Title:

Chloride ions evoke taste sensations by binding to the extracellular ligand-binding domain of sweet/umami taste receptors

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Abstract

Salt taste sensation is multifaceted: NaCl at low or high concentrations is preferably or aversively perceived through distinct pathways. Cl^- is thought to participate in taste sensation through an unknown mechanism. Here we describe Cl^- ion binding and the response of taste receptor type 1 (T1r), a receptor family composing sweet/umami receptors. The T1r2a/T1r3 heterodimer from the medaka fish, currently the sole T1r amenable to structural analyses, exhibited a specific Cl^- binding in the vicinity of the amino-acid-binding site in the ligand-binding domain (LBD) of T1r3, which is likely conserved across species, including human T1r3. The Cl^- binding induced a conformational change in T1r2a/T1r3LBD at sub- to low-mM concentrations similar to canonical taste substances. Furthermore, oral Cl^- application to mice increased impulse frequencies of taste nerves connected to T1r-expressing taste cells and promoted their behavioral preferences attenuated by a T1r-specific blocker or T1r3 knock-out. These results suggest that the Cl^- evokes taste sensations by binding to T1r, thereby serving as another preferred salt taste pathway at a low concentration.

36 **Introduction**

37 The taste sensation is initiated by specific interactions between chemicals in food and taste
38 receptors in taste buds in the oral cavity. In vertebrates, the chemicals are grouped into five
39 basic modalities: sweet, umami, bitter, salty, and sour. This sensation occurs through taste
40 receptor recognition specific to a group of chemicals representing each taste modality (Taruno
41 *et al*, 2021). Regarding the salty taste, the preferable taste, ~100 mM concentration of table
42 salt, is evoked by specific interaction between the epithelial sodium channel (ENaC) and
43 sodium ion (Chandrashekar *et al*, 2010) (Figure 1). Notably, salt sensation exhibits multifaced
44 properties (Roper, 2015), thereby suggesting the existence of an adequate concentration range
45 for salt intake to maintain the homeostasis of body fluid concentration. For example, high
46 concentrations of salt over levels perceived as a preferred taste, such as ~500 mM, stimulate
47 bitter and sour taste cells and are perceived as an aversive taste (Oka *et al*, 2013). Conversely,
48 low salt concentrations under the "preferable" concentration, such as several mM to a hundred
49 mM concentrations, are perceived as sweet by human panels (Bartoshuk *et al*, 1964;
50 Bartoshuk *et al*, 1978; Cardello, 1979). However, its mechanism has never been extensively
51 pursued. The various impacts of the salt taste sensation indicate multiple salt detection
52 pathways in taste buds (Roper, 2015). Moreover, another component of table salt, the chloride
53 ion, participates in taste sensation because of the existence of the "anion effect": the salty
54 taste is most strongly perceived when the counter anion is a chloride ion (Ye *et al*, 1991).
55 Several reports suggested a certain cellular/molecular machinery underlying anion-sensitive
56 Na^+-detection or Cl^--detection, which is independent of ENaC (Lewandowski *et al*, 2016;
57 Roebber *et al*, 2019). Indeed, a recent study indicated that transmembrane channel-like 4
58 (TMC4) expressed in taste buds involves high-concentration Cl^--sensation (Kasahara *et al*,
59 2021). Nevertheless, no candidate molecule capable of sensing low or preferable
60 concentrations of Cl^- has been elucidated. Therefore, the complete understanding of salt taste

61 sensation, including the mechanism of chloride ion detection, remains unclear.

62 Unlike salt taste sensation, those for nutrients as sugars, amino acids, and
63 nucleotides are understood as sweet and umami sensations through specific receptor proteins
64 (Li *et al*, 2002; Nelson *et al*, 2002; Nelson *et al*, 2001). Sweet and umami receptors are
65 composed of taste receptor type 1 (T1r) proteins in the class C G protein-coupled receptor
66 family. In humans, the T1r1/T1r3 heterodimer serves as the umami taste receptor and
67 responds to amino acids as L-glutamate and aspartate, and nucleotides. In contrast, the
68 T1r2/T1r3 heterodimer is the sweet taste receptor and responds to sugars. We previously
69 elucidated the crystallographic structure of the medaka fish T1r2a/T1r3 extracellular
70 ligand-binding domain (LBD) (Nuemket *et al*, 2017), which is currently the sole reported
71 structure of T1rs. In the structure, the amino acid-binding was observed in the middle of the
72 LBD of T1r2a and T1r3 subunits, which was consistent with the fact that T1r2a/T1r3 is an
73 amino-acid receptor (Oike *et al*, 2007). Furthermore, chloride ion binding was found in the
74 vicinity of the amino-acid binding site in T1r3 (Figure 2A). So far, the physiological
75 significance of Cl^--binding for T1rs functions remains unexplored. Nevertheless, chloride
76 ions regulate other receptors in class C G protein-coupled receptors (GPCRs), such as
77 metabotropic glutamate receptors (mGluRs) and calcium-sensing receptors (CaSRs), and act
78 as positive modulators for agonist binding (Eriksen & Thomsen, 1995; Kuang & Hampson,
79 2006; Liu *et al*, 2020; Tora *et al*, 2018; Tora *et al*, 2015). The potential effect of Cl^--binding
80 on T1r receptor function is of significant interest under these conditions.

81 Here, we investigated the Cl^- actions on T1rs using structural, biophysical, and
82 physiological analyses. The Cl^- binding to the LBD was investigated using the medaka fish
83 T1r2a/T1r3LBD, which is amenable to structural and biophysical analyses. Since the Cl^-
84 -binding site in T1r3 was conserved across various species, taste nerve recordings from mice
85 were used to investigate the physiological significance of Cl^-. The results suggest that Cl^-

86 induces the moderate response via T1rs, thereby implying that T1rs are involved in Cl^-
87 sensation in taste buds.
88
89 **Results**
90 **Cl^--binding site in T1r3**
91 In the previously reported structure of T1r2a/T1r3LBD crystallized in the presence of NaCl,
92 bound Cl^- was identified based on electron density and binding distances (Nuemket *et al.*,
93 2017). To verify the Cl^--binding, Cl^- in the T1r2a/T1r3LBD crystal was substituted with Br^-,
94 a halogen ion amenable for specific detection by anomalous scattering using a synchrotron
95 light source (Figure 2−figure supplement 1). The diffraction data from the crystal resulted in
96 an anomalous difference Fourier peak at 14.1 σ at the site in the vicinity of the amino-acid
97 binding site in T1r3, where Cl^- was originally bound (Figure 2B, Figure 2—figure
98 supplement 2). For further confirmation, the anomalous data of the original crystal containing
99 Cl^- was collected at 2.7 Å, where the anomalous peak for Cl and several other elements such
100 as Ca or S can be detected (Figure 2—figure supplement 1). The resultant anomalous
101 difference Fourier map showed a peak at the bound Cl^- position, while all the other peaks
102 were observed at the S atoms in the protein (Figure 2C, Figure 2—figure supplement 2).
103 These results verify that the site is able to bind halogen ions, likely accommodating Cl^- under
104 physiological conditions.
105 Cl^- was coordinated at the binding site by the side-chain hydroxyl group of Thr105
106 and the main-chain amide groups of Gln148 and Ser149 (Figure 2D). These main-chain
107 coordinating residues are followed by Ser150, a critical residue for binding amino-acid
108 ligands (Nuemket *et al.*, 2017). Furthermore, the loop regions where Thr105 and the
109 Gln148-Ser150 locate are followed by helices B and C, respectively. These helices are
110 essential structural units at the heterodimer interface (Nuemket *et al.*, 2017) (Figure 2A).

111 They are known to reorient upon agonist binding, resulting in conformation rearrangement of
112 the subunits in the dimer, likely inducing receptor activation in class C GPCRs (Koehl *et al*,
113 2019; Kunishima *et al*, 2000). In addition, the side-chain hydroxyl group of Ser149, which
114 serves as a cap for the positive helix dipole of helix C, simultaneously functions as a distal
115 ligand for Cl^- coordination. Therefore, the Cl^- binding at this site is important for organizing
116 the structure of the amino-acid binding site and the heterodimer interface.

117 The Cl^--binding site observed in the crystal structure is most likely conserved
118 among T1r3s in various organisms, such as humans (Figure 2E). Thr105, the residue that
119 provides the side-chain-coordinating ligand for Cl^--binding, is strictly conserved as either
120 serine or threonine among T1r3s. Additionally, the amino-acid sequence motifs surrounding
121 the main-chain-coordinating ligands, $FP^{45}L$ and $VIGP\zeta^{148}\zeta^{149}$, where "ζ" is a hydrophilic
122 amino acid, are well conserved to present the main-chain amide groups to coordinate Cl^- with
123 an appropriate geometry. Notably, the site structurally corresponds to the Cl^--binding site in
124 the hormone-binding domain of the atrial natriuretic peptide receptor (ANPR) (Figure 2F, 2G),
125 in which Cl^- positively regulates the peptide hormone binding (Misono, 2000). Although
126 ANPR is not a member of class C GPCR, the hormone-binding domain in ANPR shares a
127 similar structural fold with LBD of T1rs and other class C GPCRs, and bacterial
128 periplasmic-binding proteins (Kunishima *et al.*, 2000; van den Akker *et al*, 2000).
129 Accordingly, the conservation of the structure and the sequence motif at the Cl^--binding site
130 at ANPR is also observed on mGluRs (Ogawa *et al*, 2010). Indeed, Cl^- binding at the site
131 corresponding to that in T1r3 was observed in several mGluR and CaSR structures (Monn *et*
132 *al*, 2015b; Zhang *et al*, 2016) (Figure 2F, 2G) and was identified as a potential site responsible
133 for regulating agonist binding (Liu *et al.*, 2020; Tora *et al.*, 2015). These results strongly
134 imply the possibility that Cl^- has some actions on T1r receptor functions.

135 In contrast, conservation at the Thr105 position was not observed among T1r1 and

136 T1r2 (Figure 2E). Evidently, no significant anomalous peak derived from Br^-- or Cl^--binding
137 was observed in the crystal structure at the corresponding site in T1r2a (Figure 2B, 2C).
138 His100 in T1r2a, which corresponds to Thr105 in T1r3, adopted a significantly different
139 side-chain conformation from that of Thr105 in T1r3 (Figure 2—figure supplement 2).
140 Therefore, T1r1 and T1r2's ability to bind Cl^- is unlikely.

