(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
14 April 2005 (14.04.2005)

PCT

(10) International Publication Number
WO 2005/033125 A2

(51) International Patent Classification[7]: C07K

(21) International Application Number:
PCT/US2004/032678

(22) International Filing Date: 4 October 2004 (04.10.2004)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
10/679,102 2 October 2003 (02.10.2003) US

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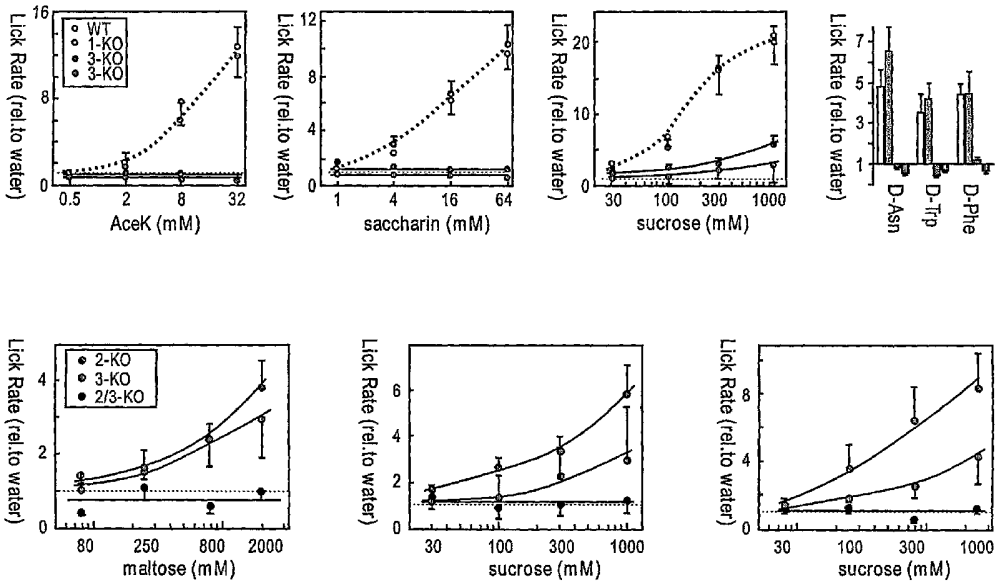
(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM),

[Continued on next page]

(54) Title: MAMMALIAN T1R3 SWEET TASTE RECEPTORS



(57) Abstract: The present invention provides isolated nucleic acid and amino acid sequences of sweet taste receptors, the receptors comprising consisting of a monomer or homodimer of a T1R3 G-protein coupled receptor polypeptide, antibodies to such receptors, methods of detecting such nucleic acids and receptors, and methods of screening for modulators of sweet and amino acid taste receptors.

WO 2005/033125 A2

European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Declaration under Rule 4.17:

— *of inventorship (Rule 4.17(iv)) for US only*

Published:

— *without international search report and to be republished upon receipt of that report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

Mammalian T1R3 Sweet Taste Receptors

CROSS-REFERENCES TO RELATED APPLICATIONS

The present application claims priority to USSN 10/679,102, filed October 2, 2003, herein incorporated by reference in its entirety.

STATEMENT AS TO RIGHTS TO INVENTIONS MADE UNDER FEDERALLY SPONSORED RESEARCH AND DEVELOPMENT

Not applicable.

FIELD OF THE INVENTION

The present invention provides isolated nucleic acid and amino acid sequences of sweet taste receptors, the receptors comprising consisting of a monomer or homodimer of a T1R3 G-protein coupled receptor polypeptide, antibodies to such receptors, methods of detecting such nucleic acids and receptors, and methods of screening for modulators of sweet taste receptors.

BACKGROUND OF THE INVENTION

The sense of taste is responsible for detecting and responding to sweet, bitter, sour, salty and umami (amino acid) stimuli. It is also capable of distinguishing between these various taste modalities to generate innate behavioral responses. For instance, animals are vigorously averse to bitter-tasting compounds, but are attracted to sweet and umami stimuli. To examine taste signal detection and information processing, we have focused on the isolation and characterization of sweet, umami and bitter taste receptors. These receptors provide powerful molecular tools to delineate the organization of the taste system, and to help define the logic of taste coding.

Two families of candidate mammalian taste receptors, the T1Rs and T2Rs, have been implicated in sweet, umami and bitter detection. The T2Rs are a family of ~30 taste-specific GPCRs distantly related to opsins, and clustered in regions of the genome genetically linked to bitter taste in humans and mice (Adler *et al.*, *Cell 100*, 693-702 (2000); Matsunami *et al.*, *Nature, 404*, 601-604 (2000)). Several T2Rs have been shown to function as bitter taste receptors in heterologous expression assays, substantiating their role as bitter sensors (Chandrashekar *et al.*, *Cell, 100*, 703-711 (2000); Bufe *et al.*, *Nat Genet, 32*, 397-401

(2002)). Most T2Rs are co-expressed in the same subset of taste receptor cells (Adler, E. *et al.*, *Cell 100*, 693-702 (2000)), suggesting that these cells function as generalized bitter detectors.

The T1Rs are a small family of 3 GPCRs expressed in taste cells of the tongue and palate epithelium, distantly related to metabotropic glutamate receptors, the calcium sensing receptor and vomeronasal receptors (Hoon *et al.*, *Cell., 96*, 541-551 (1999); Kitagawa *et al.*, *Biochem Biophys Res Commun, 283*, 236-242 (2001); Max *et al.*,| *Sac. Nat Genet, 28*, 58-63 (2001); Montmayeur *et al. Nat Neurosci, 4*, 492-498 (2001); Nelson *et al.*, *Cell, 106*, 381-390 (2001); Sainz *et al.*, *J Neurochem, 77*, 896-903 (2001)). T1Rs combine to generate at least two heteromeric receptors: T1R1 and T1R3 form an L-amino acid sensor, which in rodents recognizes most amino acids, and T1R2 and T1R3 associate to function as a broadly tuned sweet receptor (Nelson, G. *et al.*, *Cell, 106*, 381-390 (2001); Nelson, G. *et al.*, *Nature, 416*, 199-202 (2002); Li, X. *et al.*, *Proc Natl Acad Sci U S A, 99*, 4692-4696 (2002); see also WO 00/06592, WO 00/06593, and WO 03/004992).

Animals can detect a wide range of chemically distinct sweet tasting molecules, including natural sugars, artificial sweeteners, D-amino acids and intensely sweet proteins. How many different receptors does it take to taste the sweet universe? The human and rodent T1R2+3 heteromeric sweet receptors respond in cell-based assays to all classes of sweet compounds, and do so with affinities that approximate their respective *in vivo* psychophysical and/or behavioral thresholds (Nelson *et al.*, *Cell, 106*, 381-390 (2001); Li *et al.*, *Proc Natl Acad Sci U S A, 99*, 4692-4696 (2002)). At a fundamental level, the evolution of sweet taste most likely reflects the need to detect and measure sugar content in potential food sources. Therefore, a single broadly tuned receptor for natural sugars might be all that is required. On the other hand, a number of studies with various sugars and artificial sweeteners insinuate the possibility of more than one sweet taste receptor (Schiffman *et al.*, *Pharmacol Biochem Behav, 15*, 377-388 (1981); Ninomiya *et al.*, *J Neurophysiol, 81*, 3087-3091 (1999)).

In humans, monosodium L-glutamate (MSG) and L-aspartate, but not other amino acids, elicit a distinctive savory taste sensation called umami (Maga, 1983). Notably, unlike the rodent T1R1+3, the human T1R1+3 amino acid taste receptor is substantially more sensitive to L-glutamate and L-aspartate than to other L-amino acids (Li *et al.*, *Proc Natl Acad Sci U S A, 99*, 4692-4696 (2002)). These findings led to the proposal that T1R1+3 may be the mammalian umami receptor (Nelson. *et al.*, *Nature, 416*, 199-202 (2002); Li. *et al.*, *Proc Natl Acad Sci U S A, 99*, 4692-4696 (2002)). However, a number of studies, including

the recent analysis of T1R3 KO mice (Damak *et al.*, *Science, 301*, 850-853 (2003)) have suggested that umami taste is mediated by mGluR4t, a truncated variant of the metabotropic glutamate receptor (Chaudhari *et al.*, *Neurosci, 16*, 3817-3826 (1996); Chaudhari. *et al.*, *Nat Neurosci, 3,* 113-119 (2000)).

How are the different taste qualities encoded at the taste cell level? In mammals, taste receptor cells are assembled into taste buds that are distributed in different papillae in the tongue epithelium. Each taste bud contains 50-150 cells, including precursor cells, support cells, and taste receptor cells (Lindemann, *Physiol Rev, 76*, 718-766 (1996)). The receptor cells are innervated by afferent fibers that transmit information to the taste centers of the cortex through synapses in the brain stem and thalamus. In the simplest model of taste coding at the periphery, each taste modality would be encoded by a unique population of cells expressing specific receptors (e.g. sweet cells, bitter cells, salt-sensing cells, etc.). In this scenario, our perception of any one taste quality would result from the activation of distinct cell types in the tongue (labeled line model). Alternatively, individual taste cells could recognize multiple taste modalities, and the ensemble firing pattern of many such broadly tuned receptor cells would encode taste quality (across fiber model).

Recently, we showed that T1Rs and T2Rs are expressed in completely non-overlapping populations of receptor cells in the lingual epithelium (Nelson *et al.*, *Cell, 106*, 381-390 (2001)), and demonstrated that bitter-receptor expressing cells mediate responses to bitter but not to sweet or amino acid tastants (Zhang *et al.*, *Cell, 112*, 293-301 (2003)). Together, these results argued that taste receptor cells are not broadly tuned across all modalities, and strongly supported a labeled line model of taste coding at the periphery. A fundamental question we address now is how many types of cells and receptors are necessary to mediate sweet and umami, the two principal attractive taste modalities. We now show that sweet and umami tastes are exclusively mediated by T1Rs, and demonstrate that genetic ablation of individual T1R subunits selectively affects these two attractive taste modalities. The identification of cells and receptors for sweet and umami sensing also allowed us to devise a strategy to separate the role of receptor activation from cell stimulation in encoding taste responses. We show that animals engineered to express a modified k-opioid receptor in T1R2+3- expressing cells become specifically attracted to a k-opioid agonist, and prove that activation of sweet-receptor expressing cells, rather than the T1R receptors themselves, is the key determinant of behavioral attraction to sweet tastants. Finally, we now demonstrate that T1R1 alone, either as a monomer or as a homodimer, acts as a receptor for naturally occurring sugars.

BRIEF SUMMARY OF THE INVENTION

The present invention thus provides for the first time a homodimeric sweet taste receptor, the receptor comprising or consisting of two T1R3 polypeptides. The present invention also provides a monomeric sweet taste receptor comprising or consisting of one T1R3 polypeptide. The receptors transduce a signal in response to sweet taste ligands when T1R3 is expressed in a cell. In one embodiment, the sweet taste ligands are naturally occurring sweet tasting molecules. In another embodiment, the sweet taste ligands and artificial and mimic naturally occurring sweet tasting molecules. In one embodiment, the T1R3 polypeptides of the homodimer are non-covalently linked.

In one aspect, the present invention provides a sweet taste receptor comprising a T1R3 polypeptide, the T1R3 polypeptide comprising greater than about 80% amino acid sequence identity to an amino acid sequence of SEQ ID NO:15, SEQ ID NO:20, SEQ ID NO:23, SEQ ID NO:25, or SEQ ID NO:31 or encoded by a nucleotide sequence hybridizing under moderately or highly stringent hybridization conditions to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:15, SEQ ID NO:20, SEQ ID NO:23, SEQ ID NO:25, or SEQ ID NO:31.

In one embodiment, the T1R3-comprising receptor specifically binds to polyclonal antibodies generated against SEQ ID NO:15, SEQ ID NO:20, SEQ ID NO:23, SEQ ID NO:25, or SEQ ID NO:31. In another embodiment, the receptor has G-protein coupled receptor activity. In another embodiment, the T1R3 polypeptide has an amino acid sequence of SEQ ID NO:15, SEQ ID NO:20, SEQ ID NO:23, SEQ ID NO:25, or SEQ ID NO:31. In another embodiment, the receptor is from a human, a rat, or a mouse.

In another embodiment, the sweet receptor comprises a T1R3 polypeptide and recognizes natural sugars, e.g., glucose, galactose, fructose, maltose, lactose, and sucrose.

In one aspect, the present invention provides an isolated polypeptide comprising an extracellular, a transmembrane domain, or a cytoplasmic domain of a sweet T1R3-comprising homodimeric or monomeric taste receptor, the extracellular, a transmembrane domain, or a cytoplasmic domain comprising greater than about 80% amino acid sequence identity to the extracellular, a transmembrane domain, or a cytoplasmic domain of SEQ ID NO:15, SEQ ID NO:20, SEQ ID NO:23, SEQ ID NO:25, or SEQ ID NO:31. In another embodiment, the extracellular, transmembrane, or cytoplasmic domain hybridize under highly stringent conditions to an extracellular, transmembrane, or cytoplasmic domain of an amino acid sequence of SEQ ID NO:15, 20, 23, 25, or 31.

In one embodiment, the polypeptide encodes the extracellular, a transmembrane domain, or a cytoplasmic domain of SEQ ID NO:15, SEQ ID NO:20, SEQ ID NO:23, SEQ ID NO:25, or SEQ ID NO:31. In another embodiment, the extracellular, a transmembrane domain, or a cytoplasmic domain is covalently linked to a heterologous polypeptide, forming a chimeric polypeptide. In another embodiment, the chimeric polypeptide has G-protein coupled receptor activity.

In one aspect, the present invention provides an antibody that selectively binds to a homodimeric or monomeric sweet taste receptor, the receptor comprising one or two T1R3 polypeptides but no T1R1 or T1R2 polypeptides, the antibody raised against a receptor comprising a T1R3 polypeptide comprising greater than about 80% amino acid sequence identity to an amino acid sequence of SEQ ID NO:15, SEQ ID NO:20, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:31 or encoded by a nucleotide sequence hybridizing under highly stringent hybridization conditions to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:15, SEQ ID NO:20, SEQ ID NO:23, SEQ ID NO:25, or SEQ ID NO:31.

In another aspect, the present invention provides a method for identifying a compound that modulates sweet taste signaling in taste cells, the method comprising the steps of: (i) contacting the compound with a homodimeric or monomeric receptor comprising a T1R3 polypeptide but not a T1R1 or a T1R2 polypeptide, the polypeptide comprising greater than about 80% amino acid sequence identity to SEQ ID NO:15, SEQ ID NO:20, SEQ ID NO:23, SEQ ID NO:25, or SEQ ID NO:31; or encoded by a nucleotide sequence hybridizing under highly stringent hybridization conditions to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:15, SEQ ID NO:20, SEQ ID NO:23, SEQ ID NO:25, or SEQ ID NO:31; and (ii) determining the functional effect of the compound upon the receptor.

In one embodiment, the functional effect is determined *in vitro*. In one embodiment, the polypeptide is expressed in a cell or cell membrane. In another embodiment, the receptor is linked to a solid phase, either covalently or non-covalently.

In another aspect, the present invention provides a method for identifying a compound that modulates sweet taste signaling in taste cells, the method comprising the steps of: (i) contacting a cell with the compound, the cell expressing a homodimeric or monomeric receptor comprising a T1R3 polypeptide but not expressing a T1R1 or a T1R2 polypeptide, the T1R3 polypeptide comprising greater than about 80% amino acid sequence identity to SEQ ID NO:15, SEQ ID NO:20, SEQ ID NO:23, SEQ ID NO:25, or SEQ ID NO:31; or encoded by a nucleotide sequence hybridizing under highly stringent hybridization conditions to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:15, SEQ ID

NO:20, SEQ ID NO:23, SEQ ID NO:25, or SEQ ID NO:31; and (ii) determining the functional effect of the compound upon the receptor.

In one embodiment, the functional effect is determined by measuring changes in intracellular cAMP, IP3, or Ca2+. In another embodiment, the functional effect is a chemical or phenotypic effect. In another embodiment, the functional effect is a physical effect. In another embodiment, the functional effect is determined by measuring binding of the compound to the extracellular domain of the receptor. In another embodiment, the polypeptide is recombinant. In another embodiment, the cell is a eukaryotic cell, e.g., a mammalian cell, e.g., a human cell. In another embodiment, the cell expresses G protein Gα15.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1: Targeted KO of T1R1, T1R2 and T1R3.

(a) Schematic drawing showing the structure of the three T1R genes and the strategy for generating knockout animals. The targeting constructs deleted all seven predicted transmembrane helices of T1R1 and T1R2, and the entire extracellular ligand binding domain of T1R3. (b) In situ hybridization labeling demonstrating robust expression of T1Rs in taste buds of wild-type animals, but complete absence in the corresponding knock-out mice.

Figure 2: T1R mutants respond normally to sour, salty and bitter stimuli

(a) Wild-type (WT), T1R1, T1R2 and T1R3 knockout mice (1-KO, 2-KO, 3-KO) show robust neural responses to sour (100 mM citric acid), salty (100 mM NaCl) and bitter (10 mM PROP) tastants. (b) Integrated neural responses, such as those shown in (a), were normalized to the response elicited by 100 mM citric acid; control and KO animals are indistinguishable from each other. The values are means ± s.e.m. (n=4). The data represent chorda tympani responses (see Experimental Procedures for details). (c), Taste preferences of wild-type and T1R knockout animals were measured relative to water using a brief access taste test (Zhang, Y. *et al.*, *Cell, 112*, 293-301 (2003)). All four lines showed normal responses to sour, salty and bitter stimuli. The values are means ± s.e.m. (n=7). Similar results were obtained using a standard two bottle preference assay (data not shown). Cyx, cycloheximide; Den, denatonium benzoate; PROP, 6-n-propyl-thiouracil; Qui, quinine.

Figure 3: T1R1+3 functions as the mammalian umami receptor

(a-d) Taste preferences of wild-type (open circles, dashed lines), T1R1 KO (blue circles and bars), T1R2 KO (gray circles and bars) and T1R3 KO mice (brown circles and bars) were measured relative to water using a brief access taste test. T1R2 KO mice are equivalent to wild type controls. In contrast, T1R1 and T1R3 knockout animals exhibit a complete loss in preference for umami tastants (a) MSG+ 1 mM IMP, (b) MSG, (c) IMP, and (d) L-Asp (100 mM), and AP4 (30 mM). In addition, both knockout have marked impairments in other amino acid responses. L-Asn (100 mM) and L-Arg were used at 100mM each. (e-f) Integrated chorda tympani responses to umami tastants and amino acids. T1R1 and T1R3 knockouts have a complete loss of responses to (e) umami agonists and L-amino acids if salt effects are avoided by using either amiloride or the potassium salt of MSG (MPG). In contrast, (f) if high concentrations of salt are used (e.g. 100 mM MSG), residual responses are detected.

Figure 4: T1R2 and T1R3 are essential for sweet taste perception

(a) Taste preferences of wild-type (open circles, dashed lines), T1R1 KO (gray circles and bars), T1R2 KO (green circles and bars) and T1R3 KO mice (brown circles and bars) were measured relative to water using a brief access taste test. T1R1 KO mice are equivalent to wild type controls. In contrast, T1R2 and T1R3 knockout animals exhibit a complete loss in preference for artificial sweeteners and D-amino acids, but retain residual responses to high concentration of natural sugars. These are highlighted in (b) as dose responses in expanded scale for maltose, sucrose and glucose. However, T1R2/T1R3 double KO animals (red circles) have a complete loss of all sweet responses. The values are means ± s.e.m. (n=7). D-Asn and D-Phe were 100 mM each, and D-Trp was used at 30 mM.

Figure 5: T1R2 and T1R3 encode the mammalian sweet taste receptors

Panel (a) shows integrated chorda tympani responses to natural sugars, artificial sweeteners and D-amino acids in wild type (WT) and T1R knockout animals (1-KO, 2- KO, 3-KO). T1R2 and T1R3 knockouts have a complete loss of responses to artificial sweeteners and D-amino acid (red traces), but show small neural responses to high concentrations of natural sugars. These, however, are completely abolished in T1R2/T1R3 double KO mice (bottom red traces). Panel (b) shows average neural responses to an expanded panel of tastants; wild type, white bars; T1R2 KO, green bars; T1R3 KO, brown

bars; T1R2/T1R3 double KO, red bars. The values are means ± s.e.m. (n=4) of normalized chorda tympani responses.

Figure 6. T1R3 responds to high concentrations of natural sugars

HEK-293 cells co-expressing the promiscuous G protein $G_{gust-25}$ (see Experimental Procedures) and the mouse T1R3 GPCR, or co-transfected with both T1R2 plus T1R3, were stimulated with various sweet compounds. Upper panels show increases in $[Ca^{2+}]i$ upon stimulation of T1R3-expressing cells with 500 mM, but not 300 mM sucrose. No responses were detected with artificial sweeteners (300 mM saccharin, right panel), or in cells without receptors or $G_{gust-25}$; scale indicates $[Ca^{2+}]i$ (nM) determined from FURA-2 F_{340}/F_{380} ratios. As expected, control cells expressing T1R2+3 (lower panels) respond robustly to lower concentrations of natural (300 mM sucrose) and artificial sweeteners (30 mM saccharin).

Figure 7. Activation of T1R2-expressing cells triggers behavioral attraction

(a) Wild type and T1R2 KO mice expressing a human T1R2 gene under the control of the rodent T1R2-promoter were (b-d) tested for behavioral responses to a variety of human sweet tastants: (b) Ace-K, acesulfame-K, (c) aspartame, and (d) MON, monellin (~10 μM); THAU, thaumatin (~5 μM); ASP, aspartame (10 mM); GA, glycyrrhizic acid (500 μM); NH, neohesperidin dihydrochalcone (400 μM). The human T1R2 taste receptor is (a) selectively expressed in T1R2-cells, and (b) effectively rescues sweet taste responses of T1R2 KO mice. Importantly, the presence of the transgene (c-d) humanizes the sweet taste preferences of the transgenic animals. See text for details. (e) Expression of RASSL (Redfern, C. H. *et al.*, *Nat Biotechnol, 17*, 165-169 (1999)) in T1R2-cells generates animals that exhibit specific behavioral attraction to spiradoline. Note that no responses are seen in uninduced animals, or control mice, even at 100x the concentration needed to elicit strong responses in RASSL-expressing animals. The values are means ± s.e.m. (n=7)

Figure 8

Figure 8 provides a nucleotide sequence of hT1R1 (SEQ ID NO:26).

Figure 9

Figure 9 provides an amino acid sequence of hT1R1 (SEQ ID NO:27).

Figure 10

Figure 10 provides a nucleotide sequence of hT1R2 (SEQ ID NO:28).

Figure 11

Figure 11 provides a amino acid sequence of hT1R2 (SEQ ID NO:29).

Figure 12

Figure 12 provides a nucleotide sequence of hT1R3 (SEQ ID NO:30).

Figure 13

Figure 13 provides an amino acid sequence of hT1R3 (SEQ ID NO:31).

DETAILED DESCRIPTION OF THE INVENTION

INTRODUCTION

T1Rs and T2Rs are two families of G-protein-coupled receptors (GPCRs) selectively expressed in subsets of taste receptor cells (Hoon *et al.*, *Cell* 96:541-551 (1999); Adler *et al.*, *Cell* 100:693-702 (2000); Chandrashekar *et al.*, *Cell* 100:703-711 (2000); Matsunami *et al.*, *Nature* 404:601-604 (2000); Nelson *et al.*, *Cell* 106:381-390 (2001); Kitagawa *et al.*, *Biochem. Biophys. Res. Cummun.* 283:236-242 (2001); Montmayeur *et al.*, *Nature Neurosci.* 4:492-498 (2001); Max *et al.*, *Nature Genet.* 28:58-63 (2001); Sainz *et al.*, *J. Neurochem.* 77:896-903 (2001)). T2Rs are involved in bitter taste detection (Adler *et al.*, *Cell* 100:693-702 (2000); Chandrashekar *et al. Cell*, 100:703-711 (2000)); T1R2 and T1R3 combine to function as a sweet taste receptor (*see also* Nelson *et al.*, *Cell* 106:381-390 (2001); and T1R1 and T1R3 combine to function as an amino acid taste receptors, as described herein *(see also* Nelson *et al.*, *Natur*e 24 February 2002 and WO 03/004992))). We have now identified a homodimeric taste receptor, in which two T1R3 polypeptides combine to function as a sweet taste receptor. The monomeric form of T1R3 also acts as a sweet receptor.

Using a heterologous expression system, we demonstrate that T1R3 combines with itself and also acts as a monomer to function as a sweet receptor, recognizing sweet-tasting molecules such as sucrose, galactose, fructose, glucose, maltose, and lactose. Candidate receptors are expressed in human embryonic kidney (HEK) cells containing the $G\alpha_{16}$-$G\alpha_{z}$ and $G\alpha_{15}$ promiscuous G proteins (Offermanns *et al.*, *J. Biol. Chem.* 270:15175-

15180 (1995); Mody *et al.*, *Mol. Pharmacol.* 57:13-23 (2000)), and assayed for stimulus-evoked changes in intracellular calcium. In this system, receptor activation leads to activation of phospholipase Cβ (PLC-β and release of calcium from internal stores, which can be monitored at the single-cell level using calcium-indicator dyes (Chandrashekar *et al.*, *Cell* 100:703-711 (2000); Nelson *et al.*, *Cell* 106:381-390 (2001); Tsien *et al.*, *Cell Calcium* 6:145-157 (1985)).

These nucleic acids and proteins encoding the receptors provide valuable probes for the identification of taste cells, as the nucleic acids are specifically expressed in taste cells. The receptors are useful for assaying for novel tastants, such as artificial sweetener molecules. For example, probes for GPCR polypeptides and proteins can be used to identity subsets of taste cells such as foliate cells, palate cells, and circumvallate cells, or specific taste receptor cells, e.g., sweet taste receptor cells. They also serve as tools for the generation of taste topographic maps that elucidate the relationship between the taste cells of the tongue and taste sensory neurons leading to taste centers in the brain. Furthermore, the nucleic acids and the proteins they encode can be used as probes to dissect taste-induced behaviors.

The invention also provides methods of screening for modulators, e.g., activators, inhibitors, stimulators, enhancers, agonists, and antagonists, of these novel monomeric or homodimeric sweet taste receptors comprising T1R3. In one embodiment, the monomeric or homodimeric T1R3-comprising receptors of the invention can be used to screen for naturally occurring or artificial sweet tasting molecules or modulators of sweet taste transduction, e.g., small organic molecules, amino acids, peptides, carbohydrates, lipids, polysaccharides, etc. For example, homodimeric or monomeric T1R3-comprising receptors of the invention recognize naturally occurring sweet tastants, as described below in the example section. Such receptors can be used to screen for artificial sweeteners, or altered naturally occurring sweeteners, that mimic the naturally occurring sugar ligands of the homodimeric or monomeric T1R3-comprising receptor. Such modulators of sweet taste transduction are useful for pharmacological and genetic modulation of sweet taste signaling pathways, and for the discovery of novel sweet taste ligands. These methods of screening can be used to identify agonists and antagonists of sweet taste cell activity. These modulatory compounds can then be used in the food and pharmaceutical industries to customize taste. Thus, the invention provides assays for taste modulation, where the T1R3-comprising receptor acts as an direct or indirect reporter molecule for the effect of modulators on sweet taste transduction. GPCRs can be used in assays, e.g., to measure changes in ligand

binding, G-protein binding, regulatory molecule binding, ion concentration, membrane potential, current flow, ion flux, transcription, signal transduction, receptor-ligand interactions, neurotransmitter and hormone release; and second messenger concentrations, *in vitro, in vivo,* and *ex vivo*. In one embodiment, a receptor comprising T1R3 can be used as an indirect reporter via attachment to a second reporter molecule such as green fluorescent protein (*see, e.g.,* Mistili & Spector, *Nature Biotechnology* 15:961-964 (1997)). In another embodiment, a receptor comprising T1R3 is recombinantly expressed in cells that do not express either T1R1 or T1R2, and modulation of taste transduction via GPCR activity is assayed by measuring changes in Ca2+ levels.

Methods of assaying for modulators of taste transduction include *in vitro* ligand binding assays using receptors comprising T1R3, portions thereof such as the extracellular domain, or chimeric proteins comprising one or more domains of T1R3, and in *in vivo* (cell-based and animal) assays such as oocyte T1R3 receptor expression; tissue culture cell T1R3 receptor expression; transcriptional activation of T1R3; phosphorylation and dephosphorylation of GPCRs; G-protein binding to GPCRs; ligand binding assays; voltage, membrane potential and conductance changes; ion flux assays; changes in intracellular second messengers such as cAMP and inositol triphosphate; changes in intracellular calcium levels; and neurotransmitter release.

DEFINITIONS

A "T1R family taste receptor" refers to a receptor comprising a member of the T1R family of G-protein coupled receptors, e.g., T1R1, T1R2, and T1R3, or any combination thereof as a homodimer receptor, a heterodimer receptor, or a monomer receptor. In one embodiment, the T1R family receptor comprises T1R3 (a "T1R3-comprising taste receptor" or a "T1R3-comprising sweet taste receptor"). In one embodiment, the T1R family receptor comprises a first T1R3 polypeptide and a second T1R3 polypeptide, which form a homodimeric receptor, either covalently or non-covalently linked. In another embodiment, the T1R family receptor comprises a single T1R3 polypeptide and no other T1R polypeptide, and forms a monomeric receptor. In another embodiment, the T1R family receptor comprises T1R3 and a heterologous polypeptide of the T1R family. In one embodiment, the receptor comprises T1R1 and T1R3. In another embodiment, the receptor comprises T1R2 and T1R3. In one embodiment the T1R3-comprising receptor is active when the two members of the receptor are co-expressed in the same cell, e.g., T1R3 and T1R3, or T1R1 and T1R3 or T1R2 and T1R3. In another embodiment, the T1R polypeptides are co-expressed in the same cell

and form a heterodimeric or homodimeric receptor, in which the T1R polypeptides of the receptor are non-covalently linked or covalently linked. The receptor has the ability to recognize, e.g., naturally occurring and/or artificial sweet tasting molecule such as sucrose, fructose, galactose, mannose, glucose, lactose, saccharin, dulcin, acesulfame-K, as well as other molecules, sweet and non-sweet. These molecules are examples of compounds that "modulate sweet taste signal transduction" by acting as ligands for the taste-transducing G protein coupled receptor comprising T1R3.

