Opposing chemosensory functions of closely related gustatory receptors

Ji-Eun Ahn and Hubert Amrein

Department of Cell Biology and Genetics

School of Medicine

Texas A&M University

Bryan TX, 77845

Correspondence: amrein@tamu.edu

ABSTRACT

Most animals possess functionally distinct population of taste cells, expressing receptors that are tuned to compounds of different valence. This organizational feature allows for discrimination between chemicals associated with different taste modalities and facilitates sensing of foods contaminated with toxic chemicals. In the fruit fly *D. melanogaster*, primary sensory neurons express taste receptors that are tuned to distinct chemicals, thereby activating neural ensembles that elicit either feeding or avoidance behavior. Members of a family of ligand gated receptor channels, the Gustatory receptors (Gr), play a central role in these behaviors. In general, closely related, evolutionarily conserved Gr proteins are co-expressed in the same type of taste neurons, tuned to chemically related compounds and therefore triggering the same behavioral response. Here, we report that members of the Gr28 subfamily are expressed in largely non-overlapping sets of taste neurons in *Drosophila* larvae, detect chemicals of different valence and trigger opposing feeding behaviors. We determined the intrinsic properties of *Gr28* neurons by expressing the mammalian Vanilloid Receptor (VR1), which is activated by capsaicin, a chemical to which wild type *Drosophila* larvae do not respond. When VR1 is expressed in *Gr28a* neurons, larvae become attracted to capsaicin, whereas expression of VR1 in *Gr28bc* neurons triggers avoidance to capsaicin. Thus, the *Gr28* proteins, which have been evolutionarily conserved over the last 65 million years in insects, represent the first taste receptor subfamily in which specific members mediate behavior with opposite valence. We also identified denatonium benzoate, a synthetic bitter compound that shares structural similarities with natural bitter chemicals, as a ligand for a receptor complex containing a Gr28bc or Gr28ba receptor subunit. Alphafold structure prediction, combined with the limited sequence conservation in the putative binding pockets of various Gr28 proteins, creates a theoretical framework for targeted *in vivo* structure function studies to precisely map residues critical for ligand recognition.

INTRODUCTION

Meaningful animal behavior is established through cooperative engagement of multiple sensory systems. In many insects, the chemosensory system plays a central role in such integration processes. The fruit fly *Drosophila melanogaster* has served as the primary insect model system for elucidating the molecular basis and neural circuitry of both olfaction and taste, by virtue of the vast genetic resources, amenability to both neurophysiological recording and live imaging, and simple yet powerful behavioral assays, allowing investigators to link genes to chemosensory behavior and neural activity (Montell, 2021).

The gustatory system in *Drosophila* is characterized by several insect specific features with regard to anatomy and the molecular nature of taste receptors. For example, taste cells are primary sensory neurons, with dendritic projections that express taste receptors, while long axons project that convey taste information directly to the brain. In adult flies, these neurons, referred to as Gustatory Receptor Neurons (GRNs) are distributed across several appendages, such as labial palps, legs and presumably the antennae. Additionally, some GRNs reside internally, arranged in cell clusters along the pharynx (Joseph and Carlson, 2015)(Amrein, 2016)(Scott, 2018). Similarly, *Drosophila* larvae have numerous structures located both on the head surface as well as internally along the larval pharynx, that assess chemical compounds prior and during ingestion, respectively (Kwon et al., 2011)(Apostolopoulou et al., 2015)(Rist and Thum, 2017). Like most insects, *Drosophila* employs taste receptors encoded by two major gene families, the *Gustatory receptor* (*Gr*) and the *Ionotropic Receptor* (*IR*) genes, to sense all chemicals, such as appetitive food compounds, noxious and toxic chemicals as well as pheromones. Both Gr and IR based receptors are thought of form complexes composed of several different subunits, partial composition of which is known for only a few Gr-based taste receptors for sugars and bitt er compounds (Kwon et al., 2007)(Jiao et al., 2008)(Fujii et al., 2015)(Shim et al., 2015)(Gonzales et al., unpublished), as well as gaseous carbon dioxide (Jones et al., 2007) and even fewer IR-based fatty acid and carboxylic acid receptors (Ahn et al., 2017)(Tauber et al., 2017)(Chen and Amrein, 2017). Interestingly, at least some GRNs express members of

both families, although no evidence for receptor complexes consisting of both IR and Gr

subunits has been reported to date.

The *Gr* genes represent the largest taste receptor gene family in insects. In *D.*

melanogaster, it comprises 60 genes predicted to encode 68 proteins, expression of

which has been characterized (Kwon et al., 2011)(Weiss et al., 2011)(Ling et al.,

2014)(Choi et al., 2016)(Rist and Thum, 2017). Several *Gr* genes have been

functionally characterized in adult flies using genetic mutations, combined with either

electrophysiological recordings, Ca^{2+} imaging studies and behavioral analyses

(reviewed by Montell, 2021) but only a few have been studied in larvae (Mishra et al.,

2013)(Apostolopoulou et al., 2016)(Choi et al., 2016)(Mishra et al., 2018)(Choi et al.,

2020). The *Gr28* gene subfamily is of particular interest for a number of reasons: First, it

is one of the most conserved *Gr* subfamily, homologs of which can be found across all

insect families and even more distant arthropods (Eyun et al., 2017)(Suzuki et al.,

2018)(Fujii et al., 2023). Second, the *Gr28* genes are expressed not only in the

gustatory system, but in many other organs, especially the central nervous system

(CNS) and non-chemosensory neurons of the peripheral nervous system (PNS),

suggesting that they have functions beyond gustation and are important to sense

chemical signals unrelated to food (Thorne and Amrein, 2008). Notably, evidence for

such roles has been reported before any direct link to gustatory perception was

discovered. Ni and colleagues showed that *Gr28bd* is essential for high temperature

avoidance in flies (Ni et al., 2013), while Xiang and collaborators found that *Gr28* mutant

larvae were deficient in UV light avoidance (Xiang et al., 2010). Third, the only gustatory

function for any *Gr28* gene in larvae thus far is sensing of ribonucleosides and RNA in

larvae (Mishra et al., 2018), which was recently established as a novel appetitive taste

quality common to a broad range of dipteran insects (Fujii et al., 2023).

Here, we present a functional characterization of the *Gr28* genes and the

respective GRNs in *Drosophila* larvae. Four of the six *Gr28* genes (*Gr28a, Gr28ba,*

Gr28bc and *Gr28be*) are expressed in the larval taste system, subdivided into two,

functionally distinct neuronal ensembles. The first such ensemble is defined by

expression of *Gr28bc* and comprises four neurons, two of which also express *Gr28ba,*

Gr28bc, Gr28be and the bitter core receptor gene *Gr66a*, while the other two neurons

express only *Gr28bc*, *Gr28a* and *Gr66a*. The second ensemble is characterized by 12
GRNs that express *Gr28a*, including the pair of GRNs expressing the *Gr28b* genes.
When the mammalian Vanilloid Receptor 1 (VR1) was expressed under the control of
specific GAL4 drivers, we found that *Gr28a* and *Gr28bc* neurons mediate opposing
taste behavior in the presence of capsaicin, the ligand for VR1. Specifically, *Gr28a:VR1*
larvae show strong attraction for capsaicin, while *Gr28bc:VR1* larvae show strong
avoidance of capsaicin. Furthermore, inactivation experiments reveal that the *Gr28bc*
GRNs are necessary to sense bitter compounds, specifically denatonium, quinine,
lobeline, and caffeine. However, *Gr28* mutant larvae fail to avoid only denatonium, but
none of the other bitter compounds, a phenotype rescued by expression of *Gr28bc* or
Gr28ba. Thus, to our knowledge, the related *Gr28* genes represent the first subfamily
where members mediate functionally opposing taste behaviors.
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125   **RESULTS**
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127   **Expression of the *Gr28* genes in the larval taste organs**
128   The peripheral chemosensory system of the larvae is subdivided into bilaterally
symmetrical, 'external' and 'internal' taste organs (Stocker, 2008). The three external
organs reside near the tip of the head and organized as paired ganglia, the Dorsal,
Terminal and Ventral Organ Ganglia (DOGs, TOGs and VOGs) that house the GRN cell
bodies, each neuron projecting a dendrite to the sensory organ structures (DO, TO and
VO) at the head surface, while carrying information via their axons to the
subesophageal zone (SEZ) in the brain (Figure 1A). The DOG harbors 21 olfactory
neurons and 18 presumptive taste neurons. For clarity, numbers below refer to neurons
on one side of the bilaterally symmetrical structures of all organs, thus the total neuron
number in a larva is double that number. The presumptive GRNs located in the DOG fall
into two distinct groups, based on their dendritic projections: 11 presumptive GRNs, four
of which were shown to express *Gr* genes (Apostolopoulou et al., 2015), extend
dendritic projections to the base of the DO, while 7 neurons project dendrites to the TO
(the dorsolateral group, Figure 1A)(Kwon et al., 2011). The TOG contains 30 neurons,

all sending dendrites to the TO (the distal group). The internal taste structures, referred

to as the dorsal/ventral pharyngeal sense organ (DPS/VPS, 33 neurons), and the

posterior pharyngeal sense organs (PPS, 6 neurons) are located along the pharynx and

sense chemicals as they pass towards the digestive system. We note that not all these

neurons are confirmed GRNs, either by function or expression of *Gr* or *IR* genes, albeit

based on their location and anatomy, most are thought to be GRNs (Stewart et al.,

2015)(Rist and Thum, 2017)(Sánchez-Alcañiz et al., 2018).

