Pharmacology* **125**, 923–947 (1998).

202. Li, N. *et al.* Structure of a Pancreatic ATP-Sensitive Potassium Channel. *Cell* **168**, 101–110.e10 (2017).

203. Gloyn, A. L. *et al.* KCNJ11 activating mutations are associated with developmental delay, epilepsy and neonatal diabetes syndrome and other neurological features. *Eur J Hum Genet* **14**, 824–30 (2006).

204. Ribalet, B., John, S. A., Xie, L. H. & Weiss, J. N. ATP-sensitive K+ channels: Regulation of bursting by the sulphonylurea receptor, PIP2 and regions of Kir6.2. *J Physiol* **571**, 303–17 (2006).

205. Yang, H.-Q. *et al.* Palmitoylation of the KATP channel Kir6.2 subunit promotes channel opening by regulating PIP2 sensitivity. *Proceedings of the National Academy of Sciences* **117**, 10593–10602 (2020).

206. Trapp, S., Tucker, S. J. & Ashcroft, F. M. Mechanism of ATP-sensitive K Channel Inhibition by Sulfhydryl Modification. *Journal of General Physiology* **112**, 325–332 (1998).

207. Zerangue, N., Schwappach, B., Jan, Y. N. & Jan, L. Y. A New ER Trafficking Signal Regulates the Subunit Stoichiometry of Plasma Membrane KATP Channels. *Neuron* **22**, 537–548 (1999).

208. John, S. A., Monck, J. R., Weiss, J. N. & Ribalet, B. The sulphonylurea receptor SUR1 regulates ATP-sensitive mouse Kir6.2 K+ channels linked to the green fluorescent protein in human embryonic kidney cells (HEK 293). *J Physiol* **510 ( Pt 2)**, 333–45 (1998).

209. Babenko, A. P. & Bryan, J. SUR Domains That Associate with and Gate KATP Pores Define a Novel Gatekeeper\*. *Journal of Biological Chemistry* **278**, 41577–41580 (2003).

210. Gribble, F. M., Tucker, S. J., Seino, S. & Ashcroft, F. M. Tissue specificity of sulfonylureas: Studies on cloned cardiac and beta-cell K(ATP) channels. *Diabetes* **47**, 1412–1418 (1998).

211. Ashfield, R., Gribble, F. M., Ashcroft, S. J. & Ashcroft, F. M. Identification of the high-affinity tolbutamide site on the SUR1 subunit of the K(ATP) channel. *Diabetes* **48**, 1341–1347 (1999).

212. Clegg, R. M. [18] Fluorescence resonance energy transfer and nucleic acids. in *Methods in Enzymology* vol. 211 353–388 (Academic Press, 1992).

213. Ding, D., Wang, M., Wu, J. X., Kang, Y. & Chen, L. The Structural Basis for the Binding of Repaglinide to the Pancreatic KATP Channel. *Cell Rep* **27**, 1848–1857 e4 (2019).

214. Masia, R. *et al.* A Mutation in the TMD0-L0 Region of Sulfonylurea Receptor-1 (L225P) Causes Permanent Neonatal Diabetes Mellitus (PNDM). *Diabetes* **56**, 1357–1362 (2007).

215. Pratt, E. B., Zhou, Q., Gay, J. W. & Shyng, S. L. Engineered interaction between SUR1 and Kir6.2 that enhances ATP sensitivity in KATP channels. *J Gen Physiol* **140**, 175–87 (2012).

216. Doyle, D. A. *et al.* The Structure of the Potassium Channel: Molecular Basis of K+ Conduction and Selectivity. *Science* **280**, 69–77 (1998).

217. Cukras, C. A., Jeliazkova, I. & Nichols, C. G. Structural and Functional Determinants of Conserved Lipid Interaction Domains of Inward Rectifying Kir6.2 Channels. *Journal of General Physiology* **119**, 581–591 (2002).

218. Calderhead, B., Epstein, M., Sivilotti, L. & Girolami, M. Bayesian Approaches for Mechanistic Ion Channel Modeling. in *In Silico Systems Biology* (ed. Schneider, M. V.) 247–272 (Humana Press, 2013). doi:[10.1007/978-1-62703-450-0\_13](https://doi.org/10.1007/978-1-62703-450-0_13).

219. Hines, K. E., Middendorf, T. R. & Aldrich, R. W. Determination of parameter identifiability in nonlinear biophysical models: A Bayesian approach. *Journal of General Physiology* **143**, 401–416 (2014).

220. Hines, K. E. A Primer on Bayesian Inference for Biophysical Systems. *Biophysical Journal* **108**, 2103–2113 (2015).

221. Middendorf, T. R. & Aldrich, R. W. Structural identifiability of equilibrium ligand-binding parameters. *Journal of General Physiology* **149**, 105–119 (2016).

222. Puljung, M., Vedovato, N., Usher, S. & Ashcroft, F. Activation mechanism of ATP-sensitive K+ channels explored with real-time nucleotide binding. *eLife* **8**, e41103 (2019).

223. Proks, P., Wet, H. de & Ashcroft, F. M. Activation of the K(ATP) channel by Mg-nucleotide interaction with SUR1. *J Gen Physiol* **136**, 389–405 (2010).