The terms "GPCR-B3 or T1R1," "GPCR-B4 or T1R2," and "T1R3" or a nucleic acid encoding "GPCR-B3 or T1R1," "GPCR-B4 or T1R2," and "T1R3" refer to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologs that are members of the T1R family of G protein coupled receptors and: (1) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater amino acid sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acids, to an amino acid sequence encoded by SEQ ID NO:1, 2, 3, 7, 8, 9, 15, 18, 20, 23, 25, 27, or 31; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by SEQ ID NO:1, 2, 3, 7, 8, 9, 15, 18, 20, 23, 25, 27, or 31, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to an anti-sense strand corresponding to a nucleic acid sequence encoding a T1R protein, e.g., SEQ ID NO:4, 5, 6, 10, 11, 12, 13, 14, 16, 17, 19, 21, 22, 24, 26, 28, or 30, and conservatively modified variants thereof; (4) have a nucleic acid sequence that has greater than about 60% sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99%, or higher nucleotide sequence identity, preferably over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to SEQ ID NO:4, 5, 6, 10, 11, 12, 13, 14, 16, 17, 19, 21, 22, 24, 26, or 28, or 30. The T1R family polypeptide of the invention (e.g., T1R1, T1R2, or T1R3) or T1R3-comprising receptor (e.g., T1R3, T1R3+T1R3, T1R1+3 or T1R2+3) further has G protein coupled receptor activity, either alone or when co-expressed in the same cell, or when co-expressed as a monomer, homodimer, or heterodimer with another T1R family member. Accession numbers for amino acid sequences and nucleotide sequences of human, rat, and mouse T1R1, T1R2, and T1R3 can be found in GenBank (for human T1R1 amino acid sequences, *see, e.g.*, Accession No. DAA00012 and NP_619642; for human T1R1 nucleotide sequences, *see, e.g.*, Accession No. BK000153; for human T1R2 amino acid sequences, *see, e.g.*, Accession No. DAA00019,

AAM12239, and NP_619642.1, for human T1R2 nucleotide sequences, *see, e.g.,* Accession No. BK000151, NM_138697.1, AF458149S1-6; for human T1R3 amino acid sequences, *see, e.g.,* Accession No. DAA00013, for human T1R3 nucleotide sequences, *see, e.g.*, Accession NO. BK000152). See also WO 00/06592, WO 00/06593, WO 01/66563, WO 03/001876, WO 02/064631, WO 03/004992, WO 03/025137, WO 02/086079 and WO 01/83749 for amino acid and nucleotide sequences of T1R1, T1R2, and T1R3, each herein incorporated by reference in its entirety.

T1R proteins have "G-protein coupled receptor activity," e.g., they bind to G-proteins in response to extracellular stimuli, such as ligand binding (e.g., sweet ligands), and promote production of second messengers such as IP3, cAMP, and Ca2+ via stimulation of enzymes such as phospholipase C and adenylate cyclase. Such activity can be measured in a heterologous cell, by coupling a GPCR (or a chimeric GPCR) to either a G-protein or promiscuous G-protein such as Gα15 or $G\alpha_{16}$-$G\alpha_z$ and an enzyme such as PLC, and measuring increases in intracellular calcium using (Offermans & Simon, *J. Biol. Chem.* 270:15175-15180 (1995)). Receptor activity can be effectively measured, e.g., by recording ligand-induced changes in $[Ca^{2+}]_i$ using fluorescent Ca^{2+}-indicator dyes and fluorometric imaging.

Such GPCRs have transmembrane, extracellular and cytoplasmic domains that can be structurally identified using methods known to those of skill in the art, such as sequence analysis programs that identify hydrophobic and hydrophilic domains (*see, e.g.,* Kyte & Doolittle, *J. Mol. Biol.* 157:105-132 (1982)). Such domains are useful for making chimeric proteins and for *in vitro* assays of the invention (*see, e.g.*, WO 94/05695 and US Patent 5,508,384).

The phrase "functional effects" in the context of assays for testing compounds that modulate activity (e.g., signal transduction) of a sweet taste receptor or protein of the invention includes the determination of a parameter that is indirectly or directly under the influence of a GPCR or sweet taste receptor, e.g., a physical, phenotypic, or chemical effect, such as the ability to transduce a cellular signal in response to external stimuli such as ligand binding, or the ability to bind a ligand. It includes binding activity and signal transduction. "Functional effects" include *in vitro*, *in vivo*, and *ex vivo* activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a T1R GPCR protein or a sweet taste receptor comprising one or more T1R GPCR proteins, e.g.,

physical and chemical or phenotypic effect. Such functional effects can be measured by any means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index); hydrodynamic (e.g., shape); chromatographic; or solubility properties for the protein; measuring inducible markers or transcriptional activation of the protein; measuring binding activity or binding assays, e.g., binding to antibodies; measuring changes in ligand binding activity or analogs thereof, either naturally occurring or synthetic; measuring cellular proliferation; measuring cell surface marker expression, measurement of changes in protein levels for T1R-associated sequences; measurement of RNA stability; G-protein binding; GPCR phosphorylation or dephosphorylation; signal transduction, e.g., receptor-ligand interactions, second messenger concentrations (e.g., cAMP, cGMP, IP3, PI, or intracellular Ca^{2+}); neurotransmitter release; hormone release; voltage, membrane potential and conductance changes; ion flux; regulatory molecule binding; identification of downstream or reporter gene expression (CAT, luciferase, β-gal, GFP and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, and inducible markers.

"Inhibitors," "activators," and "modulators" of T1R family polynucleotide and polypeptide sequences and T1R family taste receptors are used to refer to activating, inhibitory, or modulating molecules identified using *in vitro* and *in vivo* assays of T1R polynucleotide and polypeptide sequences and T1R family taste receptors, including monomeric, homodimeric and heterodimeric receptors. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of the T1R family of taste receptors such as a receptor comprising a T1R3 polypeptide, e.g., antagonists. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate a T1R family taste receptor, such as a receptor comprising a T1R3 polypeptide, e.g., agonists. Inhibitors, activators, or modulators also include genetically modified versions of T1R family taste receptors, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, antisense molecules, ribozymes, small chemical molecules and the like. Such assays for inhibitors and activators include, e.g., expressing T1R family taste receptors *in vitro*, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. In one embodiment, taste receptor comprising a T1R3 polypeptide has the ability to recognize a sweet tasting molecule such as sucrose, glucose, fructose, lactose, mannose, galactose, saccharin, dulcin, acesulfame-K. In another

embodiment, a taste receptor comprising a T1R3 polypeptide has the ability to recognize other molecules, such as potential artificial sweeteners. These molecules are examples of compounds that modulate taste signal transduction by acting as extracellular ligands for the G protein coupled receptor and activating the receptor. In other embodiments, compounds that modulate taste signal transduction are molecules that act as intracellular ligands of the receptor, or inhibit or activate binding of an extracellular ligand, or inhibit or activate binding of intracellular ligands of the receptor.

Samples or assays comprising the T1R family of taste receptors are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a T1R family receptor is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a T1R family receptor is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more preferably 200-500% (i.e., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes any molecule, such as an artificial sweetener or naturally occurring sugar, either naturally occurring or synthetic, e.g., protein, oligopeptide (e.g., from about 5 to about 25 amino acids in length, preferably from about 10 to 20 or 12 to 18 amino acids in length, preferably 12, 15, or 18 amino acids in length), small organic molecule, polysaccharide, lipid, fatty acid, polynucleotide, oligonucleotide, etc., to be tested for the capacity to directly or indirectly modulation taste. The test compound can be in the form of a library of test compounds, such as a combinatorial or randomized library that provides a sufficient range of diversity. Test compounds are optionally linked to a fusion partner, e.g., targeting compounds, rescue compounds, dimerization compounds, stabilizing compounds, addressable compounds, and other functional moieties. Conventionally, new chemical entities with useful properties are generated by identifying a test compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

A "small organic molecule" refers to an organic molecule, either naturally occurring or synthetic, that has a molecular weight of more than about 50 daltons and less

than about 2500 daltons, preferably less than about 2000 daltons, preferably between about 100 to about 1000 daltons, more preferably between about 200 to about 500 daltons.

"Biological sample" include sections of tissues such as biopsy and autopsy samples, and frozen sections taken for histologic purposes. Such samples include blood, sputum, tissue, cultured cells, e.g., primary cultures, explants, and transformed cells, stool, urine, etc. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or a bird; reptile; or fish.

A "heterodimer" is a dimer receptor comprising two different polypeptide subunits, e.g., two different polypeptides, where the molecules are associated via either covalent, e.g., through a linker or a chemical bond, or non-covalent, e.g., ionic, van der Waals, electrostatic, or hydrogen bonds linkages. The T1R3-comprising receptors of the invention function when co-expressed in the same cell, preferably when co-expressed so that they form a heterodimer, either covalently or non-covalently linked. For example, T1R1 and T1R3 form a heteromeric receptor, and T1R2 and T1R3 form a heteromeric receptor.

A "homodimer" is a dimer receptor comprising two of the same polypeptide subunits, e.g., two T1R3 polypeptides, where the molecules are associated via either covalent, e.g., through a linker or a chemical bond, or non-covalent, e.g., ionic, van der Waals, electrostatic, or hydrogen bonds linkages. The T1R3-comprising receptors of the invention function when co-expressed in the same cell, preferably when co-expressed so that they form a homodimer, either covalently or non-covalently linked.

A "monomer" is a receptor comprising one polypeptide subunit, e.g., one T1R3 polypeptide.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (i.e., about 60% identity, preferably 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region (e.g., nucleotide sequences SEQ ID NO:1-25), when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (*see, e.g.*, NCBI web site or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the compliment of a test sequence. The definition also includes sequences that have deletions

and/or additions, as well as those that have substitutions. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *Proc. Nat'l. Acad. Sci. USA* 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (*see, e.g., Current Protocols in Molecular Biology* (Ausubel *et al.*, eds. 1995 supplement)).

A preferred example of algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al., Nuc. Acids Res.* 25:3389-3402 (1977) and Altschul *et al., J. Mol. Biol.* 215:403-410 (1990), respectively. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-

valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The terms "polypeptide," "peptide," and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers and non-naturally occurring amino acid polymer.

The term "amino acid" refers to naturally occurring and synthetic amino acids, enantiomers (D- and L- forms), and achiral amino acids, as well as amino acid analogs and amino acid mimetics that function in a manner similar to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ-carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, i.e., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs have modified R groups (e.g., norleucine) or modified peptide backbones, but retain the same basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refers to chemical compounds that

have a structure that is different from the general chemical structure of an amino acid, but that functions in a manner similar to a naturally occurring amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode any given protein. For instance, the codons GCA, GCC, GCG and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes every possible silent variation of the nucleic acid. One of skill will recognize that each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, each silent variation of a nucleic acid which encodes a polypeptide is implicit in each described sequence with respect to the expression product, but not with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention.

The following eight groups each contain amino acids that are conservative substitutions for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I),

Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (*see, e.g.*, Creighton, *Proteins* (1984)).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, *see, e.g.*, Alberts *et al.*, *Molecular Biology of the Cell* (3rd ed., 1994) and Cantor and Schimmel, *Biophysical Chemistry Part I: The Conformation of Biological Macromolecules* (1980). "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains, e.g., extracellular domains, transmembrane domains, and cytoplasmic domains. Domains are portions of a polypeptide that form a compact unit of the polypeptide and are typically 15 to 350 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β-sheet and α-helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" refers to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-stranded form, as well as the complements of any such sequence. Also included are DNA, cDNA, RNA, polynucleotides, nucleotides, and the like. The term encompasses nucleic acids containing known nucleotide analogs or modified backbone residues or linkages, which are synthetic, naturally occurring, and non-naturally occurring, which have similar binding properties as the reference nucleic acid, and which are metabolized in a manner similar to the reference nucleotides. Examples of such analogs include, without limitation, phosphorothioates, phosphoramidates, methyl phosphonates, chiral-methyl phosphonates, 2-O-methyl ribonucleotides, peptide-nucleic acids (PNAs).

A particular nucleic acid sequence also implicitly encompasses "splice variants." Similarly, a particular protein encoded by a nucleic acid implicitly encompasses any protein encoded by a splice variant of that nucleic acid. "Splice variants," as the name suggests, are products of alternative splicing of a gene. After transcription, an initial nucleic acid transcript may be spliced such that different (alternate) nucleic acid splice products encode different polypeptides. Mechanisms for the production of splice variants vary, but include alternate splicing of exons. Alternate polypeptides derived from the same nucleic acid by read-through transcription are also encompassed by this definition. Any products of a

splicing reaction, including recombinant forms of the splice products, are included in this definition.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, chemical, or other physical means. For example, useful labels include ^{32}P, fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, for example, recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein indicates that the protein comprises two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, *Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Probes*, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent conditions are selected to be about 5-10°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as

the target sequences are present in excess, at T_m, 50% of the probes are occupied at equilibrium). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is at least two times background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42°C, or, 5x SSC, 1% SDS, incubating at 65°C, with wash in 0.2x SSC, and 0.1% SDS at 65°C.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, for example, when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 1X SSC at 45°C. A positive hybridization is at least twice background. Those of ordinary skill will readily recognize that alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous reference, e.g., and *Current Protocols in Molecular Biology*, ed. Ausubel, *et al.*

For PCR, a temperature of about 36°C is typical for low stringency amplification, although annealing temperatures may vary between about 32°C and 48°C depending on primer length. For high stringency PCR amplification, a temperature of about 62°C is typical, although high stringency annealing temperatures can range from about 50°C to about 65°C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include 30-40 cycles of the following conditions: a denaturation phase of 90°C - 95°C for 30 sec - 2 min., an annealing phase lasting 30 sec. - 2 min., and an extension phase of about 72°C for 1 - 2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis *et al.*, *PCR Protocols, A Guide to Methods and Applications* (1990).

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as

gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively. Typically, the antigen-binding region of an antibody will be most critical in specificity and affinity of binding.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, for example, pepsin digests an antibody below the disulfide linkages in the hinge region to produce F(ab)'$_2$, a dimer of Fab which itself is a light chain joined to V_H-C_H1 by a disulfide bond. The F(ab)'$_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the F(ab)'$_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (*see Fundamental Immunology* (Paul ed., 3d ed. 1993). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized *de novo* either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized *de novo* using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (*see, e.g.*, McCafferty *et al.*, *Nature* 348:552-554 (1990))

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many technique known in the art can be used (*see, e.g.*, Kohler & Milstein, *Nature* 256:495-497 (1975); Kozbor *et al.*, *Immunology Today* 4: 72 (1983); Cole *et al.*, pp. 77-96 in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc. (1985); Coligan, *Current Protocols in Immunology* (1991); Harlow & Lane, *Antibodies, A Laboratory Manual* (1988); and Goding, *Monoclonal Antibodies: Principles and Practice* (2d ed. 1986)). Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric

Fab fragments that specifically bind to selected antigens (*see, e.g.*, McCafferty *et al.*, *Nature* 348:552-554 (1990); Marks *et al.*, *Biotechnology* 10:779-783 (1992)).

A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, *e.g.*, an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a portion thereof, is altered, replaced or exchanged with a variable region having a different or altered antigen specificity.

In one embodiment, the antibody is conjugated to an "effector" moiety. The effector moiety can be any number of molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the antibody modulates the activity of the protein.

The phrase "specifically (or selectively) binds" to an antibody or "specifically (or selectively) immunoreactive with," when referring to a protein or peptide, refers to a binding reaction that is determinative of the presence of the protein, often in a heterogeneous population of proteins and other biologics. Thus, under designated immunoassay conditions, the specified antibodies bind to a particular protein at least two times the background and more typically more than 10 to 100 times background. Specific binding to an antibody under such conditions requires an antibody that is selected for its specificity for a particular protein. For example, polyclonal antibodies raised to a T1R protein or a homodimeric or heterodimeric T1R3-comprising taste receptor comprising a sequence of or encoded by SEQ ID NO:1-25, polymorphic variants, alleles, orthologs, and conservatively modified variants, or splice variants, or portions thereof, can be selected to obtain only those polyclonal antibodies that are specifically immunoreactive with T1R proteins and/or homodimeric or heterodimeric T1R3-comprising taste receptors and not with other proteins. In one embodiment, the antibodies react with a homodimeric T1R3-comprising taste receptor, but not with individual protein members of the T1R family. This selection may be achieved by subtracting out antibodies that cross-react with other molecules. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select antibodies specifically immunoreactive with a protein (*see, e.g.*, Harlow & Lane, *Antibodies, A Laboratory Manual* (1988) for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity).

ISOLATION OF NUCLEIC ACIDS ENCODING T1R FAMILY MEMBERS

This invention relies on routine techniques in the field of recombinant genetics. Basic texts disclosing the general methods of use in this invention include Sambrook *et al.*, *Molecular Cloning, A Laboratory Manual* (2nd ed. 1989); Kriegler, *Gene Transfer and Expression: A Laboratory Manual* (1990); and *Current Protocols in Molecular Biology* (Ausubel *et al.*, eds., 1994)).

T1R nucleic acids, polymorphic variants, orthologs, and alleles that are substantially identical to an amino acid sequences disclosed herein can be isolated using T1R nucleic acid probes and oligonucleotides under stringent hybridization conditions, by screening libraries. Alternatively, expression libraries can be used to clone T1R protein, polymorphic variants, orthologs, and alleles by detecting expressed homologs immunologically with antisera or purified antibodies made against human T1R or portions thereof.

To make a cDNA library, one should choose a source that is rich in T1R RNA, e.g., taste buds such as circumvallate, foliate, fungiform, and palate. The mRNA is then made into cDNA using reverse transcriptase, ligated into a recombinant vector, and transfected into a recombinant host for propagation, screening and cloning. Methods for making and screening cDNA libraries are well known (*see, e.g.,* Gubler & Hoffman, *Gene* 25:263-269 (1983); Sambrook *et al., supra*; Ausubel *et al., supra*).

For a genomic library, the DNA is extracted from the tissue and either mechanically sheared or enzymatically digested to yield fragments of about 12-20 kb. The fragments are then separated by gradient centrifugation from undesired sizes and are constructed in bacteriophage lambda vectors. These vectors and phage are packaged *in vitro*. Recombinant phage are analyzed by plaque hybridization as described in Benton & Davis, *Science* 196:180-182 (1977). Colony hybridization is carried out as generally described in Grunstein *et al.*, *Proc. Natl. Acad. Sci. USA.*, 72:3961-3965 (1975).

An alternative method of isolating T1R nucleic acid and its orthologs, alleles, mutants, polymorphic variants, and conservatively modified variants combines the use of synthetic oligonucleotide primers and amplification of an RNA or DNA template (*see* U.S. Patents 4,683,195 and 4,683,202; *PCR Protocols: A Guide to Methods and Applications* (Innis *et al.*, eds, 1990)). Methods such as polymerase chain reaction (PCR) and ligase chain reaction (LCR) can be used to amplify nucleic acid sequences of human T1R directly from mRNA, from cDNA, from genomic libraries or cDNA libraries. Degenerate oligonucleotides

can be designed to amplify T1R homologs using the sequences provided herein. Restriction endonuclease sites can be incorporated into the primers. Polymerase chain reaction or other *in vitro* amplification methods may also be useful, for example, to clone nucleic acid sequences that code for proteins to be expressed, to make nucleic acids to use as probes for detecting the presence of T1R encoding mRNA in physiological samples, for nucleic acid sequencing, or for other purposes. Genes amplified by the PCR reaction can be purified from agarose gels and cloned into an appropriate vector.

Gene expression of T1R can also be analyzed by techniques known in the art, e.g., reverse transcription and amplification of mRNA, isolation of total RNA or poly A^+ RNA, northern blotting, dot blotting, *in situ* hybridization, RNase protection, high density polynucleotide array technology, e.g., and the like.

Nucleic acids encoding T1R protein can be used with high density oligonucleotide array technology (e.g., GeneChip™) to identify T1R protein, orthologs, alleles, conservatively modified variants, and polymorphic variants in this invention (*see, e.g.*, Gunthand *et al., AIDS Res. Hum. Retroviruses* 14: 869-876 (1998); Kozal *et al., Nat. Med.* 2:753-759 (1996); Matson *et al., Anal. Biochem.* 224:110-106 (1995); Lockhart *et al., Nat. Biotechnol.* 14:1675-1680 (1996); Gingeras *et al., Genome Res.* 8:435-448 (1998); Hacia *et al., Nucleic Acids Res.* 26:3865-3866 (1998)).

The gene for T1R is typically cloned into intermediate vectors before transformation into prokaryotic or eukaryotic cells for replication and/or expression. These intermediate vectors are typically prokaryote vectors, e.g., plasmids, or shuttle vectors.

EXPRESSION IN PROKARYOTES AND EUKARYOTES

To obtain high level expression of a cloned gene, such as those cDNAs encoding a T1R protein, one typically subclones T1R into an expression vector that contains a strong promoter to direct transcription, a transcription/translation terminator, and if for a nucleic acid encoding a protein, a ribosome binding site for translational initiation. The T1R nucleic acids can be co-expressed or separately expressed, preferably co-expressed on the same or a different vector. Suitable bacterial promoters are well known in the art and described, e.g., in Sambrook *et al.*, and Ausubel *et al, supra.* Bacterial expression systems for expressing the T1R protein are available in, e.g., *E. coli, Bacillus sp.,* and *Salmonella* (Palva *et al.*, *Gene* 22:229-235 (1983); Mosbach *et al.*, *Nature* 302:543-545 (1983). Kits for such expression systems are commercially available. Eukaryotic expression systems for mammalian cells, yeast, and insect cells are well known in the art and are also commercially

available. In one preferred embodiment, retroviral expression systems are used in the present invention.

Selection of the promoter used to direct expression of a heterologous nucleic acid depends on the particular application. The promoter is preferably positioned about the same distance from the heterologous transcription start site as it is from the transcription start site in its natural setting. As is known in the art, however, some variation in this distance can be accommodated without loss of promoter function.

In addition to the promoter, the expression vector typically contains a transcription unit or expression cassette that contains all the additional elements required for the expression of the T1R encoding nucleic acid in host cells. A typical expression cassette thus contains a promoter operably linked to the nucleic acid sequence encoding T1R and signals required for efficient polyadenylation of the transcript, ribosome binding sites, and translation termination. Additional elements of the cassette may include enhancers and, if genomic DNA is used as the structural gene, introns with functional splice donor and acceptor sites.

In addition to a promoter sequence, the expression cassette should also contain a transcription termination region downstream of the structural gene to provide for efficient termination. The termination region may be obtained from the same gene as the promoter sequence or may be obtained from different genes.

The particular expression vector used to transport the genetic information into the cell is not particularly critical. Any of the conventional vectors used for expression in eukaryotic or prokaryotic cells may be used. Standard bacterial expression vectors include plasmids such as pBR322 based plasmids, pSKF, pET23D, and fusion expression systems such as MBP, GST, and LacZ. Epitope tags can also be added to recombinant proteins to provide convenient methods of isolation, e.g., c-myc. Sequence tags may be included in an expression cassette for nucleic acid rescue. Markers such as fluorescent proteins, green or red fluorescent protein, β-gal, CAT, and the like can be included in the vectors as markers for vector transduction.

Expression vectors containing regulatory elements from eukaryotic viruses are typically used in eukaryotic expression vectors, e.g., SV40 vectors, papilloma virus vectors, retroviral vectors, and vectors derived from Epstein-Barr virus. Other exemplary eukaryotic vectors include pMSG, pAV009/A^+, pMTO10/A^+, pMAMneo-5, baculovirus pDSVE, and any other vector allowing expression of proteins under the direction of the CMV promoter, SV40 early promoter, SV40 later promoter, metallothionein promoter, murine mammary

tumor virus promoter, Rous sarcoma virus promoter, polyhedrin promoter, or other promoters shown effective for expression in eukaryotic cells.

Expression of proteins from eukaryotic vectors can be also be regulated using inducible promoters. With inducible promoters, expression levels are tied to the concentration of inducing agents, such as tetracycline or ecdysone, by the incorporation of response elements for these agents into the promoter. Generally, high level expression is obtained from inducible promoters only in the presence of the inducing agent; basal expression levels are minimal.

In one embodiment, the vectors of the invention have a regulatable promoter, e.g., tet-regulated systems and the RU-486 system (*see, e.g.*, Gossen & Bujard, *Proc. Nat'l Acad. Sci. USA* 89:5547 (1992); Oligino *et al., Gene Ther.* 5:491-496 (1998); Wang *et al., Gene Ther.* 4:432-441 (1997); Neering *et al., Blood* 88:1147-1155 (1996); and Rendahl *et al., Nat. Biotechnol.* 16:757-761 (1998)). These impart small molecule control on the expression of the candidate target nucleic acids. This beneficial feature can be used to determine that a desired phenotype is caused by a transfected cDNA rather than a somatic mutation.

Some expression systems have markers that provide gene amplification such as thymidine kinase and dihydrofolate reductase. Alternatively, high yield expression systems not involving gene amplification are also suitable, such as using a baculovirus vector in insect cells, with a T1R encoding sequence under the direction of the polyhedrin promoter or other strong baculovirus promoters.

The elements that are typically included in expression vectors also include a replicon that functions in *E. coli*, a gene encoding antibiotic resistance to permit selection of bacteria that harbor recombinant plasmids, and unique restriction sites in nonessential regions of the plasmid to allow insertion of eukaryotic sequences. The particular antibiotic resistance gene chosen is not critical, any of the many resistance genes known in the art are suitable. The prokaryotic sequences are preferably chosen such that they do not interfere with the replication of the DNA in eukaryotic cells, if necessary.

Standard transfection methods are used to produce bacterial, mammalian, yeast or insect cell lines that express large quantities of T1R protein, which are then purified using standard techniques (*see, e.g.*, Colley *et al., J. Biol. Chem.* 264:17619-17622 (1989); *Guide to Protein Purification*, in *Methods in Enzymology*, vol. 182 (Deutscher, ed., 1990)). Transformation of eukaryotic and prokaryotic cells are performed according to standard techniques (*see, e.g.*, Morrison, *J. Bact.* 132:349-351 (1977); Clark-Curtiss & Curtiss, *Methods in Enzymology* 101:347-362 (Wu *et al.*, eds, 1983).

Any of the well-known procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, polybrene, protoplast fusion, electroporation, biolistics, liposomes, microinjection, plasma vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (*see, e.g.*, Sambrook *et al., supra*). It is only necessary that the particular genetic engineering procedure used be capable of successfully introducing at least one gene into the host cell capable of expressing T1R .

After the expression vector is introduced into the cells, the transfected cells are cultured under conditions favoring expression of T1R , which is recovered from the culture using standard techniques identified below.

PURIFICATION OF T1R POLYPEPTIDES

Either naturally occurring or recombinant T1R polypeptides or T1R3-comprising receptors can be purified for use in functional assays. Naturally occurring T1R proteins or T1R3-comprising receptors can be purified, e.g., from human tissue. Recombinant T1R proteins or T1R3-comprising receptors can be purified from any suitable expression system. T1R polypeptides are typically co-expressed in the same cell to form T1R3-comprising receptors.

The T1R protein or T1R3-comprising receptor may be purified to substantial purity by standard techniques, including selective precipitation with such substances as ammonium sulfate; column chromatography, immunopurification methods, and others (*see, e.g.*, Scopes, *Protein Purification: Principles and Practice* (1982); U.S. Patent No. 4,673,641; Ausubel *et al., supra;* and Sambrook *et al., supra*).

A number of procedures can be employed when recombinant T1R protein or T1R3-comprising receptor is being purified. For example, proteins having established molecular adhesion properties can be reversible fused to the T1R protein or T1R3-comprising receptor. With the appropriate ligand, T1R protein or T1R3-comprising receptor can be selectively adsorbed to a purification column and then freed from the column in a relatively pure form. The fused protein is then removed by enzymatic activity. Finally, T1R protein or T1R3-comprising receptor could be purified using immunoaffinity columns.

A. Purification of T1R from recombinant bacteria

Recombinant proteins are expressed by transformed bacteria in large amounts, typically after promoter induction; but expression can be constitutive. Promoter induction with IPTG is one example of an inducible promoter system. Bacteria are grown according to standard procedures in the art. Fresh or frozen bacteria cells are used for isolation of protein.

Proteins expressed in bacteria may form insoluble aggregates ("inclusion bodies"). Several protocols are suitable for purification of T1R protein or T1R3-comprising receptor inclusion bodies. For example, purification of inclusion bodies typically involves the extraction, separation and/or purification of inclusion bodies by disruption of bacterial cells, e.g., by incubation in a buffer of 50 mM TRIS/HCL pH 7.5, 50 mM NaCl, 5 mM $MgCl_2$, 1 mM DTT, 0.1 mM ATP, and 1 mM PMSF. The cell suspension can be lysed using 2-3 passages through a French Press, homogenized using a Polytron (Brinkman Instruments) or sonicated on ice. Alternate methods of lysing bacteria are apparent to those of skill in the art (*see, e.g.*, Sambrook *et al.*, *supra*; Ausubel *et al.*, *supra*).