141 In addition to the Cl^--binding site discussed above, the Br^--substituted crystal
142 exhibited an anomalous peak at 8.5 σ in T1r2a, at a position close to the Lys265 side-chain
143 ε-amino group (Figure 2B, Figure 2—figure supplement 2). Nevertheless, Cl^--binding was
144 not observed in the original Cl^--contained crystal. This is further confirmed by the absence of
145 an anomalous peak at this position in the data collected at 2.7 Å (Figure 2C, Figure 2—figure
146 supplement 2). Therefore, the site might have the ability to bind anions such as Br^- or larger;
147 but be not specific to Cl^-. In human T1r1, the residue corresponding to Lys265 (Arg277) was
148 suggested as a critical residue for activities of inosine monophosphate, an umami enhancer
149 (Zhang *et al*, 2008).

150

151 **Cl^--binding properties in T1r2a/T1r3LBD**

152 To investigate the Cl^- actions on T1r functions, we first examined the properties of the Cl^-
153 -binding to medaka T1r2a/T1r3LBD using various biophysical techniques. For this purpose,
154 the purified T1r2a/T1r3LBD was subjected to differential scanning fluorimetry (DSF), which
155 we previously used for the amino acid-binding analysis (Yoshida *et al*, 2019). In order to
156 prepare a Cl^--free condition, Cl^- in the sample was substituted with gluconate, as it is unlikely
157 accommodated in the Cl^--site due to its much larger size. We confirmed that gluconate does
158 not serve as a ligand for T1r2a/T1r3LBD (Figure 3—figure supplement 1).

159 The addition of Cl^- to the Cl^--free T1r2a/T1r3LBD sample resulted in thermal
160 stabilization of the protein (Figure 3A), which is indicative of Cl^- binding to the protein. The

161 apparent K_d value for Cl^- estimated by the melting temperatures (T_m) at various Cl^-
162 concentrations was ~110 μM (Figure 3B, Table 1). The Cl^--dependent thermal stabilization
163 was confirmed by the fluorescence-detection size-exclusion chromatography-based
164 thermostability (FSEC-TS) assay (Hattori *et al*, 2012) (Figure 3C, Table 1). However, the Cl^-
165 -dependent stabilization was not observed on T1r2a/T1r3 with the Cl^--site mutation, T105A in
166 T1r3. In the case of this mutant, the T_m values for both in the presence and absence of Cl^- was
167 similar to the values obtained for the wild-type protein in the absence of Cl^- (Figure 3C,
168 Figure 3—figure supplement 1, Table 1). These results indicate that the Cl^- effect attributed to
169 the identical site where the Cl^--binding was observed in the crystal structure of T1r3.

170 Next, we examined the consequence of the Cl^--binding to T1r2a/T1r3LBD via
171 Förster resonance energy transfer (FRET) using the fluorescent protein-fused sample. Class C
172 GPCRs commonly exhibit agonist-induced conformational changes in LBD, such as the
173 dimer rearrangement, which is essential for receptor activation and signaling (Ellaithy *et al*,
174 2020; Koehl *et al.*, 2019; Kunishima *et al.*, 2000; Lin *et al*, 2021). Consistent with this, we
175 previously reported that T1r2a/T1r3LBD shows conformational change concomitant with the
176 binding of amino acids, which can be detected as increased FRET intensity (Nango *et al*,
177 2016). Notably, adding Cl^- to the fluorescent protein-fused T1r2a/T1r3LBD also increased
178 FRET intensities, similar to amino acids (Figure 3D). The EC_{50} for Cl^--induced FRET signal
179 change was determined as ~1 mM (Table 1). Note that both DSF and FRET estimations have
180 some degree of error: the former produced slightly lower values than the latter, particularly in
181 the case of weak affinities in the mM concentration range (Yoshida *et al.*, 2019). As such,
182 although the EC_{50} value determined by FRET was slightly higher than the apparent K_d value
183 of Cl^- determined by DSF, the two are most likely relevant. Considering that the Cl^--binding
184 site is located adjacent to the dimer interface, which exhibits reorientation upon agonist
185 binding (Figure 2D), the results suggest that the Cl^-binding to T1r2a/T1r3LBD induces a

186 conformational rearrangement of T1r2a/T1r3LBD similar to its agonist amino acid.
187 Nevertheless, the extent of the FRET change induced by Cl^- was smaller than the changes
188 induced by amino acids, such as ~1/2 of the latter (Figure 3E). Therefore, the results suggest
189 that the extent of the conformational change induced by Cl^- is smaller than the change
190 induced by amino acids. The extent of Cl^--dependent FRET index change was reduced on
191 T1r2a/T1r3 with the Cl^--site mutation, T105A in T1r3 (Figure 3E). Considering that the
192 amino-acid-dependent change in the mutant was also significantly reduced (Figure 3E), the
193 T105A mutation on T1r3 might result in losing the ability of the conformational change
194 induced by Cl^-- and amino-acid bindings, although the possibility of deactivation of the
195 protein during preparation due to its low stability cannot be excluded.

196 In addition to the Cl^--binding effect, the Cl^- effect on amino-acid binding to
197 T1r2a/T1r3LBD was investigated by FRET and isothermal calorimetry (ITC). The K_d values
198 for L-glutamine binding determined by ITC, as well as the EC_{50} values and the other
199 parameters for L-glutamine-induced conformational change determined by FRET, did not
200 differ in the presence and absence of Cl^- (Figure 3F, Figure 3—figure supplement 1, and
201 Table 1). These results indicated that the Cl^- binding had no significant effect on the binding
202 of L-glutamine, a representative taste substance, at least for T1r2a/T1r3LBD from medaka
203 fish.

204

205 **Taste response to Cl^- through T1rs in mouse**

206 Biophysical studies on T1r2a/T1r3LBD from medaka fish suggested that Cl^-binding to
207 T1r3LBD induces a conformational change similar to that of an agonist without affecting
208 agonist binding. As described above, the Cl^--binding site is likely conserved among T1r3 in
209 various species, such as those in mammals. Therefore, we analyzed single fiber responses
210 from mouse chorda tympani nerve to investigate the physiological effect of Cl^- on taste

211 sensation. While conventional cell-based receptor assay systems are affected by changes in
212 extracellular ionic components, the application of various solutions to the taste pore side of
213 the taste buds projected to taste nerve systems, are transduced exclusively as "taste" signals,
214 without inducing the other cellular responses derived from the ionic component changes in
215 the surrounding environment.

216 We first identified nerve fibers that connect to T1r-expressing taste cells in
217 wild-type (WT) mice, i.e., that receive taste information from cells likely possessing sweet
218 (T1r2/T1r3) and umami (T1r1/T1r3) receptors (Yasumatsu *et al*, 2012). The identification was
219 evidenced by responses to T1r agonists, such as sugars and amino acids, which were inhibited
220 by gurmarin (Gur), a T1r-specific blocker (Daly *et al*, 2013; Margolskee *et al*, 2007;
221 Ninomiya & Imoto, 1995; Ninomiya *et al*, 1999). Then, we examined the responses to Cl^- in
222 these fibers. Remarkably, the fibers also exhibited responses induced by Cl^-, which was
223 applied as a form of NMDG-Cl devoid of the known salty taste stimulant, sodium ion (Figure
224 4A). Cl^--induced impulse frequencies from the nerves increased in a concentration-dependent
225 manner (Figure 4B). The responses to NMDG-Cl, NaCl, and KCl at the same concentrations
226 did not differ significantly (repeated measures analysis of variance [ANOVA], $P > 0.05$),
227 whereas responses to NMDG-gluconate were significantly smaller than those to NMDG-Cl
228 (repeated measures ANOVA: $F_{(1, 43)} = 31.33$, $P < 0.001$) and did not induce explicit responses
229 up to 10 mM. These results confirmed that the observed responses were attributed to Cl^-. All
230 responses to Cl^-, regardless of the type of counter cations, were significantly decreased by
231 lingual treatment with Gur (Figure 4B, repeated measures ANOVA: $F_{(1, 42)} = 56.65$, $P < 0.001$
232 for NMDG-Cl; $F_{(1, 50)} = 24.78$, $P < 0.001$ for NaCl; and $F_{(1, 45)} = 35.72$, $P < 0.001$ for KCl).
233 Furthermore, responses to Cl^- in T1r3-KO mice were significantly lower than those in WT
234 mice (repeated measures ANOVA: $F_{(1, 43)} = 25.36$, $P < 0.001$; Figure 4C). The results indicate
235 that the observed Cl^--dependent responses were mediated by T1r. Notably, the Cl^-

236 -concentration range that induced nerve responses was lower (≤ ~10 mM) than that for
237 Na^+-detection by ENaC when applied as the NaCl form (≥ ~30 mM) (Chandrashekar *et al.*,
238 2010) but is consistent with those for Cl^--binding and Cl^--induced conformational change
239 observed on T1r2a/T1r3LBD (Table 1). These results suggest that a low Cl^- concentration is
240 sensorily detected via T1r in taste buds. Although the responses induced by known taste
241 substances for T1rs, such as sugars and amino acids, range from tens to hundreds of impulse
242 frequencies per 10 s (Yasumatsu *et al.*, 2012); the maximum response level induced by Cl^-
243 was low, ~10 per 10 s (Figure 4B). According to our observations, Cl^- likely produces a "light"
244 taste sensation compared with other known taste substances.

245 Next, to examine the physiological interaction between a canonical taste substance
246 for mouse T1r and Cl^-, we recorded responses to 20 mM L-glutamine or 100 mM sucrose
247 from T1r1/T1r3- and T1r2/T1r3-expressing cells, respectively, with or without NMDG-Cl
248 from the same T1r-connecting single fibers (Figure 4A). The concentrations for the taste
249 substances were set to induce responses greater than the baseline but less than maximum. As
250 shown in Figure 4D, the response to L-glutamine or sucrose increased significantly by adding
251 10 mM NMDG-Cl (paired *t*-test, $t2 = 7.56$, $p = 0.017$ for L-glutamine and $t2 = 5.05$, $p = 0.037$
252 for sucrose). We confirmed that these responses had been suppressed by a lingual treatment of
253 Gur in the presence ($t2 = 6.73$, $p = 0.021$ for L-glutamine and $t2 = 8.80$, $p = 0.013$ for sucrose)
254 or absence ($t2 = 8.32$, $p = 0.014$ for L-glutamine and $t2 = 11.72$, $p = 0.007$ for sucrose) of
255 NMDG-Cl to a similar extent and a similar level to the responses in T1r3-KO mice. Moreover,
256 the responses to the mixtures did not differ significantly from the summation of the responses
257 to each solution ($t2 = 2.34$, $p = 0.145$ for L-glutamine and $t2 = 2.31$, $p = 0.147$ for sucrose).
258 The results suggest that the simultaneous binding of Cl^- and a canonical taste substance, such
259 as amino acids and sugars, to T1r do not cause synergistic responses.

