## A modern ionotropic glutamate receptor with a $K^+$ selectivity signature sequence

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## Abstract

Glutamate is the major excitatory neurotransmitter in the mammalian central nervous system and gates non-selective cation channels. The origins of glutamate receptors are currently not understood as they differ structurally and functionally from simple bacterial ligand-gated ion channels. Here, we report the discovery of an ionotropic glutamate receptor that combines the typical eukaryotic domain architecture with the 'TXVGYG' signature sequence of the selectivity filter found in K<sup>+</sup> channels. This receptor exhibits functional properties intermediate between bacterial and eukaryotic glutamate-gated ion channels, suggesting a link in the evolution of ionotropic glutamate receptors.

#### Main text

Rapid signal transduction in the central nervous system of vertebrates relies on the neurotransmitter glutamate (Glu) and ionotropic glutamate receptors (iGluRs)<sup>1</sup>. Historically, iGluRs were grouped according to their responses to the small molecule agonists AMPA (α-amino-3-hydroxyl-5-methyl-4-isoxazolepropionic acid; GluA1-A4), kainate (GluK1-K5) and NMDA (*N*-methyl-D-aspartate; GluN1, GluN2A-D and GluN3A and B). The origins of iGluRs form the basis of their functional and structural diversity but are currently not understood<sup>2-4</sup>. Simple bacterial iGluRs, such as GluR0 from *Synechocystis*, presumably arose from the fusion of periplasmic binding proteins (PPBP) and K<sup>+</sup> channels (**Fig. 1a**, left)<sup>4-7</sup>. GluR0 differs in several major ways from its metazoan and plant homologues<sup>5</sup>. Structurally, it has only two transmembrane (TM) segments, instead of three, and no N-terminal domain (NTD) (**Fig. 1a**). Functionally, it distinguishes itself from the non-selective cation permeation of iGluRs in being K<sup>+</sup>-selective because of its pore loop (P-loop), which contains the 'TXVGYG' signature sequence of the K<sup>+</sup> channel selectivity filter (**Fig. 1b**). Pharmacologically, GluR0 is activated by amino acids other than Glu, but not by classical iGluR agonists.

The complex domain architecture shared by eukaryotic iGluRs (**Fig. 1a**, middle) suggests a common eukaryotic ancestor<sup>2, 8</sup> that may merge elements of GluR0, like the K<sup>+</sup> selectivity filter, with those of iGluRs, like the NTD or C-terminus. In this study, we report the discovery and functional characterization of AvGluR1, which is the first eukaryotic iGluR with the complex architecture of vertebrate iGluRs and the signature sequence of the K<sup>+</sup> channel selectivity filter. Domain organization and function seem to indicate that AvGluR1 represents the "transitional stage" between bacterial and vertebrate iGluRs.

### Results

#### Identification and structure

We searched the eukaryotic protein database of the National Center for Biotechnology Information (NCBI) with artificial sequences that combined a mammalian LBD and C-terminus (either from GluK2, GluA2 or GluN1) with a K<sup>+</sup> selectivity filter (from GluR0, **Methods**). The only protein returned by these searches that aligned to iGluRs over all domains was a putative iGluR from the fresh-water bdelloid rotifer *Adineta vaga*, a remarkable model organism for asexual reproduction and horizontal gene transfer (HGT) whose genome has been partially sequenced<sup>9</sup>. We termed this uncharacterized iGluR AvGluR1. The domain organization of AvGluR1 mirrors that of eukaryotic iGluRs (**Fig. 1a**, right). It features the 'SYTAXLA'-motif in TM2 that is conserved in all known eukaryotic iGluRs<sup>3</sup> (**Fig. 1b**) but contains a 'TXVGYG'-motif in its P-loop, as in GluR0 and K<sup>+</sup> channels. Consequently the P-loop of AvGluR1 aligns most closely to that of K<sup>+</sup> channels, while the remainder of the TM domain resembles that of iGluRs (**Supplementary Table S1**). The LBD exhibits weaker similarity to both eukaryotic iGluRs and GluR0, but an arginine residue that contacts the ligand's  $\alpha$ -carboxyl group in all mammalian iGluRs (e.g. R523 in GluK2) is conserved in AvGluR1 (R546) and so is an acidic residue contacting the  $\alpha$ -amino group (E738 in GluK2), which is an aspartic acid in AvGluR1 (D744) and in all NMDA receptors (**Supplementary Fig. S1**). Residues contacting the  $\gamma$ -carboxyl of Glu are not conserved in AvGluR1 (e.g. T690 in GluK2 is A704 in AvGluR1, like in GluN3A and B but in no other iGluR) and AvGluR1 can gate upon binding amino acid ligands other than Glu (see below). There is low conservation of the NTD of GluK2 compared to AvGluR1 (**Supplementary Table S1**) and to other lower invertebrates (data not shown), except for two marked cysteine residues (**Supplementary Fig. S1**) that stabilize the NTD in all mammalian iGluRs<sup>10</sup>. Finally, AvGluR1 has a C-terminus that is 43 amino acids in length whose sequence shows no homology to any known protein. Similarly, no homologues are found for the C-termini of many iGluRs of lower invertebrates (data not shown).

