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Abstract
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Directed evolution of a G protein-coupled receptor for expression, stability, and binding selectivity

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We outline a powerful method for the directed evolution of integral membrane proteins in the inner membrane of Escherichia coli. For a mammalian G protein-coupled receptor, we arrived at a sequence with an order-of-magnitude increase in functional expression that still retains the biochemical properties of wild type. This mutant also shows enhanced heterologous expression in eukaryotes (12-fold in Pichia pastoris and 3-fold in HEK293T cells) and greater stability when solubilized and purified, indicating that the biophysical properties of the protein had been under the pressure of selection. These improvements arise from multiple small contributions, which would be difficult to assemble by rational design. In a second screen, we rapidly pinpointed a single amino acid substitution in wild type that abolishes agonist binding while retaining agonist-binding affinity. These approaches may alleviate existing bottlenecks in structural studies of these targets by providing sufficient quantities of stable variants in defined conformational states.

protein-coupled receptors (GPCRs) comprise ~1% of the genes in mammalian genomes and constitute ~60% of all drug targets (1). Given the critical importance of this class of integral membrane proteins, there is great interest in having detailed structures of these molecules. However, in the Protein Data Bank (2), which contains ~18,000 nonredundant protein structures, the structures of only two GPCRs have been deposited, that of bovine rhodopsin (3), uniquely facilitated by its natural structures, the structures of only two GPCRs have been deposited, and that of bovine rhodopsin (3), uniquely facilitated by its natural structures. However, in the Protein Data Bank (2), which contains ~18,000 nonredundant protein structures, the structures of only two GPCRs have been deposited, that of bovine rhodopsin (3), uniquely facilitated by its natural abundance in the retina (4), and very recently that of bovine rhodopsin (3), uniquely facilitated by its natural structures. However, in the Protein Data Bank (2), which contains ~18,000 nonredundant protein structures, the structures of only two GPCRs have been deposited, that of bovine rhodopsin (3), uniquely facilitated by its natural structures. However, in the Protein Data Bank (2), which contains ~18,000 nonredundant protein structures, the structures of only two GPCRs have been deposited, that of bovine rhodopsin (3), uniquely facilitated by its natural structures. However, in the Protein Data Bank (2), which contains ~18,000 nonredundant protein structures, the structures of only two GPCRs have been deposited, that of bovine rhodopsin (3), uniquely facilitated by its natural structures. However, in the Protein Data Bank (2), which contains ~18,000 nonredundant protein structures, the structures of only two GPCRs have been deposited, that of bovine rhodopsin (3), uniquely facilitated by its natural structures. However, in the Protein Data Bank (2), which contains ~18,000 nonredundant protein structures, the structures of only two GPCRs have been deposited, that of bovine rhodopsin (3), uniquely facilitated by its natural abundance in the retina (4), and very recently that of β2 adrenergic receptor (5), whose high resolution structure determination required the replacement of a loop by a whole protein (6).

Because most GPCRs are normally produced at very low levels, an overexpression system must be set up for each GPCR of interest to obtain quantities sufficient for biophysical analyses. Many attempts have been made to increase functional membrane protein expression levels by testing various combinations of variables defining the expression system, such as host organism, expression plasmid, fusion adducts, codon usage, and expression induction conditions (7). However, even if all of these parameters could be globally optimized, they still may not yield enough functional material because of inherent limitations in the protein sequence itself. Furthermore, the limited stability of solubilized GPCRs is another bottleneck for their biophysical investigation, and this cannot be influenced by the expression system. Thus, while it may be possible to solve a limited number of new GPCR structures whose sequences are sufficiently accommodating to support such a brute-force screening for expression and solubilization conditions, this method is unlikely to have general applicability in routinely generating large amounts of stable, solubilized protein for any given GPCR.