260 Finally, we addressed whether T1r-mediated Cl^- responses observed in the taste

261 nerves involve taste perception. Thus far, most reported behavioral assays for examining the
262 gustatory detection of NaCl were performed with concentrations above ~30 mM, which can
263 induce ENaC-mediated responses. Nevertheless, a few reports have shown that NaCl solution
264 induced higher consumption relative to water even below 10 mM concentration (Dyr *et al*,
265 2014; Stewart *et al*, 1994), which is below the range inducing ENaC-mediated responses
266 (Chandrashekar *et al.*, 2010) but within what we observed in the Cl^--induced taste nerve
267 responses via T1r. For verification, we performed a mouse two-bottle choice test using
268 NMDG-Cl solution and analyzed the preference relative to water. The mouse preferred water
269 containing 10 mM NMDG-Cl, which was abolished by the application of Gur (Figure 4E, 4F).
270 These results suggest that Cl^- is preferably perceived through taste signal transduction
271 mediated by T1r.
272
273 **Discussion**
274 In this study, Cl^- is found to specifically interact with the LBD in T1r3, a common component
275 of sweet and umami taste receptors, and induces a conformational change in the receptor's
276 LBD region. The Cl^- binding to T1r in taste cells is likely further transmitted to the sweet
277 taste nervous system, resulting in a light yet preferable taste sensation. Since T1rs are
278 conserved across vertebrates and the Cl^--binding site is likely conserved among T1r3 in
279 various organisms, T1r-mediated Cl^- responses might be common in many animals, such as
280 humans. Evidently, the concentration range for the Cl^--induced conformational change of
281 medaka T1r2a/T1r3LBD and increase in murine sweet nerve impulses observed in this study
282 (i.e., ≤ ~10 mM) agrees with the NaCl concentration perceived as "sweet" by humans
283 (Bartoshuk *et al.*, 1964; Bartoshuk *et al.*, 1978; Cardello, 1979) (Figure 1). Additionally, the
284 sweet sensation induced by NaCl was reportedly suppressed by topical application of
285 *Gymnema sylvestre* (Bartoshuk *et al.*, 1978), containing Gymnemic acids, which are specific

286 inhibitors of human sweet taste receptor T1r2/T1r3 (Sanematsu *et al*, 2014). Overall, these
287 results agree with the involvement of T1rs in the Cl^--taste detection. These findings agree
288 with an earlier hypothesis by Bartoshuk and colleagues that dilute NaCl contains a sweet
289 stimulus that interacts with the same receptor molecules as sucrose (Bartoshuk *et al.*, 1978).
290 The reported "sweet" sensation by low NaCl concentration faded out at the concentrations
291 detected as "salty" (Bartoshuk *et al.*, 1964; Bartoshuk *et al.*, 1978; Cardello, 1979), thereby
292 agreeing with the fact that we might be unaware that table salt is sweet at such concentrations.
293 The phenomenon could be explained by "mixture suppression" (Bartoshuk, 1975; Keast &
294 Breslin, 2002; Stevens, 1996), such that a light sweet sensation is masked by an intense salty
295 sensation in a higher concentration range of NaCl.

296 The Cl^- perception at low salt concentrations found in this study is achieved via the
297 T1rs-mediating taste system, which transduces information as a preferred taste by nature.
298 Since Cl^- is also a component of table salt, this system might serve as another pathway for
299 preferred salt perception promoting intake along with the pathway for Na^+ perception as a
300 preferred taste via taste cells that express the Na^+ receptor ENaC and a purinergic
301 neurotransmission channel CALHM1/3 (Nomura *et al*, 2020). In contrast, the T1r-mediated
302 Cl^--sensing observed in this study shows several different properties from those of cells or the
303 molecules reportedly exhibiting anion-sensitive Na^+ detection or Cl^- detection in taste buds
304 thus far. Specifically, the anion-sensitive Na^+-responding taste cells reported by Lewandowski
305 *et al.* are type 3 cells, which include sour- but not sweet-responding cells (Lewandowski *et al.*,
306 2016). The Cl^--detection pathway reported by Roebber *et al.* was observed in type 2 cells,
307 which include both sweet- and bitter-responding cells, but was inhibited by a blocker of
308 phospholipase C, which mediates sweet- and bitter-signaling downstream of T1r and bitter
309 receptors (Roebber *et al.*, 2019). The Cl^--responses mediated by TMC4 were observed in the
310 glossopharyngeal nerve but not in the chorda tympani nerve wherein T1r-mediated responses

311 were observed (Kasahara *et al.*, 2021). Notably, responses by these reported pathways were
312 tested by much higher concentrations of NaCl, typically in the several hundred mM range
313 (Kasahara *et al.*, 2021; Lewandowski *et al.*, 2016; Roebber *et al.*, 2019), than those used in
314 this study. These results imply that there may be multiple distinct concentration-dependent
315 pathways for Cl^- detection in taste buds. Given that high NaCl concentration is transduced as
316 an aversive taste through bitter and sour taste cells (Oka *et al.*, 2013), the relevance between
317 the reported high Cl^--responsive pathways and high NaCl responses by bitter and sour cells is
318 of interest, as pointed out by the previous studies, and will require further investigation.

319 Salt taste sensation and natriuresis are critical physiological processes that regulate
320 sodium intake and excretion to maintain body fluid homeostasis. Intriguingly, both processes
321 were found to use the counter anion Cl^- to regulate the molecular functions of the receptors,
322 T1rs and ANPRs, which share a similar extracellular protein architecture with a conserved Cl^-
323 -binding site. In the case of ANPR, mGluRs, and CaSR, positive allosteric modulations by Cl^-
324 for agonist binding have been observed, with some variations in the extent of the
325 enhancement (Eriksen & Thomsen, 1995; Kuang & Hampson, 2006; Liu *et al.*, 2020; Tora *et*
326 *al.*, 2018; Tora *et al.*, 2015). Whether the Cl^- actions on T1rs of other subtypes or from other
327 organisms have some variance is yet to be examined.

328

329 **Materials and methods**

330 **Crystallography**

331 All protein samples used for structural and functional analyses were prepared using
332 Drosophila S2 cells (Invitrogen) or high-expression clones for each protein sample
333 established from S2 cells in previous studies (Nuemket *et al.*, 2017; Yamashita *et al*, 2017).
334 No authentication or test for mycoplasma contamination was performed.

335 The L-glutamine-bound T1r2a/T1r3LBD crystals, in complex with a crystallization

336 chaperone Fab16A, were prepared in the presence of NaCl as described (Nuemket *et al.*,
337 2017). For the preparation of the Br^--substituted crystals, the obtained crystals were soaked in
338 a mother liquor consisting of 100 mM MES-Tris, pH 6.0, 50 mM NaBr, 17% PEG1500, 5%
339 PEG400, 5 mM L-glutamine, 2 mM $CaCl_2$, cryoprotected by gradually increasing the
340 concentration of glycerol to 10%, incubated for 2 hours, and flash-frozen.

341 The X-ray diffraction data were collected at the SPring-8 beamline BL41XU using
342 a PILATUS6M detector (DECTRIS) at wavelength 0.9194 Å or at the Photon Factory
343 beamline BL-1A using an EIGER X4M detector (DECTRIS) at wavelength 2.7 Å. The data
344 were processed with XDS (Kabsch, 2010) (Figure 2—figure supplement 1). The phases for
345 anomalous difference Fourier map calculation were obtained by molecular replacement
346 methods with the program PHASER (McCoy *et al*, 2007), using the structures of a single unit
347 of the mfT1r2a-3LBD-Fab16A complex (PDB ID: 5X2M; ligands and water models were
348 removed) (Nuemket *et al.*, 2017) as the search model (the R/R_{free} of the model for the Br^--data
349 collected at 0.9194 Å: 0.248/0.350; the Cl^--data collected at 2.7 Å: 0.233/0.339).

350

351 **Differential scanning fluorimetry (DSF)**

352 Differential scanning fluorimetry was performed as previously described (Yoshida *et al.*,
353 2019). The purified mfT1R2a/3LBD heterodimer protein was prepared (Nango *et al.*, 2016)
354 and dialyzed with buffer A (20 mM HEPES-NaOH, 300 mM sodium gluconate, pH 7.5) to
355 remove Cl^-. 1 μg of the dialyzed protein sample was mixed with Protein Thermal Shift Dye
356 (Applied Biosystems) and 0.003 – 10 mM NaCl in 20 μL of buffer A. The mixture solutions
357 were then loaded to a MicroAmpR Fast Optical 48-Well Reaction Plate (Applied Biosystems).
358 Fluorescent intensities were measured by the StepOne Real-Time PCR System (Applied
359 Biosystems) while the temperature raised from 25 °C to 99 °C with a velocity of 0.022 °C/sec.
360 For detection, the reporter and quencher were set as "ROX" and "none," respectively. The

