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Arrestin mutations: Some cause diseases, others promise cure

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Abstract

Arrestins play a key role in homologous desensitization of G protein-coupled receptors (GPCRs) and regulate several other vital signaling pathways in cells. Considering the critical roles of these proteins in cellular signaling, surprisingly few disease-causing mutations in human arrestins were described. Most of these are loss-of-function mutations of visual arrestin-1 that cause excessive rhodopsin signaling and hence night blindness. Only one dominant arrestin-1 mutation was discovered so far. It reduces the thermal stability of the protein, which likely results in photoreceptor death via unfolded protein response. In case of the two nonvisual arrestins, only polymorphisms were described, some of which appear to be associated with neurological disorders and altered response to certain treatments. Structure-function studies revealed several ways of enhancing arrestins' ability to quench GPCR signaling. These enhanced arrestins have potential as tools for gene therapy of disorders associated with excessive signaling of mutant GPCRs.

1. Arrestins in mammals: Few subtypes, many functions

The first arrestin described was the visual subtype (systematic name arrestin-1^a). In fact, it was discovered not for its biological role as we know it today, but as an antigen causing uveitis,¹ hence it was called S-antigen. *Arrestin-1* gene is called SAG (abbreviation for S-antigen) to this day. A year later Kuhn described a “48-kDa” protein in the retina that, along with the visual G protein transducin and rhodopsin kinase, binds rhodopsin in a light-dependent manner.² A few years later Kuhn found that rhodopsin phosphorylation (also discovered by his group many years earlier³) greatly facilitates the binding of the 48-kDa protein to rhodopsin.⁴ The fact that S-antigen and 48-kDa protein are one and the same was established only in mid-1980s.^{5,6} Subsequent studies by Dr. Kuhn's group showed that the binding of the 48-kDa protein to phosphorylated rhodopsin quenches light-dependent activation of photoreceptor phosphodiesterase,⁷ which was the first evidence for the role of this protein in “arresting” rhodopsin signaling, i.e., in receptor desensitization. Subsequent discoveries of the kinase that selectively phosphorylates agonist-activated β 2-adrenergic receptor (β 2AR)⁸ and the first nonvisual arrestin⁹ demonstrated that two-step desensitization, phosphorylation of activated GPCR by a specific receptor kinase followed by arrestin binding to the active phosphorylated receptor, is a common feature of the signaling systems driven by GPCRs (reviewed in ref. 10). Mammals express between ~500

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^aWe use systematic names of arrestin proteins, where the number after the dash indicates the order of cloning: arrestin-1 (historic names S-antigen, 48 kDa protein, visual or rod arrestin), arrestin-2 (β -arrestin or β -arrestin1), arrestin-3 (β -arrestin2 or hTHY-ARRX), and arrestin-4 (cone or X-arrestin).

(dolphins) and ~3400 (elephants) different GPCRs (<http://sevens.cbrc.jp/>), but only 4 arrestin subtypes.^{11,12} Two of these four are specialized visual: arrestin-1, expressed at very high levels in both rod and cone photoreceptors,^{13–16} and cone-specific arrestin-4, constituting ~2% of total arrestin complement in cones.¹³ The other two nonvisual subtypes, arrestin-2 and –3, are ubiquitously expressed and apparently interact with hundreds of different GPCRs.^{9,17–19} In most cell types arrestin-2 greatly outnumbers arrestin-3,^{20–21} which explains why arrestin-2⁹ was cloned years before arrestin-3.^{22–24}

Arrestin-1 was shown to suppress G protein activation by phosphorylated light-activated rhodopsin via direct competition.^{25,26} Nonvisual arrestins were found to perform exactly the same function, the only difference being that they prefer other GPCRs over rhodopsin.^{22,27} Soon after their discovery, both nonvisual arrestins were shown to bind clathrin²⁸ and clathrin adaptor AP-2,²⁹ two key players in receptor internalization via coated pits. Many other nonreceptor binding partners of the two nonvisual arrestins were subsequently discovered. Interestingly, some apparently bind both arrestin-2 and –3, whereas others selectively interact with only one of the nonvisual subtypes.³⁰ Arrestins were implicated in the activation of c-Src³¹ and all three major MAP kinase classes, JNK,³² ERK,³³ and p38,³⁴ shown to bind cAMP phosphodiesterase,³⁵ calmodulin,³⁶ microtubules,^{37,38} ubiquitin ligases Mdm2,³⁹ AIP4,⁴⁰ parkin,⁴¹ and many other signaling proteins (reviewed in refs. 11,42,43). Thus, it appears that arrestins are at the crossroads of numerous vital signaling pathways in the cell.