#### **Functional characterization**

When we expressed AvGluR1 in *Xenopus leavis* oocytes we recorded large currents in response to Glu perfusion (**Fig. 2a** and **3a**). Like GluR0, AvGluR1 was gated by Glu with high potency (EC50 = 4.0 µM; 95 % confidence interval 0.8 to 20.0 µM, N = 7; **Fig. 2b**). AvGluR1 was also gated by several other amino acids, including aspartate, serine, glutamine, and, very weakly, by glycine (**Fig. 2a**). Glycine had no effect on the response to Glu (**Supplementary Fig. S2**). These amino acids do not gate AMPA and kainate receptors but serve as agonists of NMDA receptors<sup>5, 11-13</sup>. AvGluR1 was also gated by iGluR agonists kainate and AMPA (**Fig. 2a** and **Supplementary Fig. S3**), as observed for mammalian receptors, but not for GluR0<sup>5, 11, 12, 14</sup>. For aspartate and kainate, the difference in agonist response seems to be due to a shift in potency since the currents extracted from the fit at the EC50 concentration are in the same range as for Glu (**Supplementary Fig. S3**).

AvGluR1 currents activated slowly but exhibited full desensitization to prolonged agonist application (**Fig. 2a, 2c** and **3a**). The slow activation of AvGluR1 resembles the behavior of GluR0, and is distinct from the rapidly activating iGluRs (**Fig. 2c**), whereas the full desensitization resembles the behavior of iGluRs, but differs from GluR0, which only desensitizes partially<sup>5</sup>. Slow activation was also observed when agonist was presented by photolysis of caged-L-glutamate (**Fig. 2d** and **e**).

Finally, despite having a K<sup>+</sup> channel type selectivity filter sequence, AvGluR1 exhibited a poor selectivity for K<sup>+</sup> over Na<sup>+</sup>, similar to that of vertebrate iGluRs. Analysis with the Goldman-Hodgkin-Katz equation indicates a  $P_{Na+}/P_{K+}$  permeability ratio of 0.3 (*versus* 0.01 for GluR0 and0.8 for GluK2<sup>5, 15</sup>) (**Fig. 3a** and **Supplementary Fig. S4**). To test for Ca<sup>2+</sup> permeability, we

compared currents recorded in normal extracellular solution (containing 1.8 mM  $Ca^{2+}$ ) and in the absence of  $Ca^{2+}$  (zero added extracellular  $Ca^{2+}$  with 0.5 mM EGTA). Neither current amplitude nor reversal potential differed between these conditions (**Fig. 3a** and **b**). Moreover, the  $Ca^{2+}$ -activated CI<sup>-</sup>-channels of Xenopus oocytes<sup>16</sup> did not contribute to the current, since replacing external CI<sup>-</sup> did not modify either Glu-evoked current amplitude or reversal potential of AvGluR1. These data indicate that the channel has little or no permeability to  $Ca^{2+}$  (**Fig. 3a** and **b**).

Together, amino acid sequence, domain organization, and function indicate that AvGluR1 represents a functional intermediate between GluR0 and iGluRs.

#### Phylogenetic analysis

To further examine the relationship between AvGluR1 and iGluRs, we performed a phylogenetic analysis of 251 iGluRs sampled from bacteria, plants and animals (Supplementary Table S2 and S3). In particular, we collected all iGluR-like proteins from the few early branching animals that have such sequences (e.g. Trichoplax adhaerens, the cnidarian Nematostella vectensis or the mollusk Aplysia californica). Phylogeny was inferred using several methods including maximum likelihood (ML) with RAxML<sup>17</sup>. In the ML phylogeny (Fig. 4), AvGluR1 branches out early compared to all other metazoan iGluRs with bootstrap support of 77 and 85 %. Trees built using different ML methods and neighbor joining yielded the same branching order and similar bootstrap support, as did trees build on a larger dataset automatically collected by FlowerPower<sup>18</sup>, and if the GYG-sequence in AvGluR1 was replaced by three consecutive glutamines to mimic non-NMDA iGluRs (data not shown). This branching order supports the functional analysis and suggests that AvGluR1 represents a transitional stage between bacterial and metazoan iGluRs. In particular, the phylogenetic analysis allows excluding the possibility that AvGluR1 arose from the secondary acquisition of the 'TXVGYG'-sequence by a rotifer iGluR. In such a re-evolution scenario, the overall sequence of AvGluR1 should resemble that of iGluRs from animals that started to develop independently before and after rotifers. Phylogenetic analysis would then place AvGluR1 deep within the animal part of the tree, which is not observed.

#### Discussion

The origins of iGluRs are mysterious<sup>2-4</sup>. Our own database search (**Methods**) confirmed that iGluRs are absent from basal eukaryotes, such as fungi, protozoa or the sponge *Amphimedon queenslandica*<sup>2, 19</sup>. We cloned and characterized an iGluR whose amino acid sequence, domain organization and function resembles the missing intermediate between bacterial and eukaryotic iGluRs. In the *A. vaga* genome, the gene coding for AvGluR1 is located near transposable elements<sup>9</sup> and we cannot exclude that it originates from HGT<sup>20</sup>. The existence of bacterial ion

channels with an LBD but without K<sup>+</sup> selectivity motif raised the question which class of proteins developed into iGluRs<sup>21</sup>. Our findings suggest that iGluRs evolved by addition of an NTD and TM3 to a GluR0-like protein that contained a 'TXVGYG'-motif. These new domains endow new functionalities to iGluRs, in that NTDs provide for sub-type specific assembly and modulation of gating, while the third TM helix locates the C-terminus intracellularly for sorting, binding to the cytoskeleton and modulation<sup>1</sup>. The promiscuous agonist binding of AvGluR1 is divergent from typical AMPA, kainate or NMDA receptors and rather resembles that of chemosensory receptors in single cell organisms and sensory cells of multicellular organisms<sup>22</sup>. Indeed, iGluR-like chemosensors that lack an NTD were recently identified in the fruit fly, and it will be interesting to see how these proteins and AvGluR1 accommodate a chemically diverse spectrum of ligands. The low conservation of the NTD and C-terminus of AvGluR1 may not be surprising as this receptor likely serves different roles than modern neurotransmitter receptors for which cytosolic association and modulation are crucial. The identification of AvGluR1 and voltage-sensing phosphatases<sup>23</sup> thus re-emphasizes that exotic invertebrates offer a repertoire of novel proteins that remain to be discovered.

