# New hyperekplexia mutations provide insight into glycine receptor assembly, trafficking and activation mechanisms

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Running title: *New glycine receptor hyperekplexia mutations*

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**Background:** Hyperekplexia mutations have provided much information about glycine receptor structure and function.
**Results**: We identified and characterized nine new mutations. Dominant mutations resulted in spontaneous activation whereas recessive mutations precluded surface expression.
**Conclusion:** These data provide insight into glycine receptor activation mechanisms and surface expression determinants.
**Significance:** The results enhance our understanding of hyperekplexia pathology and glycine receptor structure-function.

**ABSTRACT**

**Hyperekplexia is a syndrome of readily provoked startle responses, alongside episodic and generalised hypertonia that presents within the first month of life. Inhibitory glycine receptors are pentameric ligand-gated ion channels (pLGICs) with a definitive and clinically well-stratified linkage to hyperekplexia. Most hyperekplexia cases are caused by mutations in the α1 subunit of the human glycine receptor (hGlyR) gene (*GLRA1*). Here we analysed 68 new unrelated hyperekplexia probands for *GLRA*1 mutations and identified 19 mutations of which nine were novel. Electrophysiological analysis demonstrated that the dominant mutations p.Q226E, p.V280M and p.R414H induced spontaneous channel activity indicating this is a recurring mechanism in hGlyR pathophysiology. p.Q226E, at the top of TM1, most likely induced tonic activation via an enhanced electrostatic attraction to p.R271 at the top of TM2, suggesting a structural mechanism for channel activation. Receptors incorporating p.P230S (which is heterozygous with p.R65W) desensitized much faster than wild type receptors, and represents a new TM1 site capable of modulating desensitization. The recessive mutations p.R72C, p.R218W, p.L291P, p.D388A and p.E375X precluded cell surface expression unless co-expressed with α1 wild type subunits. The recessive p.E375X mutation resulted in subunit truncation upstream of the TM4 domain. Surprisingly, on the basis of three independent assays, we were able to infer that p.E375X truncated subunits are incorporated into functional hGlyRs together with unmutated α1 or α1 plus β subunits. These aberrant receptors exhibit significantly reduced glycine sensitivity. To our knowledge, this is the first suggestion that subunits lacking TM4 domains might be incorporated into functional pLGIC receptors.**

The glycine receptor chloride channel (GlyR), a member of the pentameric ligand-gated ion channel (pLGIC) family, mediates inhibitory neurotransmission in the spinal cord, brainstem and retina (1). Functional pLGICs comprise of homo- or hetero-pentamers with subunits arranged around a central ion-conducting pore (2). Each subunit contains an extracellular domain (ECD) harbouring the neurotransmitter binding site and a transmembrane domain (TMD) comprising four transmembrane α-helices (TM1-TM4) connected by flexible loops. A total of five GlyR subunit genes exist in humans (α1 – α4, β), although the α4 (*GLRA4*) locus is considered a pseudo-gene due to a premature stop codon in the TM3-TM4 domain (3). Synaptic GlyRs comprise two α and three β subunits (4,5) although extrasynaptic homomeric α GlyRs are also found (6). Since the α1β GlyR is the sole stoichiometry responsible for inhibitory neurotransmission in motor reflex arcs of the spinal cord (6), mutations impairing the function of either the α1 or β subunit would be expected to impair motor performance.

The evidence for the neuromotor role of the GlyR is provided by the unequivocal link between glycinergic genes and hyperekplexia, a rare neurological disorder (7,8). Hyperekplexia (also known as startle disease) is characterized by readily provoked startle responses, alongside a generalised and episodic hypertonia that presents within the first month of life. A proportion of cases have an increased likelihood of delay in speech acquisition, intellectual disability and recurrent neonatal and infantile apnoeas which gradually normalise during the first years of life. During development into adulthood the condition typically evolves into a life-long predisposition to excessive startle reflexes, triggered by unexpected auditory and tactile stimuli, which then cause startle-induced falls leading to repeated injuries. Hyperekplexia is caused not only by hereditary and *de novo* mutations in the human GlyR α1 and β subunit genes (7,9-13) but also by mutations in other proteins important for the formation and maintenance of glycinergic synapses (14-16). Mutations in the α1 and β subunits result in changes in the surface expression efficiency or in the functional properties of synaptic α1β GlyRs, thereby disrupting inhibitory neurotransmission in motor reflex circuits.

We previously presented the results of a sequencing screen of the GlyR α1 subunit (*GLRA1*) in 88 unrelated hyperekplexia probands from where we identified a total of 19 mutations, twelve of which were novel (10). We demonstrated that dominant mutations typically disrupt receptor function without changing their surface expression

efficiency whereas recessive mutations generally preclude functional receptor expression when expressed either as mutated α1 homomers or as heteromers with the β subunit. In the present study, 68 new unrelated patients with a clinical diagnosis of hyperekplexia were screened for mutations in *GLRA1*. The screening revealed a total of 19 mutations of which nine were novel. All new mutations were characterized in terms of their electrophysiological properties and their cell surface localization. Additionally, a previously characterized mutation, p.R65W (10), was re-investigated due to its presumed compound heterozygosity with the new mutation, p.P230S. The subsequent functional investigation of the hyperekplexia mutations revealed three residues critical for GlyR channel opening, providing insight into pLGIC activation mechanisms, and one novel residue playing an important role in desensitization.

## EXPERIMENTAL PROCEDURES

*Patient samples* - A total of 68 unrelated probands with a clinical diagnosis of hyperekplexia were recruited for this study with appropriate ethical approval and consent procedures in place (South West Wales REC). Referral was initiated from neurologists, paediatricians, or clinical geneticists from the UK and several international centres. Diagnostic criteria for hyperekplexia included a non-habituating startle response (positive nose tap test), often with neonatal apnoea, a history of infantile hypertonicity, and clinical exclusion of phenocopies such as startle epilepsy or early encephalopathy (17,18).

*Molecular genetics* - Multiplex PCR amplification (Qiagen, UK) was employed to rapidly amplify all coding exons and flanking intronic regions of *GLRA1*. Purified PCR amplimers were Sanger sequenced using ABI™ capillary technology (Foster City, USA). The frequency of variants identified was determined by screening a panel of 100 commercial control samples using restriction fragment length polymorphism (RFLP) if a suitable restriction enzyme was available, or by high-resolution melt analysis performed on Lightscanner (Idaho Technologies, USA). Detection of large deletions or insertions was performed using Multiplex Ligation-Dependent Probe Amplification (MLPA, MRC-Holland) according to the manufacturer's protocol. Additionally, confirmation of the recurrent exon 1-7 deletion mutation was carried out using a breakpoint PCR analysis (19). Mutations were introduced into pRK5-hGlyRα1 using the QuikChange site-directed mutagenesis kit (Stratagene, UK) and confirmed by direct sequencing of the entire transgene-coding region (10).

*Fluorescence-based imaging* - Experiments were performed on HEK AD293 cells cultured in Dulbecco's modified Eagle's medium supplemented with 10% fetal calf serum and 1% penicillin/streptomycin. The α1 wild type subunit, the β wild type subunit and the plasmids containing hyperekplexia mutations were all co-transfected in equal amounts. The pcDNA3-YFP-I152L plasmid was co-transfected in an amount equal to the sum of all transfected GlyR plasmid amounts. When the transfection was terminated 16 h later by rinsing with fresh culture medium, cells were plated into the wells of a 384-well plate. Within the following 24 – 32 h, the cell culture medium was replaced by an extracellular control solution (140 mM NaCl, 5 mM KCl, 2 mM $CaCl_2$, 1 mM $MgCl_2$, 10 mM HEPES, and 10 mM glucose, pH 7.4). Cells were imaged with an automated fluorescence-based screening system using YFP-I152L fluorescence quench as an indicator of anion influx rate (20). During experiments, fluorescence images of each well were obtained twice: once before and once after the application of a sodium iodide solution (140 mM NaI, 5 mM KCl, 2 mM $CaCl_2$, 1 mM $MgCl_2$, 10 mM HEPES, and 10 mM glucose, pH 7.4) containing defined concentrations of glycine. Mean percentage quench values represent data averaged from four experiments carried out on different plates. Each experimental value was an average of the percentage quench of all fluorescent cells in three wells on the same plate, with each well containing > 200 cells. To determine the glycine dose-response curve from these data, an empirical three parameter Hill equation was fitted by a non-linear least squares algorithm using SigmaPlot 12.0 software.