Our initial expression analysis revealed that four of the six *Gr28* genes (*Gr28a*,

Gr28ba, *Gr28bc* and *Gr28be*) are expressed in larval taste organs, in addition to cells in

the gut, the brain and non-chemosensory cells of the larvae (Mishra et al., 2018). To

further delineate the putative chemosensory roles of these genes, we performed a more

detailed co-expression analysis between *Gr28* genes and with respect to the bitter

receptor gene *Gr66a*, using the bimodal expression systems *GAL4/UAS* to label *Gr28*

expressing neurons and *LexA/lexAop* to mark *Gr66a* neurons (Figure 1B and 1C; note

that the neuron numbers below refer to the number present in one of each paired

ganglion). In the TOG, we found expression of all four *Gr28* genes, along with that

Gr66a, which was expressed in 3 or 4 neurons (one neuron exhibits often stronger

expression of *Gr66a* than the two or three remaining neurons). This number slightly

smaller than the 6 neurons reported using a distinct *Gr66a-GAL4* driver (Kwon et al.,

2011). *Gr28ba*, *Gr28bc* and *Gr28be* are co-expressed in a single neuron with *Gr66a*

(Figure 1B). In contrast, *Gr28a* is expressed in a distinct TOG neuron than *Gr66a*

(Figure 1B), and by extension, in a different neuron than the co-expressed *Gr28b*

genes, which we independently confirmed using a *Gr28bc-QF* driver (Figure 1-figure

supplement 1). In the DOG, we find only a single *Gr28a* neuron, while none of the

Gr28b genes, or *Gr66a*, is expressed there (Figure 1B). Expression in the internal

sensory organs was similarly complex. *Gr66a* was found in one neuron in the DPS/VPS,

co-expressed with *Gr28bc* as well as *Gr28a* (Figure 1C). None of the *Gr28b* genes is

expressed in the PPS, but two neurons express *Gr28a*, one of which also expresses

Gr66a (Figure 1C). In summary, the internal sensory organs can be subdivided in three

distinct groups: *Gr66a/Gr28b/Gr28a* positive neurons, *Gr66a/Gr28a* positive neurons

and *Gr28a^only* neurons, which contrasts expression in the external sensory organs
where *Gr28a* and the *Gr28b* genes are mutually exclusive.

Subsets of *Gr28* neurons mediate opposing feeding behaviors

We previously showed that at least one of the six Gr28 genes is necessary for
feeding attraction to RNA, ribonucleosides and ribose using a well-established two
choice feeding assay (Mishra et al., 2018). Specifically, larvae homozygous for a *Gr28*
null allele, a deletion of the entire *Gr28a* gene and most of the coding region of all
Gr28b genes (*ΔGr28*), lose their ability to sense these compounds, a phenotype that is
restored when single *UAS-Gr28* genes are expressed in *Gr28a* neurons using *Gr28a-*
GAL4. This observation and the largely non-overlapping expression of *Gr28a* and the
Gr28b genes suggests that respective neurons represent functionally distinct entities.
To investigate this possibility, we took advantage of the mammalian Vanilloid Receptor
1 (VR1), a TRP channel that is activated by capsaicin (Caterina et al., 1997). *Drosophila*
have no *VR1* like-gene in their genome and do not respond to capsaicin behaviorally,
but flies are attracted to this chemical when a modified *VR1* gene (*VR1E600K*) is
expressed in sweet taste neurons (Marella et al., 2006). Thus, we expressed
VR1E600K (henceforth referred to *UAS-VR1*) under the control of the four *Gr28-GAL4*
drivers (*Gr28a-GAL4*, *Gr28ba-GAL4*, *Gr28bc-GAL4* and *Gr28be-GAL4*) in larvae and
tested their response to capsaicin using the two-choice preference assay. Additionally,
we expressed *UAS-VR1* in bitter neurons as well as sweet neurons using respective
GAL4 drivers (*Gr66a-GAL4* and *Gr43a^GAL4*) (Scott et al., 2001) (Miyamoto et al., 2012).
Consistent with the observation in adults (Marella et al., 2006), w^{1118} control larvae and
larvae carrying *UAS-VR1* or *Gr-GAL4* genes alone were unresponsive to 0.1 mM or 0.5
mM capsaicin (Figure 2A). However, larvae expressing *UAS-VR1* under the control of
Gr28a-GAL4 or *Gr43a-GAL4* showed strong appetitive responses to both capsaicin
concentrations (Figure 2A). In contrast, larvae expressing *UAS-VR1* under the control of
Gr28bc-GAL4 or *Gr66a-GAL4* showed robust avoidance behavior to both
concentrations of capsaicin. Lastly, expression of *UAS-VR1* with the *Gr28ba-GAL4* or
Gr28be-GAL4 driver, which is co-expressed in a single TO neuron with *Gr28bc* (Figure
1B), did cause neither attraction to nor avoidance of capsaicin.

Expression difference between *Gr28bc* and *Gr28ba/be* is a single neuron in the

DPS/VPS (Figure 1C), a neuron required to mediate avoidance of capsaicin in *Gr28bc-*

GAL4, UAS-VR1 larvae. Even though this GRN also expresses *Gr28a*, it appears

unlikely that it is necessary to mediate appetitive behavior as well. Indeed, we could

further restrict the necessary set of appetitive neurons to four *Gr28a* positive neurons

(*Gr28a^{only}* GRNs), as suppression of VR1 expression in *Gr66a* GRNs (one being the

Gr28bc expressing GRN in the DPS/VPS) did not affect capsaicin preference (Figure

2B). We further note that activation of the two *Gr28bc* neurons by capsaicin drives

repulsion to the same degree as when all seven *Gr66a* expressing neurons are

activated. Taken together, this analysis indicates that *Gr28a-GAL4* is expressed in

appetitive inducing neurons, while *Gr28bc-GAL4* neurons mediate avoidance behavior.

Wild type larvae, like adult flies, avoid bitter compounds (Apostolopoulou et al.,

2015) (Apostolopoulou et al., 2016) (Choi et al., 2016) (van Giesen et al., 2016) (Choi et

al., 2020). If *Gr28bc* neurons are indeed central to the avoidance of these chemicals in

larvae, we expect that eliminating their function would result in loss of larval avoidance

behavior to bitter chemicals. Thus, we inactivated neuronal subsets using the potassium

inward rectifying channel Kir2.1 (Baines et al., 2001) (Paradis et al., 2001). In contrast

to larvae with an intact taste neuron repertoire, larvae in which two *Gr28bc* neurons

were inactivated no longer avoided any of these bitter compounds (Figure 3). A more

subtle phenotype was observed when the single *Gr28be* neurons were inactivated,

eliminating lobeline and caffeine avoidance, but leaving denatonium and quinine

repulsion intact, a finding consistent with previous studies (Choi et al., 2020). These

data suggest that two pairs of neurons, one in the TO and one in the D/VPS are

necessary and sufficient for avoidance of all four bitter tasting chemicals.