#### Methods

#### Uniprot accession numbers

The following sequences were used for the alignment of **Fig. 1** and **Supplementary Fig. S1** (Uniprot identifiers in parentheses): *R. norvegicus* GluK2 (P42260), *A. thaliana* Glr2.1 (O04660), *Synechocystis* GluR0 (P73797), *S. lividans* KcsA (P0A334), *A. pernix* K<sub>v</sub> (Q9YDF8) and *D. melanogaster* Shaker (P08510). Sequences were aligned using Muscle  $3.8^{24}$  with the default parameters.

#### AvGluR1 identification and bioinformatics

AvGluR1 (Uniprot identifier B3G447) was identified in the NCBI non-redundant protein database using a search with PHI-Blast. The primary query sequence was a chimeric protein of GluK2 (from *R. norvegicus*, LBD, TM3 and C-terminus, residues 426 to 556 and 658 to 908) and GluR0 (from *Synechocystis* PCC 6803, pore domain, residues 154 to 246). Residues are numbered beginning with the start-methionine. The query was limited to eukaryotes (taxonomy ID 2759) and the PHI-pattern [TVIL]-G-[YF]-G-[DFLYGHKARN] that covers the K<sup>+</sup> selectivity filter of a majority of K<sup>+</sup> channels<sup>25</sup>. As of August 25 2010, AvGluR1 is the highest ranking hit for this query (27% identity) and the only hit aligning over close to the entire length of the protein. Identical queries using the LBD, TM3 and C-terminus taken from the GluA2 AMPA receptor (from *R. norvegicus*, Uniprot identifier Q9R174, residues 409 to 539 and 644 to 883) or the GluN1 NMDA receptor

(from *R. norvegicus*, Uniprot identifier P35439, residues 413 to 555 and 654 to 938) also yielded AvGluR1 as the highest ranking hit.

#### Preparation of expression constructs

The a-splice isoform of GluK2 was obtained from K. Partin (Colorado State University, Fort Collins, Co) and cloned into pGEM-HE. Genomic DNA of *A. vaga* was a kind gift of E. Gladyshev and I. Arkhipova (Marine Biology Laboratory, Woods Hole, MA and Harvard University, Cambridge, MA). Forward (TAT CCC GGG CAC CAT GAG AAT ATT TCG AGA AAA CAT CTC GTG) and reverse (ATA TCT AGA TTA TGC AAT GAT TTG TGA TAT AGT AGA CGA AG) oligonucleotide primers for polymerase chain reaction (PCR) included Xmal and Xbal restriction sites for subcloning into pGEM-HE. PCR reaction parameters were: One cycle (95 °C for 60 s); 32 cycles (95 °C for 30 s, 56 °C for 30 s, 72 °C for 180 s), one cycle (95 °C for 10 min). Several independent PCR reactions yielded the same AvGluR1 sequence that differs from that deposited in genome sequencing in 26 positions (**Accession Codes**).

#### RNA preparation and electrophysiology

RNA was transcribed by using mMessage mMachine T7 transcription kit. Surgically extracted *X. laevis* oocytes were injected with 5 ng of RNA in 50 nL volume. Cells were incubated in ND-96 solution (96 mM NaCl, 2 mM KCl, 1.8 mM CaCl<sub>2</sub>, 1 mM MgCl<sub>2</sub>, 50 mgmL<sup>-1</sup> gentamicin, 2.5 mM sodium pyruvate, and 5 mM Hepes, pH 7.4) at 18 °C for 12–36 h before experiments. Cells expressing GluK2 were pre-treated with concanavalin-A. Two-electrode voltage-clamp (TEVC) was performed at room temperature with a Dagan CA-1B amplifier, Digidata-1440A data acquisition board and pClamp10 software. Oocytes were placed in a perfusion dish and recordings were performed in ND-96 recording solution without antibiotics. For uncaging the MNI-caged-glutamate, illumination was done with a 150 W xenon lamp through a Nikon Diaphot inverted microscope with a 20× 0.75 NA fluorescence objective (Nikon). Illumination time was defined by a Uniblitz shutter (Vincent Associates) controlled by the Digidata-1440 board and pClamp10 software package (Axon Instruments).

#### Data analysis

To estimate relative permeabilities of Na<sup>+</sup> and K<sup>+</sup> we analyzed reversal potentials using the simplified Goldman-Hodgkin-Katz voltage equation,  $P_{Na^+}/P_{K^+} = \exp(\Delta E_{rev}F/RT)$ , where  $\Delta E_{rev}$  is the reversal potential difference between Na<sup>+</sup> and K<sup>+</sup>, F Faraday's constant, R the gas constant and T temperature and after correction for liquid junction potentials. To determine the EC50 (**Fig. 2** and **Supplementary Fig. S3**), dose–response data were fit in SigmaPlot with the Hill equation  $I=x^h/(x^h+EC50^h)$ , where I represents the normalized current, x represents concentration, and h is the Hill Coefficient.