If necessary, the inclusion bodies are solubilized, and the lysed cell suspension is typically centrifuged to remove unwanted insoluble matter. Proteins that formed the inclusion bodies may be renatured by dilution or dialysis with a compatible buffer. Suitable solvents include, but are not limited to urea (from about 4 M to about 8 M), formamide (at least about 80%, volume/volume basis), and guanidine hydrochloride (from about 4 M to about 8 M). Some solvents which are capable of solubilizing aggregate-forming proteins, for example SDS (sodium dodecyl sulfate), 70% formic acid, are inappropriate for use in this procedure due to the possibility of irreversible denaturation of the proteins, accompanied by a lack of immunogenicity and/or activity. Although guanidine hydrochloride and similar agents are denaturants, this denaturation is not irreversible and renaturation may occur upon removal (by dialysis, for example) or dilution of the denaturant, allowing re-formation of immunologically and/or biologically active protein. Other suitable buffers are known to those skilled in the art. Human T1R proteins or T1R3-comprising receptors are separated from other bacterial proteins by standard separation techniques, e.g., with Ni-NTA agarose resin.

Alternatively, it is possible to purify T1R protein or T1R3-comprising receptor from bacteria periplasm. After lysis of the bacteria, when the T1R protein or T1R3-comprising receptor is exported into the periplasm of the bacteria, the periplasmic fraction of the bacteria can be isolated by cold osmotic shock in addition to other methods known to skill in the art. To isolate recombinant proteins from the periplasm, the bacterial cells are

centrifuged to form a pellet. The pellet is resuspended in a buffer containing 20% sucrose. To lyse the cells, the bacteria are centrifuged and the pellet is resuspended in ice-cold 5 mM $MgSO_4$ and kept in an ice bath for approximately 10 minutes. The cell suspension is centrifuged and the supernatant decanted and saved. The recombinant proteins present in the supernatant can be separated from the host proteins by standard separation techniques well known to those of skill in the art.

B. Standard protein separation techniques for purifying T1R proteins

Solubility fractionation

Often as an initial step, particularly if the protein mixture is complex, an initial salt fractionation can separate many of the unwanted host cell proteins (or proteins derived from the cell culture media) from the recombinant protein of interest. The preferred salt is ammonium sulfate. Ammonium sulfate precipitates proteins by effectively reducing the amount of water in the protein mixture. Proteins then precipitate on the basis of their solubility. The more hydrophobic a protein is, the more likely it is to precipitate at lower ammonium sulfate concentrations. A typical protocol includes adding saturated ammonium sulfate to a protein solution so that the resultant ammonium sulfate concentration is between 20-30%. This concentration will precipitate the most hydrophobic of proteins. The precipitate is then discarded (unless the protein of interest is hydrophobic) and ammonium sulfate is added to the supernatant to a concentration known to precipitate the protein of interest. The precipitate is then solubilized in buffer and the excess salt removed if necessary, either through dialysis or diafiltration. Other methods that rely on solubility of proteins, such as cold ethanol precipitation, are well known to those of skill in the art and can be used to fractionate complex protein mixtures.

Size differential filtration

The molecular weight of the T1R proteins or T1R3-comprising receptors can be used to isolate it from proteins of greater and lesser size using ultrafiltration through membranes of different pore size (for example, Amicon or Millipore membranes). As a first step, the protein mixture is ultrafiltered through a membrane with a pore size that has a lower molecular weight cut-off than the molecular weight of the protein of interest. The retentate of the ultrafiltration is then ultrafiltered against a membrane with a molecular cut off greater than the molecular weight of the protein of interest. The recombinant protein will pass

through the membrane into the filtrate. The filtrate can then be chromatographed as described below.

Column chromatography

The T1R proteins or T1R3-comprising receptors can also be separated from other proteins on the basis of its size, net surface charge, hydrophobicity, and affinity for ligands. In addition, antibodies raised against proteins can be conjugated to column matrices and the proteins immunopurified. All of these methods are well known in the art. It will be apparent to one of skill that chromatographic techniques can be performed at any scale and using equipment from many different manufacturers (e.g., Pharmacia Biotech).

ASSAYS FOR MODULATORS OF T1R PROTEIN

A. Assays

Modulation of a T1R3-comprising taste receptor, and corresponding modulation of taste, can be assessed using a variety of *in vitro* and *in vivo* assays. Such assays can be used to test for inhibitors and activators of T1R3-comprising taste receptors, and, consequently, inhibitors and activators of taste. Such modulators of T1R3-comprising sweet taste receptors, which are involved in taste signal transduction. Modulators of T1R3-comprising taste receptors are tested using either recombinant or naturally occurring T1R3-comprising taste receptors, preferably human receptors.

In one embodiment, the monomeric or homodimeric T1R3-comprising receptors of the invention can be used to screen for naturally occurring or artificial sweet tasting molecules, e.g., small organic molecules, amino acids, peptides, carbohydrates, lipids, polysaccharides, etc. For example, homodimeric or monomeric T1R3-comprising receptors of the invention recognize naturally occurring sweet tastants, as described below in the example section. Such receptors can be used to screen for artificial sweeteners, or altered naturally occurring sweeteners, that mimic the naturally occurring sugar ligands of the homodimeric or monomeric T1R3-comprising receptor.

Preferably, the T1R3-comprising taste receptor will have a sequence as encoded by a sequence provided herein or a conservatively modified variant thereof. Alternatively, the T1R3-comprising taste receptor of the assay will be derived from a eukaryote and include an amino acid subsequence having substantial amino acid sequence identity to the sequences provided herein or is encoded by a nucleotide sequence that hybridizes under stringent conditions (moderate or high) to a nucleotide sequence as

described herein. Generally, the amino acid sequence identity will be at least 60%, preferably at least 65%, 70%, 75%, 80%, 85%, or 90%, most preferably at least 95%.

Measurement of sweet taste signal transduction or loss-of-sweet taste signal transduction phenotype on T1R3-comprising taste receptor or cell expressing the T1R3-comprising taste receptor, either recombinant or naturally occurring, can be performed using a variety of assays, *in vitro*, *in vivo*, and *ex vivo*, as described herein. A suitable physical, chemical or phenotypic change that affects activity or binding can be used to assess the influence of a test compound on the polypeptide of this invention. When the functional effects are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of signal transduction, e.g., ligand binding, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as pH changes, and changes in intracellular second messengers such as Ca^{2+}, IP3, cGMP, or cAMP.

In vitro assays

Assays to identify compounds with T1R3-comprising taste receptor modulating activity can be performed *in vitro*. Such assays can use a full length T1R3-comprising taste receptor or a variant thereof, or a fragment of a T1R3-comprising taste receptor, such as an extracellular domain, fused to a heterologous protein to form a chimera (*see, e.g.*, WO 01/66563, WO 03/001876, WO 02/064631, and WO 03/004992). Purified recombinant or naturally occurring T1R3-comprising taste receptor can be used in the *in vitro* methods of the invention. In addition to purified T1R3-comprising taste receptor, the recombinant or naturally occurring T1R3-comprising taste receptor can be part of a cellular lysate or a cell membrane. As described below, the binding assay can be either solid state or soluble. Preferably, the protein or membrane is bound to a solid support, either covalently or non-covalently. Often, the *in vitro* assays of the invention are ligand binding or ligand affinity assays, either non-competitive or competitive (with known extracellular ligands as described herein, or with a known intracellular ligand GTP). Other *in vitro* assays include measuring changes in spectroscopic (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein.

In one embodiment, a high throughput binding assay is performed in which the T1R3-comprising taste receptor or chimera comprising a fragment thereof is contacted with a potential modulator and incubated for a suitable amount of time. In one embodiment, the potential modulator is bound to a solid support, and the T1R3-comprising taste receptor is

added. In another embodiment, the T1R3-comprising taste receptor is bound to a solid support. A wide variety of modulators can be used, as described below, including small organic molecules, peptides, antibodies, and T1R3-comprising taste receptor ligand analogs. A wide variety of assays can be used to identify T1R3-comprising taste receptor-modulator binding, including labeled protein-protein binding assays, electrophoretic mobility shifts, immunoassays, enzymatic assays such as phosphorylation assays, and the like. In some cases, the binding of the candidate modulator is determined through the use of competitive binding assays, where interference with binding of a known ligand is measured in the presence of a potential modulator. Ligands for T1R3-comprising taste receptors are provided herein. Either the modulator or the known ligand is bound first, and then the competitor is added. After the T1R3-comprising taste receptor is washed, interference with binding, either of the potential modulator or of the known ligand, is determined. Often, either the potential modulator or the known ligand is labeled.

Cell-based *in vivo* assays

In another embodiment, a T1R3-comprising taste receptor is expressed in a cell (e.g., by expression or co-expression one or two members of the T1R family such as T1R1 and T1R3 or T1R2 and T1R3, preferably by expression of T1R3 alone without expression of any otherT1R family members), and functional, e.g., physical and chemical or phenotypic, changes are assayed to identify T1R3-comprising taste receptor taste modulators. Cells expressing T1R3-comprising taste receptor can also be used in binding assays. Any suitable functional effect can be measured, as described herein. For example, ligand binding, G-protein binding, and GPCR signal transduction, e.g., changes in intracellular Ca^{2+} levels, are all suitable assays to identify potential modulators using a cell based system. Suitable cells for such cell based assays include both primary cells and cell lines, as described herein. The T1R3-comprising taste receptor can be naturally occurring or recombinant. Also, as described above, chimeric T1R3-comprising taste receptors with GPCR activity can be used in cell based assays. For example, the extracellular domain of an T1R protein can be fused to the transmembrane and/or cytoplasmic domain of a heterologous protein, preferably a heterologous GPCR. Such a chimeric GPCR would have GPCR activity and could be used in cell based assays of the invention.

In another embodiment, cellular T1R polypeptide levels are determined by measuring the level of protein or mRNA. The level of T1R protein or proteins related to T1R signal transduction are measured using immunoassays such as western blotting, ELISA and

the like with an antibody that selectively binds to the T1R3-comprising taste receptor or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNAse protection, dot blotting, are preferred. The level of protein or mRNA is detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, T1R3-comprising receptor expression can be measured using a reporter gene system. Such a system can be devised using an T1R protein promoter operably linked to a reporter gene such as chloramphenicol acetyltransferase, firefly luciferase, bacterial luciferase, β-galactosidase and alkaline phosphatase. Furthermore, the protein of interest can be used as an indirect reporter via attachment to a second reporter such as red or green fluorescent protein (*see, e.g.*, Mistili & Spector, *Nature Biotechnology* 15:961-964 (1997)). The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In another embodiment, a functional effect related to GPCR signal transduction can be measured. An activated or inhibited T1R3-comprising G-coupled protein receptor will alter the properties of target enzymes, second messengers, channels, and other effector proteins. The examples include the activation of cGMP phosphodiesterase, adenylate cyclase, phospholipase C, IP3, and modulation of diverse channels by G proteins. Downstream consequences can also be examined such as generation of diacyl glycerol and IP3 by phospholipase C, and in turn, for calcium mobilization by IP3. Activated GPCR receptors become substrates for kinases that phosphorylate the C-terminal tail of the receptor (and possibly other sites as well). Thus, activators will promote the transfer of ^{32}P from gamma-labeled GTP to the receptor, which can be assayed with a scintillation counter. The phosphorylation of the C-terminal tail will promote the binding of arrestin-like proteins and will interfere with the binding of G-proteins. For a general review of GPCR signal transduction and methods of assaying signal transduction, *see, e.g., Methods in Enzymology*, vols. 237 and 238 (1994) and volume 96 (1983); Bourne *et al., Nature* 10:349:117-27 (1991); Bourne *et al., Nature* 348:125-32 (1990); Pitcher *et al., Annu. Rev. Biochem.* 67:653-92 (1998).

As described above, activation of some G-protein coupled receptors stimulates the formation of inositol triphosphate (IP3) through phospholipase C-mediated hydrolysis of

phosphatidylinositol (Berridge & Irvine, *Nature* 312:315-21 (1984)). IP3 in turn stimulates the release of intracellular calcium ion stores. Thus, a change in cytoplasmic calcium ion levels, or a change in second messenger levels such as IP3 can be used to assess G-protein coupled receptor function. Cells expressing such G-protein coupled receptors may exhibit increased cytoplasmic calcium levels as a result of contribution from both intracellular stores and via activation of ion channels, in which case it may be desirable although not necessary to conduct such assays in calcium-free buffer, optionally supplemented with a chelating agent such as EGTA, to distinguish fluorescence response resulting from calcium release from internal stores.

In one example, T1R3-comprising taste receptor GPCR activity is measured by expressing a T1R3-comprising taste receptor in a heterologous cell with a promiscuous G-protein that links the receptor to a phospholipase C signal transduction pathway (*see* Offermanns & Simon, *J. Biol. Chem.* 270:15175-15180 (1995)). Modulation of signal transduction is assayed by measuring changes in intracellular Ca^{2+} levels, which change in response to modulation of the GPCR signal transduction pathway via administration of a molecule that associates with an T1R3-comprising taste receptor. Changes in Ca^{2+} levels are optionally measured using fluorescent Ca^{2+} indicator dyes and fluorometric imaging.

In another example, phosphatidyl inositol (PI) hydrolysis can be analyzed according to U.S. Patent 5,436,128, herein incorporated by reference. Briefly, the assay involves labeling of cells with ^{3}H-myoinositol for 48 or more hrs. The labeled cells are treated with a test compound for one hour. The treated cells are lysed and extracted in chloroform-methanol-water after which the inositol phosphates were separated by ion exchange chromatography and quantified by scintillation counting. Fold stimulation is determined by calculating the ratio of cpm in the presence of agonist to cpm in the presence of buffer control. Likewise, fold inhibition is determined by calculating the ratio of cpm in the presence of antagonist to cpm in the presence of buffer control (which may or may not contain an agonist).

Other assays can involve determining the activity of receptors which, when activated, result in a change in the level of intracellular cyclic nucleotides, e.g., cAMP or cGMP, by activating or inhibiting enzymes such as adenylate cyclase. In cases where activation of the receptor results in a decrease in cyclic nucleotide levels, it may be preferable to expose the cells to agents that increase intracellular cyclic nucleotide levels, e.g., forskolin, prior to adding a receptor-activating compound to the cells in the assay.

In one example, the changes in intracellular cAMP or cGMP can be measured using immunoassays. The method described in Offermanns & Simon, *J. Biol. Chem.* 270:15175-15180 (1995) may be used to determine the level of cAMP. Also, the method described in Felley-Bosco *et al.*, *Am. J. Resp. Cell and Mol. Biol.* 11:159-164 (1994) may be used to determine the level of cGMP. Further, an assay kit for measuring cAMP and/or cGMP is described in U.S. Patent 4,115,538, herein incorporated by reference.

In one example, assays for G-protein coupled receptor activity include cells that are loaded with ion or voltage sensitive dyes to report receptor activity. Assays for determining activity of such receptors can also use known agonists and antagonists for other G-protein coupled receptors as negative or positive controls to assess activity of tested compounds. In assays for identifying modulatory compounds (e.g., agonists, antagonists), changes in the level of ions in the cytoplasm or membrane voltage will be monitored using an ion sensitive or membrane voltage fluorescent indicator, respectively. Among the ion-sensitive indicators and voltage probes that may be employed are those disclosed in the Molecular Probes 1997 Catalog. For G-protein coupled receptors, promiscuous G-proteins such as Gα15 and Gα16 can be used in the assay of choice (Wilkie *et al., Proc. Nat'l Acad. Sci. USA* 88:10049-10053 (1991)). Such promiscuous G-proteins allow coupling of a wide range of receptors.

Animal models

Animal models of taste also find use in screening for modulators of taste, such as the T1R knockout mouse strains as described herein. Transgenic animal technology including gene knockout technology, for example as a result of homologous recombination with an appropriate gene targeting vector, or gene overexpression, will result in the absence or increased expression of the T1R3-comprising receptor or components thereof. When desired, tissue-specific expression or knockout of the T1R3-comprising receptors or components thereof may be necessary. Transgenic animals generated by such methods find use as animal models of taste modulation and are additionally useful in screening for modulators of taste modulation.

B. Modulators

The compounds tested as modulators of T1R3-comprising taste receptors can be any small organic molecule, or a biological entity, such as a protein, e.g., an antibody or

peptide, an amino acid, a lipid, a fat, a sugar, e.g., a mono-, di-, or polysaccharide, a nucleic acid, e.g., an antisense oligonucleotide or a ribozyme, or a small organic molecule. Alternatively, modulators can be genetically altered versions of a T1R3-comprising taste receptor. Typically, test compounds will be small organic molecules, amino acids, peptides, lipids, and mono-, di- and polysaccharides.

Essentially any chemical compound can be used as a potential modulator or ligand in the assays of the invention, although most often compounds can be dissolved in aqueous or organic (especially DMSO-based) solutions are used. The assays are designed to screen large chemical libraries by automating the assay steps and providing compounds from any convenient source to assays, which are typically run in parallel (e.g., in microtiter formats on microtiter plates in robotic assays). It will be appreciated that there are many suppliers of chemical compounds, including Sigma (St. Louis, MO), Aldrich (St. Louis, MO), Sigma-Aldrich (St. Louis, MO), Fluka Chemika-Biochemica Analytika (Buchs Switzerland) and the like.

In one preferred embodiment, high throughput screening methods involve providing a combinatorial small organic molecule or peptide library containing a large number of potential therapeutic compounds (potential modulator or ligand compounds). Such "combinatorial chemical libraries" or "ligand libraries" are then screened in one or more assays, as described herein, to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis, by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library such as a polypeptide library is formed by combining a set of chemical building blocks (amino acids) in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks.

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (*see, e.g.,* U.S. Patent 5,010,175, Furka, *Int. J. Pept. Prot. Res.* 37:487-493 (1991) and Houghton *et al.*, *Nature* 354:84-88 (1991)). Other chemistries for generating chemical diversity libraries can also be used. Such chemistries include, but are not limited to:

peptoids (e.g., PCT Publication No. WO 91/19735), encoded peptides (e.g., PCT Publication No. WO 93/20242), random bio-oligomers (e.g., PCT Publication No. WO 92/00091), benzodiazepines (e.g., U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs *et al.*, *Proc. Nat. Acad. Sci. USA* 90:6909-6913 (1993)), vinylogous polypeptides (Hagihara *et al.*, *J. Amer. Chem. Soc.* 114:6568 (1992)), nonpeptidal peptidomimetics with glucose scaffolding (Hirschmann *et al.*, *J. Amer. Chem. Soc.* 114:9217-9218 (1992)), analogous organic syntheses of small compound libraries (Chen *et al.*, *J. Amer. Chem. Soc.* 116:2661 (1994)), oligocarbamates (Cho *et al.*, *Science* 261:1303 (1993)), and/or peptidyl phosphonates (Campbell *et al.*, *J. Org. Chem.* 59:658 (1994)), nucleic acid libraries (*see* Ausubel, Berger and Sambrook, all *supra*), peptide nucleic acid libraries (*see, e.g.,* U.S. Patent 5,539,083), antibody libraries (*see, e.g.,* Vaughn *et al.*, *Nature Biotechnology*, 14(3):309-314 (1996) and PCT/US96/10287), carbohydrate libraries (*see, e.g.,* Liang *et al.*, *Science*, 274:1520-1522 (1996) and U.S. Patent 5,593,853), small organic molecule libraries (*see, e.g.,* benzodiazepines, Baum C&EN, Jan 18, page 33 (1993); isoprenoids, U.S. Patent 5,569,588; thiazolidinones and metathiazanones, U.S. Patent 5,549,974; pyrrolidines, U.S. Patents 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent 5,506,337; benzodiazepines, 5,288,514, and the like).

Devices for the preparation of combinatorial libraries are commercially available (*see, e.g.,* 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA). In addition, numerous combinatorial libraries are themselves commercially available (*see, e.g.,* ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

C. Solid state and soluble high throughput assays

In one embodiment the invention provides soluble assays using a T1R3-comprising taste receptor, or a cell or tissue expressing a T1R3-comprising taste receptor, either naturally occurring or recombinant. In another embodiment, the invention provides solid phase based *in vitro* assays in a high throughput format, where the T1R3-comprising taste receptor is attached to a solid phase substrate. Any one of the assays described herein can be adapted for high throughput screening, e.g., ligand binding, cellular proliferation, cell surface marker flux, e.g., screening, radiolabeled GTP binding, second messenger flux, e.g., Ca^{2+}, IP3, cGMP, or cAMP, cytokine production, etc.

In the high throughput assays of the invention, either soluble or solid state, it is possible to screen up to several thousand different modulators or ligands in a single day. This methodology can be used for T1R3-comprising taste receptors *in vitro*, or for cell-based or membrane-based assays comprising T1R3-comprising taste receptors. In particular, each well of a microtiter plate can be used to run a separate assay against a selected potential modulator, or, if concentration or incubation time effects are to be observed, every 5-10 wells can test a single modulator. Thus, a single standard microtiter plate can assay about 100 (e.g., 96) modulators. If 1536 well plates are used, then a single plate can easily assay from about 100- about 1500 different compounds. It is possible to assay many plates per day; assay screens for up to about 6,000, 20,000, 50,000, or more than 100,000 different compounds are possible using the integrated systems of the invention.

For a solid state reaction, the protein of interest or a fragment thereof, e.g., an extracellular domain, or a cell or membrane comprising the protein of interest or a fragment thereof as part of a fusion protein can be bound to the solid state component, directly or indirectly, via covalent or non covalent linkage e.g., via a tag. The tag can be any of a variety of components. In general, a molecule which binds the tag (a tag binder) is fixed to a solid support, and the tagged molecule of interest is attached to the solid support by interaction of the tag and the tag binder.

A number of tags and tag binders can be used, based upon known molecular interactions well described in the literature. For example, where a tag has a natural binder, for example, biotin, protein A, or protein G, it can be used in conjunction with appropriate tag binders (avidin, streptavidin, neutravidin, the Fc region of an immunoglobulin, etc.) Antibodies to molecules with natural binders such as biotin are also widely available and appropriate tag binders; *see,* SIGMA Immunochemicals 1998 catalogue SIGMA, St. Louis MO).

Similarly, any haptenic or antigenic compound can be used in combination with an appropriate antibody to form a tag/tag binder pair. Thousands of specific antibodies are commercially available and many additional antibodies are described in the literature. For example, in one common configuration, the tag is a first antibody and the tag binder is a second antibody which recognizes the first antibody. In addition to antibody-antigen interactions, receptor-ligand interactions are also appropriate as tag and tag-binder pairs. For example, agonists and antagonists of cell membrane receptors (e.g., cell receptor-ligand interactions such as transferrin, c-kit, viral receptor ligands, cytokine receptors, chemokine receptors, interleukin receptors, immunoglobulin receptors and antibodies, the cadherein

family, the integrin family, the selectin family, and the like; *see, e.g.,* Pigott & Power, *The Adhesion Molecule Facts Book I* (1993). Similarly, toxins and venoms, viral epitopes, hormones (e.g., opiates, steroids, etc.), intracellular receptors (e.g. which mediate the effects of various small ligands, including steroids, thyroid hormone, retinoids and vitamin D; peptides), drugs, lectins, sugars, nucleic acids (both linear and cyclic polymer configurations), oligosaccharides, proteins, phospholipids and antibodies can all interact with various cell receptors.

Synthetic polymers, such as polyurethanes, polyesters, polycarbonates, polyureas, polyamides, polyethyleneimines, polyarylene sulfides, polysiloxanes, polyimides, and polyacetates can also form an appropriate tag or tag binder. Many other tag/tag binder pairs are also useful in assay systems described herein, as would be apparent to one of skill upon review of this disclosure.

Common linkers such as peptides, polyethers, and the like can also serve as tags, and include polypeptide sequences, such as poly gly sequences of between about 5 and 200 amino acids. Such flexible linkers are known to persons of skill in the art. For example, poly(ethelyne glycol) linkers are available from Shearwater Polymers, Inc. Huntsville, Alabama. These linkers optionally have amide linkages, sulfhydryl linkages, or heterofunctional linkages.

Tag binders are fixed to solid substrates using any of a variety of methods currently available. Solid substrates are commonly derivatized or functionalized by exposing all or a portion of the substrate to a chemical reagent which fixes a chemical group to the surface which is reactive with a portion of the tag binder. For example, groups which are suitable for attachment to a longer chain portion would include amines, hydroxyl, thiol, and carboxyl groups. Aminoalkylsilanes and hydroxyalkylsilanes can be used to functionalize a variety of surfaces, such as glass surfaces. The construction of such solid phase biopolymer arrays is well described in the literature. *See, e.g.*, Merrifield, *J. Am. Chem. Soc.* 85:2149-2154 (1963) (describing solid phase synthesis of, e.g., peptides); Geysen *et al., J. Immun. Meth.* 102:259-274 (1987) (describing synthesis of solid phase components on pins); Frank & Doring, *Tetrahedron* 44:60316040 (1988) (describing synthesis of various peptide sequences on cellulose disks); Fodor *et al., Science*, 251:767-777 (1991); Sheldon *et al., Clinical Chemistry* 39(4):718-719 (1993); and Kozal *et al., Nature Medicine* 2(7):753759 (1996) (all describing arrays of biopolymers fixed to solid substrates). Non-chemical approaches for fixing tag binders to substrates include other common methods, such as heat, cross-linking by UV radiation, and the like.

IMMUNOLOGICAL DETECTION OF T1R3-COMPRISING RECEPTORS

In addition to the detection of T1R genes and gene expression using nucleic acid hybridization technology, one can also use immunoassays to detect T1R3-comprising taste receptors of the invention. Such assays are useful for screening for modulators of T1R3-comprising taste receptors, as well as for therapeutic and diagnostic applications. Immunoassays can be used to qualitatively or quantitatively analyze T1R3-comprising taste receptors. A general overview of the applicable technology can be found in Harlow & Lane, *Antibodies: A Laboratory Manual* (1988).

A. Production of antibodies

Methods of producing polyclonal and monoclonal antibodies that react specifically with the T1R proteins and T1R3-comprising taste receptors are known to those of skill in the art (*see, e.g.*, Coligan, *Current Protocols in Immunology* (1991); Harlow & Lane, *supra*; Goding, *Monoclonal Antibodies: Principles and Practice* (2d ed. 1986); and Kohler & Milstein, *Nature* 256:495-497 (1975). Such techniques include antibody preparation by selection of antibodies from libraries of recombinant antibodies in phage or similar vectors, as well as preparation of polyclonal and monoclonal antibodies by immunizing rabbits or mice (*see, e.g.*, Huse *et al., Science* 246:1275-1281 (1989); Ward *et al., Nature* 341:544-546 (1989)).

A number of immunogens comprising portions of T1R protein or T1R3-comprising taste receptor may be used to produce antibodies specifically reactive with T1R protein. For example, recombinant T1R protein or an antigenic fragment thereof, can be isolated as described herein. Recombinant protein can be expressed in eukaryotic or prokaryotic cells as described above, and purified as generally described above. Recombinant protein is the preferred immunogen for the production of monoclonal or polyclonal antibodies. Alternatively, a synthetic peptide derived from the sequences disclosed herein and conjugated to a carrier protein can be used an immunogen. Naturally occurring protein may also be used either in pure or impure form. The product is then injected into an animal capable of producing antibodies. Either monoclonal or polyclonal antibodies may be generated, for subsequent use in immunoassays to measure the protein.

Methods of production of polyclonal antibodies are known to those of skill in the art. An inbred strain of mice (e.g., BALB/C mice) or rabbits is immunized with the protein using a standard adjuvant, such as Freund's adjuvant, and a standard immunization

protocol. The animal's immune response to the immunogen preparation is monitored by taking test bleeds and determining the titer of reactivity to the beta subunits. When appropriately high titers of antibody to the immunogen are obtained, blood is collected from the animal and antisera are prepared. Further fractionation of the antisera to enrich for antibodies reactive to the protein can be done if desired (*see,* Harlow & Lane, *supra*).

Monoclonal antibodies may be obtained by various techniques familiar to those skilled in the art. Briefly, spleen cells from an animal immunized with a desired antigen are immortalized, commonly by fusion with a myeloma cell (*see,* Kohler & Milstein, *Eur. J. Immunol.* 6:511-519 (1976)). Alternative methods of immortalization include transformation with Epstein Barr Virus, oncogenes, or retroviruses, or other methods well known in the art. Colonies arising from single immortalized cells are screened for production of antibodies of the desired specificity and affinity for the antigen, and yield of the monoclonal antibodies produced by such cells may be enhanced by various techniques, including injection into the peritoneal cavity of a vertebrate host. Alternatively, one may isolate DNA sequences which encode a monoclonal antibody or a binding fragment thereof by screening a DNA library from human B cells according to the general protocol outlined by Huse, *et al.*, *Science* 246:1275-1281 (1989).

Monoclonal antibodies and polyclonal sera are collected and titered against the immunogen protein in an immunoassay, for example, a solid phase immunoassay with the immunogen immobilized on a solid support. Typically, polyclonal antisera with a titer of 10^4 or greater are selected and tested for their cross reactivity against non-T1R or T1R3-comprising taste receptor proteins, using a competitive binding immunoassay. Specific polyclonal antisera and monoclonal antibodies will usually bind with a K_d of at least about 0.1 mM, more usually at least about 1 μM, preferably at least about 0.1 μM or better, and most preferably, 0.01 μM or better. Antibodies specific only for a particular T1R3-comprising taste receptor ortholog, such as human T1R3-comprising taste receptor, can also be made, by subtracting out other cross-reacting orthologs from a species such as a non-human mammal. In addition, individual T1R proteins can be used to subtract out antibodies that bind both to the receptor and the individual T1R proteins. In this manner, antibodies that bind only to a particular receptor may be obtained.