Gr28bc and Gr28ba are subunits of a taste receptor complex for denatonium

We examined whether any of the Gr28 proteins is part of a taste receptor

complex detecting these bitter chemicals (Figure 4). Surprisingly, only avoidance of

denatonium was affected in larvae without any functional *Gr28* gene (*ΔGr28*), while

responses to quinine, lobeline or caffeine was not significantly affected. Moreover,

avoidance to caffeine increased significantly (Figure 4A). We next tested which Gr28

protein is necessary for denatonium avoidance and expressed individual *Gr28* genes
under the control of the *Gr28bc-GAL4* driver. Only when either *Gr28ba* or *Gr28bc* was
expressed in these neurons, denatonium avoidance was fully recovered, whereas
expression of *Gr28bb*, *Gr28bd*, *Gr28be* or *Gr28a* failed to do so (Figure 4B). This
observation indicates that despite the high level of similarity between these receptors,
recognition of denatonium is dependent on specific Gr28b subunits, features that are
present in Gr28ba and Gr28bc, but not any of the other Gr28 proteins.

Previous work had established that *Gr66a* is required for caffeine avoidance, in
both larvae and adult flies (Moon et al., 2006)(Lee et al., 2009)(Apostolopoulou et al.,
2016). We confirmed this, as *Gr66a* mutant larvae show little if any avoidance of
caffeine, while avoidance of lobeline was not affected (Figure 4-figure supplement 1).
Somewhat surprisingly, avoidance of denatonium and quinine increased significantly.
This is likely a result of the heteromeric composition of bitter taste receptor complexes,
whereby absence of Gr66a allows Grs that tuned to denatonium (such as Gr28bc or
Gr28ba) and quinine be incorporated into multimeric receptor complexes.

Finally, we investigated neuronal responses in larvae expressing the Ca^{2+}
indicator GCaMP6m in *Gr28bc-GAL4* GRNs (Figure 5). We developed a whole larvae
imaging preparation, whereby larvae were placed in an "imaging chamber" to minimize
head movements (Figure 5A), and visualized neural activity in real time (Chen et al.,
2013) upon exposure to the four bitter compounds, as well as sucrose, ribose and
fructose (Figure 5B to 5D). All bitter compounds elicited rapid Ca^{2+} increases in *Gr28bc*
GRNs in the TO, while none of the sugars did (Figure 5C and 5D). When neural activity
was recorded in *ΔGr28* homozygous mutant larvae (Figure 5E), cellular responses to
denatonium and quinine were severely reduced, while responses to both caffeine and
lobeline were not affected. Consistent with our behavioral analysis (Figure 4B), re-
expression of either *Gr28ba* or *Gr28bc*, but not *Gr28bb*, *Gr28bd, Gr28be* or *Gr28a*
rescued cellular response to denatonium, but not to quinine (Figure 5E). Together,
these experiments identified *Gr28bc* and *Gr28ba* as redundant subunit of a denatonium
receptor complex, a complex that does not require *Gr66a* or any of the other *Gr28b*
subunits.

DISCUSSION

The Gr28 receptors comprise one of the few Gr subfamilies conserved across
diverse insect species (Engsontia and Satasook, 2021)(Agnihotri et al., 2016)(Yu et al.,
2023). Yet, they were the least characterized when compared to other conserved
subfamilies, such as the sugar receptors (Gr5a, Gr61a and Gr64a-f), the carbon dioxide
receptors Gr21a and Gr63a or the bitter taste receptors. The only ligands associated
with the Gr28 proteins were ribonucleosides and RNA, which are appetitive nutrients for
larvae and are mediated by *Gr28a* neurons (Mishra et al., 2018). Indeed, RNA has been
found to be an appetitive taste ligand across many dipteran insects, including
mosquitoes, and we showed that Gr28 homologs of both *A. aegypti* and *A. gambiae* can
rescue the preference for RNA and ribose when expressed in *Gr28a* neurons of *ΔGr28*
mutant larvae (Fujii et al., 2023). Here, we established a precedent for members of the
same subfamily for mediating both appetitive and repulsive behavior and being
expressed in largely non-overlapping sets of GRNs. In flies, members of other
conserved Gr subfamilies are either precisely (*Gr21a* and *Gr63a*)(Jones et al.,
2007)(Kwon et al., 2007), or largely (sugar *Gr* genes) (Fujii et al., 2015) co-expressed in
one type of GRNs, forming multimeric receptors that mediate a single type of behavior.
Our expression analysis in larvae is consistent with earlier reports, despite some
variation in number of neurons expressing *Gr66a* and *Gr28b* (Kwon et al., 2011)(Choi et
al., 2016), which is likely due to the use of different *GAL4* drivers and/or variability in
expression. Importantly, all *Gr28b* genes are co-expressed with the bitter marker *Gr66a*
(Figure1), while *Gr28a* is found in a largely, but not entirely distinct set of GRNs. Based
on our VR1-capsaicin experiments, the GRNs sharing expression of both *Gr28a* and
Gr66a (and by extension some *Gr28b* genes) are critical for avoidance, and not
required for appetitive behavior (Figure 2).

Distinct functions of small set of GRNs expressing specific Gr28 subunits

A key finding presented of this study is the observation that $Gr28a^{only}$ and $Gr28bc$
neurons dictate distinct behavioral programs, the former representing an ensemble of
neurons that instruct a larvae to "go towards" chemical source and consume it, while
the latter do the opposite (Figure 2). The set of "go-away" GRNs co-expressing $Gr28bc$
and $Gr66a$ is remarkably small, consisting of only two pairs, one in the TO and the other
in the DPS/VPS. It seems likely that this is the smallest, minimal subset of neurons
sufficient for avoidance, as expression of V1R in only the TO pair (under the control of
either $Gr28ba$-$GAL4$ or $Gr28be$-$GAL4$) has no behavioral effect when challenged with
capsaicin. The "go-to" neurons are characterized by expression of $Gr28a$ and represent
a slightly larger set of four GRN pairs ($Gr28a^{only}$ only GRNs). Thus, we propose that the
minimal requirement to induce "go-to" and "go-away" behavior is defined by distinct sets
of GRNs, and that each appears to be composed of neurons located in both external as
well as the internal taste organs (Figure 6).

Co-expression of a subunit for the bitter taste receptors Gr28bc/Gr28ba and
Gr28a, a receptor for RNA, a nutrient essential for larval growth (Mishra et al., 2018) in
bitter taste neurons raises interesting questions about the function of Gr28a. As these
neurons are necessary for repulsion, we propose that Gr28a might serve as a subunit
along with other Grs (possibly Gr28bc and/or Gr66a) in heteromeric bitter taste receptor
complexes, detecting yet other bitter compounds. In "go-to", $Gr28a^{only}$ GRNs, Gr28a is
likely to form a homomultimeric receptor, since its expression in fructose sensing GRNs
confers RNA recognition to these neurons, both in cellular and behavioral assays
(Mishra et al., 2018). We note that the sweet taste receptor Gr5a, a subunit of a
multimeric receptor in sweet taste GRNs in the labial palps of flies is also expressed in
non-sweet neurons of unknown function (Fujii et al., 2015). Finally, while Gr28bc was
shown to be required for detecting and avoiding 5% saponin in flies (Sang et al., 2019),
larvae showed no behavioral response to 0.1% of saponin (Choi et al., 2016)(Choi et
al., 2020), a finding we independently confirmed using both concentration of saponin
(data not shown).

Mapping ligand specificity for denatonium

Only Gr28ba and Gr28bc can rescue responses to denatonium when expressed
in *Gr28bc* GRNs of *ΔGr28* mutant larvae. Thus, sequence comparison between the
unique N-terminal halves of the Gr28 proteins might provide insights as to possible
residues important for denatonium recognition/binding, especially residues located in
extracellular loops (EL) and transmembrane (TM) regions. When interrogating TM
domains 1 to 4 and EL1 and EL2, only seven residues are identical between Gr28ba
and Gr28bc (Table 1, Figure 7). Reducing the stringency requirement by allowing one of
the remaining receptors to share the same residue, nine additional sites are identified.
Interestingly, five of these sixteen amino acid residues map to four of the nine most
probable binding pocket as predicted by Prankweb (https://prankweb.cz/), with three
residues part of the pocket with the highest probability score (Table 2, Figure 8). Thus,
targeted substitutions of single amino acids residing in predicted ligand binding pockets
in other Gr28 proteins and testing such "chimera" provides a theoretical framework for
practical experiments using either behavior analysis or Ca2+ imaging to precisely define
the specific requirement for denatonium specificity. Additional complementary
approaches can be taken to identify the critical residues in the predicted binding pockets
of other members of this family once their ligands have been identified. Thus, the Gr28
proteins might serve as model to experimentally validate the predictions created by
these powerful algorithms.