2. Naturally occurring mutations in visual arrestins

Critical role of arrestin proteins in the visual system was confirmed by abnormally prolonged photoresponses in mice lacking arrestin-1,⁴⁴ rhodopsin kinase⁴⁵ or expressing rhodopsin without phosphorylation sites necessary for its binding⁴⁶ or with insufficient number of these sites.⁴⁷ Indeed, in humans frameshift mutation in *SAG* was found to underlie Oguchi disease, a form of stationary night blindness.^{48,49} This mutation is a deletion of an adenine in codon 309, which causes a frameshift and premature termination 10 residues later.^{48,50} Thus, the resulting protein lacks about half of the C-domain⁵¹ and is unlikely to fold or become functional. Interestingly, the same mutation in the *SAG* gene caused autosomal recessive retinitis pigmentosa (a form of retinal degeneration) in some cases.⁵⁰ Although it is not known why the phenotype is so different, certain mechanisms are conceivable. All eukaryotic cells have special mechanisms of “garbage disposal,” at mRNA and protein levels. One of these is nonsense-mediated mRNA decay, i.e., the elimination of mutant or incorrectly spliced mRNA containing premature stop codons.^{52–54} The other is the degradation of misfolded and unfolded proteins via ubiquitin-proteasome system (reviewed in ref. 55). Insufficient activity of either can exacerbate the problem caused by this frameshift in the *SAG* gene. In particular, incomplete elimination of faulty mRNA would make the cell produce too much unfolded mutant arrestin-1, overwhelming ubiquitin-proteasome system and causing cell death via unfolded protein response (see below). This is particularly likely considering that arrestin-1 is the second most abundant protein in rods after rhodopsin,^{14–16} so that even if a small fraction of defective mRNA escapes the nucleus and is translated in the cytoplasm, the output of unfolded protein would be large.

Loss-of-function mutations are recessive, i.e., the production of normal arrestin-1 encoded by the second undamaged allele is usually sufficient for health of rod photoreceptors. This is consistent with the results obtained in mice, where hemizygous knockout animals and even the animals expressing arrestin-1 at ~5% of wild-type (WT) level had perfectly healthy photoreceptors and normal rate of photoresponse shutoff after moderately bright flashes.^{16,56}

Recently a dominant mutation in, *SAG*, C147F, was discovered⁵⁷ (Fig. 1A). Its dominant nature suggested that the mutant itself, rather than the absence of functional arrestin-1, causes the damage that WT arrestin-1 protein generated by the second allele cannot prevent. Although cysteine in this position is conserved in all arrestin subtypes^{11,12} and in highly homologous bovine and mouse arrestin-1 and it was shown to be important for arrestin function,⁵⁸ in and of itself this did not explain dominant nature of the C147F mutation. Careful inspection of the structure of arrestin-1 in its basal conformation,⁵¹ as well as in complex with rhodopsin^{59,60} suggested that the replacements of a cysteine with a relatively small side chain by a bulky phenylalanine in this position can affect protein folding (Fig. 1B).⁵⁷ This idea was tested experimentally, and the results turned out to be more complex. It was shown that C147F arrestin-1 folds, but demonstrates much lower thermal stability than the WT protein, denaturing within hours even at physiological temperature of 37°C.⁶¹ Similar loss of thermal stability was demonstrated in case of C147I and C147L, but not with C147A or C147V mutants with smaller side chains, clearly indicating that the bulk of the side chain underlies the problem.⁶¹ The expression of this mutant in photoreceptor-derived 661W cells,⁶² in contrast to WT human arrestin-1, was shown to induce unfolded protein response.⁶¹ Thus, considering extremely high expression of arrestin-1 in rods,^{14–16} it appears that denaturing C147F mutant overwhelms proteasome system and induces photoreceptor death via unfolded protein response (Fig. 2). It is quite likely that a mutation in the stop codon of *SAG*, which added an extra of 25 amino acids, causes late-onset hereditary retinal degeneration in dogs⁶⁴ via a similar mechanism.

Interestingly, no disease-causing mutations or polymorphisms were so far reported in cone-specific *arrestin-4* (*ARR4*), even though it appears to be necessary for proper function of cone photoreceptors.¹³

3. Nonvisual arrestins: Unexpectedly few associations with unclear functional significance

Numerous residues are highly conserved in arrestin evolution,^{11,12} which suggests their functional importance. Yet not a single disease-related change in the amino acid sequence has so far been described in human nonvisual arrestins. Several single nucleotide polymorphisms in the arrestin-2 and -3 genes (*ARRB1* and *ARRB2*), which include synonymous mutations in the coding sequence and single nucleotide polymorphisms (SNPs) in the noncoding elements of their mRNAs and in the introns, have been described. The associations of these polymorphisms with various conditions have been extensively tested.