Once the specific antibodies against T1R3-comprising taste receptors are available, the protein can be detected by a variety of immunoassay methods. In addition, the antibody can be used therapeutically as a T1R3-comprising taste receptor modulators. For a review of immunological and immunoassay procedures, see *Basic and Clinical Immunology*

(Stites & Terr eds., 7th ed. 1991). Moreover, the immunoassays of the present invention can be performed in any of several configurations, which are reviewed extensively in Enzyme Immunoassay (Maggio, ed., 1980); and Harlow & Lane, *supra*.

B. Immunological binding assays

T1R3-comprising taste receptors can be detected and/or quantified using any of a number of well recognized immunological binding assays (*see, e.g.,* U.S. Patents 4,366,241; 4,376,110; 4,517,288; and 4,837,168). For a review of the general immunoassays, see also *Methods in Cell Biology: Antibodies in Cell Biology*, volume 37 (Asai, ed. 1993); *Basic and Clinical Immunology* (Stites & Terr, eds., 7th ed. 1991). Immunological binding assays (or immunoassays) typically use an antibody that specifically binds to a protein or antigen of choice (in this case the T1R3-comprising taste receptor or antigenic subsequence thereof). The antibody (e.g., anti-T1R3-comprising taste receptor) may be produced by any of a number of means well known to those of skill in the art and as described above.

Immunoassays also often use a labeling agent to specifically bind to and label the complex formed by the antibody and antigen. The labeling agent may itself be one of the moieties comprising the antibody/antigen complex. Thus, the labeling agent may be a labeled T1R3-comprising taste receptor or a labeled anti-T1R3-comprising taste receptor antibody. Alternatively, the labeling agent may be a third moiety, such a secondary antibody, that specifically binds to the antibody/ T1R3-comprising taste receptor complex (a secondary antibody is typically specific to antibodies of the species from which the first antibody is derived). Other proteins capable of specifically binding immunoglobulin constant regions, such as protein A or protein G may also be used as the label agent. These proteins exhibit a strong non-immunogenic reactivity with immunoglobulin constant regions from a variety of species (*see, e.g.,* Kronval *et al., J. Immunol.* 111:1401-1406 (1973); Akerstrom *et al., J. Immunol.* 135:2589-2542 (1985)). The labeling agent can be modified with a detectable moiety, such as biotin, to which another molecule can specifically bind, such as streptavidin. A variety of detectable moieties are well known to those skilled in the art.

Throughout the assays, incubation and/or washing steps may be required after each combination of reagents. Incubation steps can vary from about 5 seconds to several hours, optionally from about 5 minutes to about 24 hours. However, the incubation time will depend upon the assay format, antigen, volume of solution, concentrations, and the like.

Usually, the assays will be carried out at ambient temperature, although they can be conducted over a range of temperatures, such as 10°C to 40°C.

Non-competitive assay formats

Immunoassays for detecting T1R3-comprising taste receptors in samples may be either competitive or noncompetitive. Noncompetitive immunoassays are assays in which the amount of antigen is directly measured. In one preferred "sandwich" assay, for example, the anti-T1R3-comprising taste receptor antibodies can be bound directly to a solid substrate on which they are immobilized. These immobilized antibodies then capture T1R3-comprising taste receptors present in the test sample. T1R3-comprising taste receptors thus immobilized are then bound by a labeling agent, such as a second T1R3-comprising taste receptor antibody bearing a label. Alternatively, the second antibody may lack a label, but it may, in turn, be bound by a labeled third antibody specific to antibodies of the species from which the second antibody is derived. The second or third antibody is typically modified with a detectable moiety, such as biotin, to which another molecule specifically binds, e.g., streptavidin, to provide a detectable moiety.

Competitive assay formats

In competitive assays, the amount of T1R3-comprising taste receptor present in the sample is measured indirectly by measuring the amount of a known, added (exogenous) T1R3-comprising taste receptor displaced (competed away) from an anti- T1R3-comprising taste receptor antibody by the unknown T1R3-comprising taste receptor present in a sample. In one competitive assay, a known amount of T1R3-comprising taste receptor is added to a sample and the sample is then contacted with an antibody that specifically binds to a T1R3-comprising taste receptor. The amount of exogenous T1R3-comprising taste receptor bound to the antibody is inversely proportional to the concentration of T1R3-comprising taste receptor present in the sample. In a particularly preferred embodiment, the antibody is immobilized on a solid substrate. The amount of T1R3-comprising taste receptor bound to the antibody may be determined either by measuring the amount of T1R3-comprising taste receptor present in a T1R3-comprising taste receptor/antibody complex, or alternatively by measuring the amount of remaining uncomplexed protein. The amount of T1R3-comprising taste receptor may be detected by providing a labeled T1R3-comprising taste receptor molecule.

A hapten inhibition assay is another preferred competitive assay. In this assay the known T1R3-comprising taste receptor is immobilized on a solid substrate. A known amount of anti-T1R3-comprising taste receptor antibody is added to the sample, and the sample is then contacted with the immobilized T1R3-comprising taste receptor. The amount of anti- T1R3-comprising taste receptor antibody bound to the known immobilized T1R3-comprising taste receptor is inversely proportional to the amount of T1R3-comprising taste receptor present in the sample. Again, the amount of immobilized antibody may be detected by detecting either the immobilized fraction of antibody or the fraction of the antibody that remains in solution. Detection may be direct where the antibody is labeled or indirect by the subsequent addition of a labeled moiety that specifically binds to the antibody as described above.

Cross-reactivity determinations

Immunoassays in the competitive binding format can also be used for crossreactivity determinations. For example, a T1R3-comprising taste receptor can be immobilized to a solid support. Proteins (e.g., T1R3-comprising taste receptors and homologs) are added to the assay that compete for binding of the antisera to the immobilized antigen. The ability of the added proteins to compete for binding of the antisera to the immobilized protein is compared to the ability of the T1R3-comprising taste receptor to compete with itself. The percent crossreactivity for the above proteins is calculated, using standard calculations. Those antisera with less than 10% crossreactivity with each of the added proteins listed above are selected and pooled. The cross-reacting antibodies are optionally removed from the pooled antisera by immunoabsorption with the added considered proteins, e.g., distantly related homologs.

The immunoabsorbed and pooled antisera are then used in a competitive binding immunoassay as described above to compare a second protein, thought to be perhaps an allele or polymorphic variant of a T1R3-comprising taste receptor, to the immunogen protein. In order to make this comparison, the two proteins are each assayed at a wide range of concentrations and the amount of each protein required to inhibit 50% of the binding of the antisera to the immobilized protein is determined. If the amount of the second protein required to inhibit 50% of binding is less than 10 times the amount of the T1R3-comprising taste receptor that is required to inhibit 50% of binding, then the second protein is said to specifically bind to the polyclonal antibodies generated to a T1R3-comprising taste receptor immunogen.

Other assay formats

Western blot (immunoblot) analysis is used to detect and quantify the presence of T1R3-comprising taste receptors in the sample. The technique generally comprises separating sample proteins by gel electrophoresis on the basis of molecular weight, transferring the separated proteins to a suitable solid support, (such as a nitrocellulose filter, a nylon filter, or derivatized nylon filter), and incubating the sample with the antibodies that specifically bind T1R3-comprising taste receptors. The anti-T1R3-comprising taste receptor antibodies specifically bind to the T1R3-comprising taste receptor on the solid support. These antibodies may be directly labeled or alternatively may be subsequently detected using labeled antibodies (e.g., labeled sheep anti-mouse antibodies) that specifically bind to the anti-T1R3-comprising taste receptor antibodies.

Other assay formats include liposome immunoassays (LIA), which use liposomes designed to bind specific molecules (e.g., antibodies) and release encapsulated reagents or markers. The released chemicals are then detected according to standard techniques (*see* Monroe *et al.*, *Amer. Clin. Prod. Rev.* 5:34-41 (1986)).

Reduction of non-specific binding

One of skill in the art will appreciate that it is often desirable to minimize non-specific binding in immunoassays. Particularly, where the assay involves an antigen or antibody immobilized on a solid substrate it is desirable to minimize the amount of non-specific binding to the substrate. Means of reducing such non-specific binding are well known to those of skill in the art. Typically, this technique involves coating the substrate with a proteinaceous composition. In particular, protein compositions such as bovine serum albumin (BSA), nonfat powdered milk, and gelatin are widely used with powdered milk being most preferred.

Labels

The particular label or detectable group used in the assay is not a critical aspect of the invention, as long as it does not significantly interfere with the specific binding of the antibody used in the assay. The detectable group can be any material having a detectable physical or chemical property. Such detectable labels have been well-developed in the field of immunoassays and, in general, most any label useful in such methods can be applied to the present invention. Thus, a label is any composition detectable by

spectroscopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means. Useful labels in the present invention include magnetic beads (e.g., DYNABEADS™), fluorescent dyes (e.g., fluorescein isothiocyanate, Texas red, rhodamine, and the like), radiolabels (e.g., ^{3}H, ^{125}I, ^{35}S, ^{14}C, or ^{32}P), enzymes (e.g., horse radish peroxidase, alkaline phosphatase and others commonly used in an ELISA), and colorimetric labels such as colloidal gold or colored glass or plastic beads (e.g., polystyrene, polypropylene, latex, etc.).

The label may be coupled directly or indirectly to the desired component of the assay according to methods well known in the art. As indicated above, a wide variety of labels may be used, with the choice of label depending on sensitivity required, ease of conjugation with the compound, stability requirements, available instrumentation, and disposal provisions.

Non-radioactive labels are often attached by indirect means. Generally, a ligand molecule (e.g., biotin) is covalently bound to the molecule. The ligand then binds to another molecules (e.g., streptavidin) molecule, which is either inherently detectable or covalently bound to a signal system, such as a detectable enzyme, a fluorescent compound, or a chemiluminescent compound. The ligands and their targets can be used in any suitable combination with antibodies that recognize T1R3-comprising taste receptors, or secondary antibodies that recognize anti-T1R3-comprising taste receptor.

The molecules can also be conjugated directly to signal generating compounds, e.g., by conjugation with an enzyme or fluorophore. Enzymes of interest as labels will primarily be hydrolases, particularly phosphatases, esterases and glycosidases, or oxidotases, particularly peroxidases. Fluorescent compounds include fluorescein and its derivatives, rhodamine and its derivatives, dansyl, umbelliferone, etc. Chemiluminescent compounds include luciferin, and 2,3-dihydrophthalazinediones, e.g., luminol. For a review of various labeling or signal producing systems that may be used, see U.S. Patent No. 4,391,904.

Means of detecting labels are well known to those of skill in the art. Thus, for example, where the label is a radioactive label, means for detection include a scintillation counter or photographic film as in autoradiography. Where the label is a fluorescent label, it may be detected by exciting the fluorochrome with the appropriate wavelength of light and detecting the resulting fluorescence. The fluorescence may be detected visually, by means of photographic film, by the use of electronic detectors such as charge coupled devices (CCDs) or photomultipliers and the like. Similarly, enzymatic labels may be detected by providing

the appropriate substrates for the enzyme and detecting the resulting reaction product. Finally simple colorimetric labels may be detected simply by observing the color associated with the label. Thus, in various dipstick assays, conjugated gold often appears pink, while various conjugated beads appear the color of the bead.

Some assay formats do not require the use of labeled components. For instance, agglutination assays can be used to detect the presence of the target antibodies. In this case, antigen-coated particles are agglutinated by samples comprising the target antibodies. In this format, none of the components need be labeled and the presence of the target antibody is detected by simple visual inspection.

PHARMACEUTICAL COMPOSITIONS AND ADMINISTRATION

Pharmaceutically acceptable carriers are determined in part by the particular composition being administered (e.g., nucleic acid, oligonucleotide, amino acid, protein, peptide, small organic molecule, lipid, carbohydrate, mono-, di- or polysaccharide, particle, or transduced cell), as well as by the particular method used to administer the composition. Accordingly, there are a wide variety of suitable formulations of pharmaceutical compositions of the present invention (*see, e.g., Remington's Pharmaceutical Sciences*, 17th ed., 1989). Administration can be in any convenient manner, e.g., by injection, oral administration, inhalation, transdermal application, or rectal administration.

Formulations suitable for oral administration can consist of (a) liquid solutions, such as an effective amount of the packaged nucleic acid suspended in diluents, such as water, saline or PEG 400; (b) capsules, sachets or tablets, each containing a predetermined amount of the active ingredient, as liquids, solids, granules or gelatin; (c) suspensions in an appropriate liquid; and (d) suitable emulsions. Tablet forms can include one or more of lactose, sucrose, mannitol, sorbitol, calcium phosphates, corn starch, potato starch, microcrystalline cellulose, gelatin, colloidal silicon dioxide, talc, magnesium stearate, stearic acid, and other excipients, colorants, fillers, binders, diluents, buffering agents, moistening agents, preservatives, flavoring agents, dyes, disintegrating agents, and pharmaceutically compatible carriers. Lozenge forms can comprise the active ingredient in a flavor, e.g., sucrose, as well as pastilles comprising the active ingredient in an inert base, such as gelatin and glycerin or sucrose and acacia emulsions, gels, and the like containing, in addition to the active ingredient, carriers known in the art.

The compound of choice, alone or in combination with other suitable components, can be made into aerosol formulations (i.e., they can be "nebulized") to be

administered via inhalation. Aerosol formulations can be placed into pressurized acceptable propellants, such as dichlorodifluoromethane, propane, nitrogen, and the like.

Formulations suitable for parenteral administration, such as, for example, by intraarticular (in the joints), intravenous, intramuscular, intradermal, intraperitoneal, and subcutaneous routes, include aqueous and non-aqueous, isotonic sterile injection solutions, which can contain antioxidants, buffers, bacteriostats, and solutes that render the formulation isotonic with the blood of the intended recipient, and aqueous and non-aqueous sterile suspensions that can include suspending agents, solubilizers, thickening agents, stabilizers, and preservatives. In the practice of this invention, compositions can be administered, for example, by intravenous infusion, orally, topically, intraperitoneally, intravesically or intrathecally. Parenteral administration and intravenous administration are the preferred methods of administration. The formulations of commends can be presented in unit-dose or multi-dose sealed containers, such as ampules and vials.

Injection solutions and suspensions can be prepared from sterile powders, granules, and tablets of the kind previously described. Cells transduced by nucleic acids for *ex vivo* therapy can also be administered intravenously or parenterally as described above.

The dose administered to a patient, in the context of the present invention should be sufficient to effect a beneficial therapeutic response in the patient over time. The dose will be determined by the efficacy of the particular vector employed and the condition of the patient, as well as the body weight or surface area of the patient to be treated. The size of the dose also will be determined by the existence, nature, and extent of any adverse side-effects that accompany the administration of a particular vector, or transduced cell type in a particular patient.

In determining the effective amount of the vector to be administered in the treatment or prophylaxis of conditions owing to diminished or aberrant expression of a T1R3-comprising taste receptor, the physician evaluates circulating plasma levels of the vector, vector toxicities, progression of the disease, and the production of anti-vector antibodies. In general, the dose equivalent of a naked nucleic acid from a vector is from about 1 μg to 100 μg for a typical 70 kilogram patient, and doses of vectors which include a retroviral particle are calculated to yield an equivalent amount of therapeutic nucleic acid.

For administration, compounds and transduced cells of the present invention can be administered at a rate determined by the LD-50 of the inhibitor, vector, or transduced cell type, and the side-effects of the inhibitor, vector or cell type at various concentrations, as

applied to the mass and overall health of the patient. Administration can be accomplished via single or divided doses.

CELLULAR TRANSFECTION AND GENE THERAPY

The present invention provides the nucleic acids of T1R3-comprising taste receptors for the transfection of cells *in vitro* and *in vivo*. These nucleic acids can be inserted into any of a number of well-known vectors for the transfection of target cells and organisms as described below. The nucleic acids are transfected into cells, *ex vivo* or *in vivo*, through the interaction of the vector and the target cell. The nucleic acid, under the control of a promoter, then expresses a T1R3-comprising taste receptor of the present invention, by co-expressing two members of the T1R family, thereby mitigating the effects of absent, partial inactivation, or abnormal expression of a T1R3-comprising taste receptor. The compositions are administered to a patient in an amount sufficient to elicit a therapeutic response in the patient. An amount adequate to accomplish this is defined as "therapeutically effective dose or amount."

Such gene therapy procedures have been used to correct acquired and inherited genetic defects and other diseases in a number of contexts. The ability to express artificial genes in humans facilitates the prevention and/or cure of many important human diseases, including many diseases which are not amenable to treatment by other therapies (for a review of gene therapy procedures, *see* Anderson, *Science* 256:808-813 (1992); Nabel & Felgner, TIBTECH 11:211-217 (1993); Mitani & Caskey, TIBTECH 11:162-166 (1993); Mulligan, *Science* 926-932 (1993); Dillon, TIBTECH 11:167-175 (1993); Miller, *Nature* 357:455-460 (1992); Van Brunt, *Biotechnology* 6(10):1149-1154 (1998); Vigne, *Restorative Neurology and Neuroscience* 8:35-36 (1995); Kremer & Perricaudet, *British Medical Bulletin* 51(1):31-44 (1995); Haddada *et al.*, in *Current Topics in Microbiology and Immunology* (Doerfler & Böhm eds., 1995); and Yu *et al., Gene Therapy* 1:13-26 (1994)).

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EXAMPLES

The following examples are offered to illustrate, but not to limit the claimed invention.

Example 1

Results

Generation of T1R1, T1R2 and T1R3 KO mice

Expression of T1R receptors defines three largely non-overlapping populations of taste cells in the tongue and palate: cells co-expressing T1R1 and T1R3 (T1R1+3), cells co-expressing T1R2 and T1R3 (T1R2+3), and cells expressing T1R3 alone (Nelson, G. *et al.*, *Cell, 106*, 381-390 (2001)). Heterologous expression studies of T1Rs in HEK cells demonstrated that T1R1 and T1R3 combine to form a broadly tuned L-amino acid receptor, while co-expression of T1R2 and T1R3 generates a sweet taste receptor that responds to all classes of sweet-tasting compounds (Nelson, G. *et al.*, *Cell, 106*, 381-390 (2001); Nelson, G. *et al.*, *Nature, 416*, 199-202 (2002); Li, X. *et al.*, *Proc Natl Acad Sci U S A, 99*, 4692-4696 (2002)). If T1R3 functions *in vivo* as a common component of the sweet and amino acid taste receptors, then a knockout of this GPCR should generate mice devoid of sweet and amino acid taste reception. In contrast, knockout of T1R1 or T1R2 might be expected to selectively affect a single taste modality.

To define the role of T1Rs *in vivo*, we generated knockout mice that lack each of the T1Rs by deleting exons encoding domains essential for receptor function. Figure 1 illustrates the KO strategies and shows in situ hybridization experiments demonstrating a complete lack of specific T1R staining in the corresponding homozygous KO animals. In order to ensure that loss of any one T1R did not affect the viability or integrity of taste cells, we also compared the expression of other T1Rs, T2Rs, PLCb2 (Rossler, P. *et al.*, *Eur J Cell Biol, 77*, 253-261 (1998); Zhang, Y. *et al.*, *Cell, 112*, 293-301 (2003)) and TRPM5 (Perez, C. A. *et al.*, *Nat Neurosci, 5*, 1169-1176 (2002); Zhang, Y. *et al.*, *Cell, 112*, 293-301 (2003)) in control and KO animals. No significant differences were observed in the number or distribution of T1R-, T2R, PLCb2 and TRPM5-positive cells between wild type and KO taste tissue (Figure 1 and data not shown).

Two complementary strategies were used to assay the taste responses of the genetically modified mice. First, we recorded tastant-induced action potentials from one of the major nerves innervating taste receptor cells of the tongue (chorda tympani). This physiological assay monitors the activity of the taste system at the periphery, and provides a measure of taste receptor cell function. Second, we examined taste behavior by measuring taste-choices in standard long-term two-bottle intake preference assays, or by direct counting of immediate licking responses in a multi-channel gustometer (Glendinning, J. I.. *et al.*, *Chem Senses, 27*, 461-474 (2002); Zhang, Y. *et al.*, *Cell, 112*, 293-301 (2003); see Experimental Procedures). This second method relies on very short exposures to tastants (5 s events over a total of 30 min versus 48 hrs for two-bottle preference assays), and therefore has the great advantage of minimizing the impact of other sensory inputs, and post-ingestive and learning effects from the assay.

Figure 2 shows that knockouts of T1Rs have no significant effect either on physiological or behavioral responses to citric acid, sodium chloride, and a variety of bitter tastants. These results demonstrate that bitter, salty and sour taste reception and perception operate through pathways independent of T1R receptors, and further substantiate a model of coding at the periphery in which individual modalities operate independently of each other.

T1R1+3 is the umami receptor

Previously, Chaudhari et al described a truncated variant of the metabotropic glutamate receptor-4 (mGluR4t) and suggested that it functions as the umami taste receptor (Chaudhari, N. *et al.*, *Nat Neurosci, 3,* 113-119 (2000)). We find this proposal unsatisfactory for many reasons. (1) The mGluR4t variant is missing the mGluR4 signal sequence needed for surface targeting. (2) This putative receptor also lacks large fractions of the domains essential for glutamate recognition as revealed by the crystal structure of the glutamate binding domain of mGluR (Kunishima, N., *et al.*, *Nature, 407*, 971-977 (2000)). (3) mGluR4t umami signaling has been proposed to operate via a cAMP pathway (Abaffy, T. *et al.*, *Am J Physiol Cell Physiol, 284*, C1420-1428 (2003); Chaudhari, N. *et al.*, *Nat Neurosci, 3,* 113-119 (2000)). However, amino acid/umami taste is a PLCβ2/TRPM5-dependent process (Zhang, Y. *et al.*, *Cell, 112*, 293-301 (2003)). (4) Umami taste, but not mGluR4 activity, is strongly affected by the umami enhancers IMP and GMP. (5) Finally, mGluR4 KO animals retain responses to umami stimuli (Chaudhari, N., and Roper, S. D., *Ann N Y Acad Sci, 855*, 398-406 (1998)). In contrast, recent evidence suggest that the T1R1+3 amino acid receptor may function as the mammalian umami (glutamate) taste sensor: First, the human and rodent

T1R1+3 receptors display selectivity and sensitivity differences that mimic amino acid taste differences between rodents and humans (Nelson, G. *et al.*, *Nature, 416*, 199-202 (2002); Yoshii *et al.*, 1986). Second, T1R1+3 activity is reliably enhanced by IMP and GMP, the two best known potentiators of umami taste *in vivo* (Nelson, G. *et al.*, *Nature, 416*, 199-202 (2002); Li, X. *et al.*, *Proc Natl Acad Sci U S A, 99*, 4692-4696 (2002)). Thirdly, T1R1+3 is activated by psychophysically relevant concentrations of the umami agonists L-Asp and L-AP4 (Nelson, G. *et al.*, *Nature, 416*, 199-202 (2002); Li, X. *et al.*, *Proc Natl Acad Sci U S A, 99*, 4692-4696 (2002)). In order to rigorously assess the role of T1R1+3 in umami taste, we examined T1R1 and T1R3 KO animals (see Figure 1).

Because of its Na+ content, monosodium glutamate (MSG) evokes both salty and umami taste. We therefore assayed umami responses using several strategies that allowed us to isolate salt taste from that of glutamate in behavioral and electrophysiological studies. These included testing MSG in the presence of the sodium channel blocker amiloride, using MPG, the potassium salt of glutamate, and testing the umami agonists AP4 and aspartic acid, all in the presence or absence of the umami enhancer IMP. Figure 3 shows that when salt effects are minimized, T1R3 KO mice have a dramatic loss of behavioral attraction -and a profound corresponding deficit in physiological responses to all umami tastants- including glutamate, aspartate, glutamate plus IMP, and IMP alone. Very recently, Damak et al independently generated T1R3 KO animals but concluded that multiple umami receptors must exist as significant MSG responses remained in their studies of KO mice (Damak, S. *et al.*, *Science, 301*, 850-853 (2003)). Notably, the MSG responses of the KO animals were strictly independent of IMP, a contradiction given that IMP enhancement is the hallmark of the umami modality. Since salt effects were not accounted for, we suspect that much of their remaining responses reflect Na+ content in MSG rather than umami taste (compare responses to MSG+IMP versus MPG+IMP or MSG+IMP+amiloride in Figure 3e-f).

If T1R1 combines with T1R3 (T1R1+3) to generate the mammalian umami receptor, then a knockout of T1R1 should also eliminate all umami responses. Figure 3 demonstrates that this is absolutely the case. In contrast, these very same tastants elicit normal, robust responses in control and in T1R2 KO animals. Together, these results prove that T1R1+3 is the mammalian umami receptor.

Previously, we showed that in addition to typical umami tastants, the mouse T1R1+3 receptor is also activated by other L-amino amino acids, and in the presence of IMP functions as a broadly tuned L-amino acid sensor (Nelson, G. *et al.*, *Nature, 416*, 199-202 (2002)). Therefore, we tested responses of T1R1 and T1R3 KO animals to L-amino acids in

the presence or absence of IMP. Indeed, responses to amino acid tastants are severely defective in T1R1 and T1R3, but not T1R2 KO strains (Figure 3), firmly establishing the T1R1+3 heteromeric GPCR complex as the taste receptor for a wide range of L-amino acids and IMP. Interestingly, when we assayed exceedingly high concentrations of L-amino acids that taste sweet to humans (e.g. > 300 mM Ala, Ser, and Thr), T1R1 KO animals, but not T1R3 KO mice retained a small residual attraction (see panel d in Figure 3); these trace behavioral responses likely reflect the activation of the T1R2+3 sweet taste receptor (Nelson, G. *et al.*, *Cell, 106*, 381-390 (2001); see below).

T1R2+3 and T1R3 are required for sweet reception and perception

T1R2+3 functions in cell based assays as a heteromeric receptor for diverse chemical classes of sweet compounds including natural sugars, artificial sweeteners, Damino acids and sweet-tasting proteins (Nelson, G. *et al.*, *Cell, 106*, 381-390 (2001); Li, X. *et al.*, *Proc Natl Acad Sci U S A, 99*, 4692-4696 (2002)). However, a number of studies have suggested that animals may express distinct types of sweet receptors (Schiffman, S. S. *et al.*, *Pharmacol Biochem Behav, 15*, 377-388 (1981); Ninomiya, Y. *et al.*, *J Neurophysiol, 81*, 3087-3091 (1999)). To define the role of T1R2+3 *in vivo*, we examined sweet responses of knockout mice that lack functional T1R2 and T1R3 proteins. Figures 4 and 5 demonstrate that responses to all classes of sweet tastants are dramatically impaired in T1R2 and T1R3 knockout strains. We tested a broad panel of sugars, artificial sweeteners and D-amino acids, and in all cases responses were severely defective: behavioral attraction is nearly abolished and nerve responses are greatly diminished. These results confirm T1R2+3 as the principal sweet taste sensor *in vivo*.

Notably, very high concentrations (>300 mM) of natural sugars, but not of artificial sweeteners or D-amino acids, elicited modest but detectable attractive responses in both T1R2 and T1R3 knockout strains. Thus, either there are additional sweet taste receptors (i.e. T1R-independent pathways), or T1R2 and T1R3 may also function on their own as low affinity receptors for natural sugars in the absence of their heteromeric partners. If the remaining responses are in fact due to T1R2 or T1R3, then a double knockout of these GPCRs should eliminate all sweet responses. Since T1R2 and T1R3 loci are linked at the distal end of chromosome 4 (Nelson, G. *et al.*, *Cell, 106*, 381-390 (2001)), we first generated recombinant T1R2 KO, T1R3 KO mice and then tested them physiologically and behaviorally. Figures 4 and 5 (red traces) show that T1R2,T1R3 double KO mice have lost all responses to high concentration of sugars. Together, these results illustrate the *in vivo*

significance of the combinatorial assembly of T1Rs, and demonstrate that all sweet taste reception operates via the T1R2 and T1R3 GPCRs.

Do T1R2 or T1R3 homodimeric receptors play a significant role in sweet sensing in wild type mice? T1R2 is always expressed in cells containing T1R3 (T1R2+3 cells; Nelson, G. *et al.*, *Cell, 106*, 381-390 (2001)). Therefore, even if some T1R2 were not associated with T1R3 in these cells, the much higher affinity of the T1R2+3 heteromeric receptor for sweet tastants would likely dominate the cellular response. In contrast, we previously reported that T1R3 is also found in a significant fraction of cells of the tongue and palate epithelium independent of T1R1 and T1R2 (T1R3 alone cells; Nelson, G. *et al.*, *Cell, 106*, 381-390 (2001)). This class of cells may provide animals with additional means of detecting and responding to high concentrations of sugars. To demonstrate that T1R3 alone can function as a low affinity receptor for natural sugars, we generated HEK cells stably expressing T1R3 and an optimized G protein chimera engineered to couple to T1Rs (see Experimental Procedures). Figure 6 shows that T1R3 alone in fact responds to very high concentrations of natural sugars, but not to lower concentrations (<300 mM), or to artificial sweeteners. These results confirm T1R3 as a low affinity sugar receptor, and support the postulate that T1R3 alone cells function *in vivo* as additional sweet sensors (Nelson, G. *et al.*, *Cell, 106*, 381-390 (2001)). This partial cellular segregation of sensing natural and artificial sweeteners may help explain why artificial sweeteners never attain the level of sweetness afforded by high concentrations of natural sugars (i.e. activation of T1R2+3 cells versus T1R2+3 and T1R3 alone cells).