MATERIALS AND METHODS

KEY RESOURCES TABLE

Reagent type	Designation	Source or Reference	Identifiers
Antibodies			
Rabbit polyclonal anti-GFP	Anti-GFP	Thermo Fisher Scientific	A6455; RRID: AB_221570
Rat monoclonal anti-mCD8	Anti-mCD8	Thermo Fisher Scientific	MCD0800; RRID: AB_10392843

Alexa 488 conjugated goat anti-rabbit	Green	Thermo Fisher Scientific	A11070; RRID: AB_2534114
Cy3-conjugated goat anti-rat	Magenta	Jackson Immunoresearch Laboratories Inc.	112-165-072; RRID: AB_2338248
Normal goat serum	Blocking of non-specific antibody binding in tissue staining	SouthernBiotech	0060-01
Chemical compounds			
Caffeine	Caffeine	Millipore-Sigma	C0750
Capsaicin	Capsaicin	Millipore-Sigma	M2028
Denatonium benzoate	Denatonium benzoate	Millipore-Sigma	D5765
Lobeline hydrochloride	Lobeline hydrochloride	Millipore-Sigma	141879
D-(-)-ribose	D-(-)-ribose	Millipore-Sigma	R7500
Quinine hydrochloride dihydrate	Quinine hydrochloride dihydrate	Millipore-Sigma	Q1125
Fructose	Fructose	Spectrum chemical	F1092
Agarose	Agarose	Apexbio	20-102
Sucrose	Sucrose	Macron fine chemicals	8360-06
Charcoal	Charcoal	J.T. Baker	1560-01
Experimental Models: Organisms/Strains			
D. melanogaster: w1118	Wild-type control	Bloomington *Drosophila* Stock Center	BDSC: 3605; FlyBase: FBst0003605
D. melanogaster: w*; P{Gr28a-GAL4.T}SF36S	*Gr28a-GAL4*	Thorne and Amrein, 2008	FlyBase: FBtp0056017
D. melanogaster: w*; P{Gr28a-GAL4.T}SF36B1	*Gr28a-GAL4*	Thorne and Amrein, 2008	FlyBase: FBtp0056017
D. melanogaster: w*; P{Gr28b.a-GAL4}NT42aC51a	*Gr28ba-GAL4*	Thorne and Amrein, 2008	FlyBase: FBtp0054526
D. melanogaster: w*; P{Gr28b.c-GAL4}NT21B1	*Gr28bc-GAL4*	Thorne and Amrein, 2008	FlyBase: FBtp0054528
D. melanogaster: w*; P{Gr28b.e-GAL4.4.245}Gr28a3All	*Gr28be-GAL4*	Scott et al., 2001	FlyBase: FBtp0014672
D. melanogaster: w*; Df(2L)ΔGr28	*ΔGr28/ΔGr28*	Mishra et al., 2018	FlyBase: FBab0049019

D. melanogaster: w*; P{Gr66C1-GAL4.3.153}	Gr66a-GAL4	Scott et al., 2001	FlyBase: FBtp0014661
D.melanogaster: w*; P{UAS-Gr28a.G}attP2	UAS-Gr28a	Ni et al., 2013	Flybase: FBal0344045
D.melanogaster: w*; P{UAS-Gr28b.A}attP2	UAS-Gr28ba	Ni et al., 2013	Flybase: FBal0291410
D.melanogaster: w*; P{UAS-Gr28b.B}attP2	UAS-Gr28bb	Ni et al., 2013	Flybase: FBal0291412
D.melanogaster: w*; P{UAS-Gr28b.C}attP2	UAS-Gr28bc	Ni et al., 2013	Flybase: FBal0291411
D.melanogaster: w*; P{UAS-Gr28b.D}attP2	UAS-Gr28bd	Ni et al., 2013	Flybase: FBal0291409
D.melanogaster: w*; P{UAS-Gr28b.E}attP2	UAS-Gr28be	Ni et al., 2013	Flybase: FBal0291408
D.melanogaster: w^{1118};Ti{GAL4}Gr43a^{GAL4}	Gr43a^{GAL4}	Miyamoto et al., 2012	BDSC:93447; Flybase: FBst0093447
D.melanogaster: w^{1118};P{UAS-VR1E600K}	UAS-VR1E600K	Marella et al., 2006	Flybase: FBal0215202
D. melanogaster: w*; P{lexAop-rCD2-GFP}	lexAop-rCD2:GFP	Lai and Lee, 2006	Flybase: FBst0066687
D. melanogaster: y^{1}w*;P{10XUAS-IVS-mCD8::RFP}su(Hw)attP8	UAS-mCD8:RFP	Bloomington Drosophila Stock Center	BDSC: 32220; Flybase: FBti0131987
D. melanogaster: w^{1118}; P{20XUAS-IVS-GCaMP6m}attP40	UAS-GCaMP6m	Bloomington Drosophila Stock Center	BDSC: 42748; Flybase: FBti0151346
D. melanogaster: w*; P{UAS-Hsap\KCNJ2.EGFP}1	UAS-Kir2.1-GFP	Baines et al., 2001; Paradis et al., 2001	Flybase: FBst0006596
D. melanogaster: w^{1118}; P{Gr66a-lexA.S}2;TM2/TM6B	Gr66a-LexA	Thistle et al., 2012	BDSC: 93024 Flybase: FBst0093024
Sequence-based reagents			
Gr28bc_F	5′-AATCTAGGTACCCCGGCTGCTCGTCTCCCTGGATGT-3′	This paper	PCR primers
Gr28bc_R	5′-CGTCAAACTAGTGACCGCTTCGTTTGAGCTTCAACC-3′	This paper	PCR primers
Recombinant DNA reagents			

LexA vector CMC105	Insect expression vector	This paper Larsson et al., 2004	Plasmids
Software and Algorithms			
NIS-Elements	N/A	Nikon	N/A
Prism software 9.5.1	Prism software 9.5.1	GraphPad Software	N/A
Adobe photoshop 2022	Adobe photoshop 2022	Adobe	N/A
Other			
Nikon Eclipse Ti inverted microscope	Nikon Eclipse Ti inverted microscope	Nikon	N/A
Nikon A1 confocal microscope	Nikon A1R confocal microscope system	Nikon	N/A
Pertri dish, 60 x 15 mm	Pertri culture dish	Falcon	REF353004
Microscope cover glass, 24 x 50 mm	Microscope cover glass	VWR	16004-098
Microscope cover glass, 12CIR-1	Microscope cover glass	Thermo Fisher Scientific	1254580

Drosophila Stocks

Flies were maintained on standard corn meal food in plastic vials under a 12 h light/dark cycle at 25°C. The w^{1118} strain (Bloomington Drosophila Stock Center, number 3605) was used as a wild-type control. Fly strains used: *Gr28a-GAL4(SF36S* for immunostaining and Figure 2B, and *SF36B1* for all other experiments), *Gr28ba-GAL4(NT42aC51a)*, *Gr28bc-GAL4(NT21B1)* (Thorne and Amrein, 2008); *Gr28be-GAL4(Gr28a3AII)* and *Gr66a-GAL4* (Scott et al., 2001); *ΔGr28(54B3)* (Mishra et al., 2018); *UAS-Gr28a*, *UAS-Gr28ba*, *UAS-Gr28bb*, *UAS-Gr28bc*, *UAS-Gr28bd* and *UAS-Gr28be* (Ni et al., 2013); *Gr43a^{GAL4}* (Miyamoto et al., 2012); *Gr66a-LexA* (Thistle et al., 2012); *UAS-VR1E600K* (Marella et al., 2006); *UAS-Kir2.1-GFP* (Baines et al., 2001)(Paradis et al., 2001); *lexAop-rCD2:GFP* (Lai and Lee, 2006), *UAS-GCaMP6m*, *UAS-mCD8:RFP* and *Gr66a^{ex83}* (Bloomington Drosophila Stock Center, numbers 42748, 32220 and 35528)

Chemicals

Caffeine (Cat No. C0750), capsaicin (Cat No. M2028), denatonium benzoate (Cat No. D5765) and lobeline hydrochloride (Cat No. 141879), D-(-)-ribose (Cat No. R7500) and quinine hydrochloride dihydrate (Cat No. Q1125) were purchased from Millipore-Sigma, with a purity of > 95%. Fructose (Cat No. F1092) and agarose (Cat. No. 20-102) were purchased from Spectrum chemical and Apexbio, respectively. Sucrose (Mfr. No. 8360-06) and charcoal (Cat No. 1560-01) were purchased from Macron fine chemicals and J.T. Baker, respectively. A stock solution for capsaicin (20 mM) was prepared in 70% ethanol and stored at 4° C protected from light for up to one year. Stock solutions for bitter chemicals were prepared in Millipore Q water and stored at -20° C. Stock solutions for sugars were prepared in Millipore Q water and stored at 4° C for up to one month. A stock solution for ribose was treated with charcoal (10% of the weight of ribose used for stock solution) overnight at 4° C and sterile-filtrated (0.45 μm) to remove unrelated odor. Stock solutions were diluted to the final concentration using Millipore Q water prior to each experiment.

