Molecular Insights into the Rescue Mechanism of an hERG Activator Against Severe LQT2 Mutations.

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Abstract

Mutations in the hERG potassium channel are a major cause of long QT syndrome type 2 (LQT2), which can lead to sudden cardiac death. The hERG channel plays a critical role in the repolarization of the myocardial action potential, and loss-of-function mutations prolong cardiac repolarization. In this study, we investigated the efficacy and mechanism of ICA-105574, an hERG activator, in shortening the duration of cardiac repolarization in severe LQT2 variants. We characterized the in vivo efficacy of ICA-105574 in shortening the QT duration in an animal model and the in vitro I_{Kr} current in cellular models mimicking severe hERG channel mutations (A561V, G628S, and L779P). We then used molecular dynamics simulations to investigate the molecular mechanisms of ICA-105574 action. In vivo, ICA-105574 significantly shortened the QT interval. LQT2 mutations drastically reduced I_{Kr} amplitude and suppressed tail currents in cellular models. ICA-105574 restored I_{Kr} in A561V and G628S. Finally, in silico data showed that ICA-105574 stabilizes a pattern of

interactions similar to gain-of-function SQT1 mutations and can reverse the G628S modifications, through an allosteric network linking the binding site to the selectivity filter and the S5P turret helix, thereby restoring its K^+ ion permeability. Our results support the development of hERG activators as pharmacological molecules against some severe LQT2 mutations and suggest that molecular dynamics simulations can be used to test the ability of molecules to modulate hERG function in silico, paving the way for the rational design of new hERG activators.

Significance Statement

Long QT syndrome 2 (LQT2) results from *KCNH2* gene mutations that affect the hERG channel, which is critical for cardiac repolarization. To investigate the therapeutic potential of ICA-105574, we used in vivo, in vitro and in silico models. In vivo, ICA-105574 significantly shortened the QT interval. In vitro, ICA-105574 selectively increased hERG current amplitude in severe LQT2 mutations (A561V, G628S) but not in L779P. Our *in-silico* analysis suggests a potential mechanism, similar to SQT1 mutations, modulating an allosteric network linking the ICA-105574 binding site to the selectivity filter and the S5P turret helix. These findings deepen the understanding of hERG activation and suggest a potential therapeutic approach for LQT2.

Introduction

The human *ether-à-go-go* (*hERG* or *KCNH2*) gene encodes a voltage-gated K^+ channel in neurons and cardiac cells. Its primary role involves cardiac repolarization through the rapid delayed rectifier K^+ current (I_{Kr}), which significantly influences the duration of the QT interval on the surface electrocardiogram (ECG) (1, 2). Abnormalities in the hERG channels are characterized by two distinct cardiac disorders, namely Long QT Syndrome (LQTS) and Short QT Syndrome (SQTS), which manifest as the prolongation or the shortening of the QT interval on the ECG. Congenital LQTS accounts for nearly 40% of cases (3, 4), while the majority of LQTS cases stem from pharmacological blockade by various clinically used drugs. Mutations in hERG channels can result in a loss of function due to defective trafficking, abnormal channel gating or reduced ion permeation. Notably, approximately 90% of LQT syndrome type 2 (LQT2) mutants exhibit reduced synthesis and defective trafficking (5, 6), yet certain mutations (e.g. G628S, N629D) (7, 8) near the selectivity filter (SF) can maintain normal trafficking while failing to exhibit ion selectivity and conductance in physiological solutions. On the other hand, SQT type 1 (SQT1) mutations (e.g. N588K, T618I, S631A) are often associated with reduced or loss of inactivation, resulting in a shorter QT interval (9, 10). The large number of LQT2-associated missense mutations distributed throughout the hERG sequence poses a challenge to pharmacological treatments. Of note, Priori and coworkers showed that substrate-specific therapy with mexiletine, which shortens the QT interval, confers arrhythmic protection in LQT3 (11, 12). This suggests that, in principle, QT interval shortening is an effective strategy for the treatment of LQT2. This could be achieved with hERG activators (13), which enhance the rapid component of the delayed rectifier K^+ current (I_{Kr}) and may be able to shorten the duration of cardiac repolarization in LQT2.

Structurally, hERG is a homotetramer consisting of an N-terminal cytosolic Per-Arnt-Sim (PAS) domain followed by six transmembrane segments: S1-S4, forming the voltage-sensing domain (VSD), and S5-S6, together with the S5P turret region and the P helix, forming the pore-forming domain (PD); and the C-terminal cyclic nucleotide-binding homology domain (CNBHD), all intertwined by long disordered regions (14). The hERG channel undergoes critical kinetic transitions between its closed (deactivation), active and inactivated states that regulate cardiac repolarization. Despite the recently available cryo-EM structure, the distinctive mechanism of rapid inactivation and recovery, and slow deactivation remains poorly understood due to the limited structural information available for the closed and inactivated states (15). To address this knowledge gap, recent attempts have been made to model these states, drawing on insights from the mechanism of C-type inactivation observed in the bacterial KcsA potassium channel and using the single-particle cryo-EM structure of the mammalian EAG1 channel, as a useful template for homology modeling of the closed state of the hERG channel (16–18). These studies revealed that C-type inactivation involves a structural transition of the selectivity filter to a non-conducting, constricted conformation, often characterized by changes in hydrogen bond interactions, and the role of the S4-S5 linker in the slow activation and deactivation kinetics of hERG channels (19). A recently determined cryo-EM structure for the hERG-astemizole complex has confirmed the general understanding that blockers bind to a hydrophobic pocket at the entrance of the SF, thus blocking the

passage of K^+ ions, and provides further tools for structure-based screening of hERG-related cardiotoxicity (20–23). While high-throughput virtual screening has primarily focused on the evaluation of a substantial number of drug-induced arrhythmic compounds, it has also unexpectedly revealed agonists (activators) that can induce inward rectification of I_{Kr} (24). The intricate mechanistic properties of each of these compounds show distinct differences, including delayed deactivation, inhibition of C-type inactivation, increased channel open probability, or a combination of these effects, while also indicating unique binding interactions between each activator and the channel (25). Several activators have been studied as potential candidates for different congenital LQTS mutations (25). However, they carry the risk of inducing early repolarization, leading to an excessive correction of action potential duration (APD), which could ultimately shorten the QT interval to proarrhythmic levels (i.e., SQT). It is worth noting that the behavior of these activators may vary between different mutants. Nevertheless, most activators primarily target the C-type inactivation mechanism and represent a novel approach to the prevention of ventricular arrhythmias associated with LQTS (25). One such compound is ICA-105574, a derivative of 3-nitro-n-(4-phenoxyphenyl) benzamide and is the most potent I_{Kr} activator to date (26, 27). Previous experimental and computational studies have revealed its binding site within a hydrophobic pocket located between two adjacent subunits, where it interacts with residues in the pore helix, the base of the SF, and the S6 segments (28–30). ICA-105574 is proposed to act through a subtle change in the configuration of the selectivity filter that disrupts inactivation gating, with a demonstrated stoichiometric dependence where binding of multiple ICA molecules is required for full activity of the compound (31).