T1R2 delimits species-specific sweet taste preferences

Humans can taste a number of natural and artificial sweeteners that rodents cannot. For example, monellin, thaumatin, aspartame and neohesperidin dihydrochalcone taste sweet to humans at sub-millimolar concentrations, whereas rodents show no preference even at 100 times higher concentrations (Danilova, V. *et al.*, *J Neurophysiol, 80*, 2102-2112 (1998)). Previously, we reported that rodent and human T1Rs are more than 30% dissimilar in their amino acid sequences, and hypothesized that such differences underlie the species-specific selectivity in sweet taste detection (Nelson, G. *et al.*, *Cell, 106*, 381-390 (2001); Nelson, G. *et al.*, *Nature, 416*, 199-202 (2002)). Because T1R2 participates exclusively in sweet taste detection while T1R3 is involved in both sweet and amino acid recognition, we reasoned that T1R2 would be a particularly critical determinant of sweet taste selectivity *in*

vivo. Therefore, we predicted that introducing the human T1R2 gene in T1R2 KO mice should both rescue and "humanize" sweet responses.

We generated mice that were homozygous for the T1R2 KO allele, but instead expressed a human T1R2 transgene in the native "T1R2- cells". A 12 kb genomic clone containing the T1R2 regulatory sequences was fused to a hT1R2 full length cDNA and introduced into T1R2 KO mice. Multiple independent lines were assayed for their selectivity and sensitivity to sweet tastants. To examine expression of hT1R2, we performed two-color fluorescent in situ hybridization experiments in transgenic animals carrying the wild type mT1R2 allele. Figure 7 (panel a-d) demonstrate that human T1R2 is selectively expressed in T1R2-expressing cells, and effectively restores sweet taste function. More importantly, the human transgene now confers these mice with the ability to detect and respond to several compounds that taste sweet to humans, but are not normally attractive to rodents; these include aspartame, glycyrrhizic acid and the sweet proteins thaumatin and monellin. Interestingly, the humanized T1R2 mice still do not respond to the intensely sweet compound neohesperidin dihydrochalcone, nor do HEK cells transfected with the human T1R2 and mouse T1R3 GPCRs. However, when cells are transfected with human T1R2 and human T1R3 they robustly respond to neohesperidin dihydrochalcone. Taken together, these experiments validate T1Rs as key determinants of differences in sweet taste selectivity and specificity between rodents and humans, and further substantiate T1R2+3, and T1R2-expressing cells, as an principal mediator of sweet taste *in vivo*. Finally, we propose that polymorphisms in both T1R2 and T1R3 are important determinants of human individual sweet taste preferences.

T1R2-expressing cells encode behavioral attraction *in vivo*

Activation of taste receptors trigger distinct behavioral responses in animals. For example, excitation of the T1R2+3 receptor stimulates behavioral attraction to sugars and sweet-tasting compounds in mice. Is this response a property of the receptors or the cells in which they are expressed? One way to answer this question would be to express a novel receptor unrelated to the taste system in the T1R2+3 cells and examine whether its selective stimulation elicits attractive responses (Troemel, E. R. *et al.*, *Cell 91*, 161-169 (1997)).

Our approach was to target expression of a GPCR that could couple to the endogenous signaling pathways in T1R2+3 cells, but could only be activated by a nonnatural ligand. In order to examine taste responses in the very same animals before and after receptor expression we utilized an inducible system. To accomplish this, we used transgenic mice in

which a modified k-opioid receptor activated solely by a synthetic ligand (RASSL; Redfern, C. H. *et al.*, *Nat Biotechnol, 17*, 165-169 (1999)) was targeted to the T1R2-expressing cells under the control of the Tet-on inducible system (see Experimental Procedures).

Figure 7e shows that un-induced animals, or wild type controls treated with doxycycline, are completely insensitive to the k-opioid agonist spiradoline. Remarkably, induction of RASSL expression in the T1R2-cells generates animals that are now strongly attracted to nanomolar concentrations of spiradoline (Figure 7, red trace). Thus, we conclude that activation of T1R2-expressing cells, rather than the receptors they express, determines behavioral attraction in mice. Furthermore, these results unequivocally show that activating a single cell type is sufficient to trigger specific taste responses; therefore a model requiring a combinatorial pattern of activity, or temporal coding, is not needed to account for attraction mediated by T1R2-expressing cells. By extension we suggest that activation of these taste signaling pathways in human T1R2+3 cells, regardless of the nature of the receptor, would evoke sweet taste.

Multiple receptors have been proposed to mediate sweet and umami taste in mammals. Notably, even within each of these two modalities several GPCRs, ion channels, and models invoking intracellular targets directly activated by cell-permeable tastants have been postulated (Kinnamon, S. C. *Neuron, 25*, 507-510 (2000); Margolskee, R. F., *J Biol Chem, 277*, 1-4 (2002)). We have used a combination of cell-based assays, genetic, physiological and behavioral approaches to prove that the receptors for sweet and umami taste in mammals are the T1Rs: umami taste is mediated by the T1R1+3 heteromeric GPCR, and sweet by the two T1R-based receptors, T1R2 and T1R3 (T1R2+3, and most likely, a homodimer of T1R3). Therefore, sweet and amino acid taste (umami) -two chemosensory inputs that trigger behavioral attraction, share a common receptor repertoire and evolutionary origin.

The human T1R1+3 receptor is activated by glutamate and aspartate far more effectively than by other amino acids (Li, X. *et al.*, *Proc Natl Acad Sci U S A, 99*, 4692-4696 (2002)). In contrast, the mouse T1R1+3 receptor recognizes a much broader range of L-amino acids, both in cell based assays (Nelson, G. *et al.*, *Nature, 416*, 199-202 (2002)) and *in vivo* (this paper). If the evolutionary role of the T1R1+3 receptor was to mediate attractive responses to protein-rich foods, one may question whether the tuning of receptor selectivity in primates to just two amino acids substantially altered the ability to detect diets rich these nutrients. Since amino acids are usually found as complex mixtures, detecting any one should generally be adequate, and thus this "narrowing" of tastant selectivity should not have had a

significant dietary impact. Given that the same cells and receptors recognize glutamate, other amino acids and IMP, we suggest that in rodents the umami taste modality must be generalized to include most L-amino acids and the very concept of a distinct glutamate taste in rodents (Chaudhari, N. *et al.*, *Nat Neurosci, 3,* 113-119 (2000); Lin, W. *et al.*, *J Neurophysiol, 89*, 1434-1439 (2003)) needs to be re-evaluated.

A spoonful of sugar or a few tablets of artificial sweetener? Our day to day experiences tell us that natural and artificial sweeteners do not taste the same. In this manuscript we showed that T1R2 and T1R3 are responsible for all sweet sensing. How do they account for the perceived taste differences between sweet tastants? Many sweeteners are likely to activate receptors for other taste modalities, like T2R bitter sensing cells accounting for the bitter aftertaste of saccharin (data not shown). Therefore, the "taste" of even a single sweet molecular species may reflect the combined activity of cells tuned to different taste modalities, and not just the activity of sweet sensing cells. We have also shown that at higher, but still physiologically relevant concentrations of sugars (>300 mM), natural and artificial sweeteners activate partially overlapping, yet distinct sweet receptor types (T1R2+3 and T1R3 alone).

We have shown that T1Rs are the mediators of the two principal attractive taste modalities, and demonstrated that mice expressing a RASSL opioid receptor became powerfully attracted to spiradoline, a normally tasteless and nutrionally irrelevant compound, proving that *to taste is to believe*. The discovery and functional characterization of the cells and receptors for bitter, sweet, and umami taste now provide a compelling view of how taste is encoded at the periphery: dedicated taste receptor cells mediate attractive and aversive behaviors (*see, e.g.*, Zhang, Y. *et al.*, *Cell, 112*, 293-301 (2003)).

Experimental Procedures

Gene Targeting of T1R1, T1R2 and T1R3

The strategy used to create T1R knockout animals is shown in Figure 1. For T1R1, exon 6 encoding the predicted seven transmembrane domain of the receptor was replaced by the PGK- neo^r cassette. Homologous recombination in R1 ES cells was detected by diagnostic Southern hybridization with probes outside the targeting construct. Two targeted ES clones were injected into C57BL/6 blastocysts. Chimeric mice were bred with C57BL/6 mice and progeny backcrossed to C57BL/6 mice for two generations prior to establishing a homozygous knockout colony.

For T1R2, a similar approach deleted exons 5 and 6 (see Figure 1). Chimeric animals were bred with C57BL/6 mice and progeny backcrossed to C57BL/6 mice for four generations. The T1R3 taster(C57) and non-taster (129) alleles (Nelson, G. *et al., Cell, 106,* 381-390 (2001)) were identified based on an EcoRI polymorphism ~12 kb upstream of the starting ATG of T1R3. All of the T1R2 knockout animals used in this study carried a taster allele of T1R3. However, studies with T1R2 KO mice homozygous for the non-taster T1R3 allele produced qualitatively similar results (data not shown). To generate T1R3 KO knockout animals, we replaced exons 1 to 5 encoding the N-terminal extracellular domain with the PGK- neor cassette (see Figure 1). Chimeric mice were bred with C57BL/6 mice and progeny backcrossed to C57BL/6 mice for two generations.

T1R knockouts have normal viability, body weight, overall anatomy and general behavior. Similarly, taste receptor cells appear normal morphologically and numerically in all knockout backgrounds.

In situ hybridization

Fresh frozen sections (16 μm/section) were attached to silanized slides and prepared for in situ hybridization or immunohistochemistry as previously described (Hoon, M. A. *et al., Cell., 96,* 541-551 (1999)). Single label in situ hybridization was carried out using digoxigenin labeled probes; T1R1 and T1R2 probes were to the predicted transmembrane domains, while T1R3 and RASSL (Redfern, C. H. *et al., Nat Biotechnol, 17,* 165-169 (1999)) probes utilized the full coding sequences. Double-label fluorescent detection used fluorescein (full-length hT1R2) and digoxigenin (full-length mT1R2) probes at high stringency (hybridization, 5 x SSC, 50% formamide, 65 - 72°C; washing, 0.2 x SSC, 72°C). Hybridization was detected with distinct fluorescent substrates (Adler, E. *et al., Cel,l 100,* 693-702 (2000)) and specificity of labeling was checked using T1R2-knockout and non transgenic controls.

Generation of transgenic mice expressing human T1R2 and RASSL

An approx. 12 kb genomic fragment upstream of mouse T1R2 was fused to a human T1R2 cDNA and to a reverse-tetracycline dependent transactivator (rtTA) construct (Gossen, M. *et al., Curr Opin Biotechnol, 5,* 516-520 (1994)). Transgenic lines were produced by pronuclear injection of zygotes from FVB/N mice. Three independent human T1R2 transgenic lines displayed behavioral attraction to aspartame (10 mM). One line was crossed into the T1R2 knockout background, and assayed for taste responses and transgene

expression. No expression outside T1R2-cells was detected. T1R2-rtTA transgenic lines were crossed with tetO-Ro1/tetO-lacZ transgenic animals (Redfern, C. H. *et al.*, *Nat Biotechnol, 17*, 165-169 (1999)). Doubleheterozygous progeny were induced by doxycycline treatment (6 gm / kg) (Bio-Serv) for 3 days (Gogos, J. A. *et al.*, *Cel,l* 103, 609-620 (2000)) and examined for β-galactosidase activity (Zack, D. J. *et al.*, *Neuron 6*, 187-199 (1991)) and RASSL expression in the tongue and palate. A line displaying appropriate β- galactosidase staining and RASSL expression pattern was selected for behavioral assays.

Behavioral Assays

Taste behavior was assayed using a short term assay that directly measures taste preferences by counting immediate licking responses in a multi-channel gustometer (Davis MS160-Mouse gustometer; DiLog Instruments, Tallahassee, FL). Mice were trained and tested as described previously (Zhang, Y. *et al.*, *Cell, 112*, 293-301 (2003)). Individual mice were placed in the gustometer for 30 minutes, and stimuli were presented in random order for 5s trials that were initiated by the mouse licking the stimulus spout. For sodium saccharin, glutamate and aspartate, 100 μM amiloride was added to all solutions (including the control) to minimize effects of salt taste. Data points represent the mean rate that mice licked a tastant relative to their sampling of an appropriate control tastant (ratio defined as lick rate relative to control); lick suppression is defined as 1 minus the lick rate relative to control. In most cases the control tastant was water but for amino acids + 1mM IMP, 200 mM MSG and 10 mM IMP the controls were 1 mM IMP, 200 mM sodium gluconate and 10 mM CMP, respectively.

Standard two-bottle preference assays were carried out as described previously (Nelson, G. *et al.*, *Cell, 106*, 381-390 (2001)). For mice carrying T1R2-rtTA and tetO-Ro1/tetO-lacZ transgenes, expression was induced by doxycycline treatment 3 days prior to, and during the behavioral testing. Controls included testing the same mice without induction as well as mice carrying just the T1R2-rtTA transgene treated with doxycycline. All three groups displayed normal responses to sucrose.

We noted that in 2-bottle assays T1R-KO animals appear to "learn" to identify solutions containing very high concentrations of natural sugars (>500 mM); successive exposure resulted in decreased detection threshold and increased preference ratios. Because mice are repeatedly exposed to test compounds for 48 hrs in standard twobottle assays, they may use other sensory inputs like texture or smell to distinguish tastant from water. If not properly controlled, this could be easily misunderstood as behavioral attraction via taste

pathways. To avoid this problem, we used either short term immediate lick response assays (see above) or two-bottle assays with naive knockout mice (i.e. never exposed to such tastants during either training or testing).

Nerve Recordings

Lingual stimulation and recording procedures were performed as previously described (Dahl, M. *et al.*, *Brain Res, 756*, 22-34 (1997); Nelson, G. *et al.*, *Nature, 416*, 199-202 (2002)). Neural signals were amplified (5,000x) with a Grass P511 AC amplifier (Astro-Med), digitized with a Digidata 1200B A/D converter (Axon Instruments), and integrated (r.m.s. voltage) with a time constant of 0.5 s. Taste stimuli were presented at a constant flow rate of 4 ml min^{-1} for 20 s intervals interspersed by 2 min rinses with artificial saliva (Danilova, V., and Hellekant, G., *BMC Neurosci, 4*, 5. (2003)) between presentations. All data analyses used the integrated response over a 25 s period immediately after the application of the stimulus. Each experimental series consisted of the application of 6 tastants bracketed by presentations of 0.1 M citric acid to ensure the stability of the recording. The mean response to 0.1 M citric acid was used to normalize responses to each experimental series.

Tastants used for nerve recordings (maximal concentrations) were: sucrose, glucose, maltose (600 mM); sodium saccharin (40mM); AceK (60 mM); Citric Acid (100 mM); NaCl (100 mM); NH_4Cl (100 mM); 6-n-propyl thiouracil (10mM), quinine (10mM); cycloheximide (1mM); L-Ser, L-Ala, (30mM with 0.5mM IMP added) MSG and MPG (300mM with or without 0.5mM IMP); D-Ala, D-Phe, and D-Trp (100mM). Amiloride (50 uM) was added to reduce sodium responses as indicated in the figure legends.

Heterologous expression of T1Rs and Calcium Imaging

Modified HEK-293 cells ($PEAK^{rapid}$ cells; Edge BioSystems, MD) were grown, transfected with T1Rs and promiscuous G-proteins and assayed for functional responses to tastants by Ca-imaging essentially as described previously (Nelson, G. *et al.*, *Cell, 106*, 381-390 (2001)). Minor differences in FURA-2 loading and Ca-imaging included using 199(H) Medium (Biosource) containing 0.1% BSA, 100 μM EGTA and 200 μM $CaCl_2$ as assay buffer as well as reducing the time allowed for FURA-AM ester cleavage to 10 minutes. The imaging system was an Olympus IX50 microscope equipped with a 10x/0.5 N.A. fluor objective (Zeiss), the TILL imaging system (TILL Photonics GmbH), and a cooled CCD camera. Acquisition and analysis of fluorescence images used TILL-Vision software.

To optimize coupling of T1R-responses to changes in $[Ca^{2+}]i$, C-terminal residues of human Gα16 (Offermanns, S., and Simon, M. I., *J Biol Chem, 270*, 15175-15180 (1995)) were replaced with the corresponding residues from Gz (Mody, S. M. *et al.*, *Mol Pharmacol, 57*, 13-23 (2000)), gustducin (McLaughlin, S. K. *et al.*, *Nature, 357*, 563-569 (1992)) or Gαi2. A chimera containing the C-terminal 25 residues of gustducin ($G_{gust-25}$) proved particularly effective at mediating responses of mouse T1R2+3 and T1R1+3 in transient transfection assays, and was used for further studies. Cell lines stably expressing T1R3 and $G_{gust-25}$ were established using puromycin and Zeocin (Invitrogen) selection. Three independent lines expressing T1R3 and $G_{gust-25}$ were used to examine the specificity and dose response of the T1R3 receptor. Sucrose and maltose (>300 mM) elicited dose dependent responses that were T1R3 and $G_{gust-25}$ dependent, but attempts to use high concentrations of several other sugars (glucose, fructose, trehalose and galactose) proved impractical because they induced significant receptor independent rises in $[Ca^{2+}]i$.

It is understood that the examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof will be suggested to persons skilled in the art and are to be included within the spirit and purview of this application and scope of the appended claims. All publications, patents, and patent applications cited herein are hereby incorporated by reference in their entirety for all purposes.

SEQUENCE LISTING

T1R1 SEQUENCES

Rat T1R1 amino acid sequence--SEQ ID NO:1

MLFWAAHLLLSLQLVYCWAFSCQRTESSPGFSLPGDFLLAGLFSLHGDCLQVRHRPLVTSCD
RPDSFNGHGYHLFQAMRFTVEEINNSSALLPNITLGYELYDVCSESANVYATLRVLALQGPR
HIEIQKDLRNHSSKVVAFIGPDNTDHAVTTAALLGPFLMPLVSYEASSVVLSAKRKFPSFLR
TVPSDRHQVEVMVQLLQSFGWVWISLIGSYGDYGQLGVQALEELAVPRGICVAFKDIVPFSA
RVGDPRMQSMMQHLAQARTTVVVVFSNRHLARVFFRSVVLANLTGKVWVASEDWAISTYITS
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TTDCLAGHHRVVVGSHHCCFECVPCEAGTFLNMSELHICQPCGTEEWAPKESTTCFPRTVEF
LAWHEPISLVLIAANTLLLLLLVGTAGLFAWHFHTPVVRSAGGRLCFLMLGSLVAGSCSFYS
FFGEPTVPACLLRQPLFSLGFAIFLSCLTIRSFQLVIIFKFSTKVPTFYRTWAQNHGAGLFV
IVSSTVHLLICLTWLVMWTPRPTREYQRFPHLVILECTEVNSVGFLLAFTHNILLSISTFVC
SYLGKELPENYNEAKCVTFSLLLNFVSWIAFFTMASIYQGSYLPAVNVLAGLTTLSGGFSGY
FLPKCYVILCRPELNNTEHFQASIQDYTRRCGTT

Mouse T1R1 amino acid sequence--SEQ ID NO:2

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TWNMPELGAFSMSAAYNVYEAVYAVAHGLHQLLGCTSGTCARGPVYPWQLLQQIYKVNFLLH
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Human T1R1 amino acid sequence--SEQ ID NO:3

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Rat T1R1 nucleotide sequence--SEQ ID NO:4

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Mouse T1R1 nucleotide sequence--SEQ ID NO:5

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Human T1R1 nucleotide sequence--SEQ ID NO:6

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T1R2 SEQUENCES

Rat T1R2 amino acid sequence--SEQ ID NO:7

MGPQARTLCLLSLLLHVLPKPGKLVENSDFHLAGDYLLGGLFTLHANVKSISHLSYLQVPKC
NEFTMKVLGYNLMQAMRFAVEEINNCSSLLPGVLLGYEMVDVCYLSNNIHPGLYFLAQDDDL
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SSQVMRSEEQRQLDNILDKLRRTSARVVVVFSPELSLYSFFHEVLRWNFTGFVWIASESWAI
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YVFVAFITAIKVALVVGNMLATTINPIGRTDPDDPNIMILSCHPNYRNGLLFNTSMDLLLSV
LGFSFAYMGKELPTNYNEAKFITLSMTFSFTSSISLCTFMSVHDGVLVTIMDLLVTVLNFLA
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Mouse T1R2 amino acid sequence--SEQ ID NO:8

MGPQARTLHLLFLLLHALPKPVMLVGNSDFHLAGDYLLGGLFTLHANVKSVSHLSYLQVPKC
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VPSATHHIEAMVQLMVHFQWNWIVVLVSDDDYGRENSHLLSQRLTNTGDICIAFQEVLPVPE
PNQAVRPEEQDQLDNILDKLRRTSARVVVIFSPELSLHNFFREVLRWNFTGFVWIASESWAI
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ITESFNNVLMLSGERVVYSVYSAVYAVAHTLHRLLHCNQVRCTKQIVYPWQLLREIWHVNFT
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MVPVYVGPPTVFSCFCRQAFFTVCFSVCLSCITVRSFQIVCVFKMARRLPSAYGFWMRYHGP
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LGFSFAYVGKELPTNYNEAKFITLSMTFSFTSSISLCTFMSVHDGVLVTIMDLLVTVLNFLA
IGLGYFGPKCYMILFYPERNTSAYFNSMIQGYTMRKS

Human T1R2 amino acid sequence--SEQ ID NO:9

MGPRAKTICSLFFLLWVLAEPAENSDFYLPGDYLLGGLFSLHANMKGIVHLNFLQVPMCKEY
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QEDYSNYISRVVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELRDKVRFPALLRTTPS
ADHHVEAMVQLMLHFRWNWIIVLVSSDTYGRDNGQLLGERVARRDICIAFQETLPTLQPNQN
MTSEERQRLVTIVDKLQQSTARVVVVFSPDLTLYHFFNEVLRQNFTGAVWIASESWAIDPVL
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KRCQSGQKKKPVGIHVCCFECIDCLPGTFLNHTEDEYECQACPNNEWSYQSETSCFKRQLVF
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AYMGKELPTNYNEAKFITLSMTFYFTSSVSLCTFMSAYSGVLVTIVDLLVTVLNLLAISLGY
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Rat T1R2 nucleotide sequence--SEQ ID NO:10

CACTTTGCTGTCATGGGTCCCCAGGCAAGGACACTCTGCTTGCTGTCTCTCCTGCTGCATGT
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Mouse T1R2 nucleotide sequence--SEQ ID NO:11

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Human T1R2 nucleotide sequence--SEQ ID NO:12

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TIR3 SEQUENCES

Human T1R3 genomic nucleotide sequence--SEQ ID NO:13

GCTCACTCCATGTGAGGCCCCAGTCGGGGCAGCCACCTGCCGTGCCTGTTGGAAGTTGCCTC
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Human T1R3 cds nucleotide sequence--SEQ ID NO:14

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GTGCCCAGCGACCGTGTGCAGCTGACGGCCGCCGCGGAGCTGCTGCAGGAGTTCGGCTGGAA
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CCCTGGCCGCGGCACGCGGCATCTGCATCGCGCACGAGGGCCTGGTGCCGCTGCCCCGTGCC
GATGACTCGCGGCTGGGGAAGGTGCAGGACGTCCTGCACCAGGTGAACCAGAGCAGCGTGCA
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GCAGGCTCTCGCCCAAGGTGTGGGTGGCCAGCGAGGCCTGGCTGACCTCTGACCTGGTCATG
GGGCTGCCCGGCATGGCCCAGATGGGCACGGTGCTTGGCTTCCTCCAGAGGGGTGCCCAGCT
GCACGAGTTCCCCCAGTACGTGAAGACGCACCTGGCCCTGGCCACCGACCCGGCCTTCTGCT
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GCTGCCCCGCGCAGGACCCCGTGAAGCCCTGGCAGCTCCTGGAGAACATGTACAACCTGACC
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CCTGAAGCTGTGGGTGTGGCAGGGCTCAGTGCCCAGGCTCCACGACGTGGGCAGGTTCAACG
GCAGCCTCAGGACAGAGCGCCTGAAGATCCGCTGGCACACGTCTGACAACCAGAAGCCCGTG
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GCACCTTTTGTGGCCAGGATGAGTGGTCCCCGGAGCGAAGCACACGCTGCTTCCGCCGCAGG
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GCTGGGCCTTGTGCTGGCTGCTTTGGGGCTGTTCGTTCACCATCGGGACAGCCCACTGGTTC
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GTCCTCCTGTTCCCTGGCCAGCCCAGCCCTGCCCGATGCCTGGCCCAGCAGCCCTTGTCCCA
CCTCCCGCTCACGGGCTGCCTGAGCACACTCTTCCTGCAGGCGGCCGAGATCTTCGTGGAGT
CAGAACTGCCTCTGAGCTGGGCAGACCGGCTGAGTGGCTGCCTGCGGGGGCCCTGGGCCTGG
CTGGTGGTGCTGCTGGCCATGCTGGTGGAGGTCGCACTGTGCACCTGGTACCTGGTGGCCTT

CCCGCCGGAGGTGGTGACGGACTGGCACATGCTGCCCACGGAGGCGCTGGTGCACTGCCGCA
CACGCTCCTGGGTCAGCTTCGGCCTAGCGCACGCCACCAATGCCACGCTGGCCTTTCTCTGC
TTCCTGGGCACTTTCCTGGTGCGGAGCCAGCCGGGCTGCTACAACCGTGCCCGTGGCCTCAC
CTTTGCCATGCTGGCCTACTTCATCACCTGGGTCTCCTTTGTGCCCCTCCTGGCCAATGTGC
AGGTGGTCCTCAGGCCCGCCGTGCAGATGGGCGCCCTCCTGCTCTGTGTCCTGGGCATCCTG
GCTGCCTTCCACCTGCCCAGGTGTTACCTGCTCATGCGGCAGCCAGGGCTCAACACCCCCGA
GTTCTTCCTGGGAGGGGGCCCTGGGGATGCCCAAGGCCAGAATGACGGGAACACAGGAAATC
AGGGGAAACATGAGTGA

Human T1R3 amino acid sequence--SEQ ID NO:15

MLGPAVLGLSLWALLHPGTGAPLCLSQQLRMKGDYVLGGLFPLGEAEEAGLRSRTRPSSPVC
TRFSSNGLLWALAMKMAVEEINNKSDLLPGLRLGYDLFDTCSEPVVAMKPSLMFLAKAGSRD
IAAYCNYTQYQPRVLAVIGPHSSELAMVTGKFFSFFLMPQ**VSYGASMELLSARETFPSFFRT**
VPSDRVQLTAAAELLQEFGWNWVAALGSDDEYGRQGLSIFSALAAARGICIAHEGLVPLPRA
DDSRLGKVQDVLHQVNQSSVQVVLLFASVHAAHALFNYSISSRLSPKVWVASEAWLTSDLVM
GLPGMAQMGTVLGFLQRGAQLHEFPQYVKTHLALATDPAFCSALGEREQGLEEDVVGQRCPQ
CDCITLQNVSAGLNHHQTFSVYAAVYSVAQALHNTLQCNASGCPAQDPVKPWQLLENMYNLT
FHVGGLPLRFDSSGNVDMEYDLKLWVWQGSVPRLHDVGRFNGSLRTERLKIRWHTSDNQ**KPV**
SRCSRQCQEGQVRRVKGFHSCCYDCVDCEAGSYRQNPDDIACTFCGQDEWSPERSTRCFRRR
SRFLAWGEPAVLLLLLLLSLALGLVLAALGLFVHHRDSPLVQASGGPLACFGLVCLGLVCLS
VLLFPGQPSPARCLAQQPLSHLPLTGCLSTLFLQAAEIFVESELPLSWADRLSGCLRGPWAW
LVVLLAMLVEVALCTWYLVAFPPEVVTDWHMLPTEALVHCRTRSWVSFGLAHATNATLAFLC
FLGTFLVRSQPGCYNRARGLTFAMLAYFITWVSFVPLLANVQVVLRPAVQMGALLLCVLGIL
AAFHLPRCYLLMRQPGLNTPEFFLGGGPGDAQGQNDGNTGNQGKHE

Mouse T1R3 Sac non taster 129 genomic nucleotide sequence--SEQ ID NO:16

ACATCTGTGGCTCCAACCCCACACACCCATCTATTGTTAGTGCTGGAGACTTCTACCTACC**A**
TGCCAGCTTTGGCTATCATGGGTCTCAGCCTGGCTGCTTTCCTGGAGCTTGGGATGGGGGCC
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CCTGGGCTCGACCGAGGAGGCCACTCTCAACCAGAGAGCACAACCCAACAGCACCCTGTGTA
ACAG*GTATGGAGGCTAGTAGCTGGGGTGGGAGTGAACCGAAGCTTGGCAGCTTTGGCTCCGT*
*GGTACTACCAATCTGGGGAAGGGGTGGTGATCAGTTTCCATGTGGCCTCAG***GTTCTCACCCC**
TCGGTTTGTTCCTGGCCATGGCTATGAAGATGGCTGTGGAGGAGATCAACAATGGATCTGCC
TTGCTCCCTGGGCTGCGGCTGGGCTATGACCTATTTGACACATGCTCCGAGCCAGTGGTCAC
CATGAAATCCAGTCTCATGTTCCTGGCCAAGGTGGGCAGTCAAAGCATTGCTGCCTACTGCA
ACTACACACAGTACCAACCCCGTGTGCTGGCTGTCATCGGCCCCCACTCATCAGAGCTTGCC
CTCATTACAGGCAAGTTCTTCAGCTTCTTCCTCATGCCACAG*GTGAGCCCACTTCCTTTGTG*
*TTCTCAACCGATTGCACCCATTGAGCTCTCACATCAGAAAGTGCTTCTTGATCACCACAG***GT**
CAGCTATAGCGCCAGCATGGATCGGCTAAGTGACCGGGAAACGTTTCCATCCTTCTTCCGCA
CAGTGCCCAGTGACCGGGTGCAGCTGCAGGCAGTTGTGACTCTGTTGCAGAACTTCAGCTGG
AACTGGGTGGCCGCCTTAGGGAGTGATGATGACTATGGCCGGGAAGGTCTGAGCATCTTTTC
TAGTCTGGCCAATGCACGAGGTATCTGCATCGCACATGAGGGCCTGGTGCCACAACATGACA
CTAGTGGCCAACAGTTGGGCAAGGTGCTGGATGTGCTACGCCAAGTGAACCAAAGTAAAGTA
CAAGTGGTGGTGCTGTTTGCCTCTGCCCGTGCTGTCTACTCCCTTTTTAGTTACAGCATCCA
TCATGGCCTCTCACCCAAGGTATGGGTGGCCAGTGAGTCTTGGCTGACATCTGACCTGGTCA
TGACACTTCCCAATATTGCCCGTGTGGGCACTGTGCTTGGGTTTTTGCAGCGGGGTGCCCTA
CTGCCTGAATTTTCCCATTATGTGGAGACTCACCTTGCCCTGGCCGCTGACCCAGCATTCTG
TGCCTCACTGAATGCGGAGTTGGATCTGGAGGAACATGTGATGGGGCAACGCTGTCCACAGT
GTGACGACATCATGCTGCAGAACCTATCATCTGGGCTGTTGCAGAACCTATCAGCTGGGCAA
TTGCACCACCAAATATTTGCAACCTATGCAGCTGTGTACAGTGTGGCTCAAGCCCTTCACAA