361 apparent melting transition temperature (T_m) was determined using the maximum of the
362 derivatives of the melt curve (dFluorescence/dT) by Protein Thermal Shift Software version
363 1.3 (Applied Biosystems). The apparent dissociation constant ($K_{d\text{-app}}$) for Cl^- derived from the
364 T_m values at different NaCl concentrations was estimated using a thermodynamic model
365 proposed by Schellman (Schellman, 1975) as described (Yoshida *et al.*, 2019). The sample
366 sizes for the analyses by DSF, as well as Förster resonance energy transfer and isothermal
367 titration calorimetry described below, were set to obtain reliable values based on the
368 experiences in the previous studies (Nango *et al.*, 2016; Nuemket *et al.*, 2017; Yoshida *et al.*,
369 2019).
370
371 **Förster resonance energy transfer (FRET)**
372 FRET analysis was performed as described previously (Nango *et al.*, 2016; Nuemket *et al.*,
373 2017). The WT T1r2aLBD-Cerulean and T1r3LBD-Venus fusion heterodimer proteins were
374 prepared as described (Nuemket *et al.*, 2017). For the mutant protein preparation, a
375 T1r3-T105A mutation was introduced into the vector pAc-mfT1r3aL-Ve (Nango *et al.*, 2016)
376 using polymerase chain reaction. The mutant expression vector was co-introduced with
377 pAc-mfT1r2aL-Ce (Nango *et al.*, 2016) to Drosophila S2 cells using Polyethyleneimine (PEI)
378 "MAX" (Polysciences) as previously described (Bleckmann *et al*, 2019) with a ratio of 0.5 µg
379 pAc-mfT1r2aL-Ce, 0.5-µg pAc- mfT1r3aL-Ve-T105A, and 10-µg PEI to ~1 × 10^6 cells.
380 Protein expression and purification were conducted similarly as for the WT protein.
381 For the Cl^--titration, the purified protein samples were dialyzed against buffer A in
382 the presence of 1-mM L-alanine. Afterward, the samples were diluted with buffer A to reduce
383 the remaining L-alanine concentration below 1 µM (< ~1/100 of EC_{50} (Nango *et al.*, 2016;
384 Nuemket *et al.*, 2017)), and then incubated in the presence of 0.001–10 mM NaCl or 1 mM
385 L-glutamine in buffer A at 4°C overnight. For L-glutamine titration in the presence or absence

386 of Cl^-, the protein solution was dialyzed with buffer B (20 mM HEPES-Tris, 300 mM NaCl,
387 pH 7.5) or buffer C (20 mM HEPES-Tris, 300 mM sodium gluconate, pH 7.5) in the presence
388 of 1 mM L-alanine to prepare the conditions with or without Cl^-, respectively. Then, the
389 samples were diluted with buffer B or C to reduce the remaining L-alanine concentration
390 below 1 μM and then incubated in the presence of 0.01–1000 μM L-glutamine at 4°C
391 overnight. Fluorescence spectra were recorded at 298 K with a FluoroMax4
392 spectrofluorometer (Horiba). The sample was excited at 433 nm, and FRET was detected via
393 the emission at 526 nm. The emission at 475 nm was also recorded for the FRET index
394 calculation. The FRET index (intensity at 526 nm/intensity at 475 nm) was plotted against the
395 Cl^- or L-glutamine concentration, and the titration curves were fitted to the Hill equation using
396 KaleidaGraph (Synergy Software) or ORIGIN (OriginLab).
397
398 **Isothermal titration calorimetry**
399 In order to prepare the conditions with or without Cl^-, the purified mfT1R2a/3LBD
400 heterodimer protein was dialyzed with buffers B or C, respectively. The dialyzed protein
401 solution (~50 μM) was then loaded into the sample cell in iTC200 (GE Healthcare) after the
402 removal of insoluble materials by centrifugation (10,000×*g*, 15 min, 277 K). The titration was
403 performed by injecting 2 μL of 400 μM L-glutamine at intervals of 120 s at 298 K. The
404 thermograms and the binding isotherms were analyzed with Origin software, assuming one
405 set of binding sites for fitting.
406
407 **Fluorescence-detection size-exclusion chromatography-based thermostability assay**
408 **(FSEC-TS)**
409 A T1r3-T105A mutation was introduced in the vector pAc_mfT1r3L (Yamashita *et al.*, 2017)
410 by PCR. The mutant expression vector was co-introduced with pAc_mft1r2aL (Yamashita *et*

411 *al.*, 2017) to Drosophila S2 cells to establish a stable high-expression clone cell as previously
412 described (Yamashita *et al.*, 2017). The wild-type T1r2a/T1r3LBD and mutant
413 T1r2a/T1r3-105A-LBD proteins were expressed and purified as previously described (Nango
414 *et al.*, 2016) with several modifications as listed below. After the protein binding to
415 ANTI-FLAG M2 affinity gel, the resin was washed with either buffer D (20 mM
416 HEPES-NaOH, 0.3 M NaCl, 2 mM $CaCl_2$, 5 mM L-Gln, pH 7.5) or buffer E (20 mM
417 HEPES-NaOH, 0.3 M Na gluconate, 2 mM Ca gluconate, 5 mM L-Gln, pH 7.5). Then, the
418 protein was eluted with 100 μg/mL FLAG peptide in buffer D or E.

419 The protein solutions (50 μg/mL) in buffer D or E were incubated at 4 °C, 37 °C,
420 50 °C, 70 °C, or 90 °C at 2 hours. Subsequently, the samples were loaded on an SEC-5
421 column, 500 Å, 4.6 × 300 mm (Agilent) connected to a Prominence HPLC system (Shimadzu),
422 using buffer D or E as a running buffer at a flow rate of 0.3 ml min^{-1}. The elution profiles
423 were detected with an RF-20A fluorometer (Shimadzu), using excitation and emission
424 wavelengths of 280 and 340 nm for the detection of intrinsic tryptophan fluorescence.

425 The residual ratio after incubation at each temperature was estimated using the
426 fluorescence intensity at the elution peak, which corresponded to the T1rLBD dimer, *i.e.,* the
427 peak height at ~11.6 min. The values were normalized to the intensity of the sample incubated
428 at 4 °C as 1. In order to estimate the apparent melting temperature ($T_{\text{m-app}}$) of the sample, the
429 values of residual ratio at each temperature were fitted to the Gibbs-Helmholtz equation
430 transformed as shown below (assuming that the sample protein is under equilibrium between
431 a folding and unfolding state under each condition):

$$Residual\ ratio = 1 - \frac{1}{1 + exp\left[-\frac{\Delta H\left(1 + \frac{T}{T_{m-app}}\right) - \Delta C_P\left\{\left(T_{m-app} - \mathrm{T}\right) + Tln\left(\frac{T}{T_{m-app}}\right)\right\}}{RT}\right]}$$

432 where ΔH and ΔC_p are the enthalpy and heat capacity change of unfolding, respectively; T is
433 the temperature of the sample incubation; R is the gas constant. The fittings were performed

434 with KaleidaGraph (Synergy Software), with ΔH, ΔC_p, and $T_{m\text{-app}}$ are set as valuables.

435

436 **Single fiber recording from mouse chorda tympani (CT) nerve**

437 All animal experiments were conducted following the National Institutes of Health Guide for
438 the Care and Use of Laboratory Animals and approved by the committee for Laboratory
439 Animal Care and Use and the local ethics committee at Tokyo Dental College (Permit
440 Number: 228101) and Okayama University (Permit Number: OKU-2022897) Japan. The
441 subjects were six adult male C57BL/6JCrj mice (Charles River Japan, Tokyo, Japan) and four
442 T1r3GFP-KO mice, which were obtained by mating T1r3-GFP (Damak *et al*, 2008) and
443 T1r3-KO (Damak *et al*, 2003) mice. Mice were maintained on a 12/12-h light/dark cycle and
444 fed standard rodent chow and 8–20 weeks of age ranging in weight from 20 g to 30 g.

445 The mice were anesthetized with an injection of combination anesthetic agents
446 contained midazolam (0.8 mL/kg, Sandoz, Yamagata, Japan), medetomidine (0.75 mL/kg,
447 Nippon Zenyaku Kogyo Co., Fukushima, Japan), butorphanol tartrate (1 mL/kg, Meiji Seika
448 Pharma, Tokyo, Japan) and physiologic saline (7.45 mL/kg), and maintained at a surgical
449 level of anaesthesia, with additional injections of sodium pentobarbital (Nakarai Tesque,
450 Kyoto, Japan, 8–10 mg/kg ip every hour). Under anaesthesia, each mouse was fixed in the
451 supine position with a head holder, and the trachea cannulated. The right CT nerve was
452 dissected, free from surrounding tissues, after the removal of the pterygoid muscle and cut at
453 the point of its entry to the tympanic bulla. A single or a few nerve fibers were teased apart
454 with a pair of needles and lifted onto an Ag-AgCl electrode, and an indifferent electrode was
455 placed in nearby tissue. Their neural activities were amplified (K-1; Iyodenshikagaku,
456 Nagoya, Japan) and recorded on a computer using a PowerLab system (PowerLab/sp4; AD
457 Instruments, Bella Vista, NSW, Australia). For taste stimulation of fungiform papillae, the
458 anterior half of the tongue was enclosed in a flow chamber. Taste solutions or rinses (distilled

459 water) (~24 °C) were delivered to the tongue by gravity flow at the same flow rate (~0.1 mL
460 s^{-1}). For data analysis, we used the net average frequency for 10 sec after the stimulus onset,
461 which was obtained by subtracting the spontaneous frequency for the 10 sec duration before
462 stimulation from after stimulation. In the initial survey to identify a nerve fiber connecting to
463 T1r-expressing cells, test stimuli such as 100 mM NaCl, 10 mM HCl, 500 mM sucrose, 100
464 mM monopotassium glutamate, 20 mM quinine HCl were separately applied. If the fiber
465 responded to sucrose, we applied 10 μM–100 mM NMDG-Cl, NaCl, KCl, or either of 20 mM
466 L-glutamine or 100 mM sucrose with or without 10 mM NMDG-Cl to the tongue. The criteria
467 for the occurrence of response were the following: the number of spikes was larger than the
468 mean + two standard deviations of the spontaneous discharge for three 10 sec periods before
469 stimulation, and at least three spikes were evoked by taste stimulation (Yasumatsu *et al.*,
470 2012). In the case of T1r3GFP-KO mice, as the mice showed a significant response to 0.5 M
471 sucrose, we could identify sweet-responsive fibers (impulse frequency of 13.4 ± 1.31)
472 (Yasumatsu *et al.*, 2012). The reagents used were purchased from Wako Pure Chemical
473 Industries (Osaka, Japan; others). To block responses via T1r (Daly *et al.*, 2013; Margolskee
474 *et al.*, 2007; Ninomiya & Imoto, 1995; Ninomiya *et al.*, 1999), each tongue was treated with
475 30 μg ml^{-1} (~7 μM) gurmarin (Gur) dissolved in 5 mM phosphate buffer (pH 6.8) for 10 min,
476 similarly as described by Ninomiya & Imoto (Ninomiya & Imoto, 1995). To assure the
477 detection of responses from T1r-expressing cells, recordings from Gur-insensitive
478 sweet-responsive fibers were defined as those retaining impulse frequencies to 0.5 M sucrose
479 more than 60% after the Gur treatment (Ninomiya *et al.*, 1999) were excluded from the data.
480 The number of Gur-sensitive and Gur-insensitive fibers were six and three, respectively,
481 among 0.5 M sucrose responding fibers. The sucrose application was repeated 3–6 times
482 during the recordings. Additionally, the recovery of the suppressed responses was confirmed
483 using 15 mM β-cyclodextrin, which could remove the effect of Gur from the tongue