Polymorphism in the promoter region of the *ARRB1* gene was found to be associated with the treatment outcome with antidepressant mirtazapine in Korean patients with major depressive disorder.⁶⁵ One haplotype, which includes SNPs in the promoter region and the

first intron, was found to be associated with the remission status following several weeks of mirtazapine treatment. Two SNPs in *ARRB2*, one in an intron and one in 3'-untranslated region (3'-UTR), were reported to be associated with the effects of antidepressant monotherapy in a group of mostly Caucasian patients with major depression.⁶⁶ Interestingly, the same SNP in the 3'-UTR of *ARRB2* mRNA, rs4790694, was found to be associated with two measures of nicotine dependence in European Americans.⁶⁷ There was also one major haplotype in both *ARRB2* and *ARRB1* that showed positive association with the indices of nicotine dependence. Interestingly, no such associations were seen in African Americans.⁶⁷ A study of association between polymorphism in the *ARRB2* gene and alcohol dependence found no such association in Caucasians.⁶⁸ Four SNPs spanning the entire gene were examined (rs4790694 was not included). These human data are somewhat at odds with the finding in animals that demonstrated the existence of an *Arrb2* haplotype consisting of six SNPs in different parts of the gene and one insertion (in the promoter region) that was specifically associated with ethanol preference in rats.⁶⁹ The variant haplotype in the ethanol-preferring rat line confers higher arrestin-3 expression both at mRNA and protein levels in several brain regions, but no change in the arrestin-3 protein sequence.

An extensive role of arrestins in signaling as well as in regulation of the GPCR responsiveness drove the investigation of genetic association of arrestin polymorphisms and the effects of addictive drugs. However, investigation of seven *ARRB2* SNPs, including rs4790694, failed to reveal significant association of any individual SNP or haplotype with cocaine or opioid dependence in European Americans.⁷⁰ However, polymorphism in *ARRB2* was found to impact the outcome of methadone substitution therapy in Caucasian patients addicted to opioids. The study examined four SNPs in the *ARRB2* gene, from the promoter to 3'-UTR, three of which, in intron 1, exon 11 (synonymous Ser280Ser), and 3'-UTR, were found to be significantly associated with response to methadone therapy, although no association was seen with opioid addiction.⁷¹ These three SNPs formed a haplotype block, and patients homozygous for variant alleles in the block carried an almost threefold higher risk of being nonresponders to the methadone therapy.

A study of four *ARRB2* SNPs failed to detect an association between any of them and schizophrenia in Japanese patients.⁷² However, three out of five SNPs (synonymous rs1045280 in exon 11 and rs2036657 and rs4790694 in 3'-UTR) were significantly associated with methamphetamine use disorders such as methamphetamine-induced psychosis. Additionally, a significant association was found between rs1045280 Ser280Ser SNP and tardive dyskinesia, a motor complication induced by long-term treatment with typical antipsychotics.⁷³

Overall, these association studies revealed a lot less than one would expect. Considering vital role of nonvisual arrestins in many cellular functions, one would expect to find numerous disease-associated mutations and polymorphisms. However, very few have been described so far. The major problem with interpretation of the existing findings is, of course, the lack of obvious functional significance of these genetic variants. None of the SNPs change the proteins sequence of arrestins. All known SNPs in the exons are synonymous. Many SNPs found associated with human diseases are located in introns or in 3'-UTR, with

unknown functional impact. Out of all *ARRB2* SNPs examined so far, only one SNP, rs34230287 (-159C/T), located in the gene promoter, has been shown to affect the promoter activity and *ARRB2* expression: the C variant confers a significantly higher promoter activity and is associated with higher level of *ARRB2* mRNA in Caucasians.⁷⁴ However, this SNP was either not examined or, when it was, showed no association with the outcome measures.⁷¹