CACCCTACAGTGCAATGTCTCACATTGCCACGTATCAGAACATGTTCTACCCTGGCAG*GTAA*
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*ATCATGTTGTGACTGGAGAGGCCTTACCCTGACTCCACTCCACAG*CTCCTGGAGAACATGTA
CAATATGAGTTTCCATGCTCGAGACTTGACACTACAGTTTGATGCTGAAGGGAATGTAGACA
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GACAAGACAGGCAAAAAGGATGGTGGGTAGAAGCTTGTCGGTCTTGGGCCAGTGCTAGCCAA
*GGGGAGGCCTAACCCAAGGCTCCATGTCCAG*GTGCCAGTCTCCCAGTGTTCCCGCCAGTGCA
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TGTCCACCACTGGGACAGCCCTCTTGTCCAGGCCTCAGGCGGCTCACAGTTCTGCTTTGGCC
TGATCTGCCTAGGCCTCTTCTGCCTCAGTGTCCTTCTGTTCCCAGGACGGCCAAGCTCTGCC
AGCTGCCTTGCACAACAACCAATGGCTCACCTCCCTCTCACAGGCTGCCTGAGCACACTCTT
CCTGCAAGCAGCTGAGACCTTTGTGGAGTCTGAGCTGCCACTGAGCTGGGCAAACTGGCTAT
GCAGCTACCTTCGGGGACTCTGGGCCTGGCTAGTGGTACTGTTGGCCACTTTTGTGGAGGCA
GCACTATGTGCCTGGTATTTGACCGCTTTCCCACCAGAGGTGGTGACAGACTGGTCAGTGCT
GCCCACAGAGGTACTGGAGCACTGCCACGTGCGTTCCTGGGTCAGCCTGGGCTTGGTGCACA
TCACCAATGCAATGTTAGCTTTCCTCTGCTTTCTGGGCACTTTCCTGGTACAGAGCCAGCCT
GGCCGCTACAACCGTGCCCGTGGTCTCACCTTCGCCATGCTAGCTTATTTCATCACCTGGGT
CTCTTTTGTGCCCCTCCTGGCCAATGTGCAGGTGGCCTACCAGCCAGCTGTGCAGATGGGTG
CTATCCTAGTCTGTGCCCTGGGCATCCTGGTCACCTTCCACCTGCCCAAGTGCTATGTGCTT
CTTTGGCTGCCAAAGCTCAACACCCAGGAGTTCTTCCTGGGAAGGAATGCCAAGAAAGCAGC
AGATGAGAACAGTGGCGGTGGTGAGGCAGCTCAGGAACACAATGAATGACCACTGACCCGTG
ACCTTCCCTTTAGGGA

Mouse T1R3 Sac non taster 129 cds nucleotide sequence--SEQ ID NO:17

ATGCCAGCTTTGGCTATCATGGGTCTCAGCCTGGCTGCTTTCCTGGAGCTTGGGATGGGGGC
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AACAGGTTCTCACCCCTCGGTTTGTTCCTGGCCATGGCTATGAAGATGGCTGTGGAGGAGAT
CAACAATGGATCTGCCTTGCTCCCTGGGCTGCGGCTGGGCTATGACCTATTTGACACATGCT
CCGAGCCAGTGGTCACCATGAAATCCAGTCTCATGTTCCTGGCCAAGGTGGGCAGTCAAAGC
ATTGCTGCCTACTGCAACTACACACAGTACCAACCCCGTGTGCTGGCTGTCATCGGCCCCCA
CTCATCAGAGCTTGCCCTCATTACAGGCAAGTTCTTCAGCTTCTTCCTCATGCCACAGGTCA
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GTGCCCAGTGACCGGGTGCAGCTGCAGGCAGTTGTGACTCTGTTGCAGAACTTCAGCTGGAA
CTGGGTGGCCGCCTTAGGGAGTGATGATGACTATGGCCGGGAAGGTCTGAGCATCTTTTCTA
GTCTGGCCAATGCACGAGGTATCTGCATCGCACATGAGGGCCTGGTGCCACAACATGACACT
AGTGGCCAACAGTTGGGCAAGGTGCTGGATGTGCTACGCCAAGTGAACCAAAGTAAAGTACA
AGTGGTGGTGCTGTTTGCCTCTGCCCGTGCTGTCTACTCCCTTTTTAGTTACAGCATCCATC
ATGGCCTCTCACCCAAGGTATGGGTGGCCAGTGAGTCTTGGCTGACATCTGACCTGGTCATG
ACACTTCCCAATATTGCCCGTGTGGGCACTGTGCTTGGGTTTTTGCAGCGGGGTGCCCTACT
GCCTGAATTTTCCCATTATGTGGAGACTCACCTTGCCCTGGCCGCTGACCCAGCATTCTGTG
CCTCACTGAATGCGGAGTTGGATCTGGAGGAACATGTGATGGGGCAACGCTGTCCACAGTGT
GACGACATCATGCTGCAGAACCTATCATCTGGGCTGTTGCAGAACCTATCAGCTGGGCAATT
GCACCACCAAATATTTGCAACCTATGCAGCTGTGTACAGTGTGGCTCAAGCCCTTCACAACA

CCCTACAGTGCAATGTCTCACATTGCCACGTATCAGAACATGTTCTACCCTGGCAGCTCCTG
GAGAACATGTACAATATGAGTTTCCATGCTCGAGACTTGACACTACAGTTTGATGCTGAAGG
GAATGTAGACATGGAATATGACCTGAAGATGTGGGTGTGGCAGAGCCCTACACCTGTATTAC
ATACTGTGGGCACCTTCAACGGCACCCTTCAGCTGCAGCAGTCTAAAATGTACTGGCCAGGC
AACCAGGTGCCAGTCTCCCAGTGTTCCCGCCAGTGCAAAGATGGCCAGGTTCGCCGAGTAAA
GGGCTTTCATTCCTGCTGCTATGACTGCGTGGACTGCAAGGCGGGCAGCTACCGGAAGCATC
CAGATGACTTCACCTGTACTCCATGTAACCAGGACCAGTGGTCCCCAGAGAAAAGCACAGCC
TGCTTACCTCGCAGGCCCAAGTTTCTGGCTTGGGGGGAGCCAGTTGTGCTGTCACTCCTCCT
GCTGCTTTGCCTGGTGCTGGGTCTAGCACTGGCTGCTCTGGGGCTCTCTGTCCACCACTGGG
ACAGCCCTCTTGTCCAGGCCTCAGGCGGCTCACAGTTCTGCTTTGGCCTGATCTGCCTAGGC
CTCTTCTGCCTCAGTGTCCTTCTGTTCCCAGGACGGCCAAGCTCTGCCAGCTGCCTTGCACA
ACAACCAATGGCTCACCTCCCTCTCACAGGCTGCCTGAGCACACTCTTCCTGCAAGCAGCTG
AGACCTTTGTGGAGTCTGAGCTGCCACTGAGCTGGGCAAACTGGCTATGCAGCTACCTTCGG
GGACTCTGGGCCTGGCTAGTGGTACTGTTGGCCACTTTTGTGGAGGCAGCACTATGTGCCTG
GTATTTGACCGCTTTCCCACCAGAGGTGGTGACAGACTGGTCAGTGCTGCCCACAGAGGTAC
TGGAGCACTGCCACGTGCGTTCCTGGGTCAGCCTGGGCTTGGTGCACATCACCAATGCAATG
TTAGCTTTCCTCTGCTTTCTGGGCACTTTCCTGGTACAGAGCCAGCCTGGCCGCTACAACCG
TGCCCGTGGTCTCACCTTCGCCATGCTAGCTTATTTCATCACCTGGGTCTCTTTTGTGCCCC
TCCTGGCCAATGTGCAGGTGGCCTACCAGCCAGCTGTGCAGATGGGTGCTATCCTAGTCTGT
GCCCTGGGCATCCTGGTCACCTTCCACCTGCCCAAGTGCTATGTGCTTCTTTGGCTGCCAAA
GCTCAACACCCAGGAGTTCTTCCTGGGAAGGAATGCCAAGAAAGCAGCAGATGAGAACAGTG
GCGGTGGTGAGGCAGCTCAGGAACACAATGAATGA

Mouse T1R3 Sac non taster 129 amino acid sequence--SEQ ID NO:18

MPALAIMGLSLAAFLELGMGASLCLSQQFKAQGDYILGGLFPLGSTEEATLNQRAQPNSTLC
NRFSPLGLFLAMAMKMAVEEINNGSALLPGLRLGYDLFDTCSEPVVTMKSSLMFLAKVGSQS
IAAYCNYTQYQPRVLAVIGPHSSELALITGKFFSFFLMPQVSYSASMDRLSDRETFPSFFRT
VPSDRVQLQAVVTLLQNFSWNWVAALGSDDDYGREGLSIFSSLANARGICIAHEGLVPQHDT
SGQQLGKVLDVLRQVNQSKVQVVVLFASARAVYSLFSYSIHHGLSPKVWVASESWLTSDLVM
TLPNIARVGTVLGFLQRGALLPEFSHYVETHLALAADPAFCASLNAELDLEEHVMGQRCPQC
DDIMLQNLSSGLLQNLSAGQLHHQIFATYAAVYSVAQALHNTLQCNVSHCHVSEHVLPWQLL
ENMYNMSFHARDLTLQFDAEGNVDMEYDLKMWVWQSPTPVLHTVGTFNGTLQLQQSKMYWPG
NQVPVSQCSRQCKDGQVRRVKGFHSCCYDCVDCKAGSYRKHPDDFTCTPCNQDQWSPEKSTA
CLPRRPKFLAWGEPVVLSLLLLLCLVLGLALAALGLSVHHWDSPLVQASGGSQFCFGLICLG
LFCLSVLLFPGRPSSASCLAQQPMAHLPLTGCLSTLFLQAAETFVESELPLSWANWLCSYLR
GLWAWLVVLLATFVEAALCAWYLTAFPPEVVTDWSVLPTEVLEHCHVRSWVSLGLVHITNAM
LAFLCFLGTFLVQSQPGRYNRARGLTFAMLAYFITWVSFVPLLANVQVAYQPAVQMGAILVC
ALGILVTFHLPKCYVLLWLPKLNTQEFFLGRNAKKAADENSGGGEAAQEHNE

Mouse T1R3 Sac taster SWR cds nucleotide sequence--SEQ ID NO:19

ATGCCAGCTTTGGCTATCATGGGTCTCAGCCTGGCTGCTTTCCTGGAGCTTGGGATGGGGGC
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AACAGGTTCTCACCCCTCGGTTTGTTCCTGGCCATGGCTATGAAGATGGCTGTGGAGGAGAT
CAACAATGGATCTGCCTTGCTCCCTGGGCTGCGGCTGGGCTATGACCTATTTGACACATGCT
CCGAGCCAGTGGTCACCATGAAATCCAGTCTCATGTTCCTGGCCAAGGTGGGCAGTCAAAGC
ATTGCTGCCTACTGCAACTACACACAGTACCAACCCCGTGTGCTGGCTGTCATCGGCCCCCA
CTCATCAGAGCTTGCCCTCATTACAGGCAAGTTCTTCAGCTTCTTCCTCATGCCACAGGTCA
GCTATAGCGCCAGCATGGATCGGCTAAGTGACCGGGAAACGTTTCCATCCTTCTTCCGCACA
GTGCCCAGTGACCGGGTGCAGCTGCAGGCAGTTGTGACTCTGTTGCAGAACTTCAGCTGGAA
CTGGGTGGCCGCCTTAGGGAGTGATGATGACTATGGCCGGGAAGGTCTGAGCATCTTTTCTA

GTCTGGCCAATGCACGAGGTATCTGCATCGCACATGAGGGCCTGGTGCCACAACATGACACT
AGTGGCCAACAGTTGGGCAAGGTGCTGGATGTGCTATGCCAAGTGAACCAAAGTAAAGTACA
AGTGGTGGTGCTGTTTGCCTCTGCCCGTGCTGTCTACTCCCTTTTTAGTTACAGCATCCATC
ATGGCCTCTCACCCAAGGTATGGGTGGCCAGTGAGTCTTGGCTGACATCTGACCTGGTCATG
ACACTTCCCAATATTGCCCGTGTGGGCACTGTGCTTGGGTTTTTGCAGCGGGGTGCCCTACT
GCCTGAATTTTCCCATTATGTGGAGACTCACCTTGCCCTGGCCGCTGACCCAGCATTCTGTG
CCTCACTGAATGCGGAGTTGGATCTGGAGGAACATGTGATGGGGCAACGCTGTCCACAGTGT
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GCACCACCAAATATTTGCAACCTATGCAGCTGTGTACAGTGTGGCTCAAGCCCTTCACAACA
CCCTACAGTGCAATGTCTCACATTGCCATGTATCAGAACATGTTCTACCCTGGCAGCTCCTG
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GAATGTAGACATGGAATATGACCTGAAGATGTGGGTGTGGCAGAGCCCTACACCTGTATTAC
ATACTGTGGGCACCTTCAACGGCACCCTTCAGCTGCAGCAGTCTAAAATGTACTGGCCAGGC
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CAGATGACTTCACCTGTACTCCATGTAACCAGGACCAGTGGTCCCCAGAGAAAAGCACAGCC
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GGACTCTGGGCCTGGCTAGTGGTACTGTCGGCCACTTTTGTGGAGGCAGCACTATGTGCCTG
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TGGAGCACTGCCACGTGCGTTCCTGGGTCAGCCTGGGCTTGGTGCACATCACCAATGCAATG
TTAGCTTTCCTCTGCTTTCTGGGCACTTTCCTGGTACAGAGCCAGCCTGGCCGCTACAACCG
TGCCCGTGGTCTCACCTTCGCCATGCTAGCTTATTTCATCACCTGGGTCTCTTTTGTGCCCC
TCCTGGCCAATGTGCAGGTGGCCTACCAGCCAGCTGTGCAGATGGGTGCTATCCTAGTCTGT
GCCCTGGGCATCCTGGTCACCTTCCACCTGCCCAAGTGCTATGTGCTTCTTTGGCTGCCAAA
GCTCAACACCCAGGAGTTCTTCCTGGGAAGGAATGCCAAGAAAGCAGCAGATGAGAACAGTG
GCGGTGGTGAGGCAGCTCAGGAACACAATGAATGA

Mouse T1R3 Sac taster SWR amino acid sequence--SEQ ID NO:20

MPALAIMGLSLAAFLELGMGASLCLSQQFKAQGDYILGGLFPLGSTEEATLNQRTQPNSILC
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IAAYCNYTQYQPRVLAVIGPHSSELALITGKFFSFFLMPQVSYSASMDRLSDRETFPSFFRT
VPSDRVQLQAVVTLLQNFSWNWVAALGSDDDYGREGLSIFSSLANARGICIAHEGLVPQHDT
SGQQLGKVLDVLCQVNQSKVQVVVLFASARAVYSLFSYSIHHGLSPKVWVASESWLTSDLVM
TLPNIARVGTVLGFLQRGALLPEFSHYVETHLALAADPAFCASLNAELDLEEHVMGQRCPQC
DDIMLQNLSSGLLQNLSAGQLHHQIFATYAAVYSVAQALHNTLQCNVSHCHVSEHVLPWQLL
ENMYNMSFHARDLTLQFDAEGNVDMEYDLKMWVWQSPTPVLHTVGTFNGTLQLQQSKMYWPG
NQVPVSQCSRQCKDGQVRRVKGFHSCCYDCVDCKAGSYRKHPDDFTCTPCNQDQWSPEKSTA
CLPRRPKFLAWGEPVVLSLLLLLCLVLGLALAALGLSVHHWDSPLVQASGGSQFCFGLICLG
LFCLSVLLFPGRPSSASCLAQQPMAHLPLTGCLSTLFLQAAETFVESELPLSWANWLCSYLR
GLWAWLVVLSATFVEAALCAWYLTAFPPEVVTDWSVLPTEVLEHCHVRSWVSLGLVHITNAM
LAFLCFLGTFLVQSQPGRYNRARGLTFAMLAYFITWVSFVPLLANVQVAYQPAVQMGAILVC
ALGILVTFHLPKCYVLLWLPKLNTQEFFLGRNAKKAADENSGGGEAAQEHNE

Mouse T1R3 Sac taster c57 genomic nucleotide sequence--SEQ ID NO:21

CCCACACACCCACCCATTGTTAGTGCTGGAGACTTCTACCTACC**ATGCCAGCTTTGGCTATC**
ATGGGTCTCAGCCTGGCTGCTTTCCTGGAGCTTGGGATGGGGGCCTCTTTGTGTCTGTCACA

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AGGCCACTCTCAACCAGAGAACACAACCCAACAGCATCCCGTGCAACAGGTATGGAGGCTAG
TAGCTGGGGTGGGAGTGAACCGAAGCTTGGCAGCTTTGGCTCCGTGGTACTACCAATCTGGG
AAGAGGTGGTGATCAGTTTCCATGTGGCCTCAGGTTCTCACCCCTTGGTTTGTTCCTGGCCA
TGGCTATGAAGATGGCTGTGGAGGAGATCAACAATGGATCTGCCTTGCTCCCTGGGCTGCGG
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GTTCCTGGCCAAGGTGGGCAGTCAAAGCATTGCTGCCTACTGCAACTACACACAGTACCAAC
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GGTATGGGTGGCCAGTGAGTCTTGGCTGACATCTGACCTGGTCATGACACTTCCCAATATTG
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AGAACCTATCATCTGGGCTGTTGCAGAACCTATCAGCTGGGCAATTGCACCACCAAATATTT
GCAACCTATGCAGCTGTGTACAGTGTGGCTCAAGCCCTTCACAACACCCTACAGTGCAATGT
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AGGCCTTACCCTGACTCCACTCCACAGCTCCTGGAGAACATGTACAATATGAGTTTCCATGC
TCGAGACTTGACACTACAGTTTGATGCTGAAGGGAATGTAGACATGGAATATGACCTGAAGA
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CAGCTGCAGCAGTCTAAAATGTACTGGCCAGGCAACCAGGTAAGGACAAGACAGGCAAAAAG
GATGGTGGGTAGAAGCTTGTCGGTCTTGGGCCAGTGCTAGCCAAGGGGAGGCCTAACCCAAG
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AAGCATCCAGGTGAACCGTCTTCCCTAGACAGTCTGCACAGCCGGGCTAGGGGGCAGAAGCA
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CTTTGCCTGGTGCTGGGTCTAGCACTGGCTGCTCTGGGGCTCTCTGTCCACCACTGGGACAG
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CGTGGTCTCACCTTCGCCATGCTAGCTTATTTCATCACCTGGGTCTCTTTTGTGCCCCTCCT
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TGGGCATCCTGGTCACCTTCCACCTGCCCAAGTGCTATGTGCTTCTTTGGCTGCCAAAGCTC
AACACCCAGGAGTTCTTCCTGGGAAGGAATGCCAAGAAAGCAGCAGATGAGAACAGTGGCGG
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Mouse T1R3 Sac taster C57 cds nucleotide sequence-- SEQ ID NO:22

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GCTCAACACCCAGGAGTTCTTCCTGGGAAGGAATGCCAAGAAAGCAGCAGATGAGAACAGTG
GCGGTGGTGAGGCAGCTCAGGGACACAATGAATGA

Mouse T1R3 Sac taster C57 amino acid sequence--SEQ ID NO:23

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IAAYCNYTQYQPRVLAVIGPHSSELALITGKFFSFFLMPQVSYSASMDRLSDRETFPSFFRT
VPSDRVQLQAVVTLLQNFSWNWVAALGSDDDYGREGLSIFSSLANARGICIAHEGLVPQHDT
SGQQLGKVLDVLRQVNQSKVQVVVLFASARAVYSLFSYSIHHGLSPKVWVASESWLTSDLVM
TLPNIARVGTVLGFLQRGALLPEFSHYVETHLALAADPAFCASLNAELDLEEHVMGQRCPRC

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Rat T1R3 CDS nucleotide sequence--SEQ ID NO:24

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Rat T1R3 amino acid sequence--SEQ ID NO:25

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ALGILATFHLPKCYVLLWLPELNTQEFFLGRSPKEASDGNSGSSEATRGHSE

WHAT IS CLAIMED IS:

1. An isolated homodimeric taste receptor, the receptor comprising two T1R3 polypeptides, wherein the T1R3 polypeptide is encoded by a nucleotide sequence that hybridizes under highly stringent hybridization conditions to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:15, 20, 23, 25, or 31.

2. The isolated receptor of claim 1, wherein the T1R3 polypeptide comprises an amino acid sequence of SEQ ID NO:15, 20, 23, 25, or 31.

3. The isolated receptor of claim 1, wherein the T1R3 polypeptide is encoded by a nucleotide sequence comprising SEQ ID NO:14, 19, 22, 24, or 30.

4. The isolated receptor of claim 1, wherein the T1R3 polypeptides are non-covalently linked.

5. The isolated receptor of claim 1, wherein the T1R3 polypeptides are covalently linked.

6. The isolated receptor of claim 1, wherein the receptor binds to sweet taste ligands.

7. The isolated receptor of claim 6, wherein the sweet taste ligand is a naturally occurring sugar selected from the group consisting of glucose, fructose, galactose, sucrose, maltose, and lactose.

8. The isolated receptor of claim 1, wherein the receptor has G protein coupled receptor activity.

9. The isolated receptor of claim 1, wherein the receptor specifically binds to antibodies raised against SEQ ID NO: 15, 20, 23, 25, or 31.

10. The isolated receptor of claim 1, wherein the T1R3 polypeptides are recombinant.

11. A host cell comprising the isolated receptor of claim 10, wherein the host cell does not express T1R1 or T1R2.

12. An isolated homodimeric taste receptor, the receptor consisting of two T1R3 polypeptides, wherein the T1R3 polypeptide is encoded by a nucleotide sequence that has 90% identity to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:15, 20, 23, 25, or 31.

13. An isolated monomeric taste receptor, the receptor consisting of one T1R3 polypeptide, wherein the T1R3 polypeptide is encoded by a nucleotide sequence that hybridizes under highly stringent hybridization conditions to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:15, 20, 23, 25, or 31.

14. The isolated receptor of claim 13, wherein the T1R3 polypeptide comprises an amino acid sequence of SEQ ID NO:15, 20, 23, 25, or 31.

15. The isolated receptor of claim 13, wherein the T1R3 polypeptide is encoded by a nucleotide sequence comprising SEQ ID NO:14, 19, 22, 24, or 30.

16. The isolated receptor of claim 13, wherein the receptor binds to sweet taste ligands.

17. The isolated receptor of claim 13, wherein the sweet taste ligand is a naturally occurring sugar selected from the group consisting of glucose, fructose, galactose, sucrose, maltose, and lactose.

18. The isolated receptor of claim 13, wherein the receptor has G protein coupled receptor activity.

19. The isolated receptor of claim 13, wherein the T1R3 polypeptide is recombinant.

20. A host cell comprising the isolated receptor of claim 19, wherein the host cell does not express T1R1 or T1R2.

21. A host cell expressing a recombinant taste receptor, the receptor comprising a T1R3 polypeptide, wherein the T1R3 polypeptide is encoded by a nucleotide sequence that hybridizes under highly stringent hybridization conditions to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:15, 20, 23, 25, or 31, wherein the cell does not express T1R1 or T1R2.

22. A method of identifying a compound that modulates taste signal transduction in taste cells, the method comprising the steps of

(i) contacting the compound with a homodimeric taste receptor comprising two T1R3 polypeptides, wherein the T1R3 polypeptide is encoded by a nucleotide sequence that hybridizes under highly stringent hybridization conditions to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:15, 20, 23, 25 or 31; and

(ii) determining the functional effect of the compound upon the receptor, thereby identifying a compound that modulates taste signal transduction.

23. The method of claim 22, wherein the T1R3 polypeptides are non-covalently linked.

24. The method of claim 22, wherein the T1R3 polypeptides are covalently linked.

25. The method of claim 22, wherein the receptor is recombinant.

26. The method of claim 22, wherein the receptor has G protein coupled receptor activity.

27. The method of claim 22, wherein the functional effect is measured *in vitro*.

28. The method of claim 27, wherein the functional effect is a physical effect.

29. The method of claim 27, wherein the receptor is linked to a solid phase.

30. The method of claim 27, wherein the functional effect is determined by measuring binding of a compound to the receptor.

31. The method of claim 30, wherein the functional effect is determined by measuring binding of a compound to the extracellular domain of the receptor.

32. The method of claim 22, wherein the receptor is expressed in a cell or cell membrane, wherein the cell does not express T1R1 or T1R2.

33. The method of claim 32, wherein the functional effect is a physical effect.

34. The method of claim 33, wherein the functional effect is determined by measuring ligand binding to the receptor.

35. The method of claim 34, wherein the functional effect is determined by measuring binding of a compound to the extracellular domain of the receptor.

36. The method of claim 32, wherein the functional effect is a chemical or phenotypic effect.

37. The method of claim 36, wherein the functional effect is determined by measuring changes in intracellular cAMP, IP3, or Ca^{2+}.

38. The method of claim 32, wherein the cell is a mammalian cell.

39. The method of claim 38, wherein the cell is a human cell.

40. A method of identifying a compound that modulates taste signal transduction in taste cells, the method comprising the steps of

(i) contacting the compound with cell expressing a homodimeric taste receptor comprising two T1R3 polypeptides, wherein the T1R3 polypeptide is encoded by a nucleotide sequence that hybridizes under highly stringent hybridization conditions to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:15, 20, 23, 25, or 31; wherein the cell does not express T1R1 and T1R2; and

(ii) determining the functional effect of the compound upon the receptor, thereby identifying a compound that modulates taste signal transduction.

41. The method of claim 40, wherein the T1R3 polypeptides are non-covalently linked.

42. The method of claim 40, wherein the T1R3 polypeptides are covalently linked.

43. A method of identifying a compound that modulates taste signal transduction in taste cells, the method comprising the steps of

(i) contacting the compound with a monomeric taste receptor comprising one T1R3 polypeptide, wherein the T1R3 polypeptide is encoded by a nucleotide sequence that hybridizes under highly stringent hybridization conditions to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:15, 20, 23, 25 or 31; and

(ii) determining the functional effect of the compound upon the receptor, thereby identifying a compound that modulates taste signal transduction.

44. A method of identifying a compound that modulates taste signal transduction in taste cells, the method comprising the steps of

(i) contacting the compound with cell expressing a monomeric taste receptor comprising one T1R3 polypeptide, wherein the T1R3 polypeptide is encoded by a nucleotide sequence that hybridizes under highly stringent hybridization conditions to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:15, 20, 23, 25, or 31; wherein the cell does not express T1R1 or T1R2; and

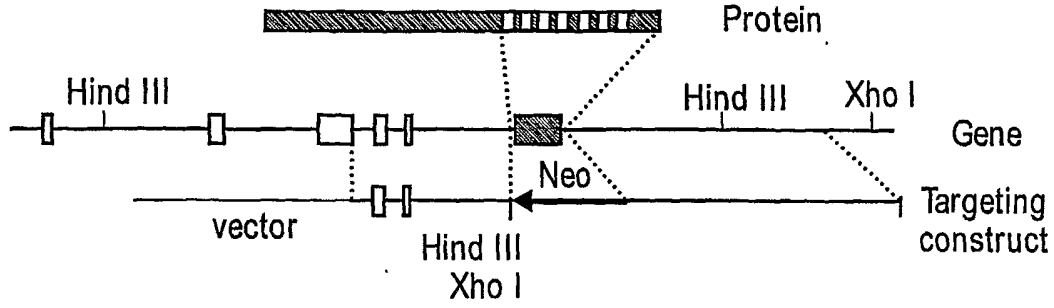
(ii) determining the functional effect of the compound upon the receptor, thereby identifying a compound that modulates taste signal transduction.