To directly address the importance of receptor sequence as an experimental variable in membrane protein expression and stability, we have developed a powerful approach, inspired by periplasmic expression with cystometric screening (8) and anchored periplasmic expression (9), in which we evolve the sequence of a GPCR, keeping all other variables constant, to yield more functionally expressed protein in a convenient heterologous host, Escherichia coli. We used as a model system the rat neurotensin receptor-1 (NTR1), which has been shown to give a detectable yield in E. coli (10, 11) but which still needs to be improved to allow more convenient preparation of milligram quantities of receptor.

Detailed characterization of the best variant from the selection reported here reveals that it exhibits an order-of-magnitude increase in expression level in both E. coli and Pichia pastoris, elevated expression in mammalian cells, and enhanced stability in detergent-solubilized form, yet it largely retains the biochemical properties of WT NTR1, including binding affinity, binding selectivity, and G protein-mediated signaling. We have further extended this approach to isolate mutants of NTR1 with altered ligand selectivity. This methodology should thus be of general utility in the directed evolution of stable variants of such proteins to high-level expression in multiple states of activity.

Results and Discussion

Setup and Optimization of Screening Methodology.

The general approach is given in Fig. 1. The expression vector containing the GPCR library of interest (e.g., from an error-prone PCR of the receptor gene) with two constant fusion partners (N-terminal maltose binding protein and C-terminal thioredoxin) is used to express the corresponding proteins in functional form in the inner membrane of E. coli DH5α (see Methods). After expression, cells are incubated at 4°C in an optimized buffer that renders the outer membrane permeable to small molecules to allow binding of fluorescent ligand to the receptors, and at the same time maximizes cell viability (see Methods). Chen and colleagues (8) have previously described conditions in which ligands as large as 10 kDa can enter the periplasmic space of E. coli without compromising cell viability. Here, the buffer was specifically optimized to allow for saturable, specific binding of fluorescently labeled agonist [BODIPY-NT(8-13)] to NTR1, while maximizing cell viability after fluorescence-activated cell sorting (FACS) [see supporting information (SI) Figs. S1–S4].


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were further randomized, and fresh bacteria were transformed.

After incubation with saturating concentrations of BODIPY-NT(8–13), bacteria expressing the largest number of functional receptors correspondingly exhibit the greatest fluorescence, and NT binding cannot be measured for the next selection. The flowchart for the selections on NTR1 is given in Fig. S5.

Selection of Variants with Increased Expression Level. For increasing expression level, the initial randomized NTR1 library was subjected to four rounds of FACS. In each round, only the most fluorescent ~0.1 to 1% of the cells were collected. Nonetheless, after these rounds, the evolved pool had a mean fluorescence intensity (MFI) no greater than that of the WT sequence. Error-prone PCR (epPCR) was used to overlay another set of random mutations on top of those that were enriched after the first four rounds of FACS, and this rerandomized library was again subjected to four rounds of sorting. In this second set of sorts, the MFI of the pool overtook that of WT NTR1. After a third randomization step followed by four more rounds of FACS, the evolved pool was split into two. One half was randomized by epPCR a fourth time and the other half was shuffled, using the staggered extension process (StEP) (12).

After these selections, the MFI was approximately five times that of WT NTR1. From the enriched pool, 96 single clones were sequenced and analyzed for receptor expression level (see Methods and Figs. S6 and S7). The clone with the best functional receptor expression level per cell, D03, exhibited approximately a 10-fold increase in specific signal, as assayed by [3H]-NT binding and flow cytometry (Table 1 and Fig. S8). D03 has 14 nucleotide substitutions scattered throughout its helices and loops (see Fig. S10 for a snake-like plot with the exact mutational positions). Five of these mutations are silent, suggesting that incorporation of nonsilent mutations was slow, approximately two amino acid substitutions per round of epPCR. This may be due to the seven-transmembrane helical topology of the protein, which limits the number and type of mutations that are possible, mandating a strategy with low mutational load.