Immunofluorescence

Immunofluorescence of larval heads was performed based on the protocol described in Croset and colleagues (Croset et al., 2016) with minor modification. Heads of third instar larvae were dissected using microscissors in phosphate buffered saline (PBS) and immediately fixed in PBS with 4% paraformaldehyde for 1 hour at 4 °C. Heads were washed six times in washing buffer (PBS with 0.1% Triton X-100) for 20 min and blocked for 1 h in washing buffer containing 5% heat-inactivated goat serum (SouthernBiotech, Cat. No. 0060-01), followed by incubation with the primary antibodies (rabbit anti–GFP, 1:1,000 dilution; rat anti–mCD8, 1:200 dilution, ThermoFisher Scientific) at 4°C overnight. Heads were washed six times for 20 min in washing buffer and blocked in washing buffer containing 5% heat-inactivated goat serum for 1 hour. Heads were incubated with the secondary antibodies (goat anti rabbit ALEXA 488, 1:500 dilution, ThermoFisher Scientific; goat anti–rat Cy3, 1:300 dilution, Jackson Immunoresearch Laboratories Inc.) at 4°C overnight. Heads were washed six times in

396 washing buffer for 20 min. Washes were carried out at room temperature under gentle
397 agitation. Heads were mounted with VectaShield (Vector Lab, Cat No. H-1200) on a
398 microscope slide and images were obtained using a Nikon A1R confocal microscope
399 system. Adobe photoshop 2022 was used further to process images.

Larval two-choice preference assay

Two-choice preference assay of larvae was conducted as described in Mishra et
al. (Mishra et al., 2013) with minor modification. Flies were placed on standard corn
meal food in plastic vials and allowed to lay eggs for 24 h under a 12 h light/dark cycle
at 25°C. Flies were removed from food vials and feeding-stage third-instar larvae were
collected. All dishes for two-choice preference assay were prepared just prior each
experiment. Petri dishes (60 x 15 mm, Falcon, Cat. No. REF353004) with two halves
marked on the bottom were filled with melted plain 1% agarose or 1% agarose
containing 1.75% ethanol (for capsaicin preference). After the agarose solidified, one
half was removed and replaced with 1% agarose solution containing taste ligands
(capsaicin or bitter compound). For each experiment, 15 larvae from food vials were
briefly rinsed twice with Millipore Q water and placed along the middle separating pure
and ligand containing agarose. After 16 min, photos were taken for record keeping and
used to calculate larval preference indices. Larvae that crawled onto the wall of a dish
or dug in the agarose were excluded. The preference index (P.I.) was calculated as
follow: PI = ($N_{tastant}$ - N_{plain}) / $N_{Total,}$ whereby N is the number of larvae in the tastant
sector, the plain agarose sector and the total number on the plate. Positive values
indicate a preference for capsaicin or bitter compound while negative values indicate
repulsion (avoidance).

Calcium imaging

Calcium imaging was performed in *Gr28bc* GRNs expressed in the terminal
organ of feeding-stage, third instar larvae, reared as described for the larval two-choice
preference assay. For each experiment, larvae from food vials were briefly rinsed twice
with Millipore Q water and were mounted dorsally on a large microscope cover glass
(24 x 50 mm, VWR, Cat. No. 16004-098) using double-sided scotch tape and covered

with a small microscope cover glass (12CIR-1, Thermo Fisher Scientific, Cat. No.
1254580). Millipore Q water (40 µl) was applied to the tip of the larval head, and the
preparation was placed on the stage of a Nikon eclipse Ti inverted microscope. Images
were obtained every 500 ms, starting 15 s before application and ending 105 s after
ligand application. Each recording was initiated by applying water (40µl) to set a
baseline. The first ligand solution (40 µl of bitter chemical or sugar) was applied
thereafter, followed by 5 washes with carrier (100 µl of water). After a 3-minute pause to
allow the preparation to recalibrate, a second ligand solution (40 µl bitter chemical or
sugar) was applied. To assure validity in experiments with *Gr28* mutants and rescues,
each recording was concluded with application of caffeine, and recordings were
included only if caffeine generated a positive response. Baseline fluorescence, which
was determined from the average of five frame measurements from a region next to the
cell immediately before ligand application, was subtracted from the actual
measurements. ∆F/F (%) = (fluorescence light intensity of the cell body –
baseline/baseline) x 100. ∆F/F (max %) is the maximum value within 40 seconds after
ligand application.

Generation of transgenic *Gr28bc-LexA* flies

To generate the *Gr28bc-LexA* driver, a 1.3 kb DNA fragment immediately
upstream of the *Gr28bc* start codon was amplified from w^{1118} flies using a forward (5′-
AATCTA<u>GGTACC</u>CCGGCTGCTCGTCTCCCTGGATGT-3′) and a reverse (5′-
CGTCAA<u>ACTAGT</u>GACCGCTTCGTTTGAGCTTCAACC-3′) primer. *Acc65I* and *SpeI*
sites included in the primer sequence (underlined) were incorporated such that the
amplified fragment was amenable to directional cloning into the LexA vector CMC105
(Larsson et al., 2004). The clone chosen was confirmed by DNA sequence analysis.
Transgenic flies were generated by standard P-element transformation of w^{1118} embryos
(Rainbow Transgenic Flies Inc., Camarillo, CA).

Statistical analysis

Statistical analyses were conducted using Prism software 9.5.1 (GraphPad
Software). Larval two-choice preference assay and Ca^{2+} imaging data were analyzed

for normal distribution using D`Agostino-Pearson omnibus and Shapiro-Wilk normality

tests. When groups did not meet the assumption for normal distribution, nonparametric

statistics was used. For comparison between multiple groups, one-way ANOVA or

Kruskal-Wallis test by ranks (nonparametric one-way ANOVA) was performed to test for

difference of mean or rank distribution. As a post hoc test, Bonferroni's or Dunn's

(nonparametric) multiple comparison tests were employed to compare two specific

groups. One-way ANOVA with Bonferroni's multiple comparison tests were used in

Figure 2. Kruskal-Wallis test by ranks with Dunn's multiple comparison tests were used

in Figures 3, 4B and 5F and 5G). For comparison between two groups, Mann-Whitney

U test (nonparametric t test, Figures 4A, 5D, 5E and Figure 4-figure supplement 1) with

two-tailed P value was used to compare means of two groups. Sample size for larval

two-choice preference assays and Ca^{2+} imaging experiments were based on Mishra et

al (Mishra et al., 2018).

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experiments, Dr. Ahn conducted all experiments, and Dr. Amrein wrote the paper.

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FIGURES

Figure 1. Expression of the *Gr28* genes in the larval sensory organs

A) **Schematic representation of larval chemosensory system** (Kwon et al.,
2011). Three external sensory organs (Dorsal Organ, DO; Terminal Organ, TO;
Ventral Organ, VO) hold collectively the dendritic projections of neuronal cell
bodies in the respective ganglia (DOG, TOG and VOG). Three clusters of
sensory neurons (Dorsa/Ventral Pharyngeal Sensory organ, D/VPS; and
Posterior Pharyngeal Sensory organ, PPS) align the pharynx. The antennal
nerve (AN) connects the DO neurons to the subesophageal zone (SEZ). The TO
and VO neurons project along the maxillary nerve (MN) to the SEZ. The DPS
and PPS neurons innervate to the SEZ via labral nerve (LRN). The VPS neurons
project to the SEZ through the labial nerve (LBN). Note that olfactory neurons
are omitted in the schematic here and in B (below).

B) **Expression of the *Gr28* genes in the external sensory organs.** Note that
images show only one of the bilaterally symmetrical organs. Possible co-
expression between *Gr66a* and different *Gr28b* genes (in B and C; left panels)
was assessed using GAL4 and LexA drivers for Gr28 genes and *Gr66a*,
respectively. Expression summary (diagram on the right) shows only one side of
the bilaterally symmetrical organs. The *Gr28b* genes and *Gr28a* are expressed
in different neurons. Likewise, no co-expression is observed between *Gr66a*
(marker for bitter GRNs) and *Gr28a,* whereas the *Gr28b* genes are co-expressed
in a subset of *Gr66a* neurons.