*Electrophysiology* - Glycine-gated currents were measured in HEK AD293 cells transfected as described above. Recordings were performed by whole-cell patch-clamp electrophysiology at a holding potential of -40 mV. Alternatively, spontaneous single-channel currents were recorded from outside-out excised patches, held at -70 mV in the absence of agonist, except for α1 wild type receptors, which opened too infrequently in glycine-free solution to obtain accurate estimates of current amplitude. Current amplitude for wild type receptors was instead estimated from recordings in the presence of 1 mM glycine. During experiments, cells were continually superfused with the extracellular control solution as detailed above. Patch pipettes were pulled to a final tip resistance of 1 – 4 MΩ (whole-cell) or 6 – 12 MΩ (outside-out) when filled with a standard intracellular solution (145 mM CsCl, 2 mM $CaCl_2$, 2 mM

$MgCl_2$, 10 mM HEPES, and 10 mM EGTA, pH 7.4). Whole-cell currents, which were filtered at 1 kHz and digitized at 2 kHz, were recorded using an Axon MultiClamp 700B amplifier (Molecular Devices). Single-channel currents, filtered at 5 kHz and digitized at 20 kHz, were recorded using an Axon Axopatch 200B amplifier (Molecular Devices). Voltage-clamp fluorometry experiments were performed as previously described (21). Briefly, oocytes were removed from the ovaries of *Xenopus laevis* frogs, incubated in OR-2 (82.5 mM NaCl, 2 mM KCl, 1 mM $MgCl_2$, and 5 mM HEPES, pH 7.4) containing 1.5 mg/ml collagenase for 2 h at room temperature on a shaker and co-injected with 5 ng pGEMHE-hGlyRα1 and 25 ng pGEMHE-hGlyRα1-R271C/E375X RNA into the cytosol. Oocytes were cultured for 2 – 3 days at 18 °C in ND96 (96 mM NaCl, 2 mM KCl, 1 mM $MgCl_2$, 1.8 mM $CaCl_2$, and 5 mM HEPES, pH 7.4) containing 275 mg/l sodium pyruvate, 110 mg/l theophylline and 0.1 % (v/v) gentamicin. For labelling, oocytes were incubated with 10 μM sulforhodamine methanethiosulfonate (MTSR) diluted in ND96 for 1 min on ice. 3 mM KCl was used as internal solution and recordings were performed at -40 mV.

*Immunofluorescence* - GlyR α1 subunits were transiently expressed in HEK293 cells using the Magnetofection™ method (Oz Biosciences). Around 24 h post-transfection, cells were fixed in 4 % (w/v) paraformaldehyde (PFA) for 5 min at room temperature. Cells were quenched with 50 mM $NH_4Cl$ in PBS. Fixed cells were permeabilised with PBS containing 0.1 % (v/v) Triton X-100 (Sigma), 10 % (v/v) fetal calf serum (Sigma) and 0.5 % (w/v) bovine serum albumin (fraction V; Sigma) to allow for intracellular immunostaining. Receptor sublocalization was determined using rabbit monoclonal anti-GlyR α1 (1:400, Millipore) primary antibody and with goat anti-rabbit secondary antibody, conjugated with AlexaFluor 488 (1:200, Invitrogen). Cell surface immunostaining was conducted using the same reagents, antibodies and dilutions but carried out prior to PFA fixation. Fixed cells were then quenched with 50 mM $NH_4Cl$ before mounting on glass slides. Cell images were acquired using a Zeiss LSM 710 confocal microscope with ZEN software. The master gain was kept constant to compare the expression of α1 GlyR mutants relative to wild type. Transfection was repeated three times.

*Molecular modelling* - Wild type and mutated forms of the human α1 GlyR were modelled by 50 % homology (69 % sequence coverage) with PDB structure 3RHW, the glutamate-gated chloride channel receptor (α GluClR) from *C. elegans* (22). Using our multi-template homology modelling pipeline, this was one of three PDB homologues that were identified and used in the assembly of the α1 GlyR models, 3RHW (chain E), 1VRY (chain A) and 1MOT (chain A). The homology modelling pipeline was built with the Biskit structural bioinformatics platform (23). Our pipeline workflow incorporates the NCBI tools platform (24), including the BLAST program for similarity searching of sequence databases. T-COFFEE (25) was used for alignment of the test sequence with the template, followed by iterations of the MODELLER-9.11 program (26) to generate the final model structure. The Chimera program (27) was used for the viewing of models and generation of images.

## RESULTS

*Mutation analysis* - A total of 68 probands with hyperekplexia were assessed for genetic variation in *GLRA1* coding regions. All sequence variations were cross-referenced with the dbSNP database and our previous *GLRA1* datasets (for recurrent mutations) and were regarded as probable mutations following exclusion from a panel of 100 control samples and exome variants server (http://evs.gs.washington.edu/EVS/). The screening revealed 19 mutations in 21 hyperekplexia probands (Table 1), a rate which is consistent with previous studies (10,28). Nine mutations were novel in the public domain and three (one novel and two recurrent) mutations were present in more than one individual. Note that p.R414H has since been reported as a very rare variant in dbSNP (rs200130685), with a heterozygosity of 0.002 and a Minor Allele Frequency (MAF) of 0.0233 from the exome variants server. Consistent with previous studies, deletion and nonsense mutations were associated with recessive inheritance (homozygous or compound heterozygous) whereas missense mutations resulted in a dominant or recessive effect depending on their position in the polypeptide. The majority of index cases showed recessive inheritance (15 / 21; 71 %) including cases 12 and 19 with confirmed compound heterozygosity as mutations were segregated back to parental DNA. It is likely that sample 5 represents a third case of compound heterozygosity; however, parental DNA was not available for confirmation. Four index cases of Turkish origin displayed a recessive homozygous deletion of exons 1-7 further confirming this deletion as a significant population-specific risk-allele (10,29). Dominant mutations were mainly located in the discrete transmembrane α-helices whereas recessive mutations were spread throughout the protein. Phylogenetic alignment of

all novel missense mutations established that they altered conserved amino acids and were protein-damaging when assessed using Sorting Intolerant from Tolerant (SIFT) tool (accessible at http://sift.jcvi.org/). The functional impact of the novel mutations was further investigated under recombinant conditions that simulated the dominant, recessive and compound heterozygous inheritance modes.

*Functional high-throughput analysis* - The first round of functional characterization involved imaging live transfected cells via an automated fluorescence-based screening system using YFP-I152L fluorescence quench as an indicator of anion influx rate (20). The advantage of this approach over electrophysiology is that responses of large cell numbers can be averaged, thus permitting the reliable quantitation of small changes in the functional expression levels of mutated GlyR isoforms. To investigate the functional properties of the mutated receptors, HEK AD293 cells were transiently transfected with wild type and mutated subunits in various combinations in an attempt to simulate dominant, recessive and compound heterozygous inheritance modes. Each mutated subunit was expressed on its own, with the β wild type subunit, with the α1 wild type subunit and with both α1 and β wild type subunits together. These experiments are summarized as: 1) mutant alone, 2) mutant + β, 3) mutant + α1, 4) mutant + α1β. For compound heterozygous mutations, the mutated subunits were also co-transfected together with and without the β wild type subunit, i.e., 5) 1$^{st}$ mutant + 2$^{nd}$ mutant, 6) 1$^{st}$ mutant + 2$^{nd}$ mutant + β. Fluorescent cells were considered as expressing functional GlyRs when the quench was a least 10 % greater than the quench from cells expressing YFP only (no receptors).

Glycine dose-response experiments showed that the glycine sensitivity was reduced for all recessive and compound heterozygous mutations relative to α1 wild type GlyRs (Fig. 1A). With the exception of the p.P230S mutation which expressed as a homomer, the recessive and compound heterozygous mutated subunits only showed a response to glycine if the α1 wild type subunit was co-expressed. Note that co-expression of these mutated α1 subunits with the β wild type subunit did not produce functional expression. Receptors incorporating both compound heterozygous mutations, p.L291P and p.D388A, showed no evidence of glycine sensitivity regardless of the presence of the β subunit. In contrast, receptors incorporating both p.R65W and p.P230S responded to glycine with and without β subunit co-expression, albeit with dramatically reduced glycine sensitivity. As the glycine sensitivity was decreased for all mutated subunits when co-expressed with the α1 wild type subunit, we concluded that all recessive and compound heterozygous mutated subunits were incorporated into functional GlyRs as heteromers, if not as homomers.

For the three novel dominant mutations, in the case of p.R414H, no significant change in glycine $EC_{50}$ was detected (Fig. 1A), and for receptors containing the dominant mutations p.Q226E and p.V280M, the glycine sensitivity could not be determined as fluorescence quench was complete in the absence of glycine. To test whether these three mutations formed spontaneously active channels, we initially bathed cells in NaCl solution and then introduced a high concentration of NaI solution containing no glycine. The results of this experiment, summarised in Fig. 1B, show that receptors containing p.Q226E, p.V280M or p.R414H subunits displayed significant quench in the absence of glycine. As iodide is highly permeant through GlyRs and quenches YFP-I152L fluorescence much more potently than chloride does, this result provides evidence that these three mutations result in spontaneously active or 'leaky' channels. Indeed, the high level of spontaneous activity was the reason why the glycine sensitivity of receptors incorporating p.Q226E and p.V280M mutations could not be quantitated (Fig. 1A).

In addition, for all functional channels, the anion influx rate was significantly reduced relative to α1 wild type receptors as indicated by their reduced maximal glycine-induced fluorescence quench magnitude (Fig. 1C). As noted above, the fluorescence quench for p.Q226E- and p.V280M-containing GlyRs was already maximal in the absence of glycine. Moreover, the percentage of quenched cells relative to the total number of fluorescent cells was significantly reduced for all functional channels relative to α1 wild type receptors (except for p.R414H) suggesting that fewer functional receptors are located at the cell surface (Fig. 1D). This observation suggests that the mutations tend to impair functional receptor expression.