Evolved Receptor Retains Biochemical and Pharmacological Properties of WT. In the membrane of both E. coli and mammalian cells, D03 binds NT with affinities comparable to WT (Table 2), as determined by radioligand binding assays (see Methods). The radioactive signal is almost entirely competed away with a 50-fold excess of either unlabeled NT (agonist) or SR 48692 (antagonist) (13), suggesting that binding specificity is also faithfully retained (Fig. 2).

We also compared the signaling properties of the evolved mutant to those of WT. NTR1 signals mainly via the Gq/11 subtype of G proteins (14), which triggers the mobilization of intracellular Ca2+ pools ([Ca2+]i) via phospholipase C (PLC)-

Although the expression conditions for WT NTR1 typically generate ~1,000 functional receptors per cell (10, 11), optimization of the binding buffer and FACS gating conditions resulted in a specific signal in the gating window that was ~900-fold above background (see Fig. S4).

After incubation with saturating concentrations of BODIPY-NT(8–13), bacteria expressing the largest number of functional receptors correspondingly exhibit the greatest fluorescence, and these cells were collected directly in growth medium and then expanded for a subsequent round. A single selection round, which consisted of library expansion, induced receptor expression, incubation with fluorescent ligand, and FACS to recover the most fluorescent bacterial cells, took approximately 1 day. The advantage of maintaining viable cells was that they could be immediately regrown after sorting, thus eliminating any preparative steps between selection rounds. Whenever additional diversity was desired after any FACS round, the sorted pool of cells was grown and harvested, the enriched plasmid collection was purified, the GPCR sequences (excluding the fusion partners) were further randomized, and fresh bacteria were transformed.

Table 1. Expression levels of NTR1, D03, and D03-L167R in multiple hosts

<table>
<thead>
<tr>
<th>Host</th>
<th>NTR1</th>
<th>D03</th>
<th>D03-L167R</th>
</tr>
</thead>
<tbody>
<tr>
<td>E. coli† no. per cell</td>
<td>705 ± 101</td>
<td>6,155 ± 777¹ (8.7 ± 1.7)</td>
<td>4,647 ± 879 (6.6 ± 1.6)</td>
</tr>
<tr>
<td>P. pastoris‡ pmol/mg</td>
<td>18.3 ± 5.4</td>
<td>216.7 ± 36.9 (11.9 ± 4.1)</td>
<td>51.1 ± 4.3 (2.8 ± 0.9)</td>
</tr>
<tr>
<td>HEK293T, no. per cell</td>
<td>18,300 ± 1,300</td>
<td>58,800 ± 6,600 (3.2 ± 0.4)</td>
<td>33,300 ± 5,400 (1.8 ± 0.3)</td>
</tr>
</tbody>
</table>

*Parenthetical terms give the ratio of mutant expression to that of NTR1.
†Expression in 1 l cultures.
‡Expression in mutated vector pRG7054G.
§Functional receptor (pmol) normalized to total membrane protein content (mg). NT binding cannot be measured with whole P. pastoris cells.

Table 2. Kd of full-length neurotensin binding to receptors on whole cells

<table>
<thead>
<tr>
<th>Host</th>
<th>NTR1</th>
<th>D03</th>
</tr>
</thead>
<tbody>
<tr>
<td>E. coli</td>
<td>0.14 ± 0.01 nM</td>
<td>0.11 ± 0.01 nM</td>
</tr>
<tr>
<td>HEK293T</td>
<td>3.7 ± 0.5 nM</td>
<td>1.9 ± 0.2 nM</td>
</tr>
</tbody>
</table>


and Fig. S11).

nM) needed to achieve strong transient and plateau responses (see Fig. S11), experiments with pooled cells cannot easily be evaluated, and we thus performed single-cell measurements of Ca\(^2+\) signaling in HEK293T cells transiently transfected with either WT or D03. It is well known that mutations in the highly conserved (D/E)R(W/Y) motif in helix III of Class A GPCRs can affect ligand binding and G protein coupling (15). While these results have been obtained with constructs missing amino acids 1 to 42 of the GPCR, no major difference in signaling between the truncated and full-length forms was detected (see Fig. S12).