484 (Ninomiya *et al.*, 1999). All Gur-sensitive fibers recovered up to 60%–150% of responses
485 before Gur. At the end of the experiment, animals were killed by administering an overdose of
486 the anaesthetic. Repeated measures ANOVA and Student's paired *t*-test were used to
487 statistically evaluate the effects of chemicals or gene deletion. The sample size was calculated
488 according to power analysis, thereby resulting in three per group due to the effect size (d) of
489 6–9.3 to detect the effects of blocking or deleting T1r3.
490

491 **Two-bottle preference tests**

492 All training and testing sessions occurred during the light phase of the light/dark cycle. On the
493 first day of training, the WT mice (adult male C57BL/6JCrj) were water deprived for 23 h and
494 then placed in a test box with two bottles: one filled with water and the other empty. The
495 amount of fluid intake was measured after a 5 min presentation. After 4 days of training, mice
496 were used for test sessions if they drank water evenly on either side (nine mice). In the test
497 sessions, they were provided with two bottles, one containing 10 mM NMDG-Cl and the
498 other containing water, with or without Gur, for 5 min. The amount of liquid consumed was
499 measured by weighing the bottles, and a preference score of NMDG-Cl was calculated using
500 the following equation:

$$Preference\ score(\%) = \frac{V_{Cl}}{V_{Cl} + V_w} \times 100$$

501 where V_{cl} and V_w are the amount of NMDG-Cl intake and water intake, respectively.
502

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Competing interests

The authors declare that they have no conflict of interest.

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672

673 **Table 1.** Properties of the Cl^--binding to T1r2a/T1r3LBD.

Cl^--binding, DSF (n = 4)		
$K_{d\text{-app}}$ (mM)	0.111 ± 0.046	
Protein thermal stability, DSF (n = 6)		
condition	$+Cl^-$	$-Cl^-$
Melting temperature (˚C)	55.2 ± 0.03	46.6 ± 0.06
Protein thermal stability, FSEC-TS		
wild type T1r2a/T1r3LBD (n = 3)		
condition	$+Cl^-$	$-Cl^-$
Melting temperature (˚C)	56.4 ± 5.1	46.0 ± 0.3
mutant T1r2a/T1r3-T105ALBD		
condition	$+Cl^-$	$-Cl^-$
Melting temperature (˚C)	42.7 ± 0.1	46.7 ± 0.7
Cl^-- binding, FRET (n = 3)		
FRET index minimum	1.00 ± 0.005	
FRET index change	0.119 ± 0.014	
EC_{50} (mM)*	1.23 ± 0.53	
L-glutamine binding, FRET (n = 3)		
condition	$+Cl^-$	$-Cl^-$
FRET index minimum	1.08 ± 0.01	0.86 ± 0.01
FRET index change	0.11	0.17
EC_{50} (μM)	3.78 ± 1.29	3.87 ± 1.76
Hill coefficient	1.20 ± 0.88	0.94 ± 0.29
L-glutamine binding, ITC		
condition	$+Cl^-$	$-Cl^-$
N (sites)	0.389 ± 0.028	0.303 ± 0.023
K_a (M^{-1})	$(2.85 \pm 0.65) \times 10^5$	$(2.12 \pm 0.46) \times 10^5$
[converted to K_d (μM)]	[3.51]	[4.72]
ΔH (kcal/mol)	−12.3 ± 1.2	–12.9 ± 1.3
ΔS (cal/mol/deg)	–16.3	−18.8

674 *Hill coefficient was fixed to 1 for fitting.

675

676 **Figure legends**

677 **Figure 1**

678 **Salt taste sensation.**

679 Approximate concentration ranges of salt taste perceptions in humans (Bartoshuk *et al.*, 1978)
680 and qualities of taste sensation with known cells and receptors responsible for their sensing
681 are summarized.

682

683 **Figure 2**

684 **Cl^--binding sites in the medaka fish taste receptor T1r2a/T1r3LBD.**

685 (**A**) Schematic drawing of the overall architecture of T1r2a/T1r3. The crystal structure (PDB
686 ID: 5X2M) (Nuemket *et al.*, 2017) is shown at the LBD region, and helices B and C in T1r3
687 are labeled. (**B**) Anomalous difference Fourier map (4.5 σ, red) of the Br^--substituted
688 T1r2a/T1r3LBD crystal. (**C**) Anomalous difference Fourier map (4.5 σ, red) of the Cl^--bound
689 T1r2a/T1r3LBD crystal derived from the diffraction data collected at the wavelength of 2.7 Å.
690 In panels B and C, the site originally identified the Cl^--binding was framed. (**D**) A close-up
691 view of the Cl^--binding site in T1r3LBD in the Cl^--bound T1r2a/T1r3LBD (PDB ID: 5X2M).
692 (**E**) Amino-acid sequence alignment of T1r proteins and the related receptors at the Cl^-
693 -binding site. The "h," "m," and "mf" prefixes to T1rs indicate human, mouse, and medaka
694 fish, respectively. The position corresponding to Thr105 in T1r3 from medaka fish is
695 highlighted. (**F**) The structures of ANPR (PDB ID: 1T34, left) (Ogawa *et al*, 2004) and
696 mGluR2 (PDB ID: 5CNI, right) (Monn *et al*, 2015a) bound with Cl^-. (**G**) Superposition of the
697 Cl^--binding site in T1r3, ANPR, and mGluR2.

698

699 **Figure 2−figure supplement 1**

700 **X-ray data collection statistics of T1r2a/T1r3LBD-Fab16A complex.**

701

702 **Figure 2−figure supplement 2**

703 **The structure of the regions relating to the Cl^--binding site in medaka fish**
704 **T1r2a/T1r3LBD.**

705 (**A**) The Br^--binding site in T1r3. The anomalous difference Fourier map (4.5 σ, red) of the
706 Br^--substituted crystal is overlayed to the Cl^--bound T1r2a/T1r3LBD structure (PDB ID:
707 5X2M). (**B**) The Cl^--binding site in T1r3. The anomalous difference Fourier map (4.5 σ, red)
708 calculated from the data collected at the wavelength of 2.7 Å is overlayed. (**C**) The region in
709 T1r2a, which corresponds to the Cl^--binding site in T1r3, in the Cl^--bound T1r2a/T1r3LBD.
710 (**D**) The Br^--binding site in T1r2. The anomalous difference Fourier map (4.5 σ, red) is
711 overlayed to the Cl^--bound T1r2a/T1r3LBD structure. (**E**) The Br^--binding site in T1r2. The
712 2.7 Å-anomalous difference Fourier map (4.5 σ, red) of the Cl^--bound T1r2a/T1r3LBD, which
713 is the same map shown in panel B, is overlayed to the Br^--binding site in T1r2. No significant
714 peak was observed.

715

716 **Figure 2—source data 1**

717 **The anomalous difference Fourier maps shown in Figure 2B and 2C.**

718 The structure factor files and the coordinate files used for anomalous difference Fourier
719 calculation, and the resultant maps were included.

720

721 **Figure 3**

722 **The Cl^--binding properties of T1r2a/T1r3LBD.**

723 (**A**) Representative thermal melt curves of T1r2a/T1r3LBD in the presence of 0.003 –10 mM
724 concentrations of Cl^- measured using DSF. (**B**) Dose-dependent T_m changes of
725 T1r2a/T1r3LBD by addition of Cl^-. (n = 4) (**C**) Thermal melting curves of WT and the

726 T1r3-T105A mutant of T1r2a/T1r3LBD in the presence and absence of Cl^-, analyzed by
727 FSEC-TS. (n = 1) (**D**) Dose-dependent FRET signal changes of the T1r2aLBD-Cerulean and
728 T1r3LBD-Venus heterodimer by addition of Cl^-. (n = 3) (**E**) FRET index increases by adding
729 10 mM Cl^- or 1 mM L-glutamine to the WT or T1r3-T105A mutant
730 T1r2aLBD-Cerulean/T1r3LBD-Venus heterodimer relative to that in the absence of any
731 ligand in the absence of Cl^-. (n = 3) (**F**) Dose-dependent FRET signal changes of the
732 T1r2aLBD-Cerulean and T1r3LBD-Venus heterodimer induced by the addition of
733 L-glutamine in the presence and absence of Cl^-. (n = 3) The experiments were performed two
734 (panels A, B, D, and E), three (C and WT), four (F and +Cl^- condition), or one (C and mutant;
735 F and –Cl^- condition) time(s), and the results from one representative experiment are shown
736 with numbers of technical replicates. Data points represent mean and s.e.m.
737
738 **Figure 3–figure supplement 1**
739 **The properties of T1r2a/T1r3LBD in the presence and absence of Cl^-.**
740 (**A**) Binding analysis of gluconate by DSF. 0.1, 1, and 10 mM of L-glutamine, as a
741 representative ligand, and sodium gluconate was added to T1r2a/T1r3LBD in 20 mM
742 HEPES-NaOH, 300 mM NaCl, pH 7.5. The mean increases of T_m (ΔT_m) from that in the
743 absence of a ligand (54.1 ˚C, measured on the same sample, n = 2) are plotted. Error bars are
744 in s.e.m. (n = 4). (**B**) Representative thermal melt curves of T1r2a/T1r3LBD in the presence
745 or absence of Cl^-, measured by DSF in the same condition in Figure 3C, and the panels C, D
746 in this figure. (**C**, **D**) The L-glutamine-binding to T1r2a/T1r3LBD was measured by
747 isothermal titration calorimetry. The upper and lower panels show the raw data and integrated
748 heat signals upon L-glutamine injection to T1r2a/T1r3LBD in the presence (C) and absence
749 (D) of Cl^-. The binding isotherms were fitted assuming 1 ligand: 1 heterodimer binding. The
750 experiments were performed one (panel A), two (B) four (C), or five (D) time(s), and the

751 results from one representative experiment are shown with numbers of technical replicates.