*Spontaneous activity as a mechanism for dominant hyperekplexia mutations* - We then employed patch-clamp electrophysiology to analyse the effects of the mutations on receptor function at greater precision. Examples of currents activated by increasing glycine concentrations at homomeric α1 GlyRs together with the averaged glycine dose-response relationship are shown in Fig. 2. The mean glycine $EC_{50}$ value of p.Q226E indicates that the glycine sensitivity was not significantly altered

(Fig. 2A, Table 2). In contrast, for receptors incorporating the dominant mutation p.V280M, the sensitivity to glycine was dramatically increased relative to wild type receptors (Fig. 2B, Table 2). The mean glycine $EC_{50}$ value of p.R414H was modestly increased (Fig. 2C; Table 2). These results are broadly consistent with the fluorescence data shown in Fig. 1.

For the three novel dominant mutations, our fluorescence assay predicted spontaneous activity for p.Q226E, p.V280M and p.R414H receptors (Fig. 1B) which was then further investigated by recording single channel activity in outside-out membrane patches bathed in glycine-free extracellular solution. Recordings revealed spontaneous activity for all three mutated homomeric receptors whereas little, if any, spontaneous activity was ever observed for wild type α1 GlyRs (Fig. 3A) consistent with previous reports (30). At a membrane potential of -80 mV, the single channel current amplitude for p.Q226E receptors was smaller (4.5 ± 0.1 pA, n = 4 patches, Fig. 3B) than for wild type α1 receptors (7.2 ± 0.1 pA, n = 3, Fig. 3A), whereas the amplitude for p.V280M receptors was unchanged (7.1 ± 0.2 pA, n = 3, Fig. 3C) and the magnitude of p.R414H receptors was larger (8.4 ± 0.2 pA, n = 3, Fig. 3D). The corresponding conductance values at −70 mV, a $Cl^-$ equilibrium potential of 0 mV, and a liquid junction potential of 4 mV, were; 97.3 pS, 60.8 pS, 95.9 pS and 110.8 pS for wild type, p.Q266E, p.V280M and p.R414H receptors, respectively. Applying a saturating concentration of glycine, measuring the peak current response and dividing that by the single channel amplitude provided an estimate of the minimum number of channels contained in each recorded patch. Open probability (Po) was determined using segments of record that contained no evidence of multiple, superimposed openings. A total of 5 - 6 minutes of recording was selected across 3 - 4 patches for each channel type. Estimated Po values determined in this way should be regarded as upper limits and were as follows: p.Q226E, 0.03; p.V280M, 0.07; p.R414H, <0.001. Wild type homomeric receptors opened too infrequently in glycine-free solution to obtain a reliable Po measurement. It was, however, dramatically reduced relative to the mutated GlyRs.

*Incorporation of TM4 truncated subunits* - Subunits incorporating the recessive mutations, p.R72C, p.R218W or p.E375X, were only functional when co-expressed with the α1 wild type subunit. The glycine sensitivities and the maximal current amplitudes of receptors incorporating these mutations were reduced relative to those of wild type receptors (Fig. 4A-D, Table 2) in agreement with the results from the fluorescence assay (Fig. 1). For all α1β heteromeric receptors, β subunit incorporation was confirmed pharmacologically by its characteristic reduction in sensitivity to lindane inhibition (31) For example, in Fig. 4D (lower panel) we confirmed that α1 wild type GlyRs are strongly inhibited by 100 μM lindane, whereas α1β wild type GlyRs are resistant. As receptors formed by co-expression of p.E375X, α1 wild type and β wild type subunits were also resistant to lindane and showed decreased glycine sensitivity relative to α1β GlyRs (Fig. 4D, Table 2), we infer that p.E375X subunits were incorporated into functional α1β heteromeric GlyRs.

We were surprised to observe that the truncation mutation, p.E375X, which has lost the TM4 domain, reduced the glycine sensitivity significantly ($p < 0.001$ relative to α1 wild type via unpaired t-test) when co-expressed with the α1 wild type subunit (Fig. 4C, D). The reduced glycine sensitivity was only partly compensated by co-expressing the β wild type subunit. This result strongly suggests that the truncated subunit is incorporated into functional receptors which is unexpected given that previous GlyR studies indicated that TM4 deletion is incompatible with the surface expression of functional α1 GlyRs (32-35). Given our unexpected result, we sought to confirm whether the p.E375X mutant subunit was incorporated into functional GlyRs using voltage-clamp fluorometry.

Voltage-clamp fluorometry involves introducing a cysteine into a receptor domain of interest and covalently tagging it with a sulfhydryl-labelled fluorophore, commonly a rhodamine derivative such as MTSR. Because the quantum efficiency of rhodamine fluorescence is proportional to the hydrophobicity of its environment, a glycine-induced fluorescence change can be interpreted as a local conformational change at the labelled site (36). Voltage-clamp fluorometry is thus able to report conformational rearrangements in real time at defined locations on the surface of the labelled subunit. These experiments were performed on receptors expressed in *Xenopus* oocytes as HEK293 cells exhibit an unacceptably high level of non-specific MTSR labelling. The MTSR-labelled p.R271C mutant α1 GlyR produces a fluorescence change of ~20 % upon activation with 10 mM (saturating) glycine (21). When the p.E375X truncation subunit, also labelled at p.R271C, was expressed together with the α1 wild type subunit, the activation of the recombinant receptors by saturating (10 mM) glycine generated currents with a mean maximal current amplitude of 4.8 ± 0.5 μA and a maximal change in fluorescence of 0.7 ± 0.1

% (n = 4; Fig. 4E). Control current and fluorescence traces from an MTSR-labelled p.R271C mutant GlyR are also shown. In contrast, unlabelled GlyRs comprising the same subunits yielded no significant glycine-induced fluorescence change (data not shown). This provides strong evidence for the surface expression of p.E375X subunits, and also suggests they experience a conformational change upon glycine-induced receptor activation. As the fluorescence change we observed is smaller than the change in fluorescence for homomeric p.R271C mutant α1 GlyRs (21), we infer that the p.E375X subunit is either incorporated into functional receptors at a low rate or that its conformational change is different from that of full length p.R271C α1 GlyRs.

*Functional effects in heterozygous state* - Receptors incorporating the compound heterozygous mutation p.R65W showed drastically decreased glycine sensitivity and decreased maximal current amplitudes independent of β subunit expression (Fig. 5A; Table 2). The p.P230S mutation also decreased glycine sensitivity and maximal current amplitudes in the presence and absence of the β subunit (Fig. 5B; Table 2). All electrophysiological results for the p.R65W and p.P230S mutations are consistent with the fluorescence data described above (Fig. 1). It is also evident in Fig. 5B that p.P230S induces fast desensitization. These receptors exhibited a mean decay time constant of 0.9 ± 0.3 s for 3 mM glycine (*c.f.,* wild type receptors: 7.2 ± 1.7 s). Receptors containing the compound heterozygous mutations p.L291P or p.D388A were only functional when each mutated α1 subunit was co-expressed with the α1 wild type subunit (Fig. 1). Electrophysiological recordings revealed that the p.L291P mutation decreased glycine sensitivity but not maximal current amplitudes (Fig. 5C; Table 2). The p.D388A mutation decreased glycine sensitivity and maximal current amplitudes (Fig. 5D; Table 2). For both mutations, the changes relative to wild type receptors were independent of β subunit expression. Again, these results are consistent with the fluorescence data presented in Fig. 1.

*Cell surface localization* - Confocal microscopy of transfected cells immunostained with an α1 GlyR antibody was performed to analyse subcellular localization of wild type and mutated receptors. Permeabilised cells were used to determine the intracellular sublocalization of receptors with all constructs showing comparable intracellular expression (Fig. 6, left hand image of each image pair). Cell surface expression was visualised in non-permeabilised cells. Cells transfected with wild type and the dominant mutations p.V280M and p.R414H showed immunoreactivity around the cellular circumference indicating localization at the surface (Fig. 6, right images), suggesting these variants do not affect integration of GlyRs into the cell membrane. The p.Q226E dominant mutation showed reduced immunoreactivity at the cell surface, suggesting it may impair integration into the surface membrane, unlike the other dominant mutations. The cell surface expression levels of recessive mutated receptors observed in this study showed partial or complete loss of cell surface accumulation. The recessive mutations p.R65W, p.P230S and p.L291P showed decreased integration into the surface membrane with only partial punctate staining, whilst p.R72C, p.R218W, p.D388A and p.E375X were completely absent from the cell membrane displaying only cytoplasmic staining (Fig. 6, right images). Surface accumulation of α1 subunits containing these mutations was not detectable with any of the three transfection procedures.