In this study, we employed a multi-pronged approach using *in vivo* and *in vitro* electrophysiology and molecular dynamics (MD) simulations to explore the therapeutic potential of ICA-105574 in LQT2 and in severe hERG mutations, specifically A561V, G628S, and L779P, derived from our cohort of LQT2 patients. First, we validated *in vivo* the ability of ICA-105574 to rescue QT prolongation in a sotalol-induced animal model mimicking LQT2. Moreover, we subcloned and expressed the above mentioned severe LQT2 hERG mutations in specific established stable cell lines to study their functional activity on current amplitude before and after ICA-105574 treatment. We then performed in silico studies to elucidate the molecular mechanisms of action of ICA-105574 in both wild-type and mutant hERG channels. Our results indicate that ICA-105574 restores I_{Kr} amplitude in cellular models (A561V and G628S). Furthermore, our *in-silico* investigation, focusing on the functionality of the active state, revealed how ICA-105574 can rescue the permeability to K^+ of the G628S mutation by stabilizing a pattern of interactions similar to that resulting from simulations of two SQT1 mutations (i.e., N588K and S631A) through an allosteric network. These results provide valuable insights into the molecular mechanisms governing hERG activation by ICA-105574. We propose an *in-silico* approach to evaluate improved activators based on their ability to maintain channel conductance and suggest a strategy for using them in patients with certain severe LQT2 mutations.

Results and Discussion

In vivo electrophysiological experiments demonstrate the shortening of the QT interval mediated by ICA-105574

To evaluate the efficacy of ICA-105574 in shortening the QT interval in LQT2 patients, we performed in vivo electrophysiological experiments. Since currently there are not knock-in animal models that recapitulate the LQT2 phenotype, we investigated the effect of the I_{Kr} activator ICA-105574 in a chemically induced LQT2 guinea pig. The LQT2 condition was mimicked by pre-treating the guinea pig with 50 mg/Kg of sotalol, with a pronounced prolongation of the QTc interval from a baseline of 255 ms (IQR: 252-259 ms) was consistently obtained in all guinea pigs (ΔQTc +41 ms, +17%; <0.001) (32–34). Despite marked QTc prolongation, during the electrocardiographic registration no spontaneous arrhythmic events were observed. Following the demonstration of successful induction of LQT2, a single intraperitoneal dose of ICA-105574 at 15 mg/Kg was administered. Immediately upon drug administration, QTc interval normalization was consistently obtained in all guinea pigs (ΔQTc -43 ms, -14%; <0.001). This effect was transient and by 30 minutes after administration QTc interval normalization waned with QTc lengthening back to values comparable to ones prior to ICA-

105574 administration. No other biologically significant effects on the principal electrocardiographic parameters were observed (**Figure 1**).

***In vitro* electrophysiological analysis of ICA-105574 with, A561V, G628S and L779P**

We then characterized the functional properties of the severe hERG mutations (A561V, G628S and L779P) and their response to ICA-105574 as an I_{Kr} activator. We generated chimeric proteins (pmCherry-N1-hERG-WT, -A561V, -G628S and -L779P) and established single stable cell lines for each condition to perform electrophysiological studies following ICA-105574 perfusion. The pmCherry-N1-hERG-WT was transiently transfected into HEK293 cells and protein expression was assessed by Western blot and localized by confocal microscopy. These preliminary analyses confirmed the correct expression of the chimera and its distribution along the cell membrane (*SI Appendix* **Figure S1**). Similarly, we generated and performed the experiments for all the hERG mutations (*SI Appendix* **Figure S2**). Western blot showed the correct molecular weights for all hERG mutants, and confocal analysis allowed to verify the different ability of the mutations to localize. Both mCherry-N1-hERG-A561V and -G628S were stained along the plasma membrane with some diffuse presence in the cytoplasm, similar to the hERG-WT, and the subcellular distribution was not affected by the ICA-105574 exposure. In contrast, the hERG-L779P was mainly localized in the cytoplasm, with enrichment around the perinuclear region, suggesting some folding defects. Again, ICA-105574 treatment did not affect its subcellular distribution.

Electrophysiological analysis was performed in HEK293 stable cell lines expressing hERG-WT and mutants (A561V, G628S, L779P). The functionality of the hERG channels was impaired by the fact that the mutations induced a suppression of the tail currents, making it impossible to evaluate the activation curve (as previously reported by Sanguinetti et al. for A561V and G628S (35)). The A561V mutation reduces the steady state pre-pulse current amplitude and only partially distort the hERG current behavior (**Figure 2**), whereas the effect of G628S and L779P leads to a drastic reduction of the I_{Kr} current (*SI Appendix* **Figure S3**). In particular, the G628S and L779P mutations produced currents that did not reach a peak and a plateau phase. These data allow us to speculate that G628S and L779P negatively alter channel opening, in agreement with previous data for G628S (8, 30, 35, 36).

The hERG stable cell lines (WT, A561V, G628S, L779P) were perfused with ICA-105574 (10 μM). The treatment induced a strong I_{Kr} activation on steady state currents in both WT and A561V (from -10 to +70 mV) and G628S (from 0 to +70 mV) partially restoring the functionality of the mutated channels (**Figure 2**). Conversely, the hERG-L779P does not respond to ICA-105574 perfusion. Notably, both the A561V and G628S mutations show a significant response to ICA-105574-induced by I_{Kr} activation with an increase in I_{Kr} amplitude (**Figure 2**).

Restrained Molecular Dynamics allow simulating the hERG active state

Having shown that ICA-105574 can rescue the activity of G628S and A561V but not that of L779P *in vitro*, we set out to understand the molecular determinants of this rescue mechanism using MD simulations. Previous work on the hERG channel showed rapid inactivation on the *ns* time scale for the wild-type protein, making it difficult to accumulate extensive statistics on the conformational dynamics of the hERG active state (16, 17, 37). Here we started with a known cryo-EM structure (PDB ID: 5VA2) determined in the active state for the wild type (**Figure 3A**), including the PAS domain (15), in a POPC bilayer with 200 mM salt concentration (KCl) and applied transmembrane voltage ranging from ~650 mV to ~750 mV. In a first round of preliminary simulations (*SI Appendix* **Table S1A**), we observed, in agreement with the work of Miranda et. al. (37), a fast inactivation on the *ns* time scale, manifested by the flipping of carbonyl oxygen atoms and subsequent SF distortion (*SI Appendix* **Figure S4**). The fast kinetics of these structural changes could be attributed to the use of a high electric field and to inaccuracies in the force field parameters. Therefore, to ensure that the selectivity filter remains stable during the simulations, we restrained the backbone torsion angles (φ, ψ). The resulting systems show a stable SF over the course of the restrained MD simulations, (*SI Appendix* **Figure S4**), with the diameter between opposite chains in agreement with cryo-EM reference values for highly flexible F627, while with a small dilation for S624 and V625 residues.