752

753 **Figure 3—source data 1**

754 **Excel file with numerical data used for Figure 3.**

755

756 **Figure 4**

757 **Electrophysiological and behavioral analyses of the T1r-mediated Cl^- responses in**

758 **mouse.**

759 (**A**–**D**) Results of single fiber recordings from the mouse chorda tympani nerve. (**A**)

760 Representative recordings of single fibers that connect to T1r-expressing taste cells. The

761 stimuli were 10 mM NMDG-Cl, 100 mM sucrose, 100 mM sucrose + 10 mM NMDG-Cl, 20

762 mM L-glutamine, or 20 mM L-glutamine + 10 mM NMDG-Cl. Lines indicate the application

763 of stimuli to the tongue. All the responses were suppressed by lingual treatment with a T1r

764 blocker, Gur (right). (**B**) Impulse frequencies in response to the concentration series of

765 NMDG-Cl, NaCl, or KCl before and after Gur treatment in WT mice. Responses to

766 NMDG-gluconate are also shown. The mean number of net impulses per 10 s (mean

767 response) ± s.e.m. in Gur-sensitive fibers (n = 5–6 from six mice). (**C**) Impulse frequencies in

768 response to the concentration series of NMDG-Cl before and after Gur treatment were

769 measured in T1r3-KO mice (n = 4–5 from three mice). Responses to NMDG-gluconate are

770 also shown. (**D**) Impulse frequencies to 20 mM L-glutamine or 100 mM sucrose in the

771 absence or presence of 10-mM NMDG-Cl before and after Gur treatment. Responses to 20

772 mM L-glutamine or 100 mM sucrose by T1r3-KO mouse are also shown. Values are mean ±

773 s.e.m. (n = 3–5 from three mice each). *, **: paired t-test; $P < 0.05$ (*) and < 0.01 (**). (**E**)

774 Amount of fluid intake for water and 10-mM NMDG-Cl in the two-bottle preference tests.

775 Values are mean ± s.e.m. (n = nine mice) (**F**) NMDG-Cl intake shown in (E) normalized to

water intake (preference score) in the two-bottle preference tests. A score > 50% indicates that the taste solution was preferred over water.

Figure 4—source data 1

Excel file with numerical data used for Figure 4.

List of Figure supplements and source data

Figure 2—figure supplement 1

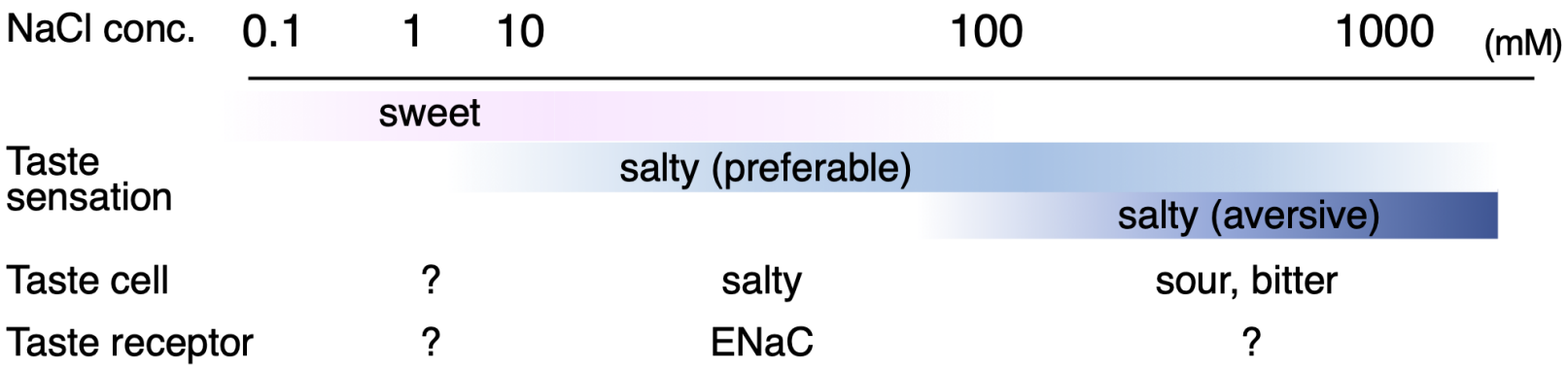
Figure 2—figure supplement 2

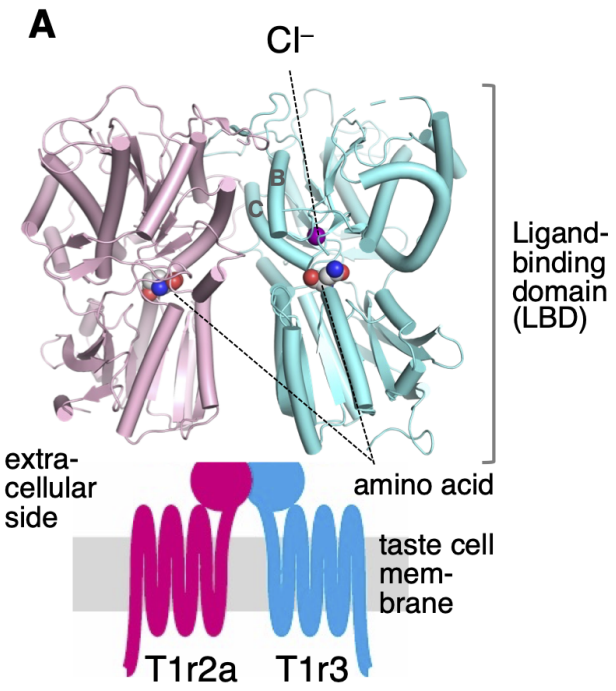
Figure 2—source data 1

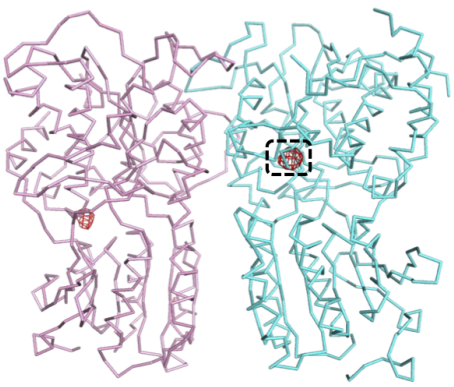
Figure 3—figure supplement 1

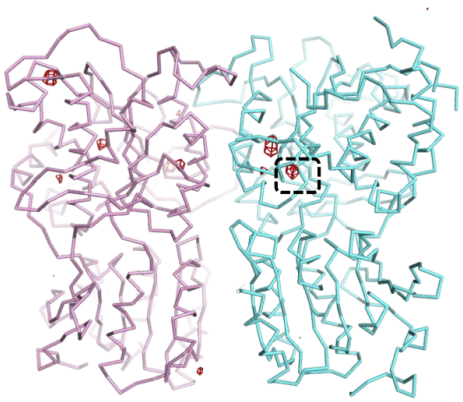
Figure 3—source data 1

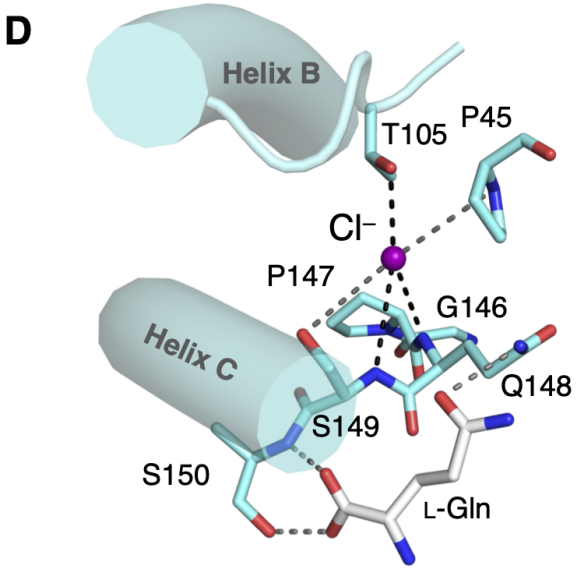
Figure 4—source data 1


NaCl conc.
0.1
1
10
100
1000
(mM)
sweet
Taste sensation
salty (preferable)
salty (aversive)
Taste cell
?
salty
sour, bitter
Taste receptor
?
ENaC
?



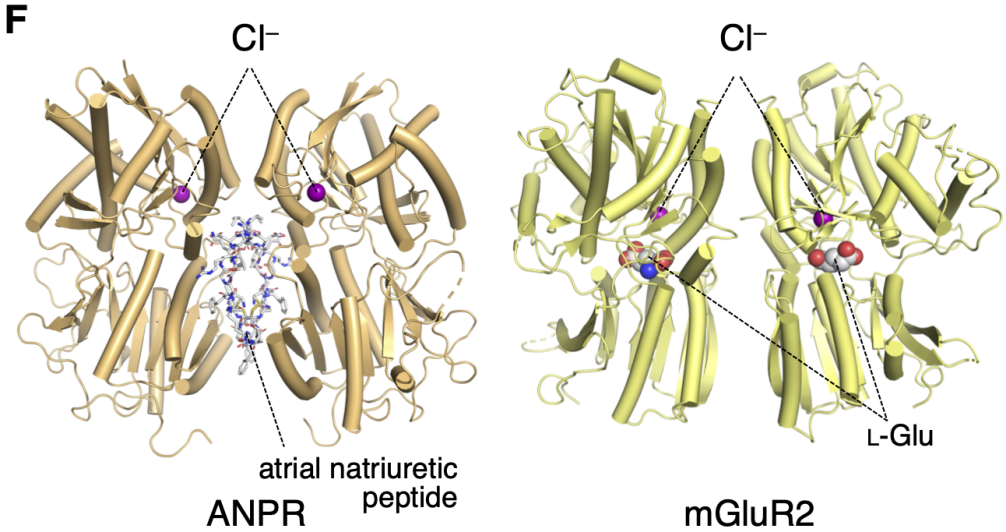


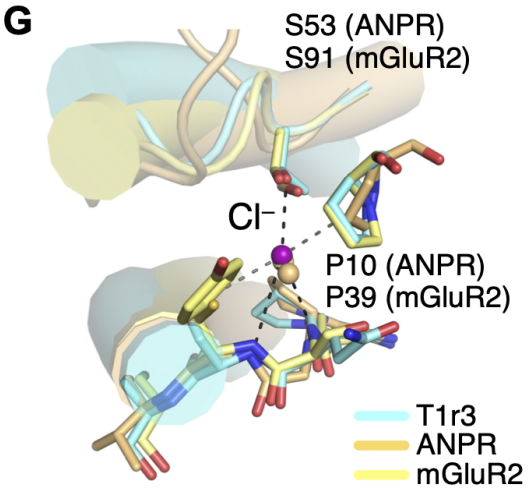




E

hT1r1	44	FPL	—	104	DVC	—	143	VIGPDSTN
mT1r1	45	FSL	—	105	DVC	—	144	LIGPDNTD
mfT1r1	14	FSL	—	104	DVC	-	147	VIGPDSSS
hT1r2	39	FSL	—	100	DVC	-	138	VIGPDNSE
mT1r2	42	FTL	—	103	DVC	-	141	VIGPDNSE
mfT1r2a	40	FNI	—	99	DHC	-	136	VIGPFTST
hT1r3	41	FPL	—	101	DTC	-	141	VIGPHSSE
mT1r3	41	FPL	—	101	DTC	-	141	VIGPHSSE
mfT1r3	44	FPL	—	104	NTC	-	144	VIGPQSSE
mGluR2	38	FPV	—	90	DSC	-	139	VIGGSYSD
ANPR	9	LPL	—	52	SSE	-	81	FLGPGCVY