*Molecular modelling* - A homology model based on the *C. elegans* α GluClR crystal structure was used to determine structural mechanisms by which novel mutations disrupted GlyR structure and function (Fig. 7). In particular, the spontaneously active channel p.Q226E affected the TM1 domain towards its extracellular end (Fig. 7A, B). Structural modelling showed extension of the TM2 and TM3 helices at their extracellular end, along with extension of the TM4 helix at its intracellular end. Given that p.Q226E faces across the subunit interface towards p.R271 of the adjacent subunit (not shown), an enhanced electrostatic attraction between these two residues may be responsible for the tonic activity induced by p.Q226E. The other spontaneous opener p.V280M affected the extracellular loop between the TM2 and TM3 domain (Fig. 7C). This mutation was also found to introduce a kink at the extracellular end of the TM1 helix, perhaps via an altered energetic or steric interaction with I225 across the subunit interface. Also, the TM2 helix was extended at its extracellular end whereas the TM4 helix was extended at its intracellular end, along with a conformational change at this site. We also observed changes to the conformation of the extracellular domain. In the p.V280M receptor, the α-helix that is found in the wild type subunit between D12 and R20 was lost and a short helix was introduced around position 72 which would explain its dramatically altered glycine sensitivity. p.R414H affected the C-terminal region at the extracellular end of the TM4 domain causing profound loss of helical conformation at the

cytoplasmic end of the TM4 domain and extension of the TM2 helix at its extracellular end (Fig. 7D). Structural modelling suggested that the truncation mutation p.E375X, which lacks the TM4 domain, caused major conformational changes in the TM2 helix via extension of the TM2 helix at its extracellular end and loss of the short helix at the top of the extracellular domain (Fig. 7E). The fast desensitizer p.P230S affected the TM1 domain, directly causing a major conformational change by introducing a profound kink at the extracellular end (Fig. 7F). In addition, a major conformational change at the cytoplasmic end of the TM3 helix was detected, producing another kink, and substantial changes to the TM4 helix. Conformational changes in the extracellular domain included loss of the short helix at the top and β sheet compression.

The impact of the novel dominant mutations upon the pore radius is shown in Fig. 7G. For the spontaneously active receptors p.Q226E and p.V280M, a channel widening of 1.3 Å and 4.3 Å, respectively, at the cytoplasmic exit was detected relative to wild type receptors which is consistent with the observations of a leaky channel. In contrast, the mutation p.R414H had no effect on the pore diameter at the cytoplasmic exit but demonstrates substantial widening towards the extracellular entry explaining the observed spontaneous channel openings.

## DISCUSSION

This study has identified a further 21 *GLRA1*-positive hyperekplexia probands (Table 1) with 19 mutations, of which nine were novel, adding to the compendium of *GLRA1* mutations. Consistent with previous studies (10,37-40), dominant mutations were expressed at the cell surface thereby causing changes to the glycine sensitivity, conductance and/or open probability. In contrast, recessive and compound heterozygous mutations mainly affected cell surface trafficking and insertion of receptors into the membrane (10,41-43). The mechanisms by which each novel mutation caused hyperekplexia will now be considered in detail.

Genetic screening identified three novel autosomal dominant mutations, p.Q226E, p.V280M and p.R414H, that each produced spontaneously active channels. Prior to this study, only one hyperekplexia mutation (Y128C) was known to produce spontaneous activity (10). This mutation was also autosomal dominant. Spontaneous activity was evident not only in mutated homomeric channels, but also in channels formed by the co-expression of mutated subunits and α1 wild type subunits and/or β wild type subunits (Fig. 1, 2). Structural modelling predicted that the mutations p.Q226E and p.V280M cause a widening of the outer channel pore leading to spontaneous activity. The p.V280M mutation dramatically increased both the level of spontaneous activity and glycine sensitivity, suggesting a drastic destabilisation of the closed channel state. The loss of the β sheet structure around the constraining loop C glycine binding domain is likely to impact upon glycine binding and retention, rendering the glycine binding site much more accessible. The kink introduced by p.V280M to the cytoplasmic end of the TM3 domain affects the close TM2-TM3 packing, reducing the stability of the closed channel, due to greater conformational freedom at the cytoplasmic end of the TM2 domain. Given that p.V280M-containing GlyRs expressed strongly at the cell surface (Fig. 6), the high level of spontaneous activity may partly explain the observed reduction in peak glycine-induced current magnitude. A reduction in the glycine-inducible current magnitude, coupled with a possible diminution of the chloride electrochemical gradient caused by the high level of spontaneous activity, may be among the mechanisms by which the p.V280M mutation disrupts glycinergic signalling.

In contrast, the glycine sensitivities of p.Q226E- and p.R414H- containing receptors were similar to that of wild type receptors and both mutations caused spontaneous activity. However, modest reductions in the single channel conductance and the cell surface expression efficiency would have reduced the chloride flux-carrying capacity of p.Q226E-containing GlyRs and therefore may have contributed to the hyperekplexia phenotype (Fig. 2D, 6). Given that p.Q226E is closely apposed with p.R271 of the adjacent subunit, we hypothesise that the enhanced electrostatic attraction between these oppositely-charged residues may be responsible for the tonic receptor activity. In the p.R414H GlyR, the extremely low spontaneous open probability seems unlikely to have caused a hyperekplexia phenotype on its own, as the expression efficiency and glycine sensitivity were not diminished relative to that of wild type receptors. One possibility is that the mutation altered TM4 orientation and thus TM3-TM4 loop structure, leading to a change in propensity of this subunit to bind clustering proteins at synapses. No effect on the predicted structure of the extracellular domain fits with wild type comparable glycine sensitivity seen for this mutation. However, the main difference to the wild type monomer is the loss of α-helical structure at the cytoplasmic end of the TM4 domain. This region is at the outside of the pentamer and contains an unusually high proportion of charged

residues for a transmembrane region, 382-QRAKKIDKISR-392, which is completely disrupted in p.R414H receptors.

The recessive p.R72C, p.R218W and p.E375X mutations all precluded the surface expression of mutated homomeric GlyRs (Fig. 1, 4). However, when each mutated subunit was co-expressed with α1 wild type or α1 and β wild type subunits, robust glycine-activated currents were observed. As the glycine sensitivity of the resultant p.E375X receptor was significantly decreased relative to homomeric α1 GlyRs, we infer that the p.E375X subunit was incorporated into functional receptors together with either α1 subunits alone or with α1 plus β subunits. Because this result was unexpected, it was substantiated using voltage-clamp fluorometry (Fig. 4E). We also attempted to confirm it using immunofluorescence, but the incorporation rate may have been too low to allow surface expression to be detected. As noted above, we were surprised that the p.E375X subunit was incorporated given that previous studies have shown that TM4 deletion is incompatible with the surface expression of functional α1 GlyRs (32-35). Indeed, the deletion of only a few residues at the C-terminal end of the TM4 domain is sufficient to render some pLGIC receptors completely non-functional (12,44,45).

To our knowledge, this is the first suggestion that a pLGIC receptor subunit may be functionally expressed without a TM4 domain. The human GlyR α4 subunit (Uniprot accession number Q5JXX5) has long been regarded as a pseudo-gene because it incorporates a stop codon that truncates the receptor prior to the TM4 domain (Simon et al., 2004). The truncation occurs at the D383 residue which corresponds to Q382 in the α1 subunit. As this is C-terminal of E375, it is possible that the α4 subunit may be incorporated into functional GlyRs suggesting it could exert a physiological role in modulating the functional properties of GlyRs. There may also be a case to reassess the pathophysiology of the other pLGIC late protein truncating events in epilepsy and related disorders, for example GABA type-A receptor mutations (46).

Genetic analysis suggested possible heterozygosity between p.R65W and p.P230S although parental DNA was not available to confirm this. We previously described p.R65W as recessive on the basis of both the genetic analysis and a trafficking defect when expressed in the homozygous state (10). The present study shows that GlyRs comprised of p.R65W plus α1 and β wild type subunits exhibited a 20-fold increase in the glycine $EC_{50}$ value (Fig. 1, 5). As this reduction in glycine sensitivity should be easily enough to cause hyperekplexia on its own (47,48), it implies that the p.R65W mutation should be inherited in an autosomal dominant manner. It therefore remains a mystery why heterozygous parents remain asymptomatic, possibly implying the existence of compensating physiological mechanisms. The p.P230S mutation produced fast desensitising receptors, reduced peak glycine-activated current magnitude and modestly reduced glycine sensitivity (Fig. 1, 5). All of these effects remained when the mutated subunit was co-expressed with α1 and/or β wild type subunits, implying that p.P230S should also exhibit an autosomal dominant inheritance mode. As expected, when p.R65W, p.P230S and β wild type subunits were co-expressed to mimic compound heterozygosity, glycine sensitivity and peak current magnitudes were drastically reduced (Fig. 1A, C), readily accounting for the hyperekplexia phenotype.

As R65 forms a crucial component of the glycine binding site (5,49), the non-conservative p.R65W mutation most likely disrupts glycine binding when functionally expressed with wild type subunits. Our finding that it is not trafficked to the surface when expressed as a homomer (Fig. 1) is most likely the result of a global structural disruption caused by this mutation (10). As GlyR desensitization involves a specific conformational change at the ECD-TMD interface (50), the effect of the p.P230S mutation on desensitization may be due to a conformational change at this interface.

Genetic analysis confirmed that the p.L291P and p.D388A mutations exhibited compound heterozygosity. Our functional analyses revealed that both mutated subunits did not express as homomers and exhibited reduced glycine sensitivity when individually co-expressed as heteromers with α1 and β wild type subunits (Fig. 1, 5). We were unable to detect functional surface expression following co-expression of both p.L291P and p.D388A with β wild type subunits which would account for the hyperekplexia phenotype.

In conclusion, this study illustrates the importance of hyperekplexia mutations in identifying new insights into the structure and function of GlyRs and other pLGIC family members. This in turn allows us to provide a more definitive explanation of the phenotype and clinical impact of the gene-positive patients through stratification of disease mechanisms.