Although in most cases this was not tested, the most likely effect of SNPs in coding and noncoding regions is a change in expression. The most extreme change in protein expression is produced by the knockout of its gene. If we look at mouse in vivo studies, the phenotypes detected in single nonvisual arrestin knockouts are fairly mild: mice lacking either *Arrb1* or *Arrb2* are overall normal, albeit demonstrate altered functional responses such as increased sensitivity to adrenergic stimulation of the heart⁷⁵ or enhanced locomotor responsiveness to amphetamine⁷⁶ in *Arrb1* knockout mice or enhanced morphine analgesia⁷⁷ and reduced locomotor response to amphetamine^{76,78} and morphine⁷⁹ in *Arrb2* knockout mice. Interestingly, simultaneous knockout of both nonvisual subtypes is embryonic lethal because of lung and heart development problems.^{80,81} The elimination of the only nonvisual arrestin, *kurtz*, in *Drosophila* is also embryonic lethal,⁸² even though in flies *kurtz* inhibits proliferative MAP kinase ERK,⁸³ in contrast to mammalian cells, where nonvisual arrestins facilitate ERK activation via c-Src³¹ and by scaffolding of c-Raf1-MEK1-ERK1/2 cascade.^{33,84}

One reason for these observations in knockout mice and humans with SNPs is that the two nonvisual subtypes in mammals can partially compensate for one another. Mild phenotypes of *Arrb1* and *Arrb2* knockout mice appear to support this argument. However, in certain aspects these two subtypes are quite different and engage distinct sets of signaling proteins.³⁰ A recent study suggests that arrestin-2 and arrestin-3 play distinct roles in amphetamine-induced hyperlocomotion and that their effects are dose dependent.⁷⁶ While the mechanistic basis for the distinct roles of the two nonvisual arrestins was not determined in that study, there are several well-known functional differences: arrestin-3 has higher affinity than arrestin-2 for clathrin²⁸ and several GPCRs,^{18,80} arrestin-3 is less selective than arrestin-2 for the active phosphorylated form of cognate GPCRs,⁸⁵ and arrestin-3, but not arrestin-2, facilitates JNK3 activation in cells.^{32,86,87} The latter difference was preserved even in short arrestin-derived N-terminal peptides.⁸⁸ One of these differences, or some functional difference that has not been elucidated yet, might underlie distinct roles of arrestin-2 and arrestin-3 in amphetamine-induced hyperlocomotion.⁷⁶ However, mild phenotypes of single subtype knockout mice suggest that either nonvisual arrestin can perform most of the biologically important functions of the other subtype.

4. Enhanced arrestins: Compensation of excessive GPCR activity

Numerous mutations in various GPCRs were reported to cause different kinds of pathological conditions in humans (reviewed in refs. 89,90). Some of these mutations are loss of function, so conceptually the strategy for gene therapy is clear: the delivery of a normal coding sequence of a functional GPCR to the affected cells should solve the problem. However, other identified disease-causing mutations are gain of function, where

the mutant gene encodes an overactive receptor. Unlike recessive loss-of-function, gain-of-function mutations are dominant, as perfectly normal second allele cannot suppress excessive signaling by the mutant. One possible therapeutic strategy is the expression of an arrestin with enhanced ability to dampen the signaling, so that, on balance, the signal might become near normal. This compensational approach was so far tested only in rod photoreceptors, where the important GPCR is rhodopsin, which is quenched exclusively by arrestin-1.⁸⁶ Extensive structure—function studies of arrestin-1 (reviewed in refs. 85,91) yielded several enhanced versions that bind both phosphorylated and unphosphorylated light-activated rhodopsin tighter than parental WT protein (Fig. 3). As usual, translation of the in vitro findings to the in vivo situation yielded both good and bad news. On the positive side, transgenic expression of enhanced arrestin-1 in mouse rods defective in rhodopsin phosphorylation improves the morphology of photoreceptors, their functional performance, and results in signal shutoff that is much faster than with WT arrestin-1.⁸⁶ Importantly, facilitation of the shutoff is also documented in mice with defects of rhodopsin phosphorylation expressing normal complement or WT arrestin-1, similar to human patients with rhodopsin mutations.⁹² However, neither parameter in “compensated” rods came even close to that of normal rods where rhodopsin was phosphorylated and quenched by WT arrestin-1.⁸⁶ As far as the visual system is concerned, with its unrivaled single photon sensitivity and subsecond shutoff of the response, these results suggested that while in principle the strategy is working, more powerful enhanced mutants are necessary for better compensation.⁹³ However, something that works only partially in rods might be sufficient to fully compensate for excessive signaling in any other GPCR-driven system, where the sensitivity is much lower and the shutoff takes minutes, rather than 200–300 ms.