#### iGluRs in archaea and unicellular eukaryotes

To identify iGluRs in archaea and unicellular eukaryotes, we searched the non-redundant protein database of the NCBI with Blast. We used GluK2 from *R. norvegicus* as the query sequence and limited the search to archaea (2157), funghi (4751), monosiga (81525), diatoms (2836), alveolata (33630), trypanosome (5690) and dictyostelium (5782; numbers in parentheses are taxonomy identifiers). As of August 25 2010, highest-ranking hits were K<sup>+</sup> channels or completely unrelated proteins with E-values near zero. No proteins that contain an iGluR-like LBD and TM domain could be identified.

#### Phylogenetic analysis

Using Blast searches, we identified 251 iGluR-like proteins in bacteria, plants and animals with special attention to early branching eukaryotes (**Supplementary Table S2**). For these organisms, we collected all proteins that aligned to AvGluR1 or GluK2 over the pore and LBD. This dataset included iGluRs that were identified previously, as well as sequences that have not yet been annotated (**Supplementary Table S3**). This search also revealed AvGluR2 (Uniprot identifier B3G464), an *A. vaga* protein that features the TXVGYG-pore motif and shares 53% sequence identity with AvGluR1. Sequences were aligned with Muscle<sup>26</sup>. Gaps and the N- and C-terminal domains only found in eukaryotic proteins were manually removed. Phylogenetic analysis was primarily performed with the maximum likelihood (ML) method and RAxML 7.2.6<sup>17</sup>. 20 ML searches were conducted to find the best ML tree (**Fig. 4**) and branch support was assessed with 100 bootstrap replicates. We observed the same branching order of AvGluR1 in trees that were built with different amino acids substitution matrices, through neighbor joining with BioNJ<sup>27</sup> and based on a dataset of 606 proteins automatically collected with FlowerPower<sup>28</sup> followed by neighbor joining.

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## **Author Contributions**

H.J. and G.S. designed and performed experiments, analyzed data and wrote the paper; E.Y.I. designed experiments, analyzed data and wrote the paper.

## **Competing Financial Interests**

The authors declare no competing financial interests.

## **Supplementary Information**

Supplementary Figures S1-4 and Supplementary Tables S1-3

## **Accession Codes**

Sequences of AvGluR1 and AvGluR2 have been deposited in GenBank under accession codes HQ901600 and HQ901601.

## **Figures**



**Figure 1.** Origins of iGluRs. (a) TM and domain organization of iGluRs, AvGluR1 and proteins resembling bacterial ancestors. Color shading is based on sequence identities of individual domains (also see **Supplementary Table S1**). (b) Sequence alignment of P-loop and TM2 for AvGluR1, iGluRs from mammals and plants, GluR0 and K<sup>+</sup> channels. Residues found in at least three sequences are highlighted in bold. Colors highlight conserved motifs.



**Figure 2.** Agonist specificity and slow gating of AvGluR1. (**a**) Agonist specificity measured for 1 mM agonist concentration. Traces of single cell responses to various agonists (bottom). Bar graphs show average current amplitudes  $\pm$  s.e.m. for multiple cells (top). \*F-test analysis of variance showed that agonist responses are significantly different at the 1% level (P < 10<sup>-10</sup>). Post-hoc analysis using the Tukey-Kramer method showed that the response to Glu is different from that of all other agonists at the 1% significance level (P < 0.0001 for each pair-wise comparison). (**b**) Peak AvGluR1 response to 15 s application of Glu at various concentrations (mean  $\pm$  s.e.m. from 7 oocytes). Data were fit as described in the Methods (EC50 = 4.0  $\mu$ M, 95 % confidence interval 0.8 to 20.0  $\mu$ M, h = 1.0, n = 7). In (a) and (b) agonists were applied at 3 min intervals to allow recovery from desensitization. (**c**) Normalized currents of GluK2 (grey trace) and AvGluR1 (black trace) elicited by prolonged 1 mM Glu application reveal slow activation of AvGluR1. (**d**) Currents elicited by 20  $\mu$ M MNI-caged-L-glutamate released by light pulses of different duration also rise slowly. (**e**) Time to peak of AvGluR1 currents elicited by Glu uncaging or perfusion (ns indicates no statistically significant differences using the Student's *t*-test, P ≥ 0.2). In (**a**) and (**e**) number of observations shown in parentheses.



**Figure 3.** Ion selectivity of AvGluR1. (**a**) Current-voltage relationship of AvGluR1 in Na<sup>+</sup> (solid circles) and K<sup>+</sup> (open circles) extracellular solution. The reversal potential shifts by 19.7 mV from - 24.3 to -2.5 mV. Inset: Representative Glu gated currents at -100, -80, -60, -40, -20 to 0 mV in Na<sup>+</sup> extracellular solution. (**b**, **c**) Reversal potentials (**b**) and current amplitudes (**c**) in normal extracellular ND96 solution (containing 1.8 mM Ca<sup>2+</sup>), Ca<sup>2+</sup>-free ND96 (zero added extracellular Ca<sup>2+</sup> with 0.5 mM EGTA) and Cl<sup>-</sup>-free ND96 (Cl<sup>-</sup> is replaced with gluconate). In (**b**) and (**c**) number of observations shown in parentheses and ns indicates no statistically significant differences using the Student's *t*-test (P ≥ 0.4).



**Figure 4.** Maximum likelihood (ML) tree of AvGluR1 and iGluRs. 251 iGluR sequences were collected from all three kingdoms of life and the ML tree was constructed as described in the Methods. Bootstrap support values are shown at the major branches. Taxa and branches are color coded with bacteria in blue, plants in green, animals in magenta and AvGluR1 and AvGluR2 in purple.