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**FIGURE LEGENDS**

**Fig. 1.** Functional characterization of novel mutations using fluorescence-based imaging. A. Normalized glycine $EC_{50}$ values for receptors comprised of the indicated subunit combinations. Results for p.Q226E and p.V280M containing GlyRs are not shown as complete quench occurred in the absence of glycine. For all other mutated receptors, the absence of a plotted result means that the indicated subunit(s) did not express. B. Mean percentage fluorescence quench observed when NaCl solution was replaced by NaI solution (without glycine). C. Normalized maximal changes in fluorescence observed upon the addition of NaI containing saturating glycine. The maximal change in fluorescence is presented as the final (quenched) fluorescence value minus the initial fluorescence value. D. Mean number of quenched cells expressed as a percentage of the total number of fluorescent cells. In panels A, C and D, all mutant values were normalised relative to the wild type value obtained from the same plate. In all panels, p-values were calculated relative to the α1 GlyR using one-way ANOVA followed by Dunnett's post-hoc test: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$.

**Fig. 2.** Functional characterization of autosomal dominant mutations by whole-cell and outside-out patch-clamp recording. A. Sample whole-cell current recording for homomeric p.Q226E GlyRs. In this and all subsequent Figures, horizontal bars indicate the duration of the glycine applications with concentrations shown in μM. The right panel represents averaged whole-cell glycine dose-response curve for the p.Q226E GlyR. The α1 GlyR dose-response curve plotted here is replicated in all panels displaying dose-response curves in this and subsequent figures. B. Sample whole-cell current recording and averaged whole-cell glycine dose-response curve for the homomeric p.V280M GlyR. C. Sample whole-cell current recording and averaged whole-cell glycine dose-response curve for the homomeric p.R414H GlyR. Averaged parameters of best fit to all individual dose-response relationships are summarized in Table 2.

**Fig. 3.** Single channel recordings of homomeric α1 wild type and spontaneously open mutant GlyRs. A. Single channel current recording of a patch expressing wild type receptors in the absence of glycine. Due to its low open probability in glycine-free solution, the higher resolution recording and accompanying amplitude histogram was obtained in 1 mM glycine. B. A sample recording of spontaneous single channel activity in an outside-out patch expressing p.Q226E, along with the amplitude histogram for the same patch. C. A sample single channel recording from a patch expressing p.V280M receptors, along with the amplitude histogram for the same patch. D. A sample single channel recording from a patch expressing p.R414H receptors, along with the amplitude histogram for the same patch. Channel openings are represented by downward deflections with the mean open current level indicated by dashed lines. The recordings in B-D were made in glycine-free solution. For these recordings, the activity above the horizontal bar in the lower resolution segment is reproduced at higher resolution below. Mean channel conductances and open probabilities are given in the text.

**Fig. 4.** Functional characterization of autosomal recessive mutations by whole-cell patch-clamp recording and voltage-clamp fluorometry. A. Sample glycine dose-response trace for p.R72C GlyRs co-expressed with the α1 wild type subunit and normalized glycine dose-response relationship. B. Sample glycine dose-response trace for p.R218W GlyRs co-expressed with the α1 wild type subunit and normalized glycine dose-response relationship. C. Sample glycine dose-response traces for p.E375X GlyRs expressed together with α1 wild type or α1 wild type plus β wild type subunits as indicated. For this and all subsequent current recordings, unfilled bars represent the application of 100 μM lindane. The lack of lindane inhibition indicates strong expression of β subunits. The α1β GlyR dose-response curve plotted here is replicated in all dose-response curve panels in Fig. 5. The bottom panel shows evidence for the efficient incorporation of β subunits into functional GlyRs. α1 homomeric GlyRs are strongly inhibited by 100 μM lindane (left), whereas α1β GlyRs are resistant (center panel). The right trace, recorded from the same cell as represented

above in panel C, shows that channels formed by the co-expression of p.E375X, α1 and β wild type subunits are also resistant to lindane. Using an unpaired t-test, mean lindane inhibition of these mutated receptors was significantly different to α1 ($p < 0.001$) but not to α1β receptors ($p = 0.393$). D. Normalized glycine dose-response curves for α1 homomeric and α1β heteromeric receptors incorporating p.E375X. Averaged parameters of best fit to all individual dose-response relationships are summarized in Table 2. E. Sample current (black) and fluorescence (grey) responses induced by the application of 10 mM glycine in receptors comprising p.R271C/E375X and α1 wild type subunits and labelled with MTSR. Averaged results are summarized in the text. Control recordings from MTSR-labelled p.R271C GlyRs are also shown.

**Fig. 5.** Functional characterization of compound heterozygous mutations by whole-cell patch-clamp recording. A. Sample glycine dose-response traces for p.R65W GlyRs expressed together with α1 wild type or α1 wild type plus β wild type subunits as indicated. Normalized glycine dose-response curves for receptors incorporating p.R65W subunits are shown below. B. Sample glycine dose-response traces for p.P230S GlyRs expressed either alone or with the β wild type subunit. Normalized glycine dose-response curves for receptors incorporating p.P230S subunits are shown below. C. Sample glycine dose-response traces for p.L291P GlyRs expressed together with α1 wild type or α1 wild type plus β wild type subunits as indicated. Normalized glycine dose-response curves for receptors incorporating p.L291P are shown below. D. Sample glycine dose-response traces for p.D388A GlyRs expressed together with α1 wild type or α1 wild type plus β wild type subunits as indicated. Normalized glycine dose-response curves for receptors incorporating p.D388A subunits are shown below. Averaged parameters of best fit to all individual dose-response relationships are summarized in Table 2.

**Fig. 6.** Expression of novel mutations using immunofluorescence. Images for intracellular expression (left) were taken as single cross-sectional confocal images and images for cell surface expression (right) as z-stack images. ++ indicates a high level of cell surface expression comparable with wild type; + indicates a reduction in cell surface expression in comparison to wild type (which was particularly dramatic in the case of p.R65W), and - indicates no visible expression. *R65W with increased master gain.

**Fig. 7.** Structural modelling of novel mutations. A – F. Major conformational changes compared to wild type receptors are indicated by arrows. TM1 is shown in green, TM2 in blue, TM3 in yellow, TM4 in orange, 0' (R252) in purple and helical extensions in red. G. Pore radius for wild type and three novel autosomal dominant mutations. Arrows indicate the limits of the membrane.

**Table 1.** Details of hyperekplexia mutations identified in this study.

| Case | Genotype | Inheritance mode | Class of mutation | Protein mutation | | | Protein position | Gender | Reference |
|---|---|---|---|---|---|---|---|---|---|
| 1 - 4 | Exons 1-7 | recessive | deletion | delEX1-7 | | | N-terminal-M2 | 2x male, 2x female | (29) |
| 5 | C573T | compound heterozygote | missense | p.R65W | } | unknown | N-terminal | male | (10) |
| | C1068T | | missense | p.P230S | | unknown | M1 | | novel |
| 6 - 7 | C594T | recessive | missense | p.R72C | | | N-terminal | 2x female | novel |
| 8 | C1032T | recessive | missense | p.R218W | | | N-terminal | male | novel |
| 9 | G687A | recessive | missense | p.E103K | | | N-terminal | male | (10) |
| 10 | C971A | recessive | nonsense | p.Y197X | | | N-terminal | male | (10) |
| 11 | C986A | recessive | nonsense | p.Y202X | | | N-terminal | male | (28) |
| 12 | G1033A | compound heterozygote | missense | p.R218Q | } | paternal | N-terminal | male | (51) |
| | C1267A | | nonsense | p.S296X | | maternal | M3 | | (52) |
| 13 | C1056G | dominant | missense | p.Q226E | | | M1 | male | novel |
| 14 | G1135A | recessive | missense | p.R252H | | | M1-M2 | | (53) |
| 15 - 16 | G1192A | dominant | missense | p.R271Q | | | M2-M3 | 2x female | (54) |
| 17 | A1216G | dominant | missense | p.Y279C | | | M2-M3 | female | (55) |
| 18 | G1218A | dominant | missense | p.V280M | | | M2-M3 | male | novel |
| 19 | T1252C | compound heterozygote | missense | p.L291P | } | paternal | M3 | female | novel |
| | A1543C | | missense | p.D388A | | maternal | M3-M4 | | novel |
| 20 | G1503T | recessive | nonsense | p.E375X | | | M3-M4 | male | novel |
| 21 | G1621A | dominant | missense | p.R414H | | | C-terminal | male | rs200130685* |

* p.R414H was a novel variant at the time of identification but since it is listed as a very rare variant in dbSNP.