The mechanism of GPCR binding is well conserved in the arrestin family,⁹¹ so both nonvisual arrestins can be enhanced by the mutations homologous to those that preactivate arrestin-1.^{94–96} Yet in case of nonvisual GPCRs there is another catch: both nonvisual arrestins are quite promiscuous and bind pretty much every GPCR tested.^{17–19,97} As virtually every cell in the body expresses numerous GPCR subtypes, only one of which is an overactive mutant in patients, introduction of a promiscuous enhanced nonvisual arrestin would likely suppress the signaling not only of the “bad guy” but of all the other perfectly normal receptors coexpressed in the same cell. This is likely to cause unwanted side effects. Thus, to make the same compensational strategy usable, mutant nonvisual arrestins with narrow receptor specificity are needed. While the receptor–arrestin interface is extensive, involving many residues on the concave sides of both arrestin domains,^{59,98–100} only select few appear to play a role in receptor preference¹⁰⁰ (Fig. 4). The results of the targeted manipulation of these putative receptor-discriminator residues suggest that the construction of nonvisual arrestins with narrow receptor specificity is feasible: certain double mutants demonstrate 50–60-fold preference for some GPCRs over others,¹⁹ and a number of mutations differentially affect arrestin interactions with distinct functional forms of several GPCRs.^{101–103} Generally speaking, preactivating mutations often reduce receptor specificity of arrestins.^{94,96} However, this is so in case of active phosphorylated receptors, whereas the same mutations enhance binding only to cognate unphosphorylated GPCRs.^{94,96} Moreover, enhanced mutants actually compete with GRKs, suppressing the phosphorylation of GPCRs they target.⁹⁵ Thus, while receptor specificity of the mutants combining preactivating

mutations with those that make them specific for particular GPCRs needs to be tested experimentally, this compensational approach appears to be a feasible method to rein in excessive signaling by many disease-causing gain-of-function receptor mutants.

5. Conclusions

Several mutations in *SAG* were reported to cause visual disorders in humans and dogs. Loss-of-function mutations are usually recessive, so that only compound heterozygotes are affected, whereas mutations causing misfolding and/or protein instability are dominant and cause severe disorders, such as retinal degeneration. Unexpectedly, no mutations in either nonvisual arrestin were associated with any disease, while polymorphisms in noncoding regions and synonymous base substitutions in exons were found to be associated with the response to treatment of several neurological disorders. The phenotypes of single nonvisual arrestin knockout in mice are mild, whereas simultaneous knockout of both, as well as the knockout of the only nonvisual arrestin in *Drosophila*, causes embryonic lethality. Thus, the most logical explanation of mild effects of single knockouts in mammals is that arrestin-2 and arrestin-3 can compensate for the missing subtype, taking over each other's duties. Preactivated arrestin mutants with enhanced ability to quench GPCR signaling appear to be a viable tool for the gene therapy of disorders caused by gain-of-function mutations in GPCRs. The use of this strategy to suppress excessive signaling by nonvisual GPCRs requires engineering of receptor-specific nonvisual arrestin mutants.

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Abbreviations

ERK	extracellular signal-regulated kinase
GPCR	G protein-coupled receptor
GRP78/BIP	glucose-regulated protein of 78 kDa/immunoglobulin binding protein
JNK	c-Jun N-terminal kinase
MAP kinase	mitogen-activated protein kinase
WT	wild type
β2AR	β2-adrenergic receptor

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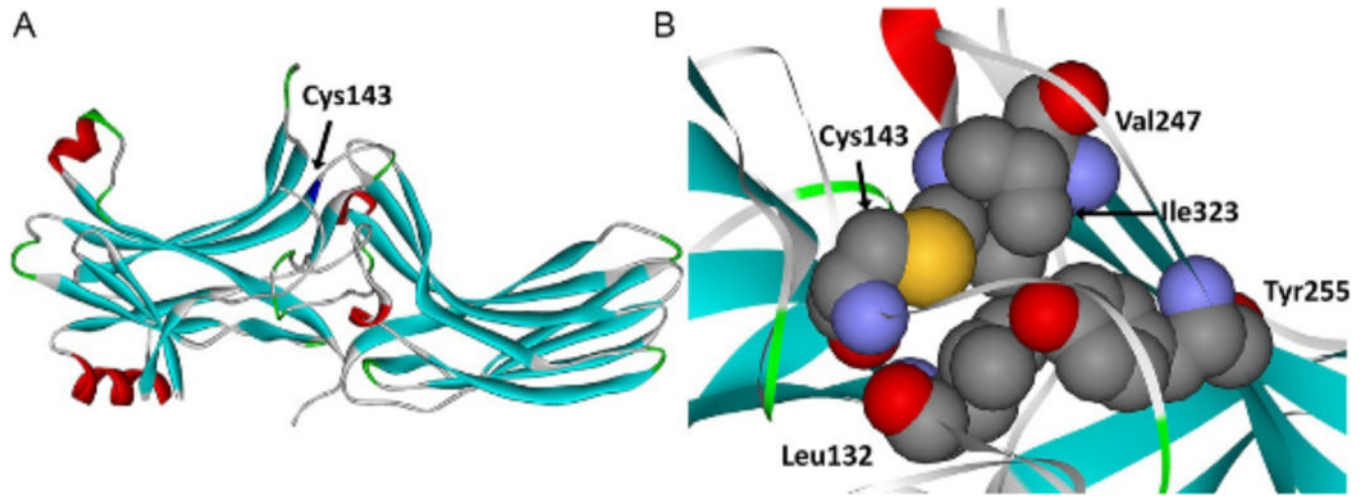