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## SUPPLEMENTARY INFORMATION

# A modern ionotropic glutamate receptor with a $K^{+}$ selectivity signature sequence

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### Supplementary Figures



**Supplementary Figure S1.** Multiple sequence alignment of iGluRs and  $K^+$  channels. Domains of iGluRs and  $K^+$  channels were aligned using Muscle. For NTD, S1, S2 and TM3 residues in bold are found in at least two sequences. For TM1, P and TM2 residues in bold are found in at least three sequences. Key functional residues are highlighted in color (see main text for details).



**Supplementary Figure S2.** No synergistic effect of glutamate gating by glycine. (a) Representative glutamate-gated currents near the EC50 concentration in the presence or absence of 200  $\mu$ M glycine. (b) Current amplitudes in the presence or absence of 200  $\mu$ M glycine. Means are not significantly different (P = 0.67, Student's *t*-test). Error bars are s.e.m.



**Supplementary Figure S3.** Dose-response curves for aspartate and kainate. (**a**) For aspartate, we measured an EC50 of 1.8 mM (95% confidence interval 0.1 to 32.5 mM, h = 1.0, n = 6). (**b**) For kainate measured an EC50 of 0.7 mM (95% confidence interval 0.1 to 4.6 mM, h = 1.5, n = 5). At the EC50 the current amplitudes extracted from the fit were 10.4, 8.2 and 12.3  $\mu$ A for glutamate, aspartate and kainate, respectively. Error bars are s.e.m.



**Supplementary Figure S4.** Current-voltage relationships obtained at the current peak. (**a**) Current amplitude at -40 mV in response to repeated short voltage ramps. (**a**, **b** and **c** mark measurements evoked by three successive ramps near the peak of the current response.) (**b**) Current-voltage relationships obtained from successive ramps a, **b** and **c**, indicated in (**a**), around the current peak. Ramps were from -100 mV to 50 mV, 70 ms in duration, applied once every 100 ms. These three voltage-ramps produce nearly identical current responses and zero-crossings.

## **Supplementary Tables**

AvGluR1 vs.	GluR6	Glr2.1	GluR0	kcsA	kvAP	Shaker
Domain						
NTD	9	12				
LBD	23	18	17			
TM1	34	23	19	19	15	16
Р	20	31	19	38	33	14
TM2	38	51	32	27	3	16
ТМЗ	21	20				

**Supplementary Table S1.** Percent sequence identity between AvGluR1 and iGluRs, GluR0 and  $K^{+}$  channels for different domains. For TM1, P and TM2 numbers in bold indicate the highest scores. Identities were determined manually after alignment.

Species name	Abbreviation	Number	Source
	in tree	of proteins	
		collected	
ANIMALS			
Adineta vaga	Av	2	NCBI
Aplysia californica	Ac	12	NCBI
Caenorhabditis elegans	Ce	10	NCBI
Capitella teleta	Ct	26	Joint Genome Institute (JGI)
Drosophila melanogaster	Dm	22	NCBI
Danio rerio	Dr	28	NCBI
Nematostella vectensis	Nv	10	NCBI
Rattus norvegicus	Rn	18	NCBI
Strongylocentrotus purpuratus	Sp	8	NCBI
Trichoplax adherens	Та	13	NCBI
PLANTS			
Arabidopsis thaliana	At	20	NCBI
Brachypodium distachyon	Bd	16	JGI
Oryza sativa japonica	Os	19	NCBI
Physcomitrella patens	Рр	2	NCBI
BACTERIA	Р	45	NCBI

Supplementary Table S2. Organisms searched for iGluRs and number of sequences identified.

Name in tree Accession number		Label		
Adineta vaga				
AvGluR1	ACD54595	AvGluR1		
AvGluR2	ACD54612	AvGluB2		
Aplysia californica				
AcGluR1	AAO46102.1	NMDA-like receptor splice form		
AcGluR3	AAP41203.1	Glutamate receptor subunit protein GluR1		
AcGluR2	ACA13599.1	NR2		
AcGluR4	AAP41204.1	Glutamate receptor subunit protein GluR2		
AcGluR5	AAP41205.1	Glutamate receptor subunit protein GluR3		
AcGluR6	AAP41206.1	Glutamate receptor subunit protein GluR4		
AcGluR7	AAP41207.1	Glutamate receptor subunit protein GluR5		
AcGluR8	AAP41208.1	Glutamate receptor subunit protein GluR6		
AcGluR9	AAP41209.1	Glutamate receptor subunit protein GluR7		
AcGluR10	ACB05517.1	Glutamate receptor 8		
AcGluR11	ACB05519.1	Glutamate receptor 10		
AcGluR12	ACV91076.1	Glutamate receptor subunit protein GluR10		
Caenorhabditis elegans	1	1		
CeGluR1	NP_492017.3	Glutamate receptor family (AMPA) family member (glr-3)		
CeGluR2	NP_495033.2	NMDA class glutamate receptor family member (nmr-1)		
CeGluR3	NP_495639.2	Glutamate receptor family (AMPA) family member (glr-4)		
CeGluR4	NP_498887.2	Glutamate receptor family (AMPA) family member (glr-1)		
CeGluR5	NP_505244.1	Glutamate receptor family (AMPA) family member (glr-5)		
CeGluR6	NP_506694.3	NMDA class glutamate receptor family member (nmr-2)		
CeGluR7	NP_508441.3	Glutamate receptor family (AMPA) family member (glr-7)		
CeGluR8	NP_509097.1	Glutamate receptor family (AMPA) family member (glr-8)		
CeGluR9	NP_741822.2	Glutamate receptor family (AMPA) family member (glr-6)		
CeGluR10 NP_001021114.1		Glutamate receptor family (AMPA) family member (glr-2)		
Capitella teleta	0			
CtGluR1	Capca1_167269	estExt_Genewise IPlus.C_7930005		
CtGluR2	Capca1_225637	estExt_rgenesh1_pg.C_6130009		
CIGIUR3	Capca1_96910	e_gw1.129.07.1		
CIGIUR4	Capca1_109025	estExt_Genewise1Plus.C_400002		
CtCluBe	Capca1_140075	estExt_Genewise1.0_2340020		
CtGluR7	Capca1_170222	estExt_Genewise1Flus.C_0130023		
	Capca1_104454	estExt_Genewise1.C_1720020		
CtGluR0	Capca1_103192	o gw1 703 5 1		
CtGluR10	Cancal 170176	estEvt Genewise1Plus C 1620047		
CtGluP11	Capca1_1/91/0	estExt_Genewise (Flus.C_1020047		
CtGluR12	Cancal 211454	frenesh1 ng C scaffold 463000011		
CtGluR13	Canca1 222580	estExt_faenesh1_pg.C_1460013		
CtGluR14	Cancal 194620	frenesh1 ng C scaffold 1131000005		
CtGluR15	Capca1_137020	e aw1 190 20 1		
CtGluR16	Capca1_02100	e gw1 50 47 1		