45. A method of identifying a compound that modulates taste signal transduction in taste cells, the method comprising the steps of

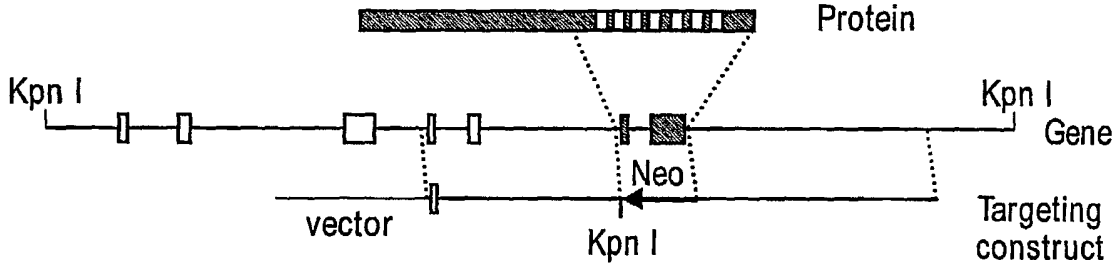
(i) contacting the compound with cell expressing a taste receptor comprising a T1R3 polypeptide, wherein the T1R3 polypeptide is encoded by a nucleotide sequence that hybridizes under highly stringent hybridization conditions to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:15, 20, 23, 25, or 31; wherein the cell does not express T1R1 and T1R2; and

(ii) determining the functional effect of the compound upon the receptor, thereby identifying a compound that modulates taste signal transduction.

T1R1



T1R2



T1R3

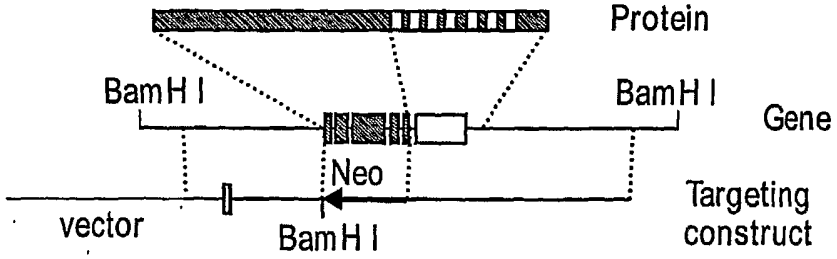


FIG. 1A

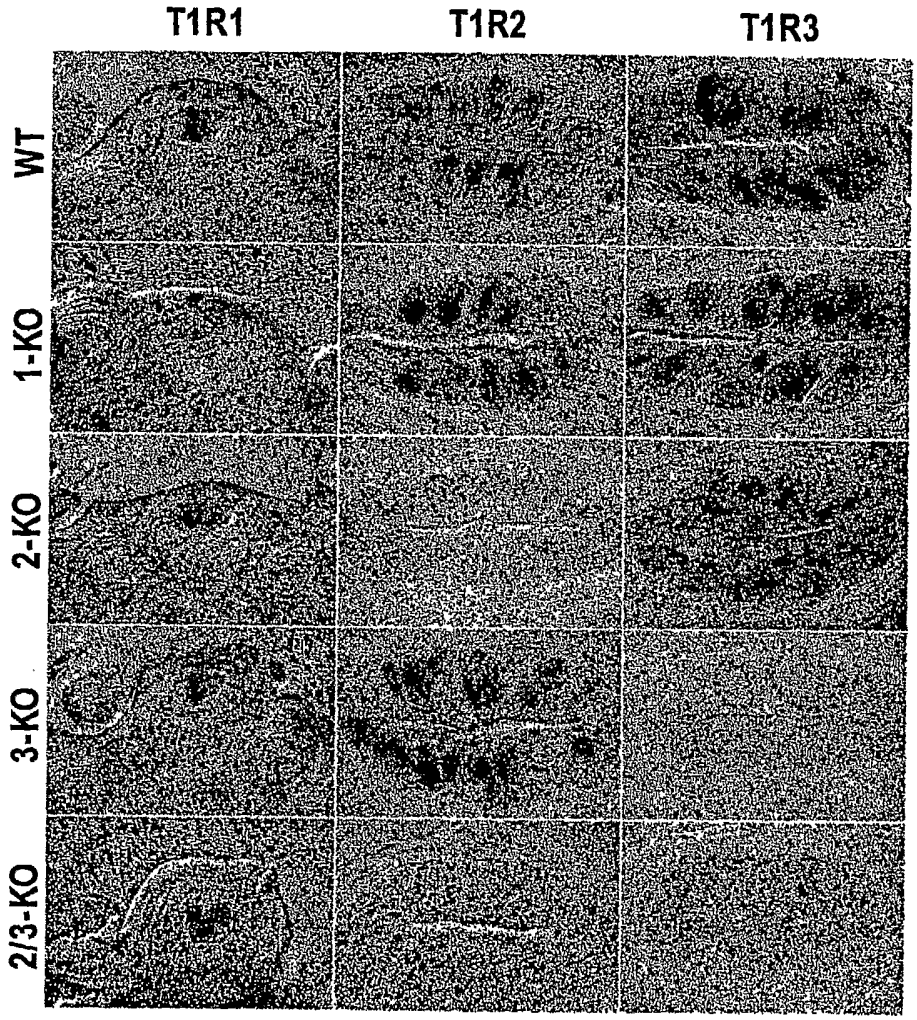


FIG. 1B

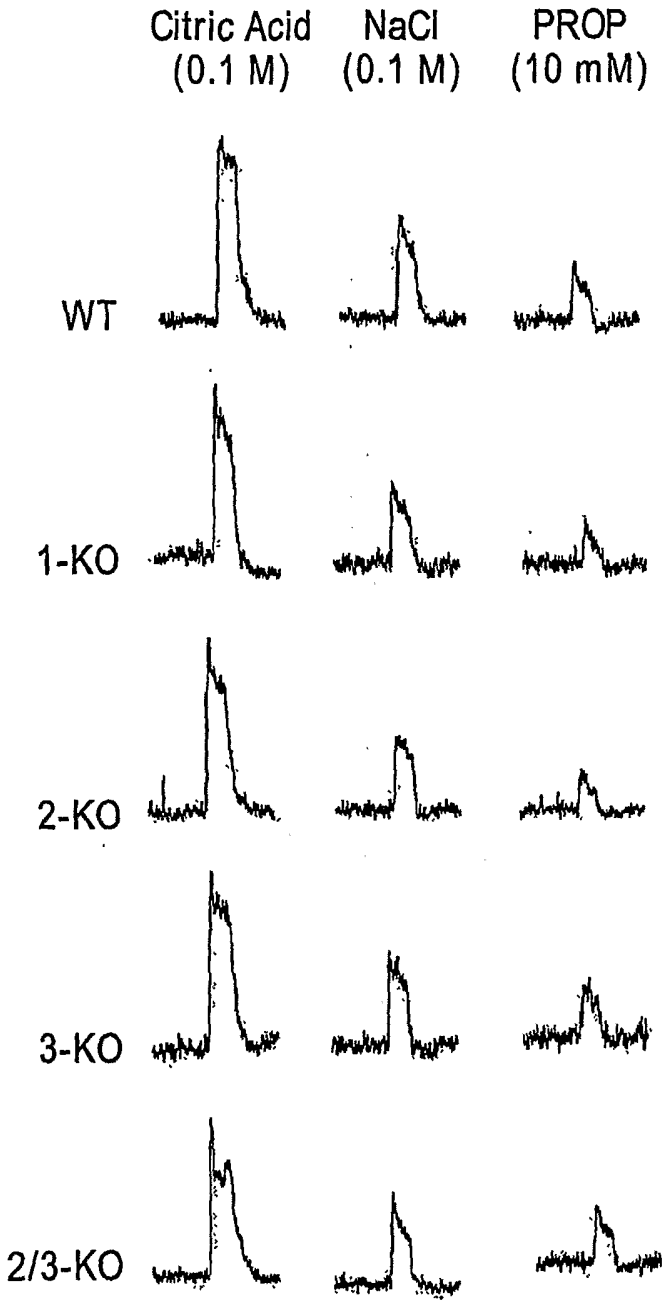


FIG. 2A

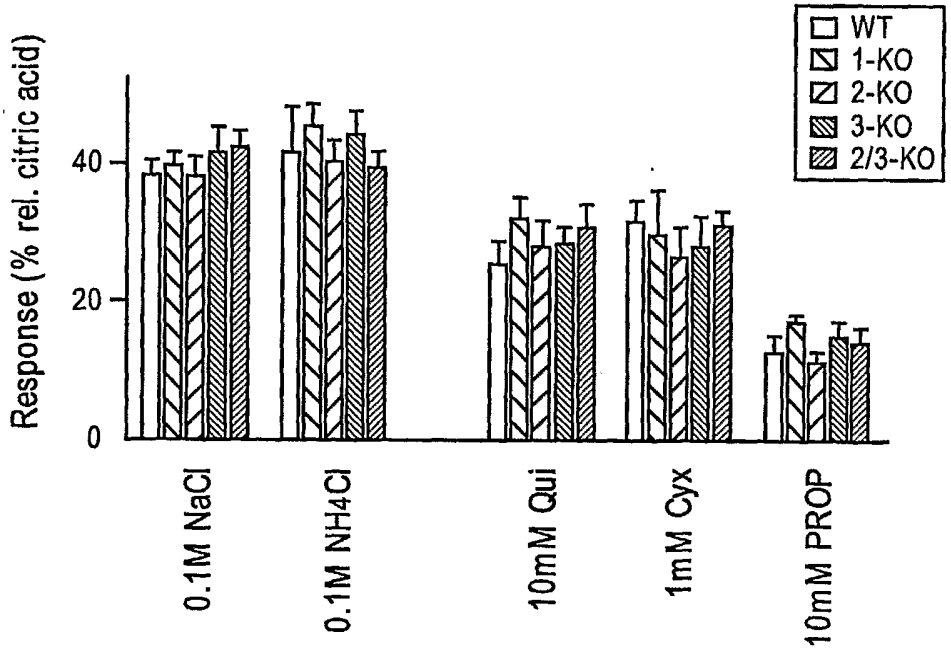

WT
1-KO
2-KO
3-KO
2/3-KO
Response (% rel. citric acid)
40
20
0
0.1M NaCl
0.1M NH4Cl
10mM Qui
1mM Cyx
10mM PROP

FIG. 2B

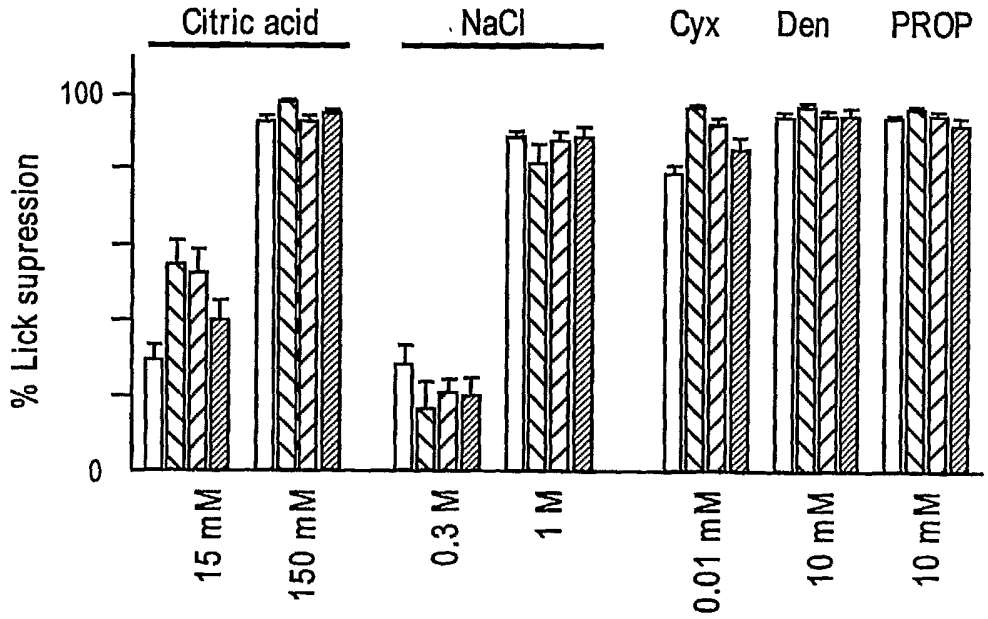
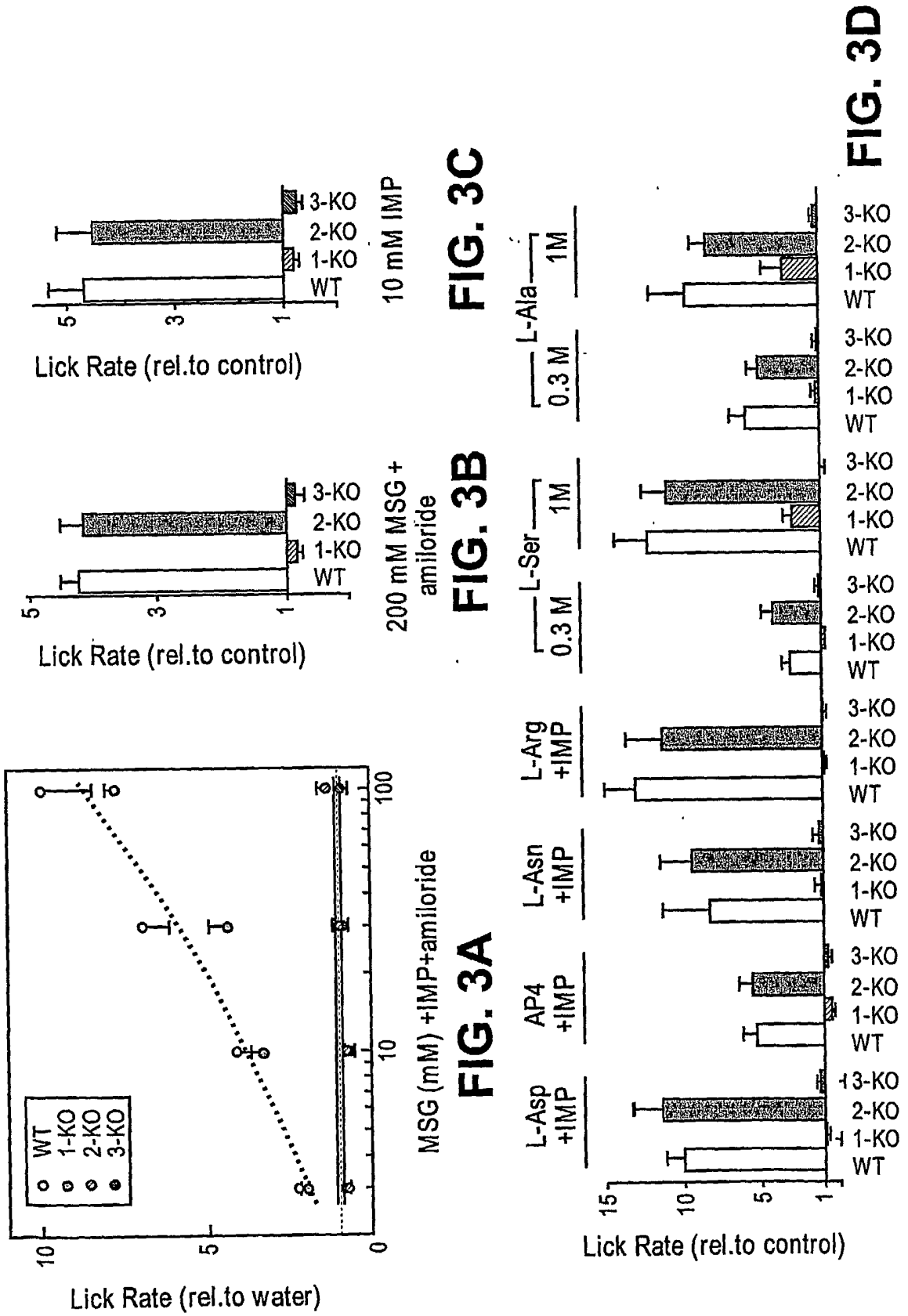

Citric acid
NaCl
Cyx
Den
PROP
% Lick supression
100
0
15 mM
150 mM
0.3 M
1 M
0.01 mM
10 mM
10 mM

FIG. 2C


Lick Rate (rel.to water)
WT
1-KO
2-KO
3-KO
MSG (mM) +IMP+amiloride
FIG. 3A
Lick Rate (rel.to control)
200 mM MSG + amiloride
FIG. 3B
Lick Rate (rel.to control)
10 mM IMP
FIG. 3C
L-Asp +IMP
AP4 +IMP
L-Asn +IMP
L-Arg +IMP
L-Ser 0.3 M
L-Ser 1M
L-Ala 0.3 M
L-Ala 1M
Lick Rate (rel.to control)
FIG. 3D

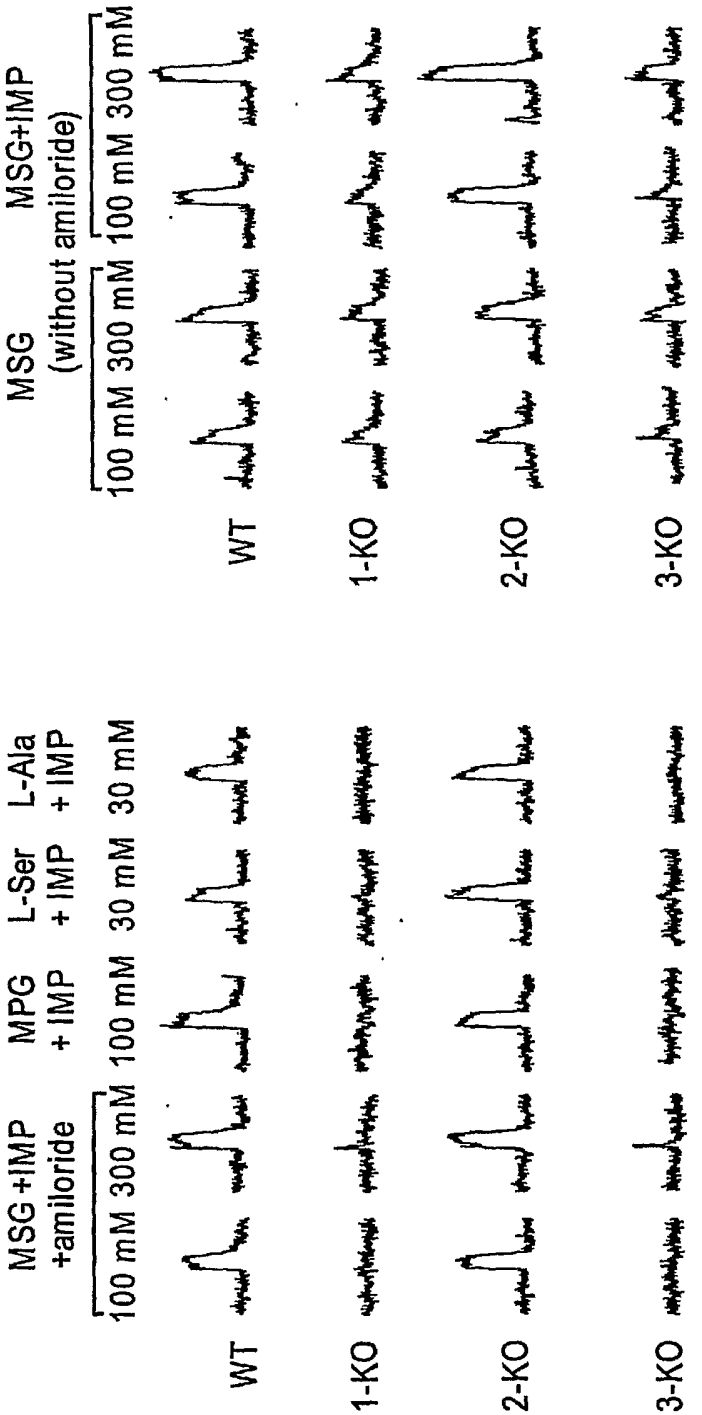
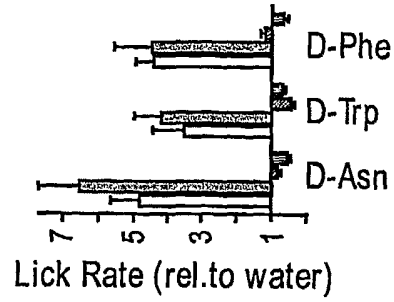
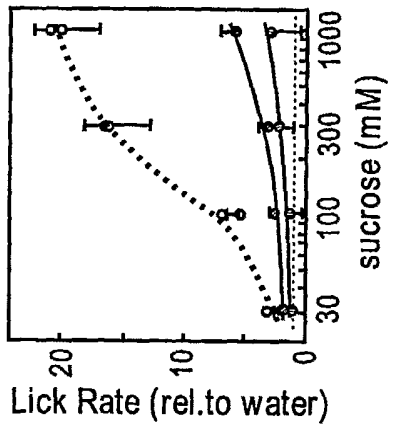

MSG (without amiloride)
MSG+IMP
100 mM 300 mM 100 mM 300 mM
WT
1-KO
2-KO
3-KO

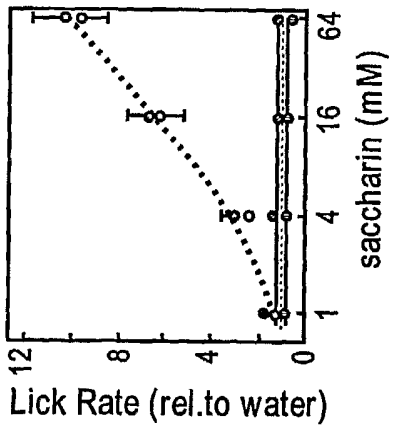
FIG. 3F

MSG +IMP +amiloride
MPG + IMP
L-Ser + IMP
L-Ala + IMP
100 mM 300 mM 100 mM 30 mM 30 mM
WT
1-KO
2-KO
3-KO

FIG. 3E


D-Phe
D-Trp
D-Asn
7
5
3
1
Lick Rate (rel.to water)


sucrose (mM)
30
100
300
1000
0
10
20
Lick Rate (rel.to water)


saccharin (mM)
1
4
16
64
0
4
8
12
Lick Rate (rel.to water)

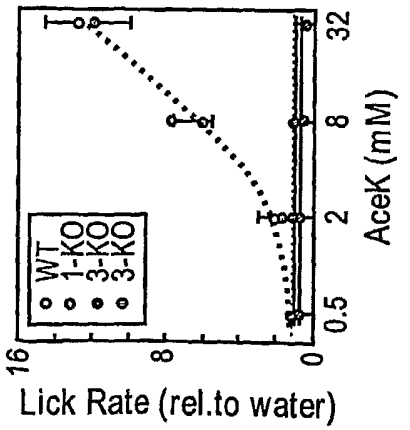
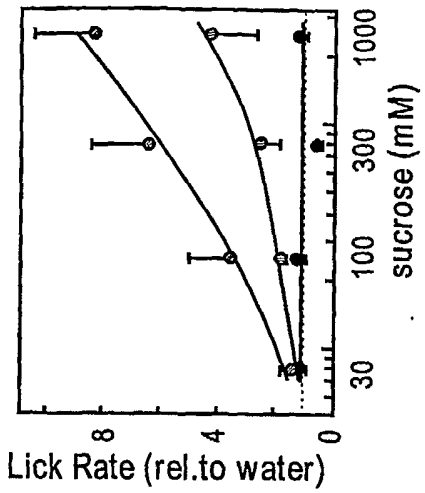
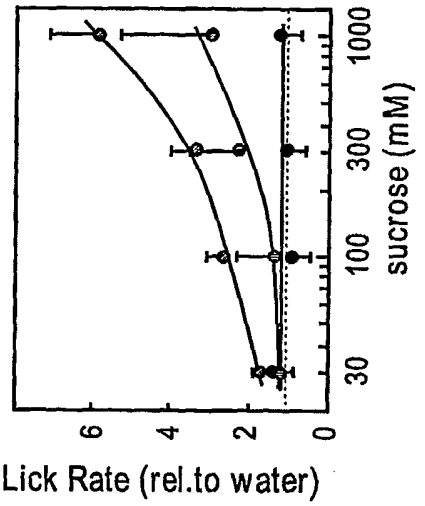

AceK (mM)
0.5
2
8
32
WT
1-KO
3-KO
3-KO
0
8
16
Lick Rate (rel.to water)

FIG. 4A


sucrose (mM)
30
100
300
1000
0
4
8
Lick Rate (rel.to water)


sucrose (mM)
30
100
300
1000
0
2
4
6
Lick Rate (rel.to water)

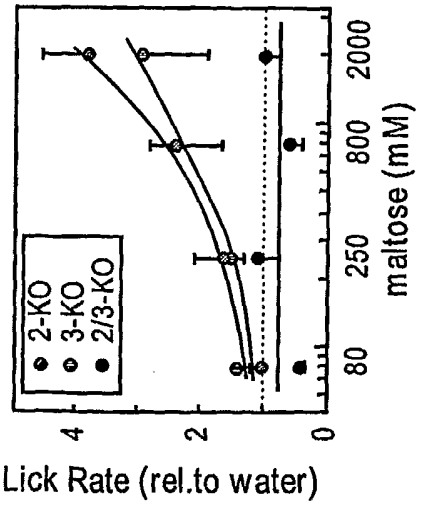

maltose (mM)
80
250
800
2000
2-KO
3-KO
2/3-KO
0
2
4
Lick Rate (rel.to water)

FIG. 4B

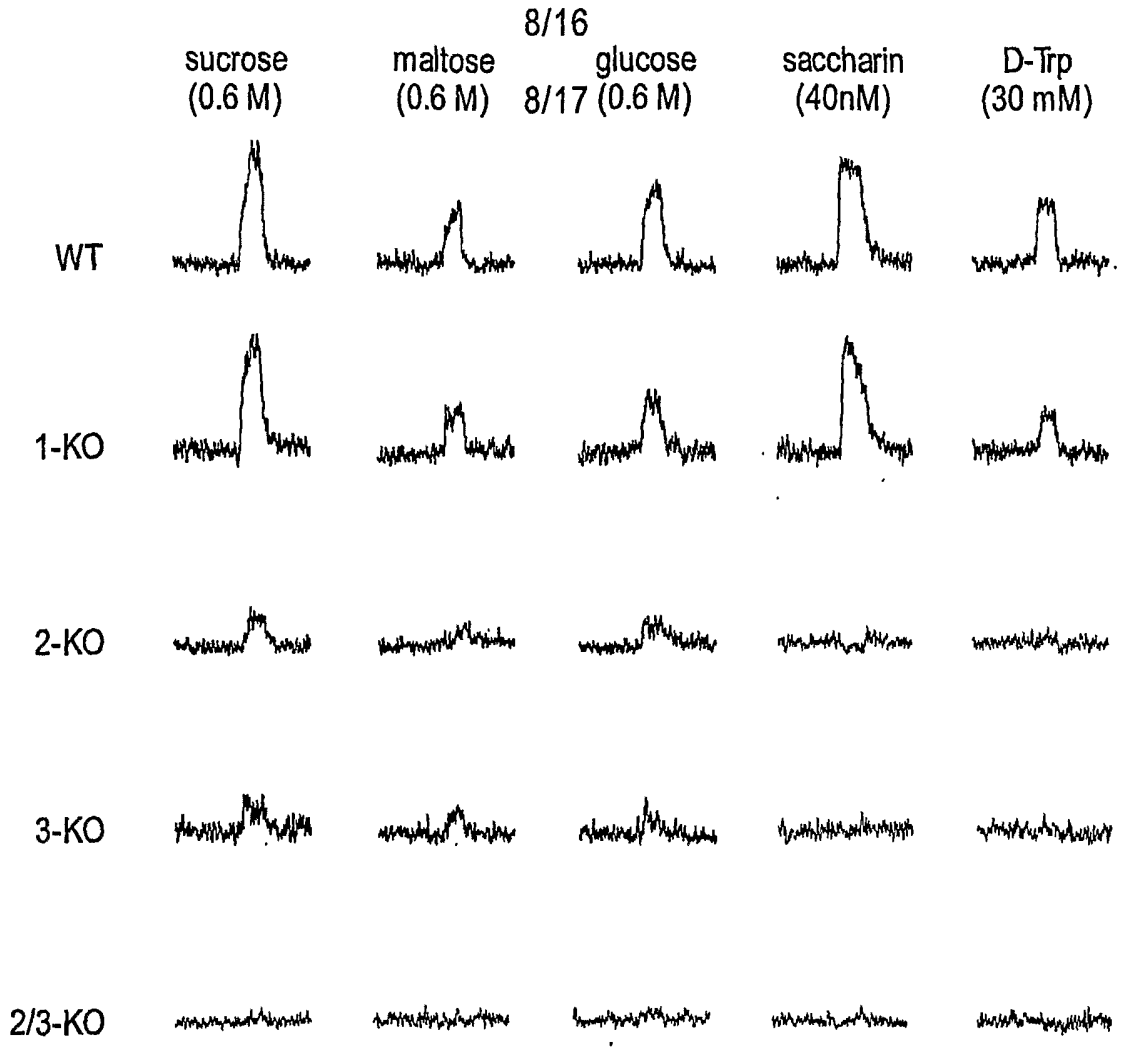

sucrose (0.6 M)
maltose (0.6 M)
glucose (0.6 M)
saccharin (40nM)
D-Trp (30 mM)
WT
1-KO
2-KO
3-KO
2/3-KO