Fig. 1. Dominant mutation in visual arrestin-1 causing retinal degeneration. (A) The position of Cys-147 in the arrestin-1 molecule (panels A and B are based on the crystal structure of bovine arrestin-1, PDB ID:1CF1,⁵¹ so the homologous bovine Cys-143 is shown). (B) Cys-143 and its neighbors (indicated) are shown as CPK models, with the atoms colored, as follows: carbon, *gray*; oxygen, *red*; nitrogen, *blue*; sulfur, *yellow*. Note close packing, which would make the introduction of much bulkier side chain destabilizing.

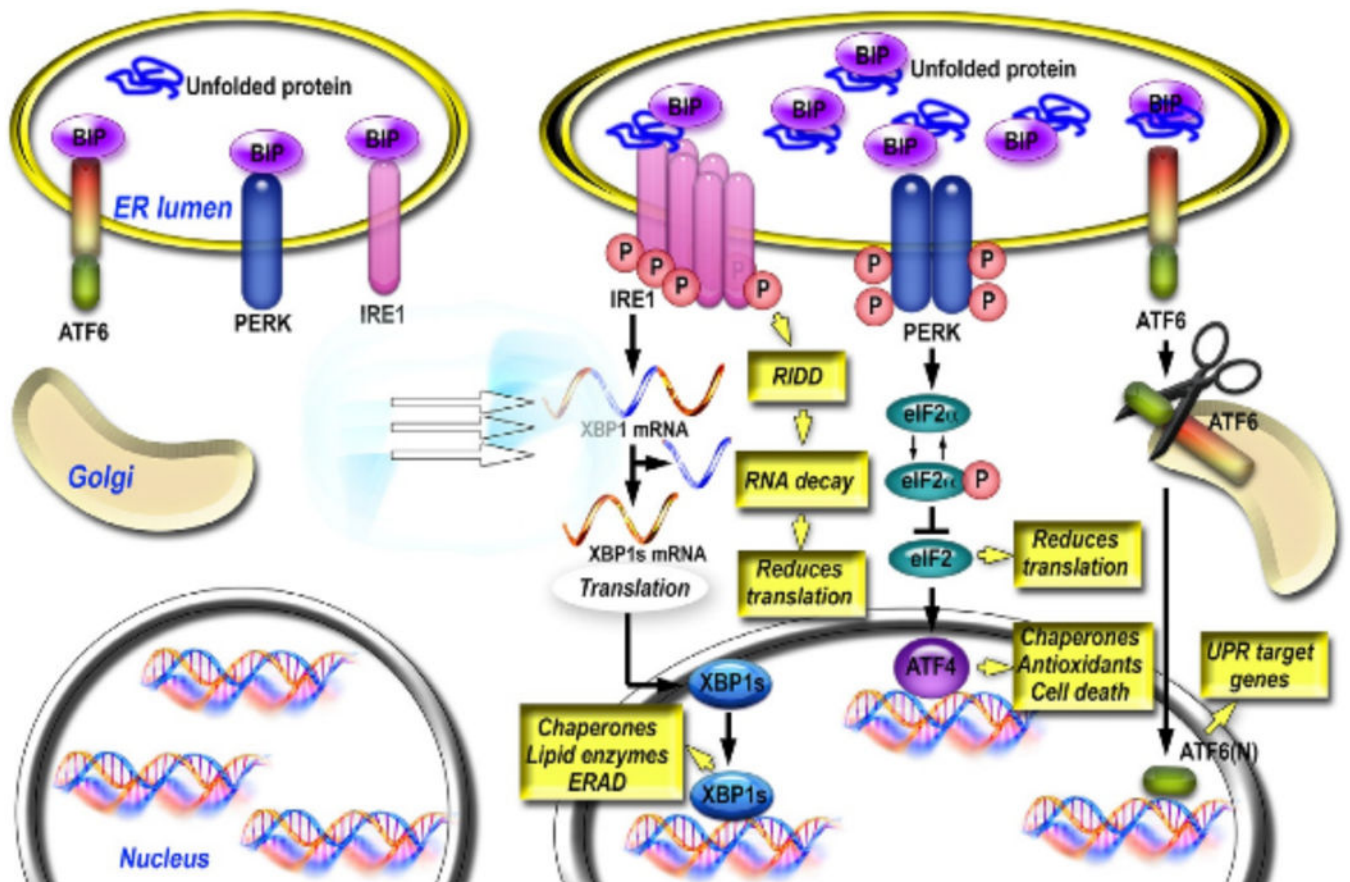


Fig. 2. Mutant arrestin-1 induces unfolded protein response. Experimental data suggest that C147F mutant is significantly less stable than WT arrestin-1.⁶¹ As arrestin-1 is the second most abundant protein in the rod photoreceptors after rhodopsin, its unfolding likely induces unfolded protein response, which eventually leads to rod death.⁶³ An increase in GRP78/BIP, which manifests the first step of the unfolded protein response, was detected in photoreceptor-derived 661W cells expressing this mutant, but not in cells expressing WT human arrestin-1.⁶¹ The schematic is based on the mechanisms described earlier (see ref. 63 and references therein). Abbreviations: *ATF4*, activating transcription factor 4; *ATF6*, activating transcription factor 6; *BIP*, same as GPR78, a major ER chaperone, a.k.a. 78-kDa glucose-regulated protein; *eIF2α*, eukaryotic translation initiation factor 2α; *ER*, endoplasmic reticulum; *ERAD*, ER-associated protein degradation; *IRE1*, inositol-requiring enzyme 1; *PERK*, PKR-like ER kinase; *RIDD*, regulated IRE1-dependent decay of mRNA; *UPR*, unfolded protein response; *XBPI*, X-box binding protein 1.