CiGuR18     Capa1_10366     eutilit_Genevasi C_B3002       CiGuR20     Capa1_13072     eutilit_Genevasi C_B3002       CiGuR21     Capa1_107912     eutilit_Genevasi C_B3002       CiGuR23     Capa1_107912     eutilit_Genevasi C_B3002       CiGuR23     Capa1_107912     eutilit_Genevasi C_B30002       CiGuR23     Capa1_10871     Igenesh1_p_G_Scatfol_11000020       CiGuR25     Capa1_108985     Igenesh1_p_G_Scatfol_11000010       CiGuR25     Capa1_108985     Igenesh1_p_G_Scatfol_162000017       CiGuR25     Capa1_108980     Igenesh1_p_G_Scatfol_1700010       OrduR1     AA225751     Cidumate receptor subunit       DmGluR3     AA225751     Cidumate receptor Subunit Namato subtype       DmGluR4     AA3331     CH25739       DmGluR5     AM46171     A730129_1       DmGluR6     AP403951     HUB0300       DmGluR8     AP7309A01     NMA0 receptor 1       DmGluR1     AV308051     RE09730p       DmGluR10     NP_27323.1     Iontopic receptor 2       DmGluR10     NP_27323.1     Iontopic receptor 1       DmGluR11	CtGluR17	Capca1_43271	gw1.20.62.1
CiGlinP30     Capar1_12072     cellsL_genewier 1, 29.0.962005       CiGlinP21     Capar1_21867     cellsL_genewier 1, 29.0.962005       CiGlinP21     Capar1_16871     fignesht_p.g.0.safdkl_27100033       CiGlinP23     Capar1_168971     fignesht_p.g.0.safdkl_271000020       CiGlinP23     Capar1_164900     fignesht_p.g.0.safdkl_27100010       CiGlinP23     Capar1_164900     fignesht_p.g.0.safdkl_27100010       CiGlinP23     Capar1_164900     eilEst_Genewise1.0.3140016       CiGlinP23     Capar1_164900     eilEst_Genewise1.0.3140016       CiGlinP24     Capar1_164900     eilEst_Genewise1.0.3140016       CiGlinP24     Capar2471     Cidliamate receptor subunit       DmGluR3     AAC60712.1     Gidliamate receptor DGluR18       DmGluR4     AA03031.1     Cidliamate receptor DGluR18       DmGluR5     AAM4057.1     R2590p       DmGluR4     AA03031.1     R2590p       DmGluR5     AAM49854.1     H003030       DmGluR6     NP_70940.1     NIDA receptor 1       DmGluR4     AA03951.1     R259730       DmGluR5     AA71127.1     R271430 <td>CtGluR18</td> <td>Capca1_103666</td> <td>e_gw1.20.60.1</td>	CtGluR18	Capca1_103666	e_gw1.20.60.1
CKGNR20     Capca1_248871     estExt_genesht_pg.C.g520005       CKGNR21     Capca1_107912     e.gw1.488.11       CGNR22     Capca1_186771     fgenesht_pg.C.gcafbd.Z71000033       CKGNR24     Capca1_186870     fgenesht_pg.C.gcafbd.Z71000030       CKGNR24     Capca1_186870     fgenesht_pg.C.gcafbd.J1900020       CKGNR24     Capca1_18695     fgenesht_pg.C.gcafbd.J57000010       CKGNR24     Capca1_18696     fgenesht_gg.C.gcafbd.J57000010       CKGNR24     Capca1_164990     fgenesht_gg.C.gcafbd.J57000010       CKGNR24     Capca1_164990     fgenesht_gg.C.gcafbd.J57000010       CKGNR24     CA22675.1     Glutamate receptor subunit       DmGUR3     AA22675.1     Glutamate receptor DGNR1B       DmGUR4     AA23053.1     Glotamate receptor DGNR1B       DmGUR5     AAM4675.1     A531242_1 MMD receptor 2       DmGUR6     AAM4965.1     HL05030       DmGUR6     AAM4965.1     H000767       DmGUR6     AAM4965.1     H000767       DmGUR6     AA7127.1     A731773       DmGUR6     AA7127.1     R5134736       DmGUR61	CtGluR19	Capca1_152072	estExt_Genewise1.C_8280002
CHGMP21     Capaca 1.07912     e_gw1.1488.1.1       CHGMP23     Capaca 1.188771     fgnesh1_ps_C_scaffold_27000033       CHGMP23     Capaca 1.204860     fgnesh1_ps_C_scaffold_4200007       CHGMP23     Capaca 1.204860     fgnesh1_ps_C_scaffold_4500007       CHGMP23     Capaca 1.204860     fgnesh1_ps_C_scaffold_4500007       CHGMP23     Capaca 1.194990     cellst_Genewise1.C_3140018       CHGMP33     Capaca 1.194990     cellst_Genewise1.C_3140018       DmGUR3     AAC00192.1     Glutamate receptor subunit       DmGUR4     AAL3954.1     CH00030       DmGUR5     AAM4057.1     AF381242_1 NMCA receptor JGURIB       DmGUR4     AAM3965.1     HE0030p       DmGUR5     AAM4057.1     AF381242_1 NMCA receptor 1       DmGUR6     APA7127.1     AF38757.9       DmGUR4     AAM3965.1     HE0030p       DmGUR5     AAM4065.1     HE30970p       DmGUR6     NP_70394.0.1     NDA receptor 1       DmGUR4     NP_70394.0.1     RE07345p       DmGUR4     NP_70394.0.1     RE07345p       DmGUR1     AV39812.1	CtGluR20	Capca1_218867	estExt_fgenesh1_pg.C_9520005