**Table 2.** Properties of novel mutations using whole-cell patch-clamp electrophysiology.

| | $EC_{50}$ (μM) | $n_H$ | $I_{max}$ (nA) | n |
|---|---|---|---|---|
| **wild type** | | | | |
| **α1** | 64 ± 8 | 3.8 ± 0.3 | 19 ± 3 | 10 |
| **α1β** | 39 ± 4 | 2.4 ± 0.2 | 14 ± 3 | 5 |
| **dominant mutations** | | | | |
| **p.Q226E** | 32 ± 6 | 3.5 ± 0.7 | 10 ± 5 | 3 |
| **p.V280M** | 2.4 ± 0.3 | 1.1 ± 0.2*** | 5 ± 4** | 3 |
| **p.R414H** | 110 ± 12 | 2.3 ± 0.2* | 13 ± 1 | 4 |
| **recessive mutations** | | | | |
| **p.R72C + α1** | 189 ± 14 | 2.9 ± 0.1 | 8 ± 3* | 4 |
| **p.R218W + α1** | 235 ± 26 | 2.4 ± 0.2 | 6 ± 2** | 4 |
| **p.E375X + α1** | 243 ± 20 | 1.8 ± 0.2** | 1.2 ± 0.4**** | 4 |
| **p.E375X + α1β** | 140 ± 22 | 2.2 ± 0.2 | 9 ± 4 | 3 |
| **compound heterozygous mutations** | | | | |
| **p.R65W + α1** | 1468 ± 557**** | 1.0 ± 0.1**** | 2.9 ± 1.3**** | 6 |
| **p.R65W + α1β** | 1281 ± 315**** | 1.1 ± 0.2** | 1.2 ± 0.9*** | 5 |
| **p.P230S** | 172 ± 50 | 1.6 ± 0.1**** | 1.6 ± 0.5**** | 6 |
| **p.P230S + β** | 155 ± 26 | 2.4 ± 0.3 | 2.2 ± 1.0*** | 6 |
| **p.L291P + α1** | 198 ± 15 | 3.1 ± 0.5 | 9 ± 1* | 5 |
| **p.L291P + α1β** | 180 ± 22 | 2.2 ± 0.3 | 7 ± 1 | 4 |
| **p.D388A + α1** | 173 ± 11 | 2.8 ± 0.7 | 6 ± 2** | 5 |
| **p.D388A + α1β** | 170 ± 16 | 2 ± 0.2 | 9 ± 3 | 4 |

* $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$ relative to the corresponding homo- or heteromeric wild type GlyR via one-way ANOVA followed by Dunnett's post-hoc test.

Figure 1

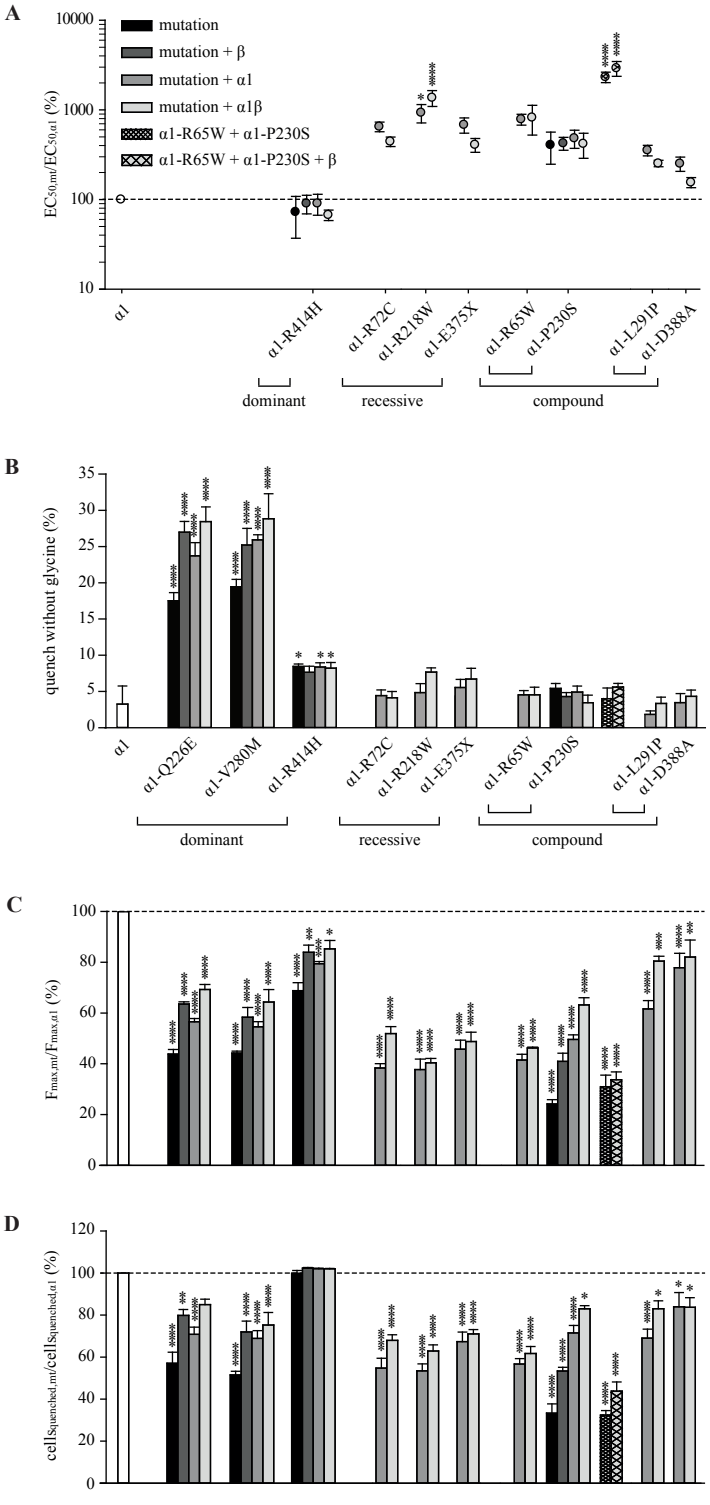

A
mutation
mutation + β
mutation + α1
mutation + α1β
α1-R65W + α1-P230S
α1-R65W + α1-P230S + β
EC50,mt/EC50,α1 (%)
α1
α1-R414H
α1-R72C
α1-R218W
α1-E375X
α1-R65W
α1-P230S
α1-L291P
α1-D388A
dominant
recessive
compound
B
quench without glycine (%)
α1
α1-Q226E
α1-V280M
α1-R414H
α1-R72C
α1-R218W
α1-E375X
α1-R65W
α1-P230S
α1-L291P
α1-D388A
dominant
recessive
compound
C
Fmax,mt/Fmax,α1 (%)
D
cellsquenched,mt/cellsquenched,α1 (%)

Figure 2

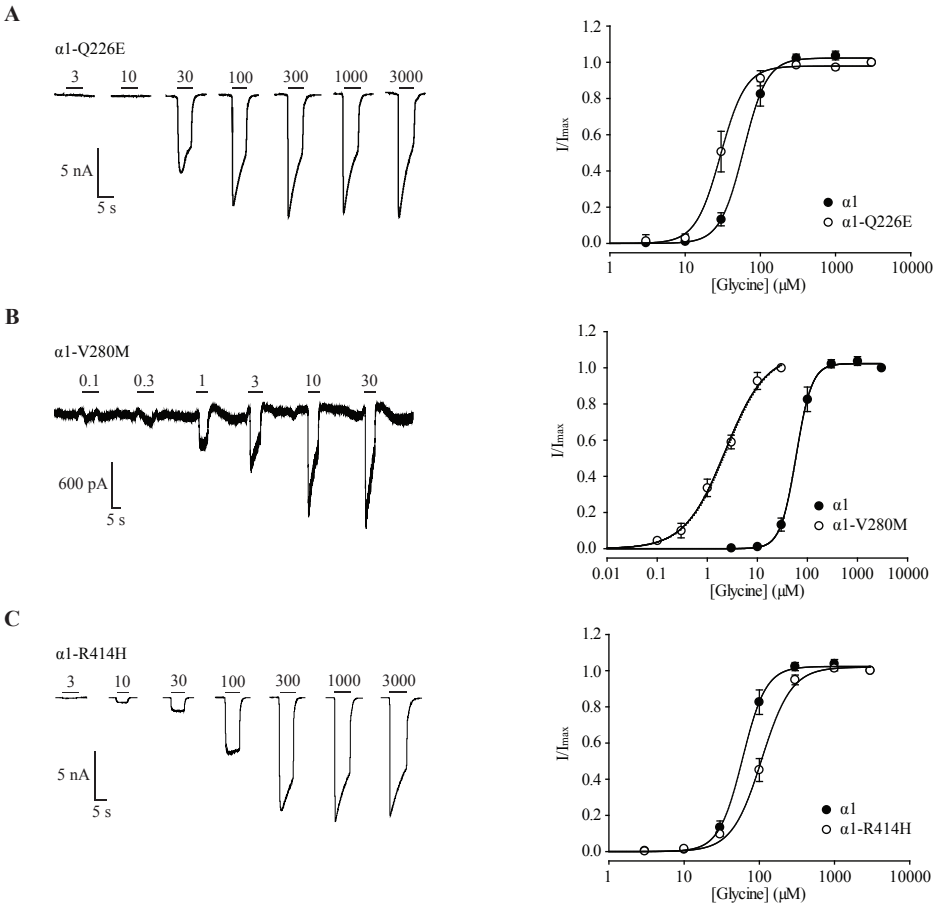

A
α1-Q226E
3
10
30
100
300
1000
3000
5 nA
5 s
I/Imax
[Glycine] (μM)
α1
α1-Q226E
B
α1-V280M
0.1
0.3
1
3
10
30
600 pA
5 s
α1
α1-V280M
C
α1-R414H
3
10
30
100
300
1000
3000
5 nA
5 s
α1
α1-R414H