That these evolved receptors can qualitatively mimic the signals generated by WT, including similar agonist concentration-dependent signaling of D03-L167R, is pleasantly surprising for two reasons: (i) the variants are significantly mutated (8–9 amino acid substitutions) and (ii) the ability to efficiently signal was never under the pressure of selection. More generally, this suggests that it is indeed possible to partially decouple the biophysical properties of a GPCR from its biochemical and pharmacological properties through mutagenesis, which thus enables the use of protein engineering approaches such as the present methodology to improve the robustness of these membrane proteins for structural studies.

**Evolved Receptor Shows Increased Expression in Both Prokaryotic and Eukaryotic Hosts.** There are at least two conceivable mechanisms by which more functional D03 is obtained in E. coli as a result of selection: (i) the total amount of NTR1 and D03 per cell is comparable, but the fraction of properly folded and inserted D03 is significantly greater, or (ii) the total amount of D03 per cell is significantly greater than that of NTR1, but the fraction of functional receptor is similar. Whole-cell Western blots of E. coli proteins reveal that more D03 molecules are detected per cell (see Fig. S13). While this would be consistent with a greater rate of biosynthesis of D03, it more likely reflects the fact that noninserted and dysfunctional WT is degraded. Thus, the quantity of properly inserted, functional GPCR seems to correlate well with the total amount of receptor detected.

To determine whether D03 may have merely adapted to the biosynthetic pathway or the membrane of E. coli during selection or may have actually acquired traits of generally improved biophysical properties, we also expressed WT NTR1, D03, and D03-L167R in the methylotrophic yeast P. pastoris and compared functional and total expression yields. The functional expression level for D03, as assayed by specific radioligand binding to membrane preparations, was nearly 12-fold higher than that for WT NTR1 (Table 1), while the improvement for the backmutated D03-L167R was more modest. This is in contrast to E. coli, where the effect of the back mutation was very small (Table 1). When total receptor protein levels in P. pastoris are compared by Western blot (Fig. 4), the increased expression of D03 is confirmed by the strong intensity of the band at \(\approx 43\) kDa (see Methods). In contrast, WT NTR1 shows a strong band that has not properly entered the gel, suggesting that this receptor is more aggregation-prone than the evolved D03 and D03-L167R. We found that the precursor form [unprocessed prepro- or pro-alpha factor fusion (16)] is detected at about equal intensity for WT and mutants (see Fig. S14), suggesting that protein biosynthesis is not changed, but that the expression level in E. coli depends on the biosynthetic pathway or the membrane of P. pastoris.

To test whether this improvement is also seen in mammalian cells, we transiently transfected HEK293T cells with NTR1 or D03. The evolved mutant was approximately threefold better expressed, as measured in whole-cell radioligand binding assays (see Table 1). Again, the effect of the back mutation L167R on expression is small (Table 1). Similar experiments in CHO cells and COS cells also revealed a two- to threefold increase in functional D03 expression relative to WT NTR1 (data not shown). In all of the experimentally

![Graph](image-url)

**Fig. 3.** Ca\(^2+\) signaling in HEK293T cells expressing NTR1, D03, or D03-L167R. Single-cell measurements were performed and the resulting signal was classified as an oscillatory, plateau, or transient response (see Methods, SI Text, and Fig. S11).
tested hosts, neither the growth rate nor the final cell density was detectably different when expressing NTR1 and D03 in parallel cultures (data not shown). These results thus suggest that D03 is an intrinsically more robust protein in expressing and folding not only in E. coli, but also in multiple eukaryotic hosts. It should be noted that all receptors were expressed as fusion proteins with N-terminal maltose binding protein (MBP) and C-terminal thioredoxin (TrxA) fusions in E. coli, whereas these fusion partners were not present for expression in eukaryotic hosts (P. pastoris and HEK293T cells). Therefore, the similar trends in functional expression (Table 1) and biochemical affinity (Table 2) across different hosts suggest that the fusion partners used in bacteria are not involved in causing these evolutionary improvements.

