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An efficient Escherichia coli expression system for the production of a functional N-terminal domain of the T1R3 taste receptor

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Vertebrate chemosensory receptors are able to recognize diverse chemical compounds, including ions, tastants, odorants and pheromones. The first step of this detection is mostly accomplished by the activation of G protein-coupled receptors (GPCRs). These receptors share a common seven transmembrane motif and are encoded by < 1% of the mammalian genes. One particular GPCR family, GPCR class C, contains receptors for sweet and amino acid taste compounds, some pheromone molecules, and the odorants in fish.1,2 The most studied receptors of this class are the homodimeric metabotropic glutamate receptors (mGlur), the heterodimeric γ-aminobutyric acid type B receptor (GABA BR), and the homodimeric extracellular calcium-sensing receptor (CaSR). Class C GPCRs share a large N-terminal domain (NTD), comprising 500–600 amino acids, which is composed of two lobes separated by a large cleft in which the agonists bind (for a review, see refs. 3 and 4). Except for GABABR, this domain is connected to a transmembrane heptahelical domain (HD), typical of all GPCRs, via a cysteine-rich region (CRR). Numerous studies have revealed the importance of the NTD in the functionality of class C GPCRs.5-7 This domain, which qualifies as an orthosteric site, is responsible for agonist recognition. Indeed, when produced as a soluble protein in insect cells, this domain was found to retain its ability to bind ligands, as demonstrated for mGlur,2 GABA BR, and CaSR.8

Sweet taste is mediated by a dimeric receptor composed of two distinct subunits, T1R2 and T1R3, whereas the T1R1/T1R3 receptor is involved in umami taste perception. The T1R1, T1R2, and T1R3 subunits are members of the small family of class C G protein-coupled receptors (GPCRs). The members of this family are characterized by a large N-terminal domain (NTD), which is structurally similar to bacterial periplasmic-binding proteins and contains the primary ligand-binding site. In a recent study, we described a strategy to produce a functional dimeric human T1R3-NTD. Although the protein was expressed as inclusion bodies (IBs) using the Escherichia coli system, the conditions for the refolding of functional hT1R3-NTD were determined using a fractional factorial screen coupled to a binding assay. Here, we report that this refolding strategy can be used to produce T1R1- and T1R2-NTDs in large quantities. We also discuss that our findings could be more generally applicable to other class C GPCR-NTDs, including the γ-aminobutyric acid type B receptor (GABA BR), the extracellular calcium-sensing receptor (CaSR) and the large family of pheromone (V2R) orphan receptors.

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form homodimers that are able to function as low-affinity receptors for sugars.12,13 The presence of multiple binding sites has been revealed for both umami and sweet taste receptors. Natural and artificial sugars (e.g., sucrose, glucose and sucralose) bind to both T1R2- and T1R3-NTDs,10,15 whereas dipeptide sweeteners (e.g., aspartame and neotame) bind only to T1R2-NTD.16,17 The binding sites of two other non-caloric sweeteners (cyclamate and neohesperidin dihydrochalcone) and lactulose, a human sweet-taste inhibitor, are located within the HD of human T1R3.18-21 Lastly, T1R1-NTD has been identified as the primary binding site of t-glutamate.19 Although the binding properties of T1R1- and T1R2-NTD have been demonstrated, the role of T1R3-NTD and its relative contribution to the heterodimeric receptor function remains to be elucidated.

There is a great interest in discovering new sweeteners or umami compounds. These compounds can be identified by the screening of large compound libraries for molecules that are able to bind to T1R1-, T1R2- or T1R3-NTDs, a technique requiring large quantities of functional proteins. In addition, the rational design of new tasting molecules and the elucidation of the molecular mechanisms, which are critical for detection and discrimination, relies on obtaining high-resolution X-ray crystal structures of these domains, which also requires high-quality protein. Mouse T1R2- and T1R3-NTDs have been successfully expressed in E. coli as protein fusions with maltose-binding protein or the chitin-binding domain.14 However, the level of soluble protein expression was low (< 0.5 mg/L), and the presence of the fusion partner complicated the functional analyses of the ligand interactions. The baculovirus expression system has been shown to efficiently secrete a functionally active mGluR-NTD that is amenable to crystallization.1,2 In contrast, a recent study aimed at expressing mouse T1R-NTDs fused to green fluorescent protein demonstrated that the protein fusion remained almost completely in the cellular space of the insect cells, exhibiting polydisperse hydrodynamic states with large aggregated fractions and without the formation of homodimers.22