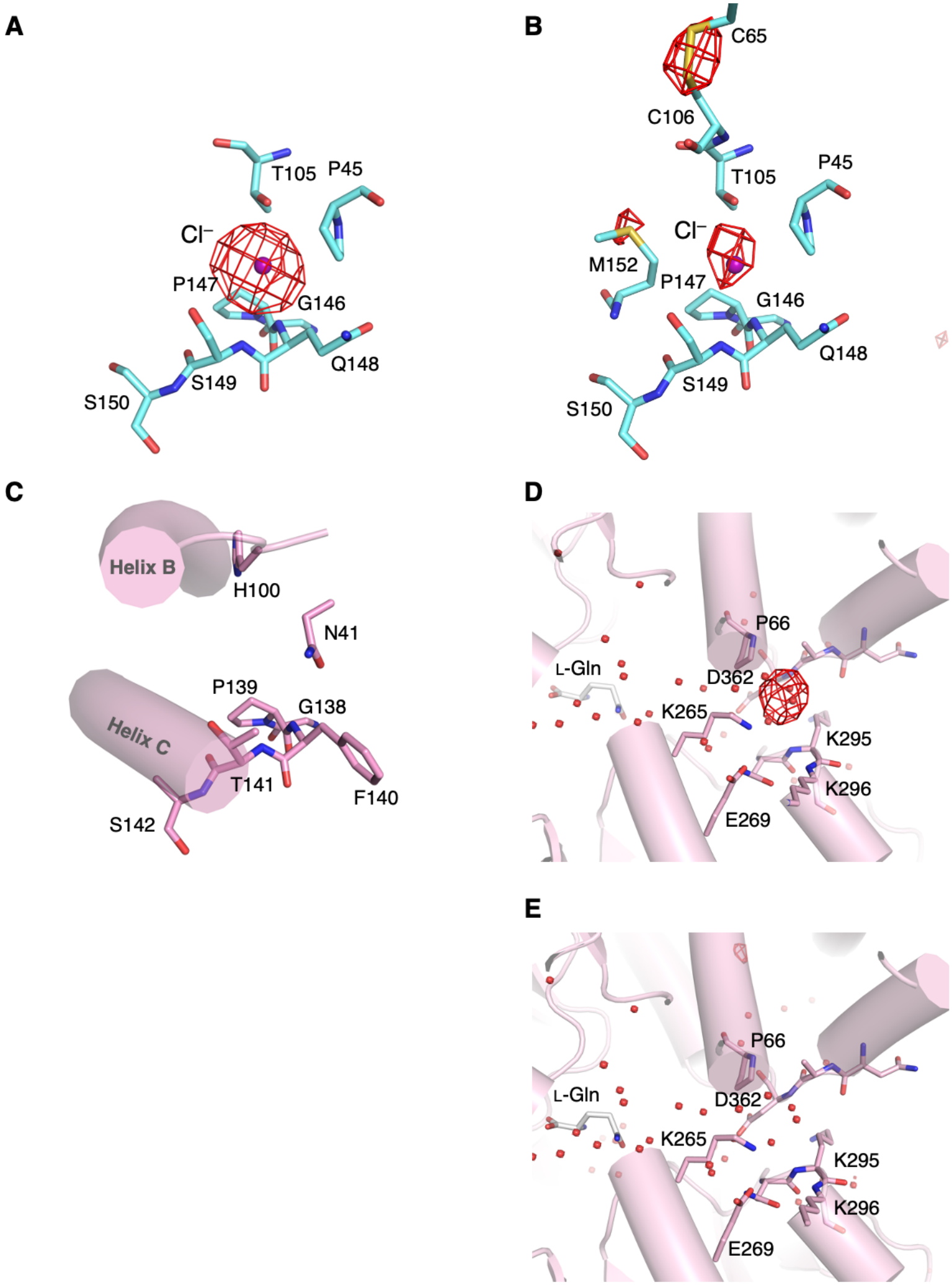


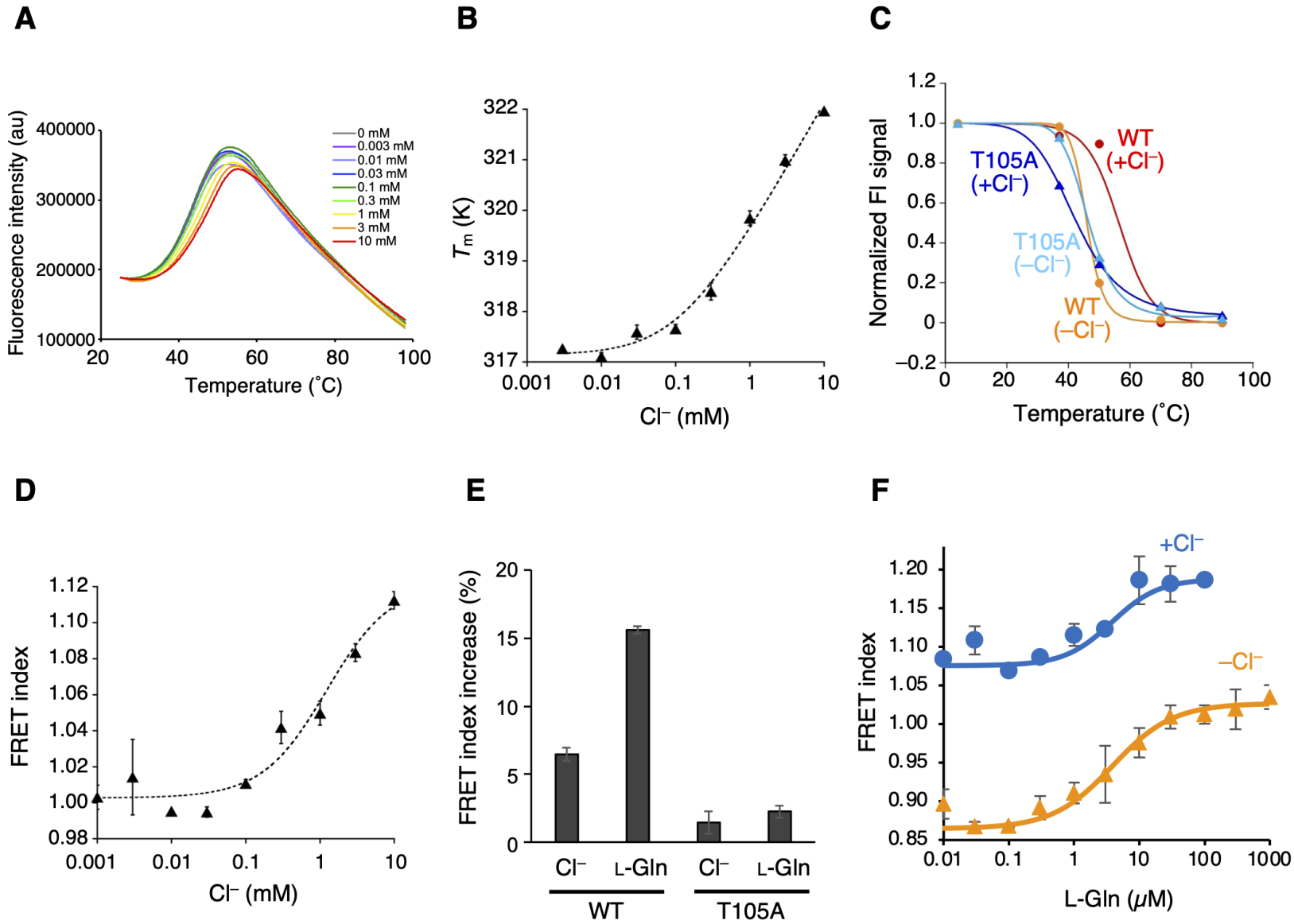


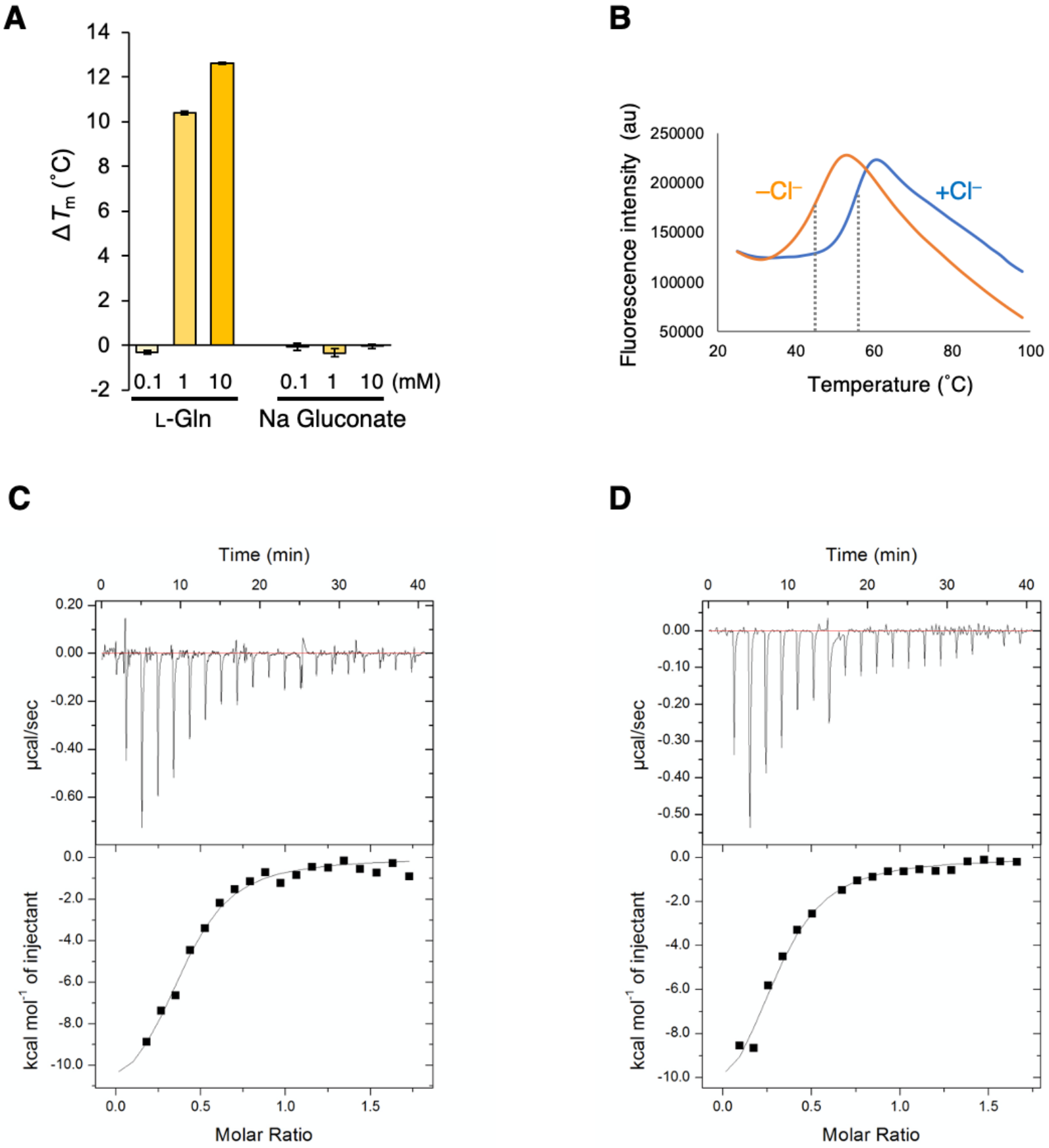
X-ray data collection statistics of T1r2a/T1r3LBD-Fab16A complex.

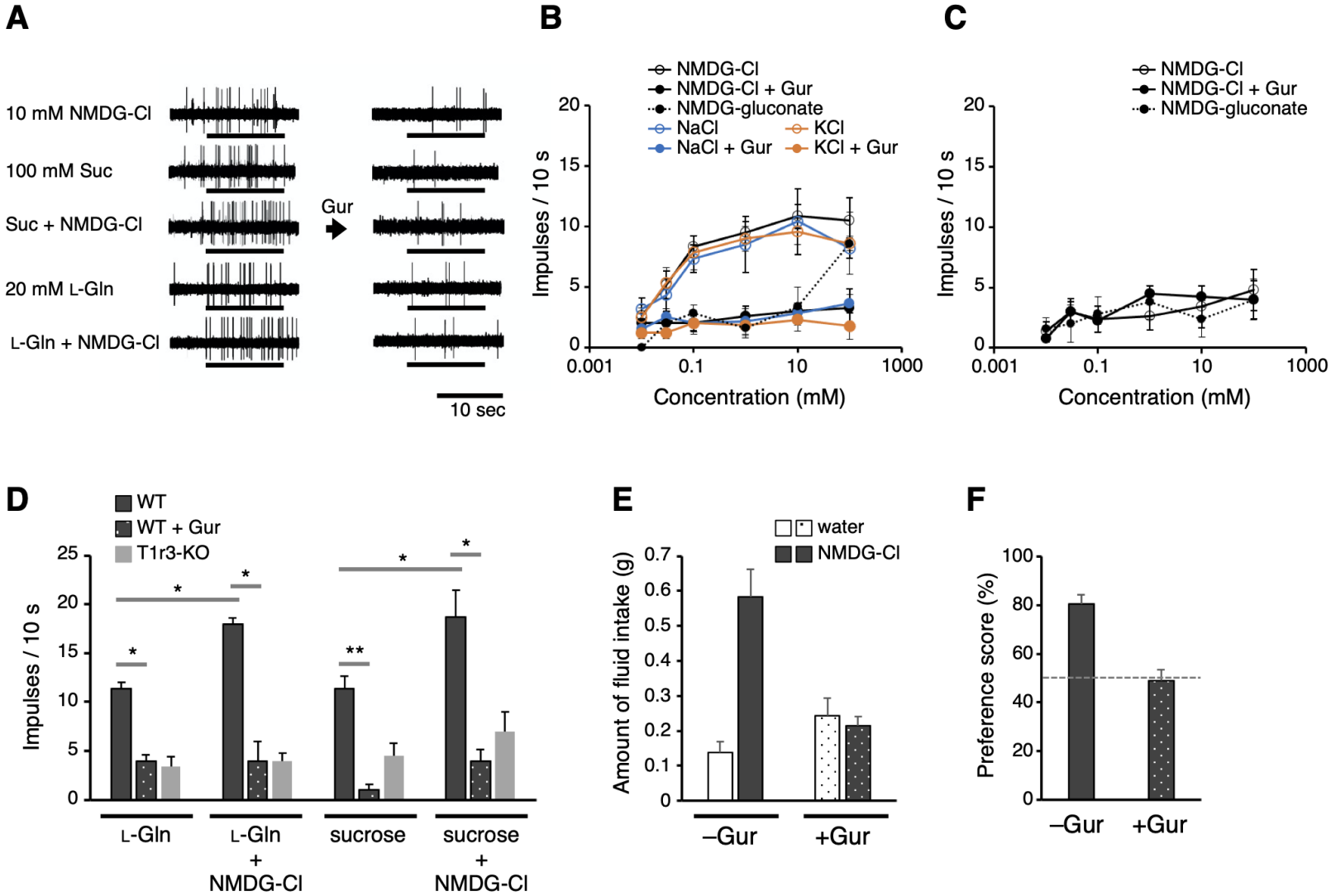
	Br^--bound	**Cl^--bound**
Beamline	SPring-8	Photon Factory
	BL41XU	BL-1A
Detector	PILATUS6M	EIGER X4M
Wavelength (Å)	0.9194	2.7
Space group	$P2_12_12_1$	$P2_12_12_1$
Cell dimensions		
a (Å)	102.8	102.8
b (Å)	121.6	120.8
c (Å)	129.9	129.1
Resolution (Å)	50-3.41 (3.43-3.41)	49.8-3.32 (3.33-3.32)
R_{sym} (%)*	0.094 (0.808)	0.089 (0.865)
$I/\sigma(I)$*	16.4 (2.3)	15.1 (2.45)
Completeness (%)*	99.8 (99.2)	99.6 (97.8)
Redundancy*	7.0 (7.0)	6.9 (6.8)

*Values in parentheses refer to data in the highest resolution shells.


A
T105
P45
Cl⁻
P147
G146
Q148
S149
S150
B
C65
C106
T105
P45
Cl⁻
M152
P147
G146
Q148
S149
S150
C
Helix B
H100
N41
P139
G138
Helix C
T141
F140
S142
D
P66
L-Gln
D362
K265
K295
K296
E269
E
P66
L-Gln
D362
K265
K295
K296
E269


A
Fluorescence intensity (au)
400000
300000
200000
100000
20
40
60
80
100
Temperature (˚C)
0 mM
0.003 mM
0.01 mM
0.03 mM
0.1 mM
0.3 mM
1 mM
3 mM
10 mM
B
T_m (K)
322
321
320
319
318
317
0.001
0.01
0.1
1
10
Cl⁻ (mM)
C
Normalized FI signal
1.2
1.0
0.8
0.6
0.4
0.2
0
−0.2