CHGLIR22     Capcal _ 18871     Tgenesh1_p3_C_scaffol_271000033       CIGUR23     Capcal _ 186470     Fgenesh1_p3_C_scaffol_27000020       CIGUR24     Capcal _ 186985     Igenesh1_p3_C_scaffol_26200007       CIGUR25     Capcal _ 186985     Igenesh1_p3_C_scaffol_26200007       CIGUR26     Capcal _ 186985     Igenesh1_p3_C_scaffol_26200007       DmGluR1     AA28575.1     Glutamate receptor subunit       DmGluR2     AA28575.1     Glutamate receptor Subunit Kainate subtype       DmGluR3     AA40697.1     A7381249_1 NMDA receptor 2       DmGluR4     AA2837.1     RE03730       DmGluR5     AA4487.1     RE03730       DmGluR6     NAV172.1     A736730       DmGluR1     AV3690.1     RE03730       DmGluR1     AV3690.1     RE079450       DmGluR1     AV3690.1     RE079450       DmGluR1     AV3690.1     RE079450	CtGluR21	Capca1_107912	e_gw1.1488.1.1
CRGuR23     Capca1_18470     fignesh1_pG_c_setRidi_19000020       CRGuR24     Capca1_204960     fignesh1_pG_c_setRidi_L51700010       CRGuR25     Capca1_184990     estExt_Genewise1.C_3140018       DroGuR26     Capca1_184990     estExt_Genewise1.C_3140018       DroGuR2     AA2857.1     Glutamate receptor subunit       DmGUR2     AA2857.1     Glutamate receptor Subunit       DmGUR3     AAC00192.1     Glutamate receptor DGUR118       DmGUR4     AA4885.1     H1080305       DmGUR5     AAM48167.1     AF3512.9_1 NMOA receptor 2       DmGUR5     AAM48167.1     R1080305       DmGUR6     AAM4806.1     R1080305       DmGUR6     AAM4806.1     R1080305       DmGUR6     AAM4985.1     R1080305       DmGUR7     AAM985.1     R1080305       DmGUR6     AA7712.1     A7316739       DmGUR7     AA999.1     R607345       DmGUR7     AA51647.1     R213792       DmGUR18     NP_5017360     R007456       DmGUR18     NP_5017366     R113410       DmGUR18     NP_5	CtGluR22	Capca1_188571	fgenesh1_pg.C_scaffold_271000033
CIGUR24     Capca1_284980     fgenesh1_pgC_scaffold_45200007       CIGUR25     Capca1_188995     fgenesh1_pgC_scaffold_5700010       CIGUR26     Capca1_188995     setExt_Genewlse1C_3140016       Drosophile melanogater     Dirosophile melanogater     Dirosophile melanogater       DmGUR3     AA28575.1     Glutamate receptor subunit kainats subtype       DmGUR3     AA28575.1     Glutamate receptor Subunit kainats subtype       DmGUR3     AA28575.1     Glutamate receptor DGURIB       DmGUR4     AA138343.1     GH25591p       DmGUR4     AA38343.1     FE68730p       DmGUR8     AM48667.1     A7381249_1 NMOA receptor 1       DmGUR8     AAM50983.1     FE68730p       DmGUR8     AAV127.1     A73673p       DmGUR8     AAV36902.1     FE617403p       DmGUR10     NP_72732.1     Ionofropic receptor 76b       DmGUR11     AA28690.1     FE24732p       DmGUR14     NP_60173769.1     Ionofropic receptor 76b       DmGUR14     NP_60173769.1     Ionofropic receptor 76b       DmGUR14     NP_60169769.1     Ionofropic receptor 76b	CtGluR23	Capca1_185470	fgenesh1_pg.C_scaffold_119000020
CiGluR25     Capca1_189895     fgenesh1_gp_C_scaffold_517000010       CiGluR26     Capca1_164990     etExt_Genewise1.C_3140016       Drosphil melanogaster     Discompt and and acceptor subunit       DmGluR1     AA28975.1     Gutamate receptor subunit kainate subtype       DmGluR3     AAC00192.1     Gutamate receptor DGluR118       DmGluR4     AA28975.1     Gutamate receptor DGluR118       DmGluR5     AAM46167.1     AF381242_1 MMDA receptor 2       DmGluR4     AA3934.3     EK6730p       DmGluR5     AAM46167.1     AF381242_1 MMDA receptor 1       DmGluR6     AAM49854.1     HL08030p       DmGluR6     AAM49854.1     HL08030p       DmGluR6     AAM5085.1     REC6730p       DmGluR6     AA7127.1     A731673p       DmGluR7     AA30901.1     RE07450p       DmGluR11     AA30901.1     RE07450p       DmGluR12     AA3091.2     RE07450p       DmGluR13     AA9991.1     Iontorpic receptor 76       DmGluR14     NP_501795.1     Iontorpic receptor 76       DmGluR18     NP_00103975.1     Coffee1 <td>CtGluR24</td> <td>Capca1 204960</td> <td>fgenesh1 pg.C scaffold 452000007</td>	CtGluR24	Capca1 204960	fgenesh1 pg.C scaffold 452000007