In our previous study, we described a strategy to produce large quantities of the NTD of the human T1R3 subunit (hT1R3-NTD).23 We overexpressed hT1R3-NTD using an E. coli prokaryotic system because this expression system offers the advantages that include the ability to grow rapidly at high densities utilizing inexpensive substrates. The well-characterized genetics of E. coli and the availability of a large number of expression vectors and mutant host strains also constitute the advantages of this system. We found that large quantities of hT1R3-NTD can be expressed in the form of inclusion bodies (IBs); using a fractional factorial screen coupled to a functional fluorescent assay, we determined conditions for the refolding of the protein. Using size-exclusion chromatography, spectroscopic techniques and microcalorimetry, we have shown that hT1R3-NTD behaves as a functional dimer that is capable of binding sucralose, a chlorodeoxysugar sweetener, with an affinity in the millimolar range. Here, we extend this previous study to report detailed strategies for obtaining other taste receptor NTDs using bacterial expression systems and discuss the benefit of using this expression system.

**Construction of the Expression Plasmid**

As previously described for hT1R3-NTD,1 we expressed hTIR1- and hTIR2-NTD, minus a short putative signal peptide and the CRR, independently of the seven-transmembrane domain (Fig. 1A and B). The cDNA coding for hTIR1- or hTIR2-NTD was cloned into the bacterial expression vector pET28a. The resulting expression plasmid encodes a fusion protein comprising an N-terminal His6-tag that can be cleaved with thrombin, followed by hTIR3-NTD and a C-terminal Strep-tag II. The thrombin cleavage site is represented with an arrow.

**Figure 1. Expression of T1R-NTD proteins.** (A) The NTDs of the T1R1, T1R2 and T1R3 proteins, minus a putative signal peptide and without the CRR, were expressed independently of the seven-transmembrane domain. (B) The construct pET28-NTRI3-NTD encodes a protein comprising an N-terminal His6-tag that can be cleaved by thrombin, followed by hTIR3-NTD and a C-terminal Strep-tag II. (C) The pET28-hTIR1-NTD/pET28-hTIR2-NTD plasmid encodes a fusion protein that contains an N-terminal His6-tag that can be cleaved with thrombin, followed by hTIR1- or hTIR2-NTD and a C-terminal Strep-tag to facilitate the purification of the heterodimers. (D) The pET22-hTIR3-NTD plasmid encodes hTIR3-NTD with an additional N-terminal Met residue and a C-terminal Strep-tag II. The thrombin cleavage site is represented with an arrow.
produced using E. coli BL21 (DE3). Both constructs showed a good level of overexpression of the recombinant proteins similar to that of hT1R3-NTD as demonstrated by SDS-PAGE analysis (Fig 2). As previously observed with hT1R3-NTD, both proteins entirely precipitated in the form of insoluble IBs in the E. coli cytosol. IBs were purified and solubilized in a denaturing buffer containing 6 M guanidinium chloride (GuCl) as previously described. The quantity of purified protein was determined using UV absorbance at 270 nm. Approximately 80 and 120 mg of hT1R1- and hT1R2-NTD were obtained from 1 L of bacterial culture, respectively. A second hT1R1-NTD expression construct was also generated to evaluate the impact of the hT1R3-NTD N-terminus on the protein expression level and to avoid the use of thrombin for the proteolytic cleavage of the N-terminal His6-tag. The sequence coding for hT1R3-NTD was PCR amplified and subcloned into the NdeI and EcoRI restriction sites of the pET22b vector (Novagen), allowing removal of the pETB leader peptide sequence encoded by the expression plasmid. This construct encodes hT1R3-NTD (Ala21-Ser497) containing an additional N-terminal Met residue and a C-terminal Stop-tag II to facilitate its purification (Fig 1D). The resulting construct, named pET22-hT1R3-NTD, was sequenced (Cogenics) and expressed in E. coli BL21 (DE3) cells. Unfortunately, no hT1R3-NTD protein was detectable in the bacterial lysate, as previously observed with mouse T1R3-NTD. We observed the removal of the N-terminal His6-tag encoded by the pET28 vector is essential to the production of a large amount of hT1R3-NTD as IBs.