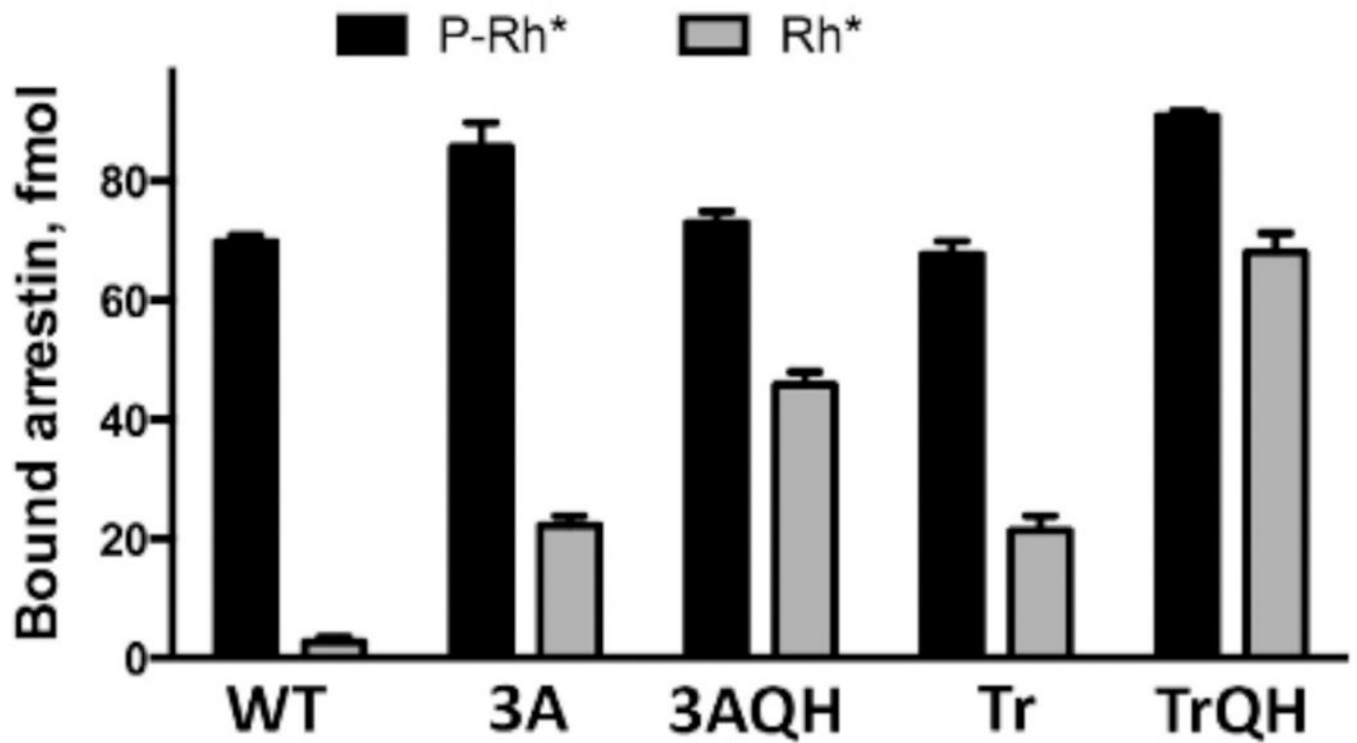


Fig. 3. Phosphorylation dependence of the binding of WT arrestin-1 and its enhanced mutants. The binding in the in vitro assay of translated radiolabeled arrestins to purified phosphorylated (P-Rh*) and unphosphorylated (Rh*) light-activated rhodopsin (performed as described¹⁷) is shown.

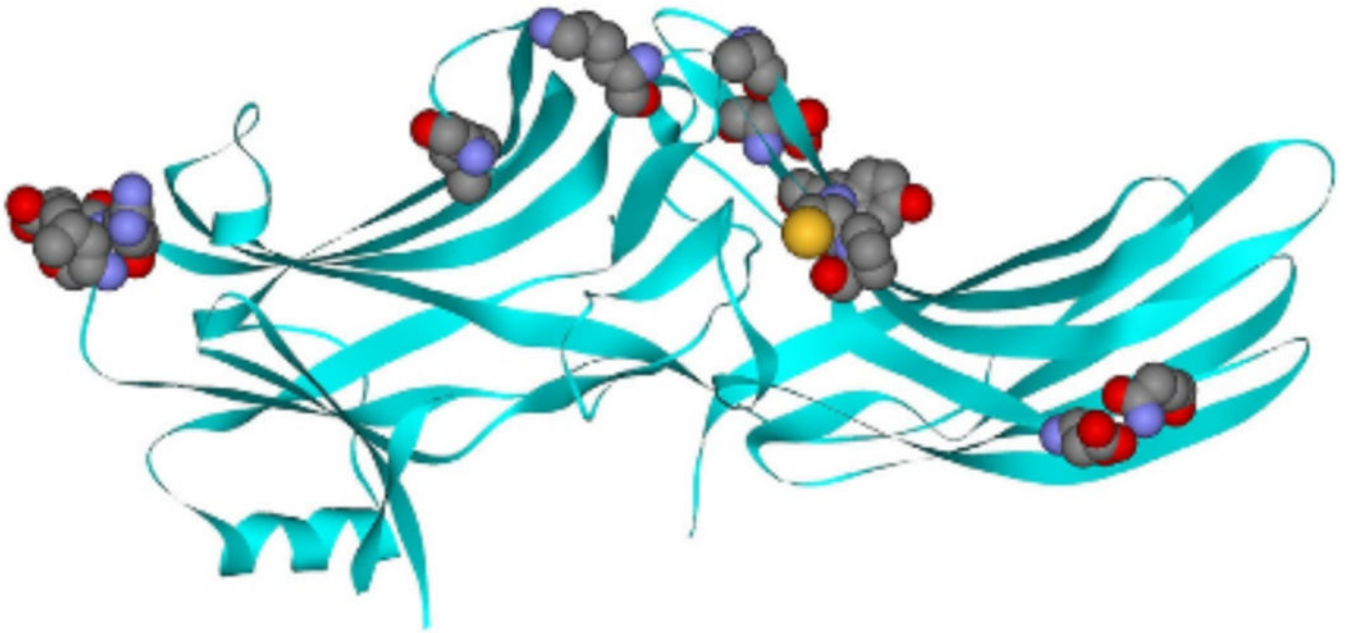


Fig. 4. Arrestin-3 residues that determine receptor preference. The residues found to change receptor preference of nonvisual arrestin-3 in the in-cell BRET-based assay^{19,101–103} are shown as CPK models on the crystal structure of the basal state of bovine arrestin-3 (PDB ID: **3P2D**⁸⁵), with the atoms colored, as follows: *gray*, carbon; *red*, oxygen; *blue*, nitrogen; *yellow*, sulfur. Note the localization of these residues on the concave sides of both arrestin domains, with clustering on the central crest of the receptor-binding side of the molecule.