Figure 3

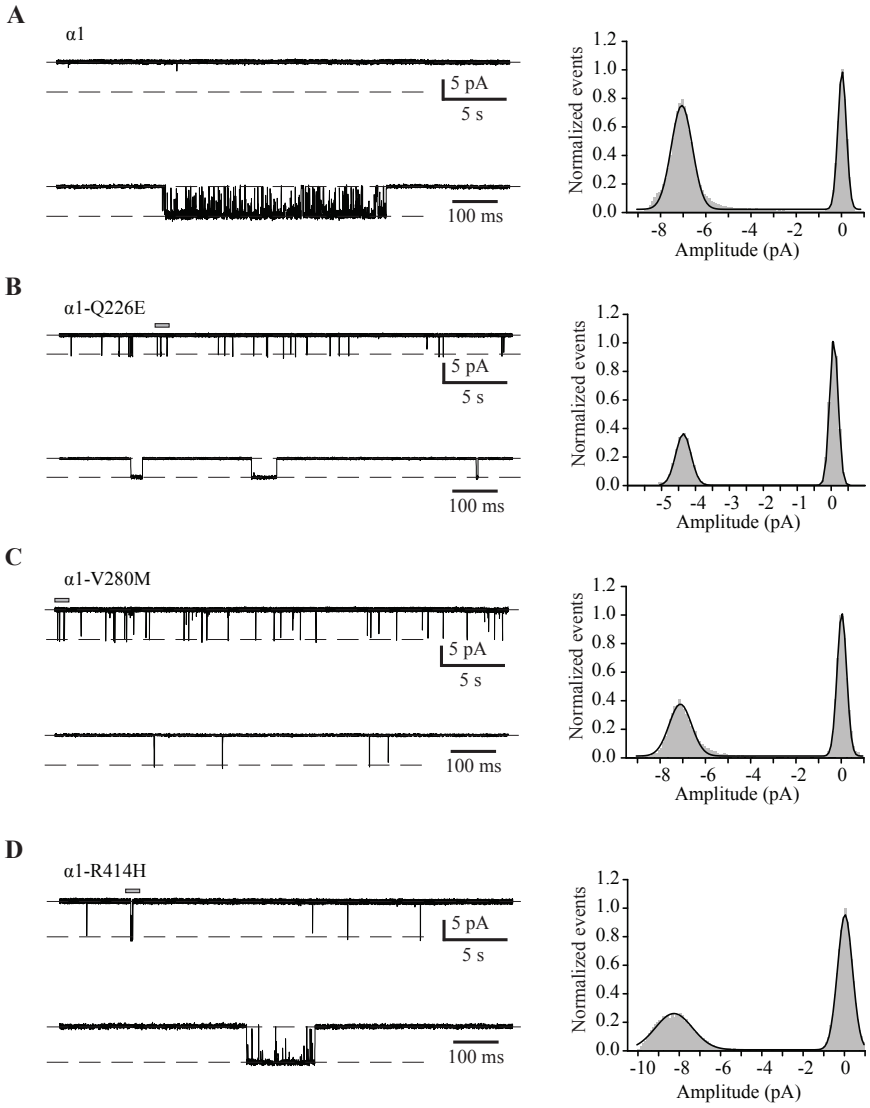

A
α1
5 pA
5 s
100 ms
Normalized events
Amplitude (pA)
B
α1-Q226E
5 pA
5 s
100 ms
Normalized events
Amplitude (pA)
C
α1-V280M
5 pA
5 s
100 ms
Normalized events
Amplitude (pA)
D
α1-R414H
5 pA
5 s
100 ms
Normalized events
Amplitude (pA)

Figure 4

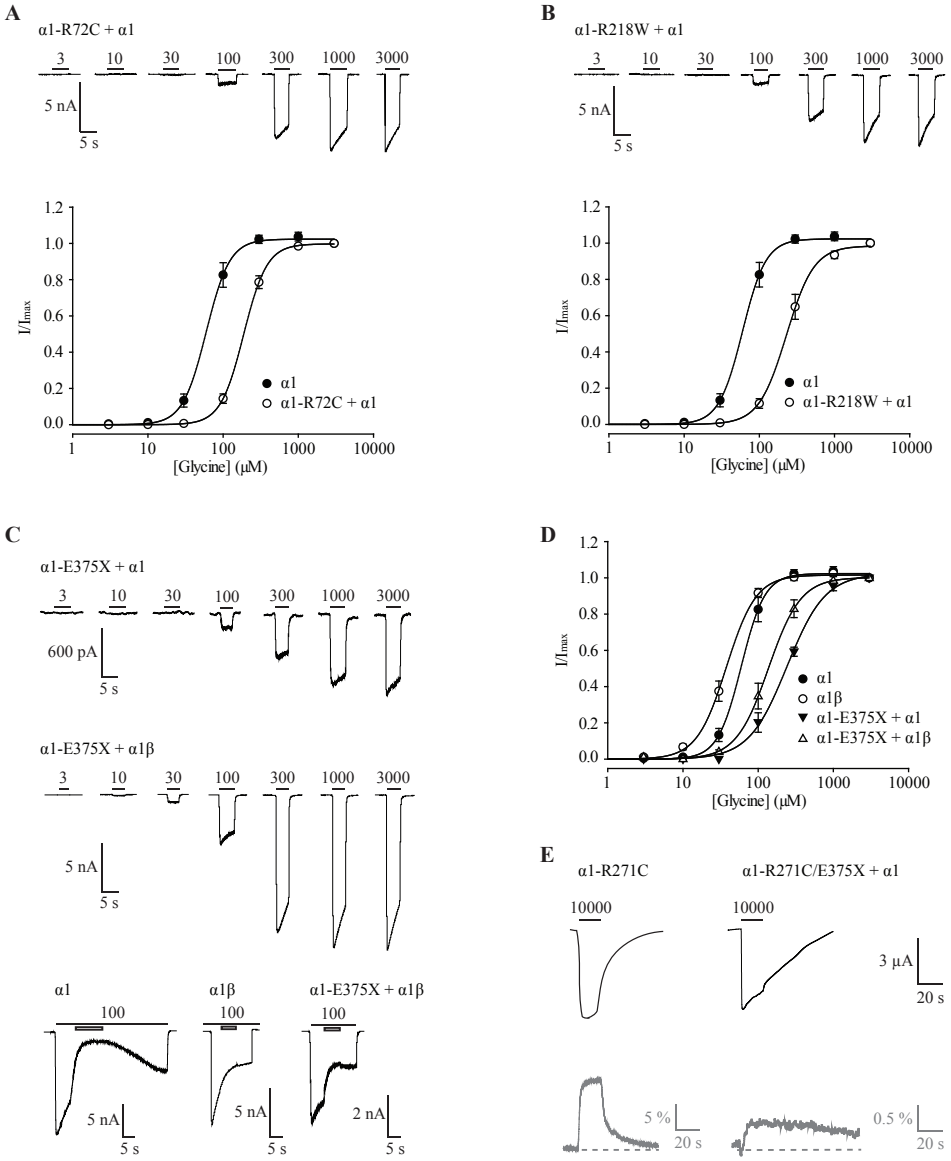

A
α1-R72C + α1
3
10
30
100
300
1000
3000
5 nA
5 s
I/Imax
α1
α1-R72C + α1
[Glycine] (μM)
B
α1-R218W + α1
α1
α1-R218W + α1
C
α1-E375X + α1
600 pA
α1-E375X + α1β
α1
α1β
α1-E375X + α1β
2 nA
D
α1
α1β
α1-E375X + α1
α1-E375X + α1β
E
α1-R271C
α1-R271C/E375X + α1
10000
3 μA
20 s
5 %
0.5 %