Ion permeation mechanisms in potassium ion channels have been found to be ambiguous in nature, depending on the type of force field considered, the membrane potential, and the charge corrections for the ions (38). In

preliminary simulations with dihedral restraints (*SI Appendix* **Table S1B**), we observed mostly a soft knock-on mechanism for the ion permeations using the CHARMM force field with NBFIX parameters (39), regardless of the initial configuration of the ions ([KKKKK] or [KWKWK]). In addition, the mixed KCl and NaCl simulations for the wild-type system established the ion selectivity with outward K^+ ion movement and no inward/outward Na^+ ion movement in the presence of torsional restraints. Therefore, subsequent production simulations were run with [KWKWK] ion configuration and KCl salt only for uninterrupted ion permeations (see *SI Appendix* **Movie S1** and **Table S2**).

Production simulations were performed for six systems containing LQT2 and SQT1 mutations, namely WT, G628S, WT-ICA, G628S-ICA, S631A, and N588K. WT and G628S simulations, with and without ICA-105574, were performed to observe and characterize the molecular determinants of ICA-105574-induced hERG rescue. While N588K and S631A represent SQT1 mutations used in this work to investigate whether the effect of ICA-105574 is structurally comparable to that of these pathological mutations, given their associated attenuated inactivation (9, 10). To demonstrate the effect of ICA-105574, two molecules were docked into the opposite subunit fenestrations based on the previously identified binding site residues (28–30) (**Figure 3B**, cf. *SI Appendix* for the molecular docking protocol). ICA-105574 is found to be stable in WT-ICA and G628S-ICA systems over the course of simulations (*SI Appendix* **Figure S5A, B**). Our energetic analysis reveals that ICA-105574 molecules forms favorable polar and non-polar interactions in the form of H-bond (S649) and pi-pi interactions (F557, Y652, F656) in the respective fenestrations (*SI Appendix* **Figure S5C, D**).

Ion permeation and selectivity filter stability as a feature of active state

Because of the stable SF resulting from our restrained MD simulations, we recorded continuous K^+ ion permeation events in multiple trajectories for all systems except, remarkably, the LQT2-G628S system. Based on these trajectories, we calculated the ion occupancy probability at different sites in the selectivity filter described previously for K^+ ion channels (**Figure 4A**). All ion-permeable systems show higher ion occupancy at the S2 site, which in turn prevents the collapse of SF (40). In contrast, the ion occupancy at S2 decreases in LQT2-G628S, which is restored in the presence of ICA-105574 in the G628S-ICA system. The number of ion permeations varies in the multiple replicates of each system (*SI Appendix* **Table S2**). Therefore, we estimated an average transition time (τ) for an ion to permeate through the SF from S_{cavity} to the escape of the ion from the S0 site (**Figure 4B**). The average transition time of a single ion permeation event for WT, S631A, and ICA-bound systems (WT-ICA, G628S-ICA) is in the range of 100-150 *ns,* with the exception of 260 *ns* for N588K (**Figure 4B**, inset), suggesting that our MD simulations cannot fully capture the differences in conductance, possibly due to a combination of force field limitations and the high applied membrane potential. Despite these approximations, our model can capture the loss of conductance in terms of ion permeations across the SF in G628S and, remarkably, the rescue effect of ICA-105574 in the G628S-ICA system in agreement with our *in vitro* electrophysiological data (**Figure 2**). These observations suggest that we can interrogate our MD simulations to obtain relevant structural information on the rescue mechanism. Importantly, previous *in silico* studies (28, 41) of hERG activators have never explicitly demonstrated the effect of these molecules on conductance.

The helicity of the S5P turret as a signature of activation propensity

Structural and computational studies suggest that the active state of the hERG channel differs from inactivation in terms of the diameter of the SF and the heterogeneity in the dihedral angles of F627 (19, 37). In a recent preprint, Vanderberg and coworkers report the narrowing of the SF in the cryo-EM structure of hERG in the inactivated state (42). In our simulations, the average diameter for the SF residues is found to be stable and similar for wild-type, SQT mutations (N588K, S631A), and WT-ICA systems (**Figure 4C**). While, in the presence of LQT mutation (G628S), there is a notable increase in the diameter around F627 (0.80 ± 0.1 nm) and S628 (1.13 ± 0.08 nm) showing the effect of the mutation. Of note, the G628S-ICA bound system showed only a small decrease in the SF diameter with respect to G628S, suggesting that in this range of values, SF diameter is not a clear signature of activation. To access any major conformational rearrangements and flexibility in the pore domain (PD) upon mutation or ligand binding, we analyzed the inter-residue pairwise distances for different systems with respect to the wild type (*SI Appendix* **Figure S6 A-E**). Overall, no major conformational changes in the pore domain were observed, except for a higher flexibility in the extracellular loops in the wild type and G628S as compared to the other systems (*SI Appendix* **Figure S6F**), suggesting that the differences we are looking for may be subtle and related to the conformational dynamics of the system.

In hERG, experimental evidence emphasizes on the role of the S5P turret helix (residues 584-592) in the c-type inactivation mechanism (43–45), and the S5P segment has been observed to exist between helical and unstructured conformations in MD simulations. Interestingly, we observe a clear trend in the helicity of this region within SQT mutations and ligand-bound hERG channel as compared to the wild type (**Figure 4D**). Importantly, the G628S mutation has the least helical propensity, which is restored in the presence of ICA-105574. The activator is proposed to act primarily by attenuating rapid inactivation by increasing the stability of SF and channel conductance; it is intriguing how the binding of ICA-105574 below the SF can exert its function via conformational changes at long distance in the S5P turret helix. In contrast both SQT mutations are localized within or in contact with this region (**Figure 3A**) and may alter its role in c-type inactivation.