Cigur26     Capcat_164990     estExt_Genewise1C_3140016       DroSophila melanogastr     Uncomposition and the second subunit       DmGluR1     AA28575.1     Glutamate receptor subunit       DmGluR2     AA28575.1     Glutamate receptor Subunit Anate subtype       DmGluR3     AAC00192.1     Glutamate receptor Subunit Anate subtype       DmGluR4     AA3933.1     CH2591p       DmGluR5     AM46167.1     AF381242.1 MUDA receptor 2       DmGluR6     AAM9854.1     H.08030p       DmGluR6     AAM9854.1     H.08030p       DmGluR7     AAM50963.1     REG6730p       DmGluR8     Nr_73940.1     NUDA receptor 1       DmGluR8     Nr_73940.1     NUDA receptor 8a       DmGluR10     Nr_72732.1     Ionotropic receptor 76b       DmGluR10     Nr_72732.1     Ionotropic receptor 76b       DmGluR14     Nr_6017310     Ionotropic receptor 76b       DmGluR14     Nr_601137080.1     Ionotropic receptor 76b       DmGluR14     Nr_601137080.2     Ir56       DmGluR20     Nr_00103703.1     CG6221       DmGluR20     Nr_00103703.1	CtGluR25	Capca1_189895	fgenesh1_pg.C_scaffold_517000010
Drosophila melanogaster     Av28574.1     Glutamate receptor subunit       DmGluR1     Av28575.1     Glutamate receptor subunit kainate subtype       DmGluR2     Av28575.1     Glutamate receptor Subunit kainate subtype       DmGluR3     Av28575.1     Glutamate receptor Subunit kainate subtype       DmGluR4     AL3934.1     GH2591.0       DmGluR5     Av46167.1     AF381249.1 MIDA receptor 2       DmGluR6     Av466167.1     AF381249.1 MIDA receptor 2       DmGluR6     Av466167.1     AF381249.1 MIDA receptor 2       DmGluR6     NP_30940.1     NIDA receptor 1       DmGluR6     NP_27308.1     Inotoropic receptor 6a       DmGluR7     Av436003.1     RE134159       DmGluR10     NP_272738.1     Inotoropic receptor 76       DmGluR14     NP_349176.1     Inotoropic receptor 76       DmGluR15     NP_57241.1     Inotoropic receptor 76       DmGluR16     NP_57241.1     Inotoropic receptor 76       DmGluR18     NP_001137066.2     Ir756       DmGluR19     NP_00136736.1     Glotarmate receptor       DmGluR2     Al6250.1     Glutarmate receptor <td>CtGluR26</td> <td>Capca1_164990</td> <td>estExt_Genewise1.C_3140016</td>	CtGluR26	Capca1_164990	estExt_Genewise1.C_3140016
Dresophile melanogaster       DmGluR2     AA2857.1     Glutamate receptor subunit kainate subtype       DmGluR3     AA28575.1     Glutamate receptor DGluRIIB       DmGluR4     AA29343.1     GH25991p       DmGluR5     AAM6065.1     AF381249_11MDA receptor 2       DmGluR6     AAM99854.1     HL08030p       DmGluR7     AAM6065.1     RE06730p       DmGluR8     NP_30940.1     NNDA receptor 1       DmGluR10     NP_27238.1     Ionotropic receptor 8a       DmGluR11     AX36902.1     RE1349p       DmGluR13     AAX51947.1     RE24732p       DmGluR14     NP_649176.1     Ionotropic receptor 76b       DmGluR16     NP_57295.1     Ionotropic receptor 75d       DmGluR16     NP_001137968.2     Ir76b       DmGluR18     NP_00103763.1     Ionotropic receptor 75d       DmGluR21     NP_001036735.1     Glutamate receptor       DrGluR2 <t< td=""><td></td><td></td><td></td></t<>			
DmGluR1     AAA2857.1     Glutamate receptor subunit       DmGluR2     AAA2857.1     Glutamate receptor GluRilB       DmGluR3     AC00192.1     Glutamate receptor OluRilB       DmGluR4     AAL33343.1     GH25591p       DmGluR5     AAM40167.1     H20303p       DmGluR6     AM49085.1     H00303p       DmGluR6     AM49085.1     H00303p       DmGluR6     AM49085.1     RE06730p       DmGluR7     AM50963.1     RE06730p       DmGluR6     AN1127.1     AT31673.9       DmGluR7     AM50963.1     RE0473.9       DmGluR8     NP_730840.1     RE0745.9       DmGluR10     NP_72738.1     Ionotropic receptor 8a       DmGluR14     AV308012.1     RE0745.9       DmGluR15     NP_57296.1     Ionotropic receptor 76       DmGluR18     NP_00137066.2     I756       DmGluR18     NP_00137066.2     I756       DmGluR20     NP_00137066.2     I756       DmGluR21     NP_00103735