C) **Expression of the *Gr28* genes in internal taste organs.** Note that images for
the DPS/VPS show both side of the bilaterally symmetrical ganglion, while
images of the PPS show only one side of the bilaterally symmetrical organ.
Gr28a and *Gr66a* are partially co-expressed, but each gene is also expressed
exclusively in a subset of neurons in the PPS. *Gr28bc* but none of the other
Gr28b genes is co-expressed with *Gr66a* in a single neuron in the DPS/VPS.
Expression summary (diagram on the right) shows only one of the bilaterally

677	symmetrical organs. Immunostaining with anti-GFP (green) and anti-mCD8
678	(magenta) antibodies was carried out on whole-mount preparations from larvae
679	heads of the following genotypes: (1) *UAS-mCD8:RFP lexAop-*
680	*rCD2:GFP;Gr66a-LexA/Gr28a-GAL4* or *Gr28bc-GAL4* or *Gr28be-GAL4* (2) *UAS-*
681	*mCD8:RFP lexAop-rCD2:GFP;Gr66a-LexA/+; Gr28ba-GAL4/+*. Asterisks refer
682	to a GRN expressing both *Gr66a* and the indicated *Gr28* gene. Scale bars are 5
683	μm.

Figure 2. Taste behavior of larvae mediated by different *Gr28* GRNs

A) *Gr28a* GRNs mediate capsaicin preference, while *Gr28bc* GRNs elicit capsaicin avoidance in larvae. Control larvae (w^{1118}, *UAS-VR1/+* and *Gr* (indicated *Gr* genes)-*GAL4/+*) show no preference for or avoidance to 0.1 mM (top) or 0.5 mM (bottom) capsaicin. When expressing *UAS-VR1* in *Gr28a* GRNs (*Gr28a-GAL4/UAS-VR1*), larvae display robust taste preference for capsaicin for both 0.1 and 0.5 mM capsaicin. In contrast, when expressed in *Gr28bc* GRNs (*Gr28bc-GAL4/UAS-VR1*), larvae strongly avoid both 0.1 and 0.5 mM capsaicin. Neither avoidance nor preference was observed when VR1 was expressed in the *Gr28ba* or *Gr28be* GRNs. For comparison, expression of VR1 in sweet taste neurons (*Gr43a^{GAL4}/UAS-VR1*) or bitter taste neurons (*Gr66a-GAL4/UAS-VR1*) led to strong preference for or strong avoidance of capsaicin. Each bar represents the mean ± SEM of P.I. (n = 11- 42 assays). The taste behavior of *Gr-GAL4 > UAS-VR1E600K* larvae is compared with 3 controls (w^{1118}, *UAS-VR1E600K/+* & *Gr-GAL4/+*) by using one-way ANOVA with Bonferroni's multiple comparison tests (p < 0.05), whereby different letters indicate statistically significant difference. Dashed lines delineate groups for ANOVA. A short solid line indicates control groups.

B) *Gr28a^{only}* GRNs are necessary and sufficient for inducing capsaicin preference of larvae. When VR1 expression is restricted to GRNs not co-expressing *Gr66a* or *Gr28bc* (*Gr28a^{only}* GRNs) by means of *lexAop-GAL80* under control of *Gr66a-LexA*, larvae show strong preference for capsaicin. Each bar

represents the mean ± SEM of P.I. (n = 13- 18 assays). Bars with different letters
are significantly different (one-way ANOVA with Bonferroni's multiple comparison
tests (p < 0.05). Fly genotypes: wild-type: w^{1118} (black), w^{1118};UAS-VR1E600k/+
(light gray), w^{1118};Gr28a-GAL4/+ (dark grey), w^{1118};Gr28a-GAL4/UAS-VR1E600K
(white), w^{1118};+;Gr28ba-GAL4/+ (dark grey), w^{1118};UAS-VR1E600K/+;Gr28ba-
GAL4/+ (white), w^{1118};Gr28bc-GAL4/+ (dark grey), w^{1118};Gr28bc-GAL4/UAS-
VR1E600K (white), w^{1118};Gr28be-GAL4/+ (dark grey), w^{1118};Gr28be-GAL4/UAS-
VR1E600K (white), w^{1118};Gr43a^{GAL4}/+ (dark grey), w^{1118};Gr43a^{GAL4}/UAS-
VR1E600K (white), w^{1118};Gr66a-GAL4/+ (dark grey), w^{1118};Gr66a-GAL4/UAS-
VR1E600K (white), w^{1118};UAS-VR1E600k/+;lexAop-GAL80/+ (light gray),
w^{1118};Gr66a-LexA/+;Gr28a-GAL4/+ (dark grey) and w^{1118};Gr66a-LexA/UAS-
VR1E600K;Gr28a-GAL4/lexAop-GAL80 (white).

Figure 3. The *Gr28b* neurons mediate avoidance behavior to bitter compounds

Inactivation of *Gr28bc* GRNs (*Gr28bc-GAL4/UAS-Kir2.1*) elicits significantly reduced
avoidance of larvae to all four bitter compounds tested: denatonium, quinine, lobeline
and caffeine, while control larvae carrying either the driver or the reporter only showed
strong avoidance of these compounds. In contrast, flies with inactivated *Gr28be* GRNs
(*Gr28be-GAL4/UAS-Kir2.1*) still avoid denatonium and quinine (top), but no longer avoid
lobeline and caffeine (bottom). Each bar represents the mean ± SEM of P.I. (n = 11- 20
assays). The taste behavior of *Gr-GAL4 > UAS-Kir2.1* larvae is compared with 2
controls *(UAS-Kir2.1/+* & *Gr28b-GAL4/+*) by using Kruskal-Wallis test by ranks with
Dunn's multiple comparison tests (p < 0.05). Bars with different letters are significantly
different. Dashed lines delineate groups for ANOVA. A short solid line indicates a
control. Fly genotypes: w^{1118}; UAS-Kir2.1/+ (light grey), w^{1118}; Gr28bc-GAL4/+ (dark
grey), w^{1118}; Gr28bc-GAL4/UAS-Kir2.1 (white), w^{1118}; Gr28be-GAL4/+ (dark grey), w^{1118};
Gr28be-GAL4/UAS-Kir2.1 (white).

Figure 4. Role of individual *Gr28* genes in bitter taste avoidance

A) Some of the *Gr28* genes are strictly required for sensing denatonium. Wild-type (w^{1118}) larvae, but not *Gr28* mutant larvae, strongly avoid denatonium. In contrast, *Gr28* mutant (w^{1118};*ΔGr28/ΔGr28*) larvae do not show significantly reduced avoidance of quinine, lobeline and caffeine. Each bar represents the mean ± SEM of P.I. (n = 12- 22 assays). Asterisks indicate a significant difference between the *Gr28* mutant and wild-type larvae (Two-tailed, Mann-Whitney U test, **** $p < 0.0001$, *** $p < 0.001$, ns: not significant).

B) Single *Gr28b* genes can rescue avoidance response to denatonium when expressed in *Gr28bc* neurons of *Gr28* mutant larvae. Each bar represents the mean ± SEM of P.I. (n = 11- 22 assay). The behavior of *Gr28* mutant larvae expressing *UAS-Gr28* transgenes under control of the *Gr28bc-GAL4* driver was compared to $Gr28^{+/+}$ control (w^{1118}, filled bar), and three *Gr28* mutant controls (*ΔGr28*, *ΔGr28* plus driver, and *ΔGr28* plus respective *UAS-Gr28* reporter, plain bar) using Kruskal-Wallis test by ranks with Dunn's multiple comparison tests ($p < 0.05$). Bars with different letters are significantly different. Fly genotypes: wild-type: w^{1118} (black), mutants: w^{1118};*ΔGr28/ΔGr28*, w^{1118};*ΔGr28/ΔGr28 Gr28bc-GAL4*, w^{1118};*ΔGr28/ΔGr28;UAS-Gr28* (indicated *Gr28* genes)/+ and w^{1118};*ΔGr28/ΔGr28 UAS-GCaMP6m;UAS-Gr28 (*for *Gr28bb* or *Gr28bc* genes)/+ (white), rescues: w^{1118};*ΔGr28/ΔGr28 Gr28bc-GAL4;UAS-Gr28* (indicated *Gr28* genes)/+ and w^{1118};*ΔGr28 UAS-GCaMP6m/ΔGr28 Gr28bc-GAL4;UAS-Gr28* (for *Gr28bb* or *Gr28bc* genes)/+ (grey).