ICA-105574 promotes molecular interactions and hydrogen bond rearrangement in the rescue state

So far, our observations suggest the signatures of the rescue effect in the G628S-ICA system; therefore, we now investigate the molecular mechanism of the rescue effect of the ICA-105574 in the G628S mutation. We calculated the variation of the hydrogen bond (H-bond) occupancy in the pore domain of the hERG channel in the wild-type, G628S, and activator-bound G628S-ICA systems to identify changes in molecular interactions upon different perturbation perturbations (mutation or ligand binding). The net H-bond occupancy (%) between two residues *i* and *j* is given by $\Delta HB_{ij} = HB_{ij}^{perturbation} - HB_{ij}^{reference}$ where the perturbation factor could be mutation or ligand binding while the reference could be either WT or G628S. As shown in **Figure 5**, red lines indicate residue pairs with higher H-bond occupancy (%) in the perturbed system, while blue lines indicate the same in the reference system (H-bond loss in perturbed system). When comparing G628S with WT, the analysis is the result of an averaging over the four chains (**Figure 5A**), whereas when comparing G628S with G628S-ICA, we had to take into account the asymmetric docking of the activator across two adjacent monomers, so we have analyzed the change in the H-bond occupancy in these chains separately (**Figure 5B**). Our analysis showed that the G628S mutation decreases the H-bond occupancy around the SF (F617-S621, S620-G626, S631-N633) and in the S5P turret helix spanning from G584 to Q592 as compared to the WT (**Figure 5A**). Notably, binding of ICA-105574 to the G628S system resulted in a marked increase in H-bond occupancy, in both adjacent chains, for residues around SF (Y616-S620, S620-G626) and in the S5P turret helix residues (G584-Q592). The asymmetric positioning of ICA-105574 also resulted in different H-bonding patterns in adjacent chains. For example, one chain had higher H-bond occupancy near SF (F617-S621, S621-S624) and W568-W585, while another chain with more ICA-105574 contacts had increased H-bond occupancy in the S6 helical subunit. In addition, some residue pairs (e.g. Y616-N629, E637-S641, M645-S649 and at the S6 helix end) have higher H-bond occupancy in G628S than in WT (**Figure 5A**, red lines). However, this difference is reversed when ICA-105574 binds to G628S (**Figure 5B**, red lines). Notably, we also observed a similar H-bond rearrangement in the S5P turret region when comparing the wild-type and WT-ICA systems (*SI Appendix* **Figure S8A**), supporting that this is a robust feature of ICA-105574 binding. Furthermore, a similar pattern is observed when comparing the WT with the S631A and N588K SQT variants (*SI Appendix* **Figure S8B, C**). Overall, the increase in turret helicity (**Figure 4D**) and the decrease in RMSF (*SI Appendix* **Figure S6F**) observed above for both ICA-105574 bound and SQT systems can be attributed to a rearrangement of H-bonds occupancy, although the mechanism of stability may differ between systems. For example, the mutation of the polar amino acid (N588) to a charged amino acid (K588) increases helix stability by forming a salt bridge with D591, whereas mutation of S631A replaces the wild-type S631-N633 H-bond with an N588-A631 H-bond.

While these observations further highlight a similarity between the binding of ICA-105574 and two SQT mutations under study, they still do not fully describe how ICA-105574 may exert its long-range effect on the conformational dynamics of hERG. To this end, we focused on a single monomer chain and shortlisted residues with either higher net H-bond occupancy in G628S-ICA or $E_{i,ICA} < -2.5\ kcal/mol$ (*SI Appendix* **Figure S5D**). We identified S624 as a common residue in this list and defined it as the starting point of the allosteric network, coupling ICA-105574 to the SF and the S5P turret helix. Specifically, we observed that the nitro group of ICA-105574, located behind the SF, formed favorable interaction with the hydroxyl group of S624 (**Figure 6A**). This resulted in a population shift of the chi (χ_1) dihedral angle of S624, which describes the orientation of its side chain (**Figure 6B**). We hypothesize that this favorable interaction may trigger a domino effect in the form of an increase in the H-bond occupancy of several neighboring residue pairs behind the SF (Y616-S620, S620-G626), as previously shown in **Figure 5**, including A561-T618, F617-S621, S621-S624, with some of

these occupancy changes manifesting as a significant shift in side chain orientation (e.g. T618, S620) upon ICA-105574 binding (**Figure 6C**). In particular, the changes observed for the region S620-S624 and the S5P turret helix are associated with a population shift in the χ-dihedral distribution of F617 and the tryptophan clamp (W568-W586). In **Figure 6**, we have shown a 2D distribution of the χ_1/ χ_2 angle in the residue pairs W568-F617 (**Figure 6D, E**) and W568-W585 (**Figure 6F, G**). Here, we observed that the population density of the chi dihedrals for W568-F617 increases for a basin (F617(χ_2) ~ -100°, W568(χ_1) ~180°) without changing the overall shape of the distribution. While in the case of W568-W585, there is a marked shift for W585 (χ_1) towards exclusively side chain orientation upon ICA-105574 binding, whereas the population for W568 (χ_1) dihedral is significantly higher in one state (~180°) in G628S-ICA compared to the G628S system. Thus, the pairing in the side chain orientations of these three residues may enhance the interaction between the S5, pore helix, and turret region in the activated state. These results are consistent with what we have observed *in vitro* for A561V and L779P. Indeed, the A561V mutation is located within the network identified here and its effect is consistently rescued by ICA-105574. In contrast, the L779P mutation is located in the cyclic nucleotide-binding homology domain (CNBHD), its effect cannot thus be interpreted by our conformational analysis, and it cannot be rescued by ICA-105574 (**Figure 2**). To test the extent to which MD simulations can capture the effect of additional mutations, we performed an additional round of simulations on the A561V and L779P systems.

MD simulations of A561V and L779P highlight strengths and limitations of our *in silico* approach

Regarding the A561V mutation located in the S5 helix of the pore domain, in our *in-silico* model, both the A561V and A561V-ICA systems exhibited ion permeation comparable to the WT and all conducting systems studied here, with ion occupancy in the selectivity filter consistent with the above observations (**Figure 4** and *SI Appendix* **Figure S9**). Interestingly, the permeation rate for A561V-ICA is the same as that observed for the WT-ICA and G628S-ICA systems, indicating some robustness. No obvious differences were observed in the SF due to this mutation (*SI Appendix* **Figures S10, S11, and S12A**). In addition, the helicity of the SP5 turret suggests a conducting system with values greater than the WT system. Notably, the A561V and A561V-ICA systems also show an increase in H-bond occupancy in the helical residues of the S5P turret (G584-Q592) and around SF (Y616-S620, S620-G626). These results suggest that the A561V mutation does not affect the active state. On the one hand, this may be consistent with our in vitro electrophysiological data showing that A561V reduces but does not drastically alter the steady state pre-pulse current amplitude and only partially distorts hERG current behavior. On the other hand, it highlights the limitations of our *in-silico* model to capture the complexity of ionic conductance and current changes in mutant hERG channels by focusing only on the open state. Previous work on this mutation has already hypothesized that the A561V mutation may not primarily affect conductance, but rather localization (46, 47).

For the L779P mutation, located in the cyclic nucleotide-binding homology domain (CNBHD), we focused on simulating only the CNBHD of hERG channels (48) in both the wild-type and mutant states (*SI Appendix* for Materials and Methods). The L779 residue is strategically positioned within the central beta-strand of the beta-roll, which is a common fold among canonical cyclic nucleotide-binding proteins. It establishes favorable hydrophobic and backbone H-bond interactions with neighboring residues, thus contributing to the overall stability of this domain. However, the introduction of a proline mutation at position L779 can have a significant impact on the overall structure of the CNBHD. Interestingly, our simulations showed a significant increase in the RMSF for the CNBHD in the presence of the L779P mutation (*SI Appendix* **Figure S12B**). The dramatic increase in fluctuations observed here, coupled with the loss of interactions in the inner core of the CNBHD, suggests a loss of stability in this domain, potentially increasing the risk of misfolding and a putative loss of functionality. This is consistent with our in vitro observations, where most of the protein is localized in the cytoplasm, with enrichment around the perinuclear region, suggesting some folding defects. Having observed that the effect of ICA-105574 is primarily localized to the SF region, its inability to rescue such a mutation is therefore expected.