Characterization of Solubilized and Purified Receptor. To ascertain whether the observed enhancement in functional receptor expression in E. coli translates into a corresponding increase in pure, soluble material, we performed a side-by-side purification of the NTR1 and D03 fusion proteins (see Methods). Briefly, after detergent solubilization and purification by immobilized metal ion affinity chromatography (IMAC), the amount of functional GPCR was monitored at each step by a radiolabeled ligand-binding assay (see Fig. S19) and the impact of each single substitution was individually reintroduced into the WT sequence, and (ii) each of the existing substitutions in D03 was individually reverted back to the corresponding WT nucleotide. The first approach should elucidate whether individual mutations can substantially increase the expression level on their own, whereas the second approach should reveal any additional mutations that also may be beneficial but whose effect may be masked by unfavorable WT amino acids. For the 28 variants that were generated in this manner, the receptor expression level was determined by saturation radioligand binding (see Fig. S19) and the impact of each single mutation—whether added to WT or subtracted from D03—is relatively small. We refer to this phenomenon as a “staircase effect,” because the improved phenotype of D03 is the sum of many incremental enhancements that leads to an increase in expression level.

In addition to the R167L mutation discussed previously, other unusual substitutions in NTR1 and one unintended mutation in the expression vector arose during the evolution of D03. Five of the nucleotide substitutions in NTR1 were silent, but two of these surprisingly introduced rare leucine codons (CTA) into the sequence (see Fig. S10). While it was recently shown that a synonymous single-nucleotide polymorphism in the MDR1 gene can change the conformation of the corresponding protein because of altered kinetics of cotranslational folding and insertion (18), in our case none of the rare codons appears to alter protein expression (see Fig. S19) (although we cannot rigorously exclude that they might subtly influence protein conformation by altering biosynthesis kinetics). This result suggests that codon optimization or the use of rare tRNA-overexpressing strains may not be fruitful if other, inherently larger bottlenecks exist in heterologous protein expression.

Lastly, an unintentional mutation arose in the origin of...
replication in the plasmid harboring D03. This mutation (C7054G, for numbering see Fig. S15), close to the origin of replication and close to a previously identified mutation influencing the copy number (19), increases the copy number of the plasmid by 100%, as determined by measuring the total amount of DNA from plasmid isolation experiments from standard expressions at 20°C (see Fig. S16). However, when D03 is expressed in the mutated pRG vector (pRG(C7054G)), its expression level increases by only ~25% as compared to the original vector (pRGWT), and when WT NTR1 is expressed in the mutated vector, there is even no noticeable increase in its expression level (see Fig. S16). We hypothesize that the major bottlenecks in functional protein expression for WT NTR1 are cotranslational folding and insertion and, therefore, any other improvements along the expression pathway remain masked.

**Selection of Variants with Altered Ligand Selectivity.** For selections of ligand selectivity on NTR1 (see Fig. 1), two ligands were used, agonist BODIPY-NT(8–13) and antagonist SR 48692. In principle, selectivity selections could be performed independently of selections for expression level. However, in the case of NTR1, the FACS signal of the WT receptor was so weak with BODIPY-NT(8–13) alone, that the addition of excess SR 48692 would drop the signal of any positive clones into the background. Thus, the selectivity screen was only used after an initial selection for expression level to ensure that the MFI of the pool was significantly above background (after the fourth epPCR; see Fig. S5). Sequencing of the library before the fourth epPCR revealed expression-specific mutations; thus, any mutations that were enriched after the fourth epPCR in this screen could be readily identified as selectivity mutations and not expression mutations. After performing selections for NTR1 sequences that still bound BODIPY-NT(8–13) in the presence of 100-fold excess SR 48692, 96 single clones were sequenced and analyzed for receptor expression level. The best expressing clone, G10, exhibited approximately a fivefold higher expression level than the WT, could be fully competed by NT, but could not be fully competed by 100-fold excess SR 48692 (see Fig. 2 and Fig. S9).