FIG. 5A

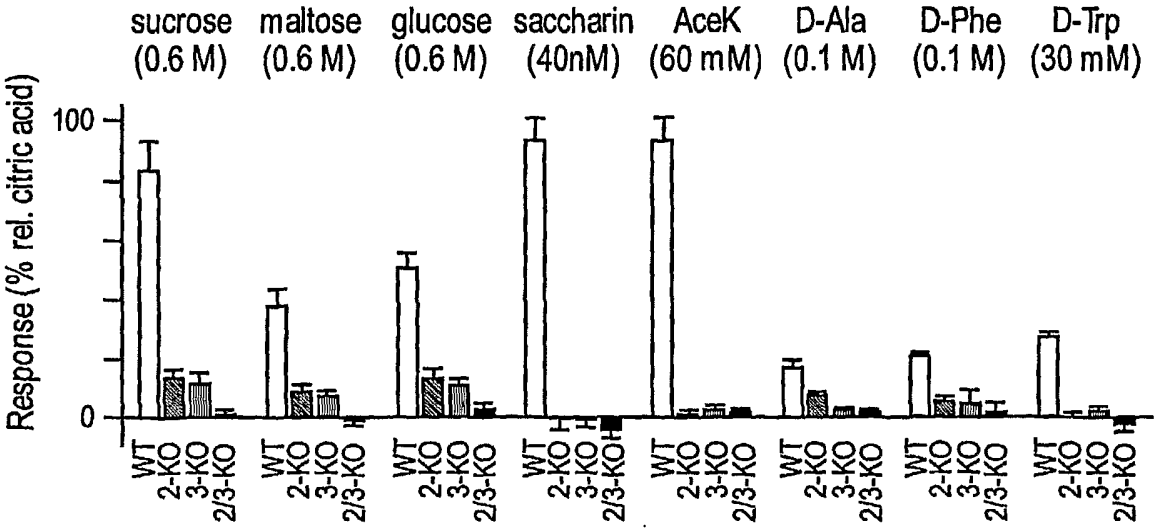

sucrose (0.6 M)
maltose (0.6 M)
glucose (0.6 M)
saccharin (40nM)
AceK (60 mM)
D-Ala (0.1 M)
D-Phe (0.1 M)
D-Trp (30 mM)
Response (% rel. citric acid)
100
0
WT
2-KO
3-KO
2/3-KO

FIG. 5B

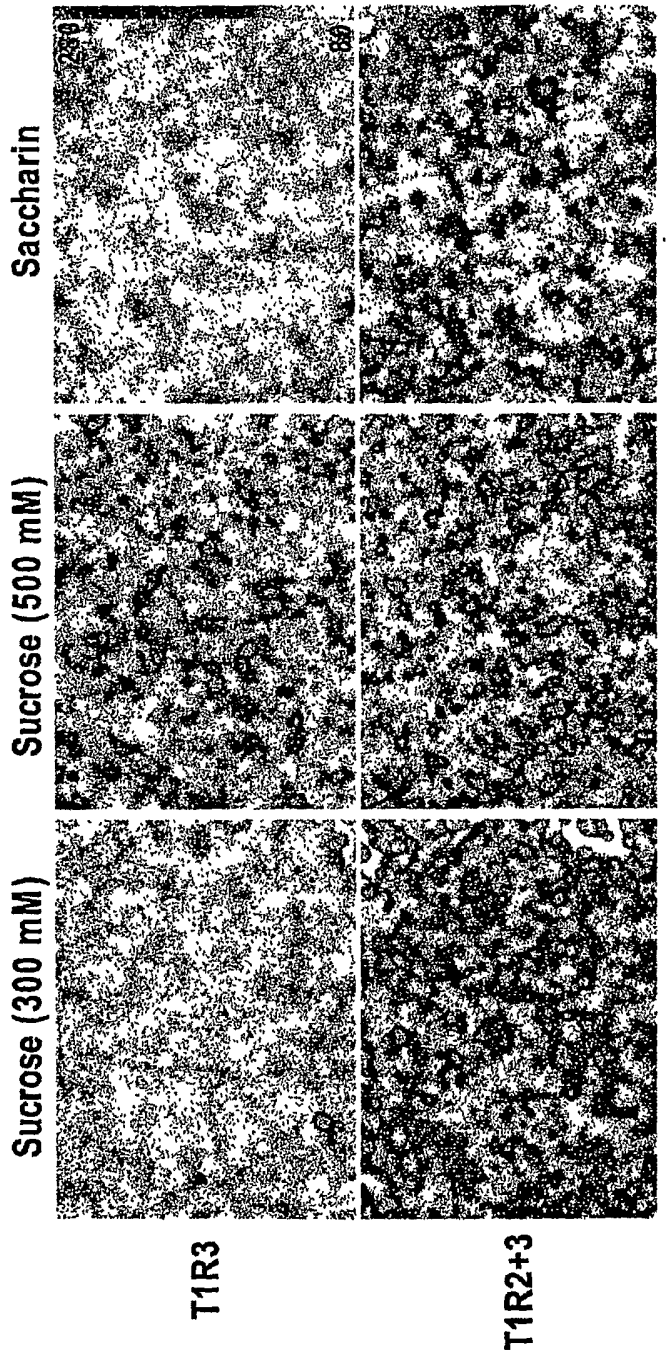


FIG. 6

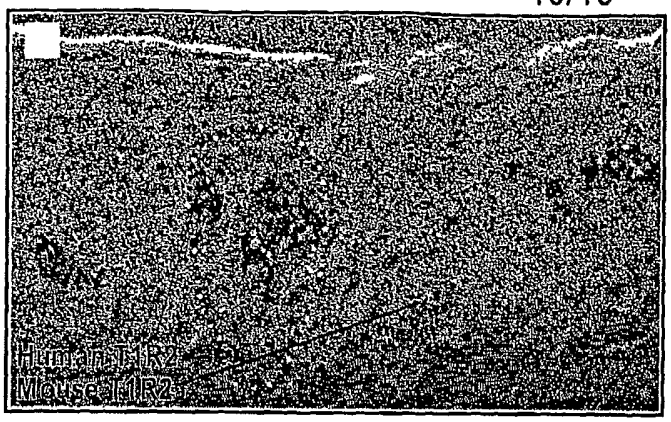


FIG. 7A

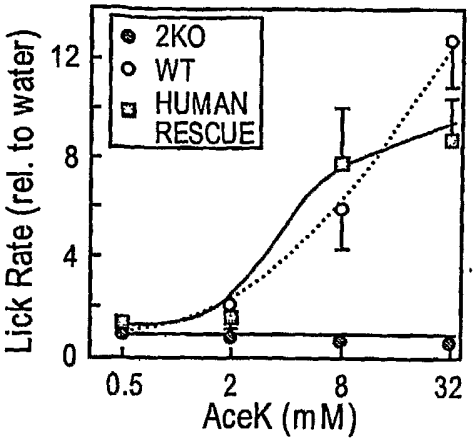


FIG. 7B

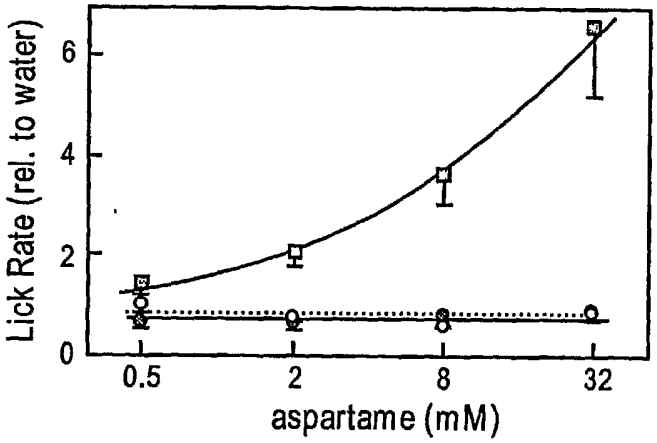


FIG. 7C

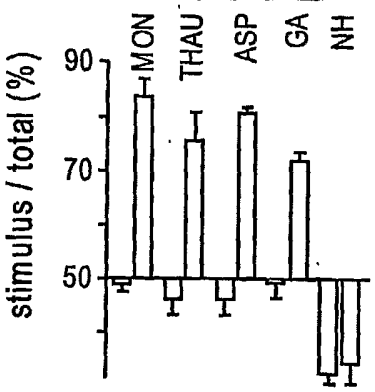


FIG. 7D

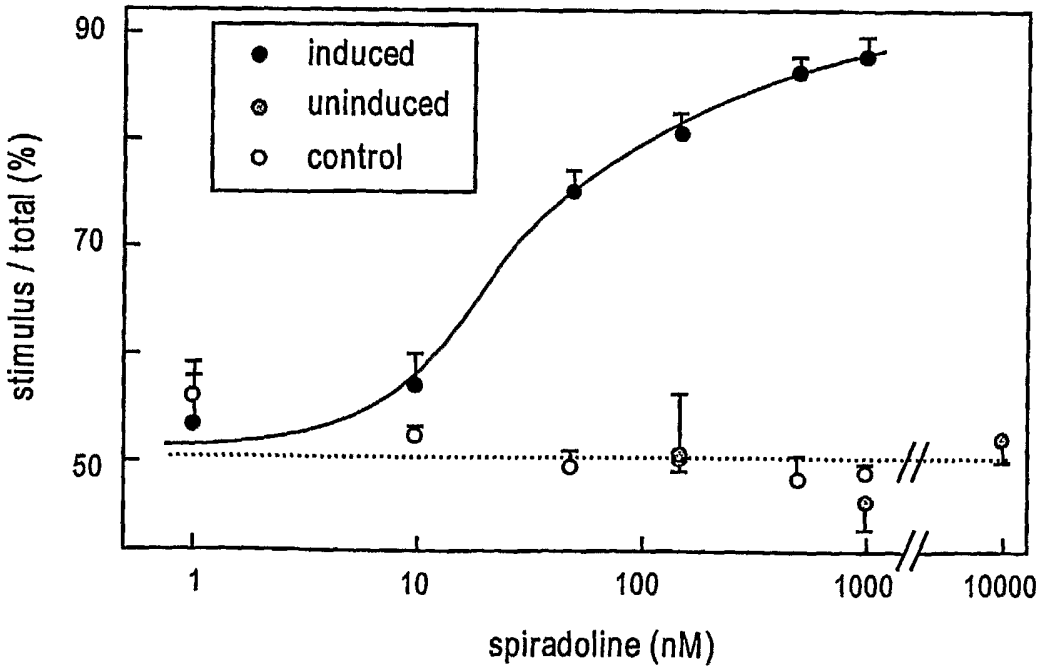


FIG. 7E

hT1R1 SEQ ID NO: 26

ATGCTGCTCTGCACGGCTCGCCTGGTCGGCCTGCAGCTTCTCATTTCCTGCTGCTGGGCC
TTTGCCTGCCATAGCACGGAGTCTTCTCCTGACTTCACCCTCCCCGGAGATTACCTCCTG
GCAGGCCTGTTCCCTCTCCATTCTGGCTGTCTGCAGGTGAGGCACAGACCCGAGGTGACC
CTGTGTGACAGGTCTTGTAGCTTCAATGAGCATGGCTACCACCTCTTCCAGGCTATGCGG
CTTGGGGTTGAGGAGATAAACAACTCCACGGCCCTGCTGCCCAACATCACCCTGGGGTAC
CAGCTGTATGATGTGTGTTCTGACTCTGCCAATGTGTATGCCACGCTGAGAGTGCTCTCC
CTGCCAGGGCAACACCACATAGAGCTCCAAGGAGACCTTCTCCACTATTCCCCTACGGTG
CTGGCAGTGATTGGGCCTGACAGCACCAACCGTGCTGCCACCACAGCCGCCCTGCTGAGC
CCTTTCCTGGTGCCCATGATTAGCTATGCGGCCAGCAGCGAGACGCTCAGCGTGAAGCGG
CAGTATCCCTCTTTCCTGCGCACCATCCCCAATGACAAGTACCAGGTGGAGACCATGGTG
CTGCTGCTGCAGAAGTTCGGGTGGACCTGGATCTCTCTGGTTGGCAGCAGTGACGACTAT
GGGCAGCTAGGGGTGCAGGCACTGGAGAACCAGGCCACTGGTCAGGGGCATCTGCATTGC
TTTCAAGGACATCATGCCCTTCTCTGCCCAGGTGGGCGATGAGAGGATGCAGTGCCTCAT
GCGCCACCTGGCCCAGGCCGGGGCCACCGTCGTGGTTGTTTTTTCCAGCCGGCAGTTGGC
CAGGGTGTTTTTCGAGTCCGTGGTGCTGACCAACCTGACTGGCAAGGTGTGGGTCGCCTC
AGAAGCCTGGGCCCTCTCCAGGCACATCACTGGGGTGCCCGGGATCCAGCGCATTGGGAT
GGTGCTGGGCGTGGCCATCCAGAAGAGGGCTGTCCCTGGCCTGAAGGCGTTTGAAGAAGC
CTATGCCCGGGCAGACAAGAAGGCCCCTAGGCCTTGCCACAAGGGCTCCTGGTGCAGCAG
CAATCAGCTCTGCAGAGAATGCCAAGCTTTCATGGCACACACGATGCCCAAGCTCAAAGC
CTTCTCCATGAGTTCTGCCTACAACGCATACCGGGCTGTGTATGCGGTGGCCCATGGCCT
CCACCAGCTCCTGGGCTGTGCCTCTGGAGCTTGTTCCAGGGGCCGAGTCTACCCCTGGCA
GCTTTTGGAGCAGATCCACAAGGTGCATTTCCTTCTACACAAGGACACTGTGGCGTTTAA
TGACAACAGAGATCCCCTCAGTAGCTATAACATAATTGCCTGGGACTGGAATGGACCCAA
GTGGACCTTCACGGTCCTCGGTTCCTCCACATGGTCTCCAGTTCAGCTAAACATAAATGA
GACCAAAATCCAGTGGCACGGAAAGGACAACCAGGTGCCTAAGTCTGTGTGTTCCAGCGA
CTGTCTTGAAGGGCACCAGCGAGTGGTTACGGGTTTCCATCACTGCTGCTTTGAGTGTGT
GCCCTGTGGGGCTGGGACCTTCCTCAACAAGAGTGACCTCTACAGATGCCAGCCTTGTGG
GAAAGAAGAGTGGGCACCTGAGGGAAGCCAGACCTGCTTCCCGCGCACTGTGGTGTTTTT
GGCTTTGCGTGAGCACACCTCTTGGGTGCTGCTGGCAGCTAACACGCTGCTGCTGCTGCT
GCTGCTTGGGACTGCTGGCCTGTTTGCCTGGCACCTAGACACCCCTGTGGTGAGGTCAGC
AGGGGGCCGCCTGTGCTTTCTTATGCTGGGCTCCCTGGCAGCAGGTAGTGGCAGCCTCTA
TGGCTTCTTTGGGGAACCCACAAGGCCTGCGTGCTTGCTACGCCAGGCCCTCTTTGCCCT
TGGTTTCACCATCTTCCTGTCCTGCCTGACAGTTCGCTCATTCCAACTAATCATCATCTT
CAAGTTTTCCACCAAGGTACCTACATTCTACCACGCCTGGGTCCAAAACCACGGTGCTGG
CCTGTTTGTGATGATCAGCTCAGCGGCCCAGCTGCTTATCTGTCTAACTTGGCTGGTGGT
GTGGACCCCACTGCCTGCTAGGGAATACCAGCGCTTCCCCCATCTGGTGATGCTTGAGTG
CACAGAGACCAACTCCCTGGGCTTCATACTGGCCTTCCTCTACAATGGCCTCCTCTCCAT
CAGTGCCTTTGCCTGCAGCTACCTGGGTAAGGACTTGCCAGAGAACTACAACGAGGCCAA
ATGTGTCACCTTCAGCCTGCTCTTCAACTTCGTGTCCTGGATCGCCTTCTTCACCACGGC
CAGCGTCTACGACGGCAAGTACCTGCCTGCGGCCAACATGATGGCTGGGCTGAGCAGCCT
GAGCAGCGGCTTCGGTGGGTATTTTCTGCCTAAGTGCTACGTGATCCTCTGCCGCCCAGA
CCTCAACAGCACAGAGCACTTCCAGGCCTCCATTCAGGACTACACGAGGCGCTGCGGCTC
CACCTGA

FIG. 8

hT1R1 SEQ ID NO:27

MLICTARLVGLQLLISCCWAFACHSTESSPDFTLPGDYLLAGLFPLHSGCLQVRHRPEVTLCDR
SCSFNEHGYHLFQAMRLGVEEINNSTALLPNITLGYQLYDVCSDSANVYATLRYLSLPGQHHIE
LQGDLLHYSPTVLAVIGPDSTNRAAITAALSPFLVPMISYAASSETLSVKRQYPSFLRTIPNDK
YQVEIMVLLLQKFGWTWISLVGSSDDYGQLGVQALENQATGQGICIAFKDIMPFSAQVGDER
MQCLMRHLAQAGATVVVVFSSRQLARVFFESVVLTNLTGKVWVASEAWALSRHITGVPGIQR
IGMVLGVAIQKRAVPGLKAFEEAYARADKKAPRPCHKGSWCSSNQLCRECQAFMAHTMPKL
KAFSMSSAYNAYRAVYAVAHGLHQLLGCASGACSRGRVYPWQLLEQIHKVHFLLHKDTVAF
NDNRDPLSSYNIIAWDWNGPKWTFTVLGSSTWSPVQLNINETKIQWHGKDNQVPKSVCSSDC
LEGHQRVVTGFHHCCFECVPCGAGTFLNKSDLYRCQPCGKEEWAPEGSQTCFPRTVVFLALRE
HTSWVLLAANTLLLLLLLIGTAGLFAWHLDTPVVRSAGGRLCFLMLGSLAAGSGSLYGFFGEPT
RPACLLRQALFALGFTIFLSCLTVRSFQLIIIFKFSTKVPTFYHAWVQNHGAGLFVMISSAAQLLI
CLTWLVVWTPLPAREYQRFPHLVMLECTEINSLGFILAFLYNGLLSISAFACSYLGKDLPENYN
EAKCVTFSLLFNFVSWIAFFTTASVYDGKYLPAANMMAGLSSLSSGFGGYFLPKCYVILCRPDL
NSTEHFQASIQDYTRRCGST

FIG. 9

ATGGGGCCCA GGGCAAAGAC CATCTGCTCC CTGTTCTTCC TCCTATGGGT CCTGGCTGAG
CCGGCTGAGA ACTCGGACTT CTACCTGCCT GGGGATTACC TCCTGGGTGG CCTCTTCTCC
CTCCATGCCA ACATGAAGGG CATTGTTCAC CTTAACTTCC TGCAGGTGCC CATGTGCAAG
GAGTATGAAG TGAAGGTGAT AGGCTACAAC CTCATGCAGG CCATGCGCTT CGCGGTGGAG
GAGATCAACA ATGACAGCAG CCTGCTGCCT GGTGTGCTGC TGGGCTATGA GATCGTGGAT
GTGTGCTACA TCTCCAACAA TGTCCAGCCG GTGCTCTACT TCCTGGCACA CGAGGACAAC
CTCCTTCCCA TCCAAGAGGA CTACAGTAAC TACATTTCCC GTGTGGTGGC TGTCATTGGC
CCTGACAACT CCGAGTCTGT CATGACTGTG GCCAACTTCC TCTCCCTATT TCTCCTTCCA
CAGATCACCT ACAGCGCCAT CAGCGATGAG CTGCGAGACA AGGTGCGCTT CCCGGCTTTG
CTGCGTACCA CACCCAGCGC CGACCACCAC GTCGAGGCCA TGGTGCAGCT GATGCTGCAC
TTCCGCTGGA ACTGGATCAT TGTGCTGGTG AGCAGCGACA CCTATGGCCG CGACAATGGC
CAGCTGCTTG GCGAGCGCGT GGCCCGGCGC GACATCTGCA TCGCCTTCCA GGAGACGCTG
CCCACACTGC AGCCCAACCA GAACATGACG TCAGAGGAGC GCCAGCGCCT GGTGACCATT
GTGGACAAGC TGCAGCAGAG CACAGCGCGC GTCGTGGTCG TGTTCTCGCC CGACCTGACC
CTGTACCACT TCTTCAATGA GGTGCTGCGC CAGAACTTCA CGGGCGCCGT GTGGATCGCC
TCCGAGTCCT GGGCCATCGA CCCGGTCCTG CACAACCTCA CGGAGCTGGG CCACTTGGGC
ACCTTCCTGG GCATCACCAT CCAGAGCGTG CCCATCCCGG GCTTCAGTGA GTTCCGCGAG
TGGGGCCCAC AGGCTGGGCC GCCAC

FIG. 10

Human T1R2 amino acid sequence--SEQ ID NO: 29

MGPRAKTICSLFFLLWVLAEPAENSDFYLPGDYLLGGLFSLHANMKGIVHLNFLQVPMCKEY
EVKVIGYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQPVLYFLAHEDNLLPI
QEDYSNYISRVVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELRDKVRFPALLRTTPS
ADHHVEAMVQLMLHFRWNWIIVLVSSDTYGRDNGQLLGERVARRDICIAFQETLPTLQPNQN
MTSEERQRLVTIVDKLQQSTARVVVVFSPDLTLYHFFNEVLRQNFTGAVWIASESWAIDPVL
HNLTELGHLGTFLGITIQSVPIPGFSEFREWGPQAGPPPLSRTSQSYTCNQECDNCLNATLS
FNTILRLSGERVVYSVYSAVYAVAHALHSLLGCDKSTCTKRVVYPWQLLEEIWKVNFTLLDH
QIFFDPQGDVALHLEIVQWQDRSQNPFQSVASYYPLQRQLKNIQDISWHTVNNTIPMSMCS
KRCQSGQKKKPVGIHVCCFECIDCLPGTFTLNHTEDEYECQACPNNEWSYQSETSCFKRQLVF
LEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAGGPMCFLMLTLLLVAYMVVPV
YVGPPKVSTCLCRQALFPLCFTICISCIAVRSFQIVCAFKMASRFPRAYSYWVRYQGPYVSM
AFITVLKMVIVVIGMLARPQSHPRTDPDDPKITIVSCNPNYRNSLLFNTSLDLLLSVVGFSF
AYMGKELPTNYNEAKFITLSMTFYFTSSVSLCTFMSAYSGVLTIVDLLVTVLNLLAISLGY
FGPKCYMILFYPERNTPAYFNSMIQGYTMRRD

FIG. 11

hT1R1 SEQ ID NO: 30

ATGCTGGGCCCTGCTGTCCTGGGCCTCAGCCTCTGGGCTCTCCTGCACCCTGGGACGGGG
GCCCCATTGTGCCTGTCACAGCAACTTAGGATGAAGGGGGACTACGTGCTGGGGGGGCTG
TTCCCCCTGGGCGAGGCCGAGGAGGCTGGCCTCCGCAGCCGGACACGGCCCAGCAGCCCT
GTGTGCACCAGGTTCTCCTCAAACGGCCTGCTCTGGGCACTGGCCATGAAAATGGCCGTG
GAGGAGATCAACAACAAGTCGGATCTGCTGCCCGGGCTGCGCCTGGGCTACGACCTCTTT
GATACGTGCTCGGAGCCTGTGGTGGCCATGAAGCCCAGCCTCATGTTCCTGGCCAAGGCA
GGCAGCCGCGACATCGCCGCCTACTGCAACTACACGCAGTACCAGCCCCGTGTGCTGGCT
GTCATCGGGCCCCACTCGTCAGAGCTCGCCATGGTCACCGGCAAGTTCTTCAGCTTCTTC
CTCATGCCCCAGGTCAGCTACGGTGCTAGCATGGAGCTGCTGAGCGCCCGGGAGACCTTC
CCCTCCTTCTTCCGCACCGTGCCCAGCGACCGTGTGCAGCTGACGGCCGCCGCGGAGCTG
CTGCAGGAGTTCGGCTGGAACTGGGTGGCCGCCCTGGGCAGCGACGACGAGTACGGCCGG
CAGGGCCTGAGCATCTTCTCGGCCCTGGCCGCGGCACGCGGCATCTGCATCGCGCACGAG
GGCCTGGTGCCGCTGCCCCGTGCCGATGACTCGCGGCTGGGGAAGGTGCAGGACGTCCTG
CACCAGGTGAACCAGAGCAGCGTGCAGGTGGTGCTGCTGTTCGCCTCCGTGCACGCCGCC
CACGCCCTCTTCAACTACAGCATCAGCAGCAGGCTCTCGCCCAAGGTGTGGGTGGCCAGC
GAGGCCTGGCTGACCTCTGACCTGGTCATGGGGCTGCCCGGCATGGCCCAGATGGGCACG
GTGCTTGGCTTCCTCCAGAGGGGTGCCCAGCTGCACGAGTTCCCCCAGTACGTGAAGACG
CACCTGGCCCTGGCCACCGACCCGGCCTTCTGCTCTGCCCTGGGCGAGAGGGAGCAGGGT
CTGGAGGAGGACGTGGTGGGCCAGCGCTGCCCGCAGTGTGACTGCATCACGCTGCAGAAC
GTGAGCGCAGGGCTAAATCACCACCAGACGTTCTCTGTCTACGCAGCTGTGTATAGCGTG
GCCCAGGCCCTGCACAACACTCTTCAGTGCAACGCCTCAGGCTGCCCCGCGCAGGACCCC
GTGAAGCCCTGGCAGCTCCTGGAGAACATGTACAACCTGACCTTCCACGTGGGCGGGCTG
CCGCTGCGGTTCGACAGCAGCGGAAACGTGGACATGGAGTACGACCTGAAGCTGTGGGTG
TGGCAGGGCTCAGTGCCCAGGCTCCACGACGTGGGCAGGTTCAACGGCAGCCTCAGGACA
GAGCGCCTGAAGATCCGCTGGCACACGTCTGACAACCAGAAGCCCGTGTCCCGGTGCTCG
CGGCAGTGCCAGGAGGGCCAGGTGCGCCGGGTCAAGGGGTTCCACTCCTGCTGCTACGAC
TGTGTGGACTGCGAGGCGGGCAGCTACCGGCAAAACCCAGACGACATCGCCTGCACCTTT
TGTGGCCAGGATGAGTGGTCCCCGGAGCGAAGCACACGCTGCTTCCGCCGCAGGTCTCGG
TTCCTGGCATGGGGCGAGCCGGCTGTGCTGCTGCTGCTCCTGCTGCTGAGCCTGGCGCTG
GGCCTTGTGCTGGCTGCTTTGGGGCTGTTCGTTCACCATCGGGACAGCCCACTGGTTCAG
GCCTCGGGGGGGCCCCTGGCCTGCTTTGGCCTGGTGTGCCTGGGCCTGGTCTGCCTCAGC
GTCCTCCTGTTCCCTGGCCAGCCCAGCCCTGCCCGATGCCTGGCCCAGCAGCCCTTGTCC
CACCTCCCGCTCACGGGCTGCCTGAGCACACTCTTCCTGCAGGCGGCCGAGATCTTCGTG
GAGTCAGAACTGCCTCTGAGCTGGGCAGACCGGCTGAGTGGCTGCCTGCGGGGGCCCTGG
GCCTGGCTGGTGGTGCTGCTGGCCATGCTGGTGGAGGTCGCACTGTGCACCTGGTACCTG
GTGGCCTTCCCGCCGGAGGTGGTGACGGACTGGCACATGCTGCCCACGGAGGCGCTGGTG
CACTGCCGCACACGCTCCTGGGTCAGCTTCGGCCTAGCGCACGCCACCAATGCCACGCTG
GCCTTTCTCTGCTTCCTGGGCACTTTCCTGGTGCGGAGCCAGCCGGGCTGCTACAACCGT
GCCCGTGGCCTCACCTTTGCCATGCTGGCCTACTTCATCACCTGGGTCTCCTTTGTGCCC
CTCCTGGCCAATGTGCAGGTGGTCCTCAGGCCCGCCGTGCAGATGGGCGCCCTCCTGCTC
TGTGTCCTGGGCATCCTGGCTGCCTTCCACCTGCCCAGGTGTTACCTGCTCATGCGGCAG
CCAGGGCTCAACACCCCCGAGTTCTTCCTGGGAGGGGGCCCTGGGGATGCCCAAGGCCAG
AATGACGGGAACACAGGAAATCAGGGGAAACATGAGTGA

FIG. 12

hT1R3 SEQ ID NO: 31

MLGPAVLGLSLWALLHPGTGAPLCLSQQLRMKGDYVLGGLFPLGEAEEAGLRSRTRPSSPVCT
RFSSNGLLWALAMKMAVEEINNKSDLLPGLRLGYDLFDTCSEPVVAMKPSLMFLAKAGSRDI
AAYCNYTQYQPRVLAVIGPHSSELAMVTGKFFSFFLMPPHYGASMELLSARETFPSFFRTVPSDR
VQLTAAAELLQEFGWNWVAALGSDDEYGRQGLSIFSALAAARGICIAHEGLVPLPRADDSRLG

KVQDVLHQVNQSSVQVVLLFASVHAAHALFNYSISSRLSPKVWVASEAWLTSDLVMGLPGM
AQMGTVLGFLQRGAQLHEFPQYVKTHLALATDPAFCSALGEREQGLEEDVVGQRCPQCDCIT
LQNVSAGLNHHQTFSVYAAVYSVAQALHNTLQCNASGCPAQDPVKPWQLLENMYNLTFHVG
GLPLRFDSSGNVDMEYDLKLWVWQGSVPRLHDVGRFNGSLRTERLKIRWHTSDNQKPVSRCS
RQCQEGQVRRVKGFHSCCYDCVDCEAGSYRQNPDDIACTFGQDEWSPERSTRCFRRRSRFLA
WGEPAVLLLLLLLSLALGLVLAALGLFVHHRDSPLVQASGGPLACFGLVCLGLVCLSVLLFPG
QPSPARCLAQQPLSHLPLTGCLSTLFLQAAEIFVESELPLSWADRLGCLRGPWAWLVVLLAML
VEVALCTWYLVAFPPEVVTDWHMLPTEALVHCRTRSWVSFGLAHATNATLAFLCFLGTFLVR
SQPGCYNRARGLTFAMLAYFITWVSFVPLLANVQVVLRPAVQMGALLLCVLGILAAFHLPRCY
LLMRQPGLNTPEFFLGGGPGDAQGQNDGNTGNQGKHE

FIG. 13