Conclusions

LQTS predisposes young patients to develop ventricular fibrillation leading to sudden cardiac death. QT interval duration is a strong predictor of arrhythmic events, with each 10 ms increase conferring a 15% increased risk (49). We decided to test whether ICA-105574, an hERG activator, could be a good candidate

to shorten the duration of cardiac repolarization in LQT2, by gaining an insight at three different levels: *in vivo, in vitro and in silico.* Our combined *in vitro* and *in silico* data allow to suggest that A561V, G628S and L779P mutants act on different aspects of hERG function, with A561V possibly stabilizing states other than the active one, G628S clearly disrupting the conductivity of the open state and L779P by strongly destabilizing the CNBHD domain. Importantly, our data showed that the I_{Kr} activator ICA-105574 can rescue the function of A561V and G628S hERG LQT2 mutations by a mechanism similar to that of some known SQT1 mutations (i.e., S631A and N588K). ICA-105574 binding stabilizes a network of amino acids in the SF, pore helix and S6 helix, allowing its effects to propagate ~2 nm away to the S5P turret helix. Interestingly, a significant number of LQT2 mutations fall in the pore region identified in this work (50, 51) and may be consistently rescued by ICA-105574. At the same time, we cannot exclude the efficacy of ICA-105574 against other mutations in heteromeric wild-type/mutant combinations that were not the focus of this work. Finally, the stabilization mechanism observed here is also compatible with the increased potency of the drug with increasing stoichiometry, as previously observed (31).

In conclusion, the *in vivo* experiments confirmed that administration of ICA-105574 induced a pronounced and statistically significant shortening of the QT interval in LQT2 and, importantly, no arrhythmic events were observed. In parallel, our *in vitro* analyses showed that the I_{Kr} activator can partially rescue and restore the functionality of some hERG LQT2 mutations. Thus, we support the hypothesis that hERG channel activators may represent a potentially very powerful novel therapeutic strategy for LQT2 patients. Furthermore, we note that molecular dynamics simulations such as the one performed here, which focus on the functional effect of a drug, despite all their approximations, are optimally positioned to provide an *in-silico* platform to test the functionality of hERG activators even in the difficult case of testing a drug rescue mechanism.

Materials and Methods

A brief summary of the different materials and methods used in this study is given below. More detailed descriptions are provided in the supplementary information.

ICA-105574 preparation

ICA-105574 was synthesized following a recently reported procedure by Zangerl-Plessl et al. (28), which is also employed in our recently published study (52).

In vivo electrophysiological experiments

The procedures employing Guinea pigs (Dunkin Hartley) were approved by the Ministero Italiano della Salute (Rome, Italy; 854/2019-PR). We used D,L-Sotalol (50 mg/Kg) to develop a drug-induced model of LQT2. The ECG signal was recorded for 90 minutes, ICA-105574 (15 mg/Kg) was intraperitoneally administered and the ECG signal was recorded for 90 minutes after injection. The QTc interval value was corrected for heart rate by the Bazett's formula (32). The ECG parameters were evaluated by a mixed effects model, using RStudio 11 Version 4.1.1 (Boston, MA, USA). The significance level was considered at $p < 0.05$.

Cloning of hERG-WT and mutants in heterologous systems

The commercial clone of full-length human hERG (NM_000238.3) cloned in pCMV6-XL4 (Origene) was subcloned in pmCherry-N1 (Clontech) to generate a functional chimera. Site-direct mutagenesis was performed using QuickChange II XL kit (Agilent Technologies) to generate the single hERG mutations: pmCherry-N1-hERG-A561V, pmCherry-N1-hERG-G628S and pmCherry-N1-hERG-L779P. All the plasmids were entirely sequenced. Primers are indicated in the Supplementary information.

Cell culture and transfection

The HEK293 stable cell lines were generate by a transfection with Effectene (Qiagen) and 1µg plasmid (pmCherry-N1-hERG-WT and -A561V, -G628S and -L779P, respectively) and selected by Gentamicin sulfate salt and the hERG-mCherry-positive cells were sorted by BD FACS Aria III (Becton Dickinson).

Immunofluorescence

HEK293 cells with pmCherry-N1-hERG-WT or mutants (A561V, G628S or L779P) were stained with antibodies indicated in the supplementary materials and analysed by confocal microscopy.

Protein extraction and Immunoblotting

48h after transient transfection, HEK293 cells have been lysated in RIPA buffer; 30 µg of total proteins, were quantified and resolved by SDS-gel electrophoresis and blotted on 0.2 µm nitrocellulose membrane.

***In vitro* electrophysiological experiments**

Electrophysiological recordings were performed on stable HEK293 cell lines expressing the single mutation and expressing the red mCherry signal were chosen for current recordings. The solutions are the same used in previous study as reported by Milani et al. (54). All the data were tested by two-tailed Student's paired t-test. The significance level was considered at $p < 0.05$.

Molecular docking and simulations details

MD simulations were performed for six systems. These systems included wild type (WT, PDB: 5VA2), two SQT mutations (N588K and S631A (PDB: 5VA3)), two LQT2 mutations (A561V and G628S), and complexes of ICA-105574 with WT and LQT2 mutated channels. The ICA-105574 molecules were positioned within the channel using the Schrödinger Glide software for molecular docking. In addition, MD simulations for the Cyclic Nucleotide-Binding Homology Domain (CNBHD, PDB: 2N7G) were performed to assess the impact of the LQT2 mutation L779P on the domain's stability and conformation. All the simulations in the present study were performed using GROMACS (55) with the CHARMM36 forcefield (56) and the TIP3P water model (57). Further details about molecular docking and simulations are described in the Supplementary Information. The data generated and analyzed in the current study can be accessed on Zenodo: https://zenodo.org/records/8349178