In stark contrast to the staircase effect observed with D03 and other expression variants, there was only one consensus mutation observed in G10 and other selectivity variants. This “elevator effect” in changing selectivity arose from a single mutation, F358S (see Fig. S10). The effects of mutation at Phe-358 have been studied by others (20), and reveal that a substitution to alanine at this position results not only in decreased antagonist affinity, but also in spontaneous basal inositol phosphate production in a receptor-dependent manner (21). Based upon a sequence alignment with bovine rhodopsin, Phe-358 may play an important role in maintaining the interaction between transmembrane helices 6 and 7, which in turn keeps NTR1 in an inactive conformation (21). Disruption of this residue leads to the observed constitutive activity. Thus, more generally, the present methodology has the ability to rapidly isolate mutations that may trap receptors in the active or inactive state, an approach that is complementary to previous work in engineering GPCR selectivity and activity (22, 23).

**Conclusion**

There have been recent advances in membrane protein engineering, including technologies for the screening of high-expressing members in a diverse pool of eukaryotic membrane proteins (24), identification of functionally critical amino acids in a GPCR (25–27), manual blot screening of randomly mutated membrane proteins for increased expression (28), and introduction of thermostabilizing mutations, individually identified by trial and error, in a GPCR (29). Complementary to such approaches, we present here a powerful, high-throughput platform for the directed evolution of a GPCR to enhance both expression level and stability while retaining function and to tailor ligand selectivity. This methodology should be applicable to other integral membrane proteins as well, for which specific binding ligands are available, and may help to facilitate biophysical studies by allowing milligram-level production of these proteins in multiple states of activity. Importantly, no basal heterologous expression of a WT GPCR sequence is necessary for the approach to work, as long as there exist expressing mutants that can be recovered by FACS. In the present study, a highly expressing, stable NTR1 variant displays WT biochemical properties—as assayed by binding affinity, binding selectivity, and G protein mediated signaling—and therefore provides a biologically meaningful template for structural studies. Such evolved membrane proteins may facilitate X-ray crystallography trials not only because they can be produced more abundantly but also because they remain functional in detergent micelles for significantly longer periods of time. If the proteins are more stable because of enhanced rigidity, they may also be more likely to generate properly diffracting crystals for structural determinations. The ability to obtain such high-resolution structures may help to elucidate the molecular basis for activation, inactivation, or pathology associated with that receptor, and may also provide templates for drug design.

**Methods**

**Library Design and Selection.** The rat neurotensin receptor-1 gene (NTR1; amino acids 43–424) has previously been expressed in *E. coli* using a vector that generates an N-terminal fusion of the receptor to MBP and C-terminal fusion to TrxA to enhance expression. The fusion protein contains tobacco etch virus (TEV) protease cleavage sites on both ends of the receptor and a C-terminal His$_{10}$ tag. This derivative of the expression vector pGIII-hs-MBP containing the NTR1 gene with these fusions was a kind gift from R. Grisham (National Institutes of Health). Expression of NTR1 in *E. coli* DH5$_{\alpha}$ was essentially as described in ref. 30. Details of the preparation of fluorescently labeled neurotensin [BODIPY-NT(8–13)] and construction of NTR1 libraries are given in the *SI Text*. To allow binding of BODIPY-NT(8–13) to NTR1 in the inner membrane of *E. coli* while maximizing cell viability, an optimized binding buffer (50 mM Tris-HCl, pH 7.4, and 150 mM KCl) was identified (see *SI Text*). During each round of FACS, only the most fluorescently labeled clones were sorted directly into 96-well plates during FACS and regrown to perform single clone analysis of expression levels by radioligand binding assays.