0
20
40
60
80
100
Temperature (˚C)
WT (+Cl⁻)
T105A (+Cl⁻)
T105A (−Cl⁻)
WT (−Cl⁻)
D
FRET index
1.12
1.10
1.08
1.06
1.04
1.02
1.00
0.98
0.001
0.01
0.1
1
10
Cl⁻ (mM)
E
FRET index increase (%)
20
15
10
5
0
Cl⁻
L-Gln
Cl⁻
L-Gln
WT
T105A
F
FRET index
1.20
1.15
1.10
1.05
1.00
0.95
0.90
0.85
0.01
0.1
1
10
100
1000
L-Gln (μM)
+Cl⁻
−Cl⁻


A
14
12
10
8
6
4
2
0
-2
Δ T_m (˚C)
0.1 1 10
0.1 1 10 (mM)
L-Gln
Na Gluconate
B
Fluorescence intensity (au)
250000
200000
150000
100000
50000
20 40 60 80 100
Temperature (˚C)
–Cl⁻
+Cl⁻
C
Time (min)
0 10 20 30 40
0.20
0.00
-0.20
-0.40
-0.60
µcal/sec
0.0
-2.0
-4.0
-6.0
-8.0
-10.0
kcal mol^{-1} of injectant
0.0 0.5 1.0 1.5
Molar Ratio
D
Time (min)
0 10 20 30 40
0.00
-0.10
-0.20
-0.30
-0.40
-0.50
µcal/sec
0.0
-2.0
-4.0
-6.0
-8.0
-10.0
kcal mol^{-1} of injectant
0.0 0.5 1.0 1.5
Molar Ratio


A
10 mM NMDG-Cl
100 mM Suc
Suc + NMDG-Cl
20 mM L-Gln
L-Gln + NMDG-Cl
Gur
10 sec
B
NMDG-Cl
NMDG-Cl + Gur
NMDG-gluconate
NaCl
NaCl + Gur
KCl
KCl + Gur
Impulses / 10 s
Concentration (mM)
C
NMDG-Cl
NMDG-Cl + Gur
NMDG-gluconate
Impulses / 10 s
Concentration (mM)
D
WT
WT + Gur
T1r3-KO
Impulses / 10 s
L-Gln
L-Gln + NMDG-Cl
sucrose
sucrose + NMDG-Cl
E
water
NMDG-Cl
Amount of fluid intake (g)
–Gur
+Gur
F
Preference score (%)
–Gur
+Gur