Acknowledgments

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Figures and Tables

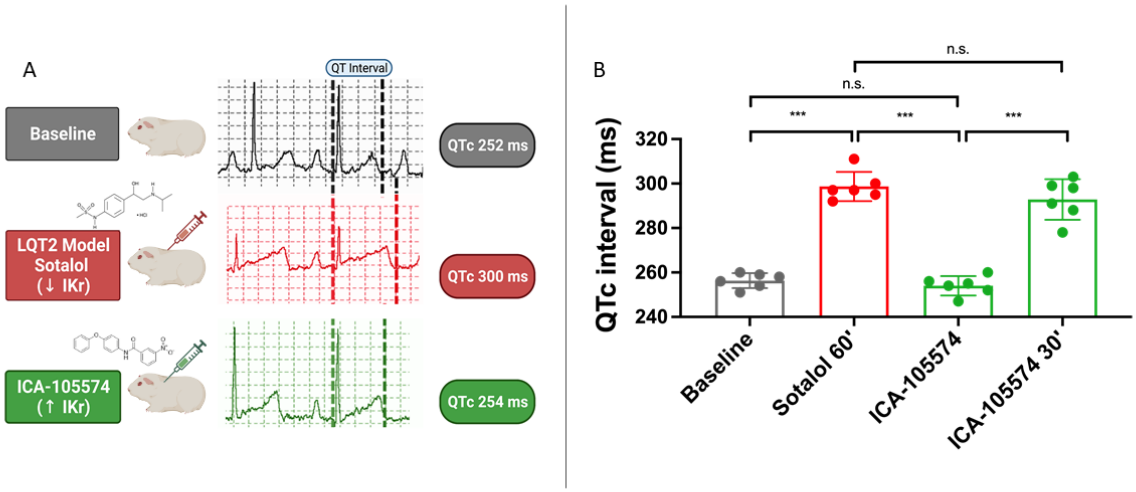

Figure 1. (A) In vivo LQT2 ECG recordings. LQTS was successfully induced in all animals after sotalol treatment (252±10 ms *vs*. 295±9 ms for the baseline and sotalol treated guinea pigs, respectively; $p<0.001$). Importantly, a pronounced and statistically significant shortening of the QTc interval was consistently obtained in guinea pigs after ICA-105574 administration, normalizing the QTc in all animals (295±9 ms *vs.* 254±4 ms, before and after ICA administration, respectively). Importantly, despite the marked QTc shortening, no arrhythmic events were observed in the study animals after ICA-105574 administration. (B) Pairwise comparisons were performed and the main relevant comparisons regarding the ECG values, are shown as histograms.

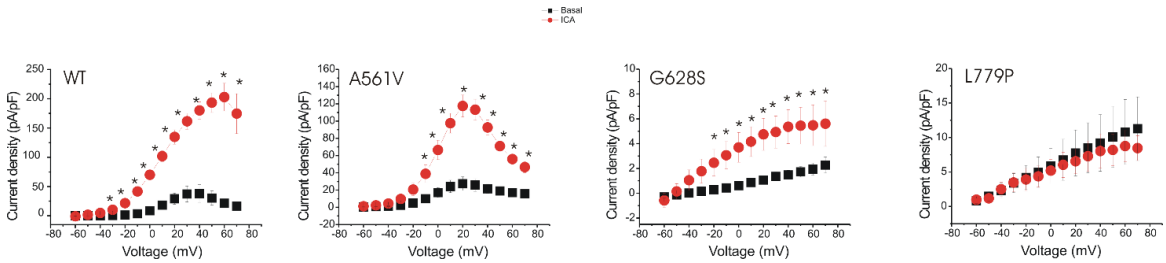

Figure 2. I/V relationships in hERG WT and mutants. The I/V graphs are derived by voltage clamp recordings showing WT, A561V, G628S and L779P activation currents recorded in basal condition (black square) and after the perfusion of 10 μM ICA-105574 (red dot). The asterisk indicates a statically significant difference ($p \leq 0.05$, Student t-test, WT: n=5, A561V: n=6, G628S: n=6, L779P: n=4).

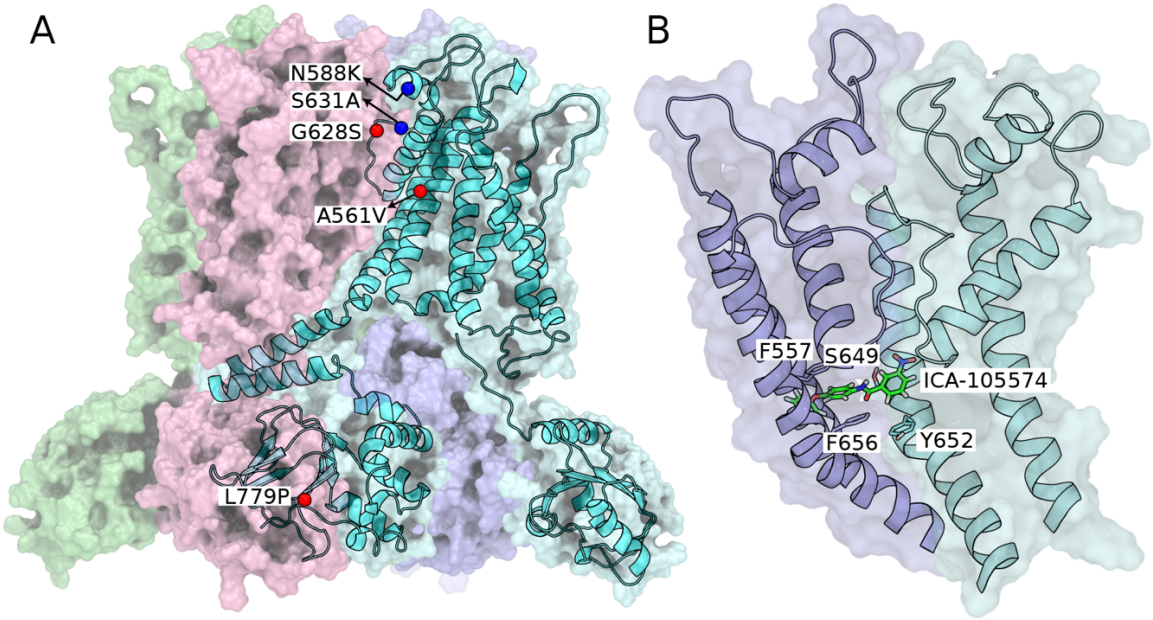

Figure 3. (A) Structural representation of the hERG tetramer with the SQT (N588K and S631A) and LQT (A561V, G628S and L779P) mutations highlighted in blue and red spheres respectively. A single monomer is shown with different domains identified in the cryo-EM structure (PDB: 5VA2). The SQT mutations, N588K and S631A, are located near the selectivity filter and are known to attenuate the inactivation state, whereas the LQT mutation G628S directly affects the selectivity filter. (B) ICA-105574 was docked into the hERG tetramer based on the previous mutagenesis study by Sanguinetti and co-workers (28–30). The docked structure is subjected to molecular dynamics (MD) simulations to obtain an equilibrated protein-ligand structure embedded in the lipid bilayer. The position of ICA-105574 in the equilibrated structure is consistent with previous findings and suggestions.