Figure 5. Cellular activation of *Gr28bc* GRNs by bitter compounds that require Gr28ba or Gr28bc function.

A) **Diagram of Ca^{2+} imaging experimental set up.**

B) **Representative still images of Ca^{2+} response in the *Gr28bc* expressing TO neuron.** Ca^{2+} responses of the *Gr28bc* GRNs upon stimulation with indicated ligands. ΔF indicates the changes in fluorescence light intensity of the cell body before/after ligand application.

C & D) Representative traces (C) and quantified Ca²⁺ responses (D) of the
Gr28bc GRNs after stimulation with indicated ligands. Fly genotype: w^{1118};
Gr28bc-GAL4/UAS-GCaMP6m. Each bar represents the mean ± SEM of Ca²⁺
imaging with 12 – 16 larvae. Asterisks indicate a significant difference between
carrier (water) and indicated ligands (Two-tailed, Mann-Whitney U test, *** p <
0.001, ns: not significant).

(E) Neurons of larvae lacking the Gr28 genes exhibit significantly reduced
responses to denatonium and quinine. The Gr28bc expressing TO GRN of
Gr28 mutant larvae (ΔGr28) display significantly reduced Ca²⁺ responses to
denatonium and quinine but not to lobeline or caffeine when compared to Gr28bc
expressing TO of wild type controls. Responses to denatonium, but not quinine,
is restored by expression of single Gr28b (Gr28ba or Gr28bc) genes (grey).
Larvae genotypes: $Gr28^+$ control (black bar): w^{1118}; Gr28bc-GAL4/UAS-
GCaMP6m. Gr28⁻ control (white bar): w^{1118}; ΔGr28 Gr28bc-GAL4/ΔGr28 UAS-
GCaMP6m. Each bar represents the mean ± SEM with 13 – 16 larvae. Asterisks
indicate a significant difference between $Gr28^+$ control and Gr28 mutant (ΔGr28)
larvae (Two-tailed, Mann-Whitney U test, *** p < 0.001, ** p < 0.01 ns: not
significant).

(F and G) Gr28bc or Gr28ba rescues denatonium responses in GRNs of ΔGr28
larvae. Expression of Gr28bc or Gr28ba in under control of Gr28bc-GAL4
restores responses to denatonium, but not quinine in GRNs of ΔGr28 larvae.
Each bar represents the mean ± SEM of Ca²⁺ imaging with 12 – 17 larvae. The
Ca²⁺ responses of Gr28 mutant larvae expressing UAS-Gr28 transgenes under
Gr28bc-GAL4 driver is compared to $Gr28^+$ (black) and Gr28⁻ (white) controls by
using Kruskal-Wallis test by ranks with Dunn's multiple comparison tests (p <
0.05). Bars with different letters are significantly different. Dashed lines delineate
groups for ANOVA. A short solid line indicates control groups. Fly genotypes:
$Gr28^+$ control (black bar): w^{1118}; Gr28bc-GAL4/UAS-GCaMP6m. Gr28⁻ control
(white bar): w^{1118}; ΔGr28 Gr28bc-GAL4/ΔGr28 UAS-GCaMP6m. Gr28 rescues
(grey bar): w^{1118}; ΔGr28 Gr28bc-GAL4/ΔGr28 UAS-GCaMP6m; UAS-Gr28/+.

Concentrations of ligands were 100 mM for sugars, 50 mM for caffeine and 5 mM

for denatonium, quinine and lobeline.

Figure 6 Role of different GRN subsets in taste behavior of larvae

GRNs mediating avoidance behavior express *Gr28bc*, while GRNs necessary for

feeding preference express *Gr28a* alone (*Gr28a^only^* GRNs). Note that each ensemble is

composed of at least a pair of neurons located in the external taste organs and a pair of

neurons in the internal taste organs.

Figure 7 Amino acid alignment of the six Gr28 proteins

The sequence alignment was generated using Clustal Omega tool from ClustalW2

(https://www.ebi.ac.uk/Tools/msa/clustalo/). IL and EL indicate intracellular loop and

extracellular loop, respectively. Note that the C terminal region starting at the IL3 is

identical in the Gr28b proteins. Red highlighted letters indicate amino acids identical

only in Gr28ba and Gr28bce. Green highlighted letters indicate amino acids conserved

in Gr28ba, Gr28bc and one other Gr28 protein. An asterisk below the sequences

indicates residues identical in all Gr28 proteins; a colon a strongly conserved residue

(STA, NEQK, NHQK, NDEQ, QHRK, MILV, MILF, HY, FYW); and a period moderately

conserved residue (CSA, ATV, SAG, STNK, STPA, SGND, SNDEQK, NDEQHK,

NEQHRK, FVLIM, HFY). TM1-7 indicates helical transmembrane segment predicted by

HMMTOP 2.0 software (http://www.enzim.hu/hmmtop).

Figure 8. Identification of candidate amino acids for ligand binding pockets of

Gr28bc.

Top: Sixteen amino acids conserved in both Gr28ba and Gr28bc are mapped on 3D

structure of Gr28bc using Alphafold (https://www.alphafold.ebi.ac.uk/). Red circles

indicate amino acid locations of residues identical in Gr28ba and Gr28bc. Green circles

indicate amino acid locations of residues identical in one additional Gr28 protein

(Gr28bb or Gr28a).

Bottom: Prediction of putative ligand binding pocket in of Gr28bc with highest probability
using Prankweb (https://prankweb.cz/). The three resides part of this pocket and
identical between Gr28ba and Gr28bc are indicated in green (V177, I218 & I222). The
color displayed in the protein structure indicates a per-residue confidence score
(pLDDT) between 0 and 100 as predicted by Alphafold.

Figure 1-figure supplement 1. Co-expression analysis between *Gr28* genes in
larval sensory organs
Immunostaining with anti-GFP (green) and anti-mCD8 (magenta) antibodies on whole-
mount preparations of the heads from larvae of the genotypes: (1) *UAS-mCD8:RFP*
lexAop-rCD2:GFP;Gr28a-GAL4 or *Gr28be-GAL4* or *Gr66a-GAL4/+;Gr28bc-LexA/+*: (2)
UAS-mCD8:RFP lexAop-rCD2:GFP;+; Gr28ba-GAL4/Gr28bc-LexA. Asterisks refer to
GRN expressing both *Gr28bc* and the indicated *Gr66a* or *Gr28* gene. Note that images
show only one of the bilaterally symmetrical external organs in the DOG/TOG (A) and
both bilaterally symmetrical organs in the DPS/VPS (B).

Figure 4-figure supplement 1. *Gr66a* gene is necessary for caffeine avoidance of
larvae
Gr66a null mutant larvae are unable to avoid of caffeine but none of other bitter
compounds. Each bar represents the mean ± SEM of P.I. (n = 11- 12 assays). Asterisks
indicate a significant difference between the *Gr66a* mutant (*Gr66a*^{ex83}) and control
larvae (*w*^{1118}) (Two-tailed, Mann-Whitney U test, ** p < 0.01, ns: not significant).

SOURCE DATA FILES

Figure 2-Source Data 1. (A) Taste preference assay of larvae expressing VR1 in
different *Gr28* GRNs for 0.1 mM (top) or 0.5 mM (bottom) capsaicin. (B) Taste
preference assay of larvae with expression of VR1 in *Gr28a*^{only} GRNs using *lexAop-*
GAL80 under control of *Gr66a-LexA*.

Figure 3-Source Data 1. Taste preference assay for bitter compounds of larvae with
inactivated *Gr28bc* or *Gr28be* GRNs using expression of *UAS-Kir2.1*.

Figure 4-Source Data 1. (A) Taste preference assay of wild type and *Gr28* mutant
larvae for bitter compounds. (B) Taste preference assay of *Gr28* mutant larvae for
denatonium expressing single *Gr28* genes in *Gr28bc* GRNs.

Figure 5-Source Data 1. (D) Ca^{2+} responses of *Gr28bc* GRNs in the TO to bitter
compounds and sugars. (E) Ca^{2+} responses of *Gr28* mutant larvae to bitter compounds.
(F&G) Ca^{2+} responses of *Gr28* mutant larvae to denatonium (F) or quinine (G)
expressing single *Gr28* genes in *Gr28bc* GRNs.

Figure 4-figure supplement 1-Source Data 1. Taste preference assay of *Gr66a*
mutant larvae for bitter compounds.