Expression and Purification of hT1R3-NTD

As many biophysical studies are made possible by the availability of large amounts of pure protein, we have focused on designing strategies to recover folded and biologically active molecules from protein overexpressed as insoluble IBs. After washing and solubilizing the IBs, approximately 110 mg of hT1R3-NTD was obtained from 1 L of bacterial culture for refolding studies. At this stage, the protein was pure to apparent homogeneity (i.e., ~90%) by simply washing the IBs with an aqueous solution containing NaCl and urea, supplemented with Triton X-100. The IBs of hT1R3-NTD were solubilized using 6 M GuCl. In our previous work, we elaborated a strategy for the production of hT1R3-NTD using a refolding screen, which is outlined in Figure 4. To test a variety of refolding additives in a minimal number of experiments, we compared the effects of 12 well-known refolding reagents with 16 experiments. The screening for the optimal refolding buffer was performed with an incubation at 20°C and included a change of the pH, a variation of the pH-buffer, and the addition of varying amounts of different salts and the presence of a chaotrope (urea), ligands (sucralose and glucose) and polar additives. We also tested the impact of three detergents (nonionic and zwitterionic) on hT1R3-NTD refolding. To evaluate the functionality of the refolded hT1R3-NTD rapidly, we measured its intrinsic tryptophan fluorescence in the absence and presence of 10 mM sucrose. Based on our analysis, we observed that the presence of a zwittergent, Zw3-14, had the largest impact on the refolding of hT1R3-NTD. We also determined the demixing state using size-exclusion chromatography and the presence of secondary structures using circular dichroism (as shown in Fig. 5 of our previously published paper). We determined the binding activity of hT1R3-NTD using the tryptophan fluorescence and isothermal titration calorimetry. We found that hT1R3-NTD binds sucrose with a Ka value in the low millimolar range, which is in good agreement with the value measured for mouse THR3-NTD by Nie and coworkers. Moreover, we digested hT1R3-NTD with thrombin to evaluate further that the protein was properly refolded. As detected by SDS-PAGE, we observed the removal of the N-terminal His6-tag, giving another indication of the correct refolding of hT1R3-NTD. We tested hT1R1 and hT1R2-NTD proteins in our refolding strategy. Size-exclusion chromatography indicated that both proteins were mainly produced as aggregates with a low proportion of properly refolded protein (data not shown). Extension of folding screens for improving the refolding yields of hT1R1- and hT1R2-NTDs by the inclusion of other factors such as receptor ligands (glutamate or sweeteners), other detergents or additives, are in progress. Our produced proteins can be also used to generate antibodies against hT1R1 are of poor quality, we recently

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detergent (Zw3-14) that we used for the protein refolding could be exchanged with n-dodecyl-β-D-maltopyranoside or n-octyl-β-D-glucopyranoside detergents. Our approach should also offer a method for the reconstruction of the heterodimeric T1R2/T1R3 and T1R1/T1R3 taste receptors at a quality that is suitable for the detailed study of its structure, dynamics, and interactions with taste molecules. It has been shown that the activation of the human T1R2/T1R3 receptor by the sweet-tasting protein brazzein is dependent on the CRR.24 Our approach should allow the production of the entire extracellular region (i.e., comprising the CRR). The availability of large amounts of recombinant hT1R3-NTD will enable detailed studies of its interactions with sweet-tasting proteins, such as brazzein, monellin or thaumatin and gurmarin,25 a sweet-taste-suppressing protein.

The class C GPCR family consists of 22 human proteins, including the receptor for GABA, CaSR, GPRC6A and seven orphan receptors, which may constitute drug targets. In addition, the mouse genome contains approximately 120 genes coding orphan pheromone (V2R) receptors that seem to be activated by peptides or proteins.26 We anticipate that our method will also be more generally applicable to all of these class C GPCR-NTDs.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

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Conclusion
In this paper, we provide additional information about the production of recombinant hT1R3-NTD. We show that the presence of a His6-tag in the N-terminal position is essential to obtain a high level of expression of our protein of interest in E. coli. Our data indicate that our developed strategy is applicable for other protein members of this family, such as hT1R1- and hT1R2-NTD.

Owing to this high amount of functional hT1R3-NTD protein, biochemical tests and the screening of large compound libraries are now possible. In addition, the rational design of sweeteners and elucidation of the molecular mechanisms, which are critical for detection and discrimination, rely on obtaining high-resolution X-ray crystal structures of T1R2- and T1R3-NTD, a technique that also requires high-quality protein. Current experiments with the in vitro refolded hT1R3-NTD include crystalization trials and NMR spectroscopic analyses to gather the desired structural information for hT1R3-NTD in the near future. Certain detergents, such as maltosides and glucosides, have been used more often than others for crystallization and NMR experiments to gather the desired structural information for hT1R3-NTD in the near future. Certain detergents, such as maltosides and glucosides, have been used more often than others for crystallization and NMR spectroscopic analyses to gather the desired structural information for hT1R3-NTD in the near future. Certain detergents, such as maltosides and glucosides, have been used more often than others for crystallization and NMR spectroscopic analyses to gather the desired structural information for hT1R3-NTD in the near future. Certain detergents, such as maltosides and glucosides, have been used more often than others for crystallization and NMR spectroscopic analyses to gather the desired structural information for hT1R3-NTD in the near future.

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