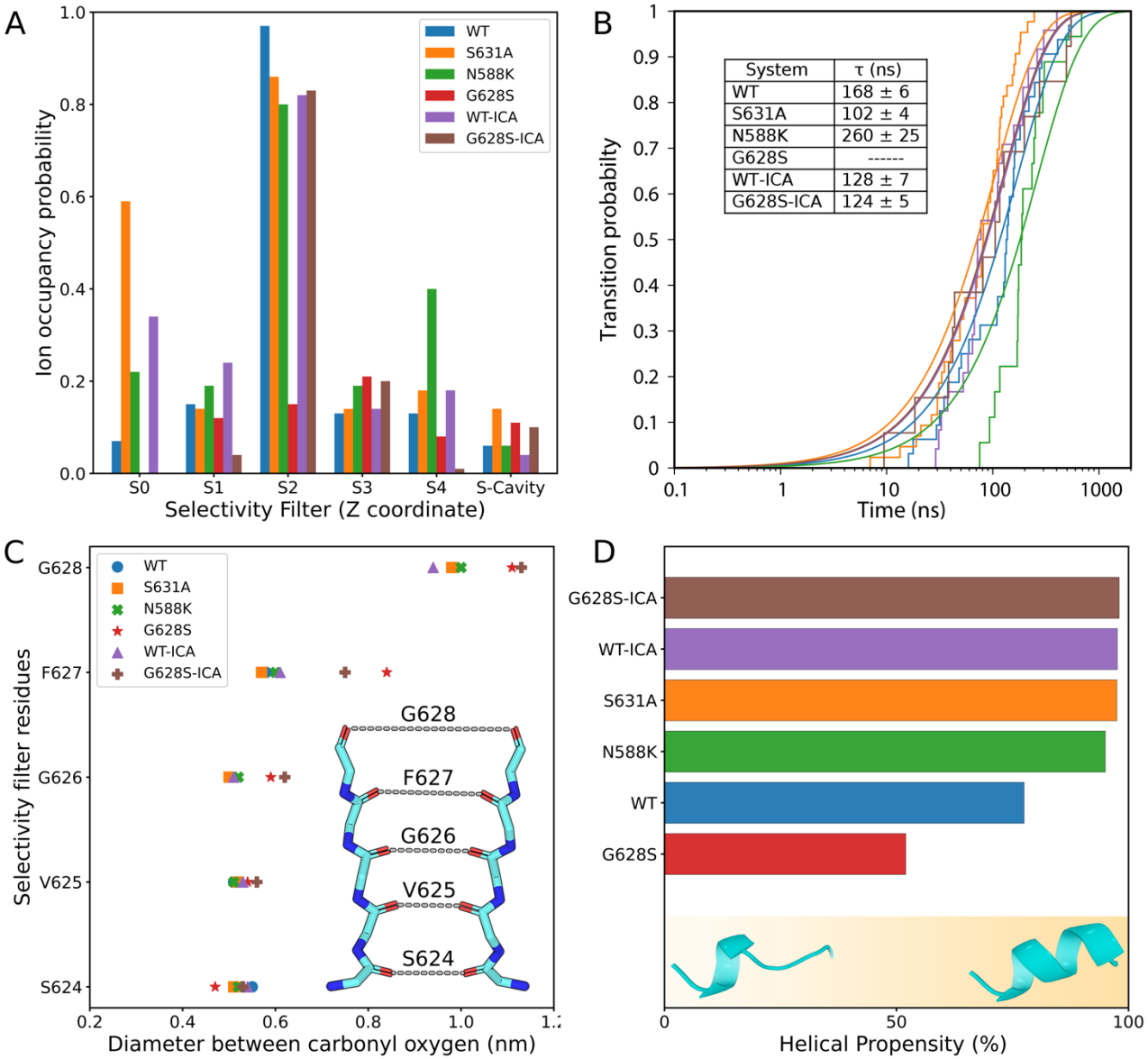

Figure 4. (A) The plot represents the ion occupancy probability at different sites in the selectivity filter over the simulations. The selectivity filter is divided into six different sites namely S0 to S4 and S_{cavity}. (B) The plot describes the transition probability of an ion crossing event and the average transition time for a single permeation event. No new ion permeation event was observed for the LQT2-G628S system except for the ions initially placed to prevent SF collapse. The inset table shows the average transition time for an ion permeation event in the hERG channel. (C) Open state definition of SF: The plot shows the diameter of the SF averaged over all replica trajectories. The diameter is calculated by averaging over the interchain distance between the opposite carbonyl oxygens of the SF residues. The Mutation G628S increases the diameter of the SF at the extracellular side. (D) The plot shows the helical propensity (%) of the S5P turret helix (residue number 584 to 592) in different systems. The values were averaged over the monomers for the replicated trajectories. Two distinct population clusters were observed for the helical region. The lower helical propensity around 30% is a weakly ordered structure which is prominent in the G628S mutation, whereas the higher helical propensity (> 90%) is represented as a well-structured helix in WT, SQTs (N588K, S631A) and ICA-bound systems. For comparison, see in *SI Appendix* **Figure S7,** which shows the population density of helical propensity in different systems.