Figure 5

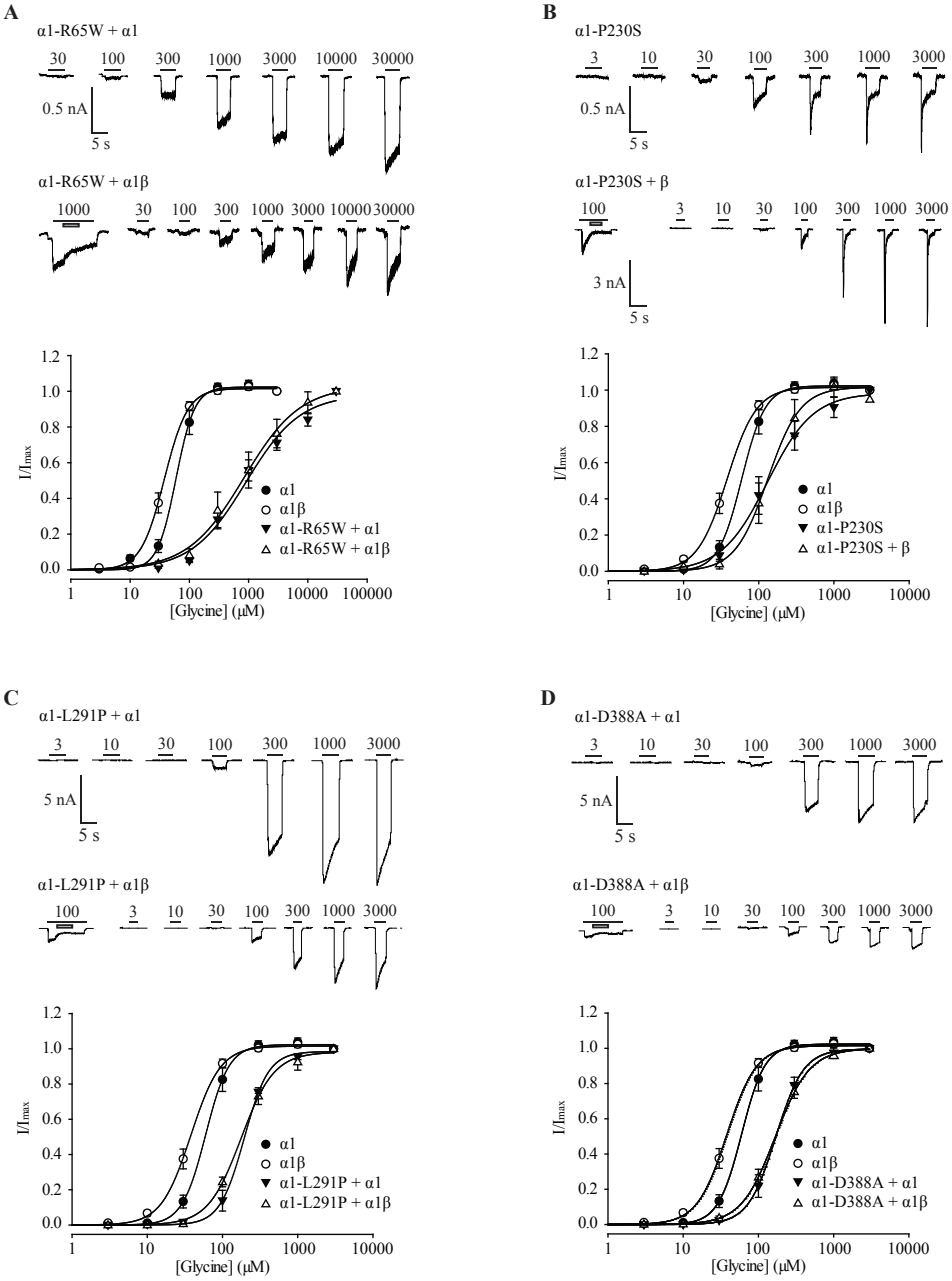
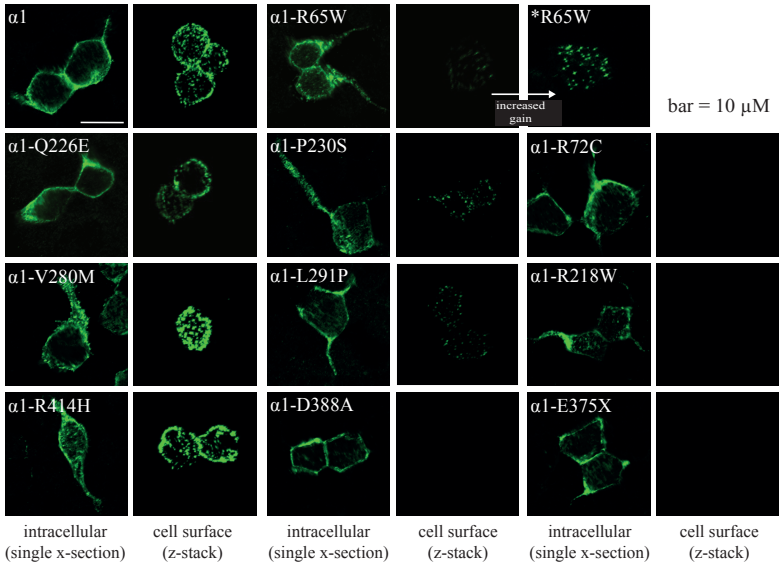
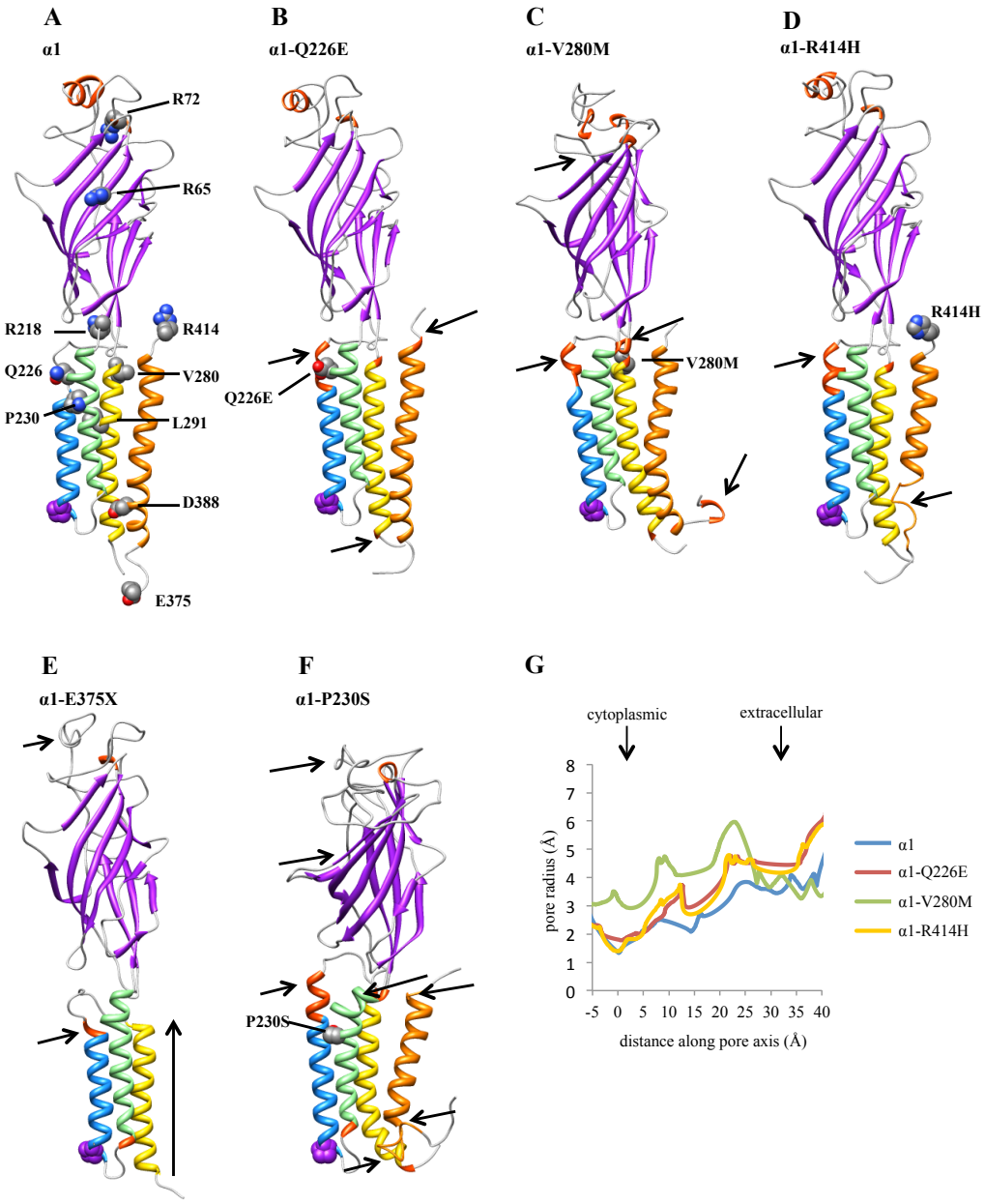

A
α1-R65W + α1
30 100 300 1000 3000 10000 30000
0.5 nA
5 s
α1-R65W + α1β
1000 30 100 300 1000 3000 10000 30000
I/Imax
α1
α1β
α1-R65W + α1
α1-R65W + α1β
[Glycine] (μM)
B
α1-P230S
3 10 30 100 300 1000 3000
0.5 nA
5 s
α1-P230S + β
100 3 10 30 100 300 1000 3000
3 nA
5 s
α1
α1β
α1-P230S
α1-P230S + β
[Glycine] (μM)
C
α1-L291P + α1
3 10 30 100 300 1000 3000
5 nA
5 s
α1-L291P + α1β
100 3 10 30 100 300 1000 3000
α1
α1β
α1-L291P + α1
α1-L291P + α1β
[Glycine] (μM)
D
α1-D388A + α1
3 10 30 100 300 1000 3000
5 nA
5 s
α1-D388A + α1β
100 3 10 30 100 300 1000 3000
α1
α1β
α1-D388A + α1
α1-D388A + α1β
[Glycine] (μM)

Figure 6




| | intracellular | cell surface |
|---|---|---|
| α1 | + | ++ |
| α1-Q226E | + | + |
| α1-V280M | + | ++ |
| α1-R414H | + | ++ |
| α1-R65W | + | + |
| α1-P230S | + | + |
| α1-L291P | + | + |
| α1-D388A | + | - |
| α1-R72C | + | - |
| α1-R218W | + | - |
| α1-E375X | + | - |

Figure 7


A
α1
R72
R65
R218
R414
Q226
V280
P230
L291
D388
E375
B
α1-Q226E
Q226E
C
α1-V280M
V280M
D
α1-R414H
R414H
E
α1-E375X
F
α1-P230S
P230S
G
cytoplasmic
extracellular
pore radius (Å)
distance along pore axis (Å)
α1
α1-Q226E
α1-V280M
α1-R414H