**Radioligand Binding Assays.** Details of the experimental protocols are given in the *SI Text*. Briefly, quantitative measurements of receptor number in *E. coli*, *P. pastoris*, *H. krausii* cells, and detergent solution were performed using a saturating concentration of radioactive agonist $[^{3}H]$-NT (10 nM) (PerkinElmer). For determining equilibrium binding affinities, a dilution series of radioligand was used (0.04–20 nM). Nonselective binding was determined in the presence of 5$nM$ unlabeled NT. For competition experiments, antagonist SR 48692 (Sanofi Aventis) was used at a concentration of 5$nM$.

**Mammalian Cell Culture and Transfection.** For expression in mammalian cells, receptors were cloned into the vector pcDNA3.1 (Invitrogen) encoding C-terminal Myc and His$_{6}$ tags. The HEK293T cell line (31) (a clonal line of HEK293 cells stably expressing SV40 large T antigen) was grown as described in ref. 32. Cells were routinely seeded into 6-well culture plates or 10 mm Petri dishes and grown for 24 h, reaching 70 to 80% confluence before transfection. Cells for binding assays were transiently transfected with DNA using calcium phosphate precipitation as described in ref. 32.

**Single-Cell Monitoring of Variations in Intracellular Free Calcium, [Ca$^{2+}$].** Changes in [Ca$^{2+}$], in response to NT were measured in individual HEK293T cells using the indicator Fura2-acetoxymethyl ester, as described in ref. 33. Different types of Ca$^{2+}$ responses were observed and were classified as transient, oscillatory, or plateau (see *SI Text*).

**Expression in *Pichia pastoris*.** The *P. pastoris* strain SMD1163 (Invitrogen) was used for all experiments. A modified version of the yeast shuttle vector pPICZa/C (Invitrogen) was previously designed in which the *Sacharomyces cerevisiae* alpha-factor prepro sequence (34), under the control of the AOX

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Immunoblot Analysis. For immunoblot analysis, yeast membranes (20 µg of total membrane protein) were diluted with TBS to a concentration of 4 µg/ml and an equivalent volume of 2× SDS loading buffer was added. The samples were incubated at 42°C for 30 min in the presence of 10 mM DTT before separating the proteins by SDS/PAGE (4–12% Bis-Tris gels; Invitrogen). Proteins were transferred to Immobilon-P transfer membranes (Millipore), and membranes were blocked in TBST (TBS with 0.5% Tween-20) with 5% milk powder for 1 h at room temperature. The C-terminal biotinylation was detected with a streptavidin–alkaline phosphate conjugate (Roche Diagnostic GmbH). While the expected size of the GPCR is ~55 kDa, results from N-terminal sequencing and from in-gel digestions followed by mass spectrometry of the P. pastoris construct showed that the band at ~43 kDa indeed corresponds to the full-length GPCR, correctly processed at the N terminus (data not shown).

Receptor Solubilization and Purification. This was performed essentially as published by Grishammer and Tucker (30). The detailed protocol is provided in the SI Text.

Thermal Stability. Receptors were expressed as fusion proteins (MBP-GPCR-TrxA-His10) in E. coli and purified by IMAC and size exclusion chromatography (Superdex 200). Thermal stability was assayed in buffer STA830 [50 mM Tris-HCl, pH 7.4, 30% glycerol, 200 mM NaCl, 1 mM EDTA, 0.05% dodecyl-β-D-maltopyranoside (DDM), 0.5% (wt/vol) 3-(3-cholamidopropyl)-dimethylammonio)-1-propanesulfonate (CHAPS), 0.1% (wt/vol); cholesterol hemisuccinate (CHS)]. Samples were incubated at 45°C for the indicated period (up to 175 min) and were then gel-filtered. Radioligand binding assays were performed as described in the SI Text.

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