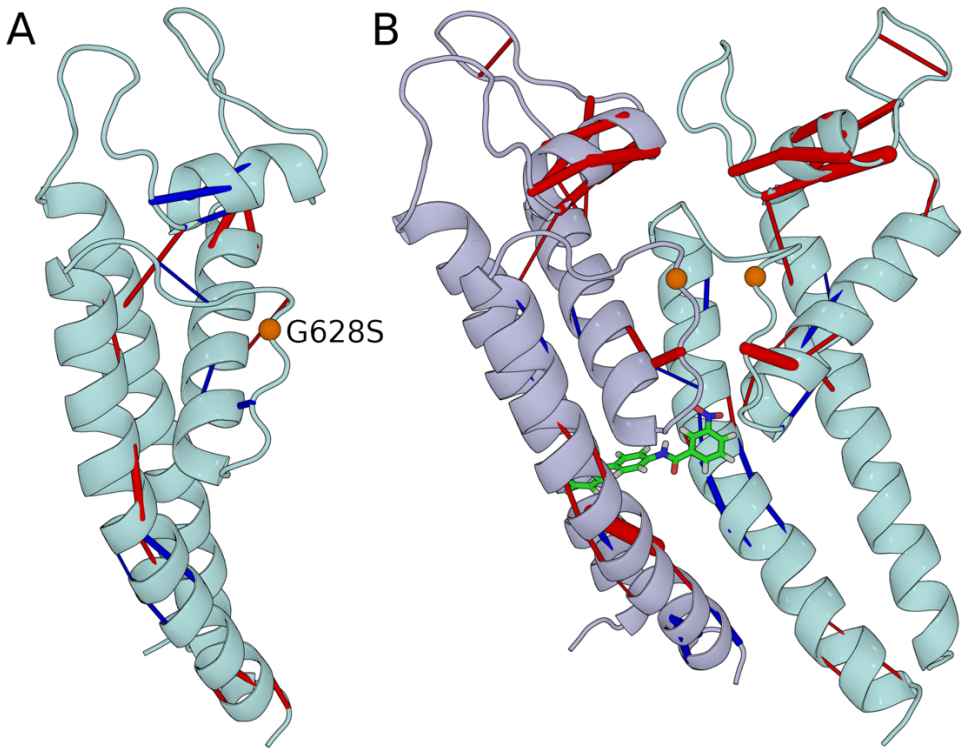

Figure 5. Hydrogen bond rearrangement upon perturbation in the form of mutation (G628S) or ligand binding (ICA-105574). The net H-bond occupancy (%) is highlighted in blue and red lines for the reference and the perturbed systems, respectively. The thickness of the lines represents the magnitude of the change. The G628S mutation is shown as an orange sphere. (A) Net H-bond occupancy (%) between G628S and WT ($\Delta HB_{ij} = HB_{ij}^{G628S} - HB_{ij}^{WT}$) shows the effect of the mutation in wild-type hERG: Blue lines show H-bonds that are lost in the mutant around the SF and the S5P turret helix, while red lines show H-bonds that are gained in the mutant at some residue pairs and the S6 helix end. (B) Net H-bond occupancy (%) between G628S-ICA and G628S ($\Delta HB_{ij} = HB_{ij}^{G628S-ICA} - HB_{ij}^{G628S}$) shows the rescue effect of ICA-105574: The figure shows two adjacent chains to represent different H-bonding patterns following the asymmetric binding of the activator in the hERG channel. ICA-105574 binding increases the H-bond occupancy around SF (Y616-S620, S620-G626) and S5P turret helix (G584-Q592) in both chains, while some residue pairs have opposite H-bond occupancy changes in G628S and ICA-105574 systems (e.g., E637-S641, M645-S649).

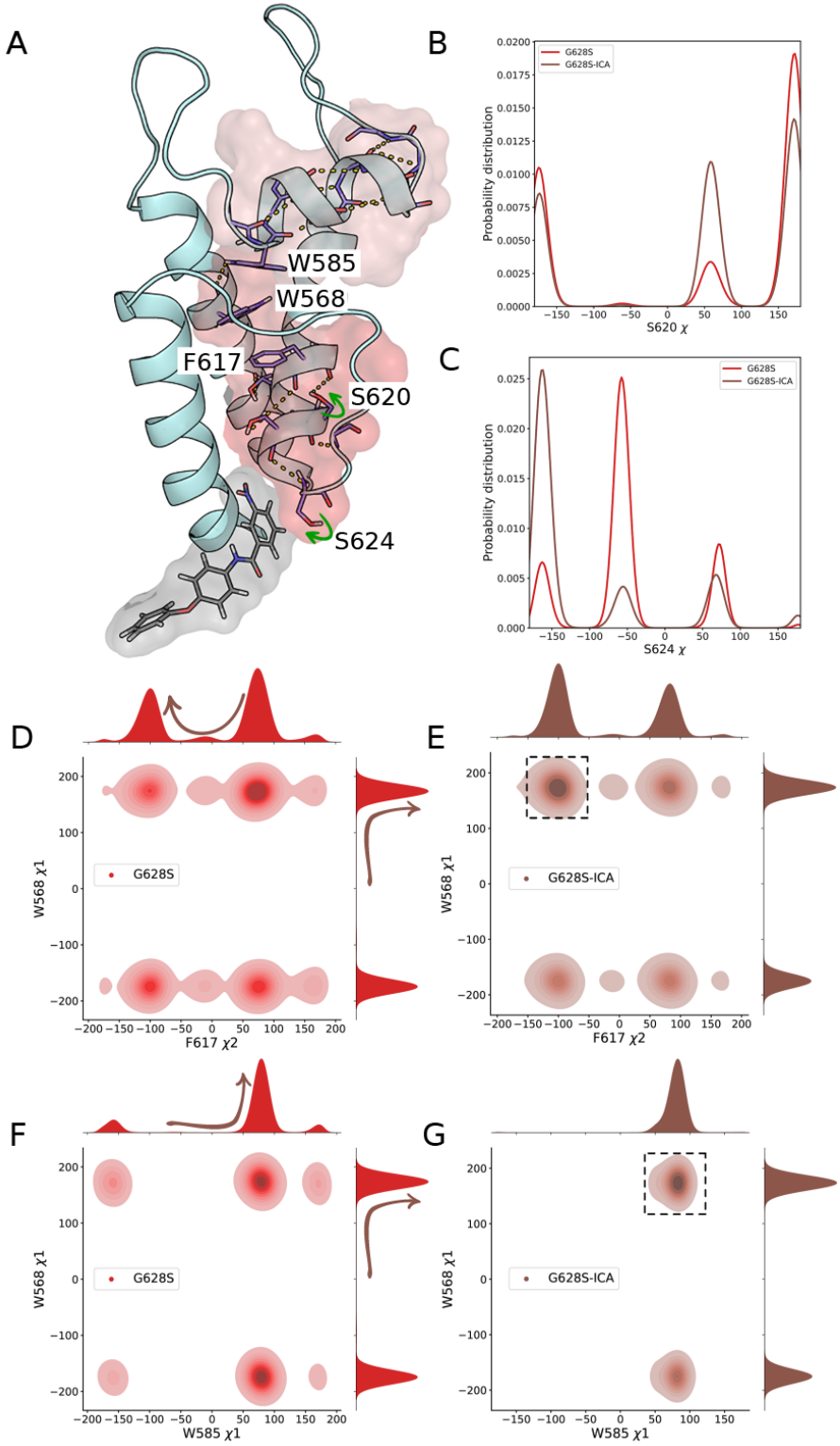

Figure 6. Mechanism of the rescue effect of the I_{kr} activator ICA-105574 in the G628S mutation. (A) The figure shows a schematic representation of the allosteric network linking ICA-105574 binding to the SF and the S5P turret helix in a single monomer chain of the G628S mutant. ICA-105574 and the residues with higher net H-bond occupancy in the G628S-ICA system are highlighted as sticks, with H-bonds indicated by dashed lines. The surface representation shows the propagation path, with the gradual decrease in color indicating increasing distance from the ligand binding site. (B, C) S624 is defined as the starting point of the network because it forms a favorable interaction with the nitro group of ICA-105574. The Chi *(χ)1* dihedral angle

distributions of S620 and S624 are shown as 1D histograms, indicating significant population shifts or changes in the side chain orientations upon ICA-105574 binding. (D-G) *χ2* dihedral distributions of residue pairs W568-F617 and W568-W585 in the G628S and G628S-ICA systems. The color opacity indicates the population density of each bin. The figure is plotted jointly for each axis variable with a 1D histogram to represent the population shift in the dihedrals. The arrows indicate the changes in the distribution upon ICA-105574 binding, while the dashed square box indicates the most populated basin in 2D distribution upon ICA-105574 binding. (D, E) show the 2D distribution of W568-*χ1* and F617-*χ2* angles, and (F, G) show the 2D distribution of *χ1* angle for W585-W568.