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875

876 **Table 1. Conserved amino acids in the amino termini of Gr28ba and Gr28bc**

Location	Residue (Gr28bc)	Other (if applicable)
EL1	E103	Gr28bb
	R111	Gr28bb
EL2	**E200**	**none**
	Y94	Gr28bb
	S95	**none**
TM2	**V124**	**none**
	I128	Gr28bb
TM3	**V170**	**none**
	V177	Gr28bb
TM4	**L207**	**none**
	F209	**none**
	I218	Gr28a
	I220	Gr28bb
	I222	Gr28bb
	T229	Gr28a
	V232	**none**

879 The 7 amino acid residues identical in the amino-terminal region of Gr28bc and Gr28ba

880 are shown in bold. The nine additional amino acids also identical in one additional Gr28

881 proteins are also listed. These residues are considered potentially critical for recognition

882 of denatonium, since only Gr28ba and Gr28bc can rescue response to denatonium

883 when expressed in *Gr28bc* neurons of *ΔGr28/ΔGr28* mutant larvae.

Table 2. Prediction of ligand binding sites from protein structure of Gr28bc

Name	Score	Probability	Residue_ids
Pocket 1	10.35	0.533	F173, **V177**, S180, M181, V184, N185, F188, H215, **I218**, A219, **I222**, S226, L357, Y358, I360, A361, S364, G368, R371
Pocket 2	4.54	0.172	F117, M121, F318, L319, V322, F323, Y436, I439, L440
Pocket 3	4.44	0.166	S104, V105, A106, Q122, I123, ***L207***, T210, F211, Q214, F350, Q354
Pocket 4	3.47	0.11	I314, S315, F318, F419, L425, T428, I429, A432, T436
Pocket 5	3.17	0.093	L178, M181, F182, N185, T216, **I220**, V151, H55
Pocket 6	2.36	0.05	V105, T192, L196, L207, H208, F211, F350
Pocket 7	2.01	0.037	L359, I362, I363, Y426, I429, S430, L433
Pocket 8	1.45	0.017	I213, T216, H55, H86
Pocket 9	1.07	0.007	R46, F49, H50, Y53, Y61, I62, F78

Probability and expansion of predicted ligand binding sites in Gr28bc as predicted by Prankweb (https://prankweb.cz/). Amino acid residues identical in Gr28ba and Gr28bc alone are in ***bold & italic***, or in **bold** only if a residue is conserved in one additional Gr28 protein.

Figure 1

A

B

External sensory organs

C

Internal sensory organs

Figure 2

Figure 3

Figure 4

A

B

Gr28	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Gr28b.c-GAL4	-	-	+	-	+	-	+	-	+	-	+	-	+	-	+
UAS-Gr28	-	-	-	a		ba		bb		bc		bd		be	

Figure 5

Figure 6

Figure 7

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                                                                    IL1
Gr28ba  -----------------MIRCGLDIFRGCRGRFRYWLSARDCYDSISLMVAIAFALGITPFLVR    47
Gr28bc  MDIEMAKEPVNPTDTPDIEVTPGLCQPLRRRFRRFVTAKQLYECLRPVFHVTYIHGLTSFYIS    63
Gr28bb  -----------------------MSALRRVRKYFISSQVYEALRPLFFLTFLYGLTPFHVV    38
Gr28bd  ------------------------MSFYFCEIFKPRDAFGAEQTLLLYTYLLGLTPFRL-    35
Gr28be  ----------------------MWLLRRSVGKSGNRPHDVYTCYRLTIFMALCLGIVPYYVS    40
Gr28a   ------------------------MAFKLWERFSQADNVFQALRPLTFIS-LLGLAPFRLN    36
                                         : :  .         :          *:. : :

                               TM1                     EL1           TM2
Gr28ba  -RNALGENSLEQSWYGFLNAIFRWLLLAYCYSYI-NLRNESLIGYFMRNHVSQISTRVHDVGG   108
Gr28bc  CDTKTGKKAIKKTIFGYINGIMHIAMFVFAYSLTIYNNCESVASYFFRSRITYFGDLMQIVSG   126
Gr28bb  -RRKMGESYLKMSCFGVFNIFIYICLCGFCYIS-SLRQGESIVGYFFRTEISTIGDRLQIFNG    99
Gr28bd  -RGQAGERQFHLSKIGYLNAFLQLSFFSYCFLAA-LIEQQSIVGYFFKSEISQMGDSLQKFIG    96
Gr28be  -ISSEGRGKLTSSYIGYINIIIRMAIYMVNSFYG-AVNRDTLMSNFFLTDISNVIDALQKING   101
Gr28a   L---NPRKEVQTSKFSFFAGIVHFLFFVLCFGIS-VKEGDSIIGYFFQTNITRFSDGTLRLTG    95
          .    :   : :  : . :     . ::: .  *: .  ::  .          . *

                        IL2                          TM3
Gr28ba  IIAAVFTFILPLLLRKYFLKSVKNMVQVDTQ-LERLRSPVNFNTVVGQVVLVILAVVLLDTVL   170
Gr28bc  FIGVTVIYLTAFVPNHRLERCLQKFHTMDVQ-LQTVGVKIMYSKVLRFSYMVLISMFLVNVLF   188
Gr28bb  LIAGAVIYTSAILKRCKLLGTLTILHSLDTN-FSNIGVRVKYSRIFRYSLLVLIFKLLILGVY   161
Gr28bd  MTGMSILFLCSSIRVRLLIHIWDRISYIDDR-FLNLGVCFNYPAIMRLRLLQIFLINGVQLGY   158
Gr28be  MLGIFAILLISLLNRKELLKLLATFDRLETEAFPRVGVAMHQVAANKKMNRLVIILVGSMVAY   164
Gr28a   ILAMSTIFGFAMFKRQRLVSIIQNNIVVDEI-FVRLGMKLDYRRILLSSFLISLGMLLFNVIY   157
         : . :      .       :         ::      :    :          :

                EL2           TM4                       IL3
Gr28ba  LTTGLVCLAKME-VYASWQLTFIFVYELLAISITICMFCLMTRTVQRRITCLHKVLKNLAHQW   232
Gr28bc  TGGTFSVLYSSE-VAPTMALHFTFLIQHTVIAIAIALFSCFTYLVEMRLVMVNK          241
Gr28bb  FVGVFRLLVSLD-VTPSFCVCMTFFLQHSVVSIAICLFCVIAFSFERRLSIINQ          214
Gr28bd  LISSNWMLLGND-VRPIYTAIVAFYVPQIFLLSIVMLFNATLHRLWQHFTVLNQ          211
Gr28be  ITCSFLMISLRDTTTFSISAVISFFSPHFIVCAVSFLAGNVMIKLRIYLSALNE          218
Gr28a   LCVSYSLLVSAT-ISPSFVTFTTFALPHINISLMVFKFLCTTDLARSRFSMLNEILQDILDAH   219
          :                 *         :                 :    :*::: .

Gr28ba  DT----R---SLKA-VNQKQRS-------LQCLDSFSMYTIVTKDPAEIIQESMEIHHLICEA   280
Gr28a   IEQLSALELSPMHSVVNHRRYSHRLRNLISTPMKRYSVTSVIRLNPEYAIKQVSNIHNLLCDI   282
             :::  **::: *        :. :*: ::: :*    *::  :**:*:*:

                TM5                 EL3              TM6
Gr28ba  AATANKYFTYQLLTIISIAFLIIVFDAYYVLETLLGKSKRESKFKTVEFVTFFSCQMILYLIA   343
Gr28a   CQTIEEYFTYPLLGIIAISFLFILFDDFYILEAILN-PKRLDVFEADEFFAFFLMQLIWYIVI   344
         . *  ::****.**:.** **:*:**:*:** :*:*:**::.   ** . *:: **.:** *:* *::

                               IL4
Gr28ba  IISIVEGSNRAIKKSEKTGGIVHSLLNKTKSAEVKEKLQQFSMQLMHLKINFTAAGLFNIDRT   406
Gr28a   IVLIVEGSSRTILHSSYTAAIVHKILNITDDPELRDRLFRLSLQLSHRKVLFTAAGLFRLDRT   407
         *: *****.*:* :*. *..***.:** *.. *:::* ::*:** * *: ******* .:***

                TM7                      EL4
Gr28ba  LYFTISGALTTYLIILLQFTSNSPNNGYGNGSSCCETFNNMTNHTL--               452
Gr28a   LIFTITGAATCYLIILIQFRFTHHMDDTSSNS-----TNNLHSIHLGD               450
         * ***:** * *****:** .   :. ...*       **:  .   *
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Figure 8

Figure 1-figure supplement 1

Figure 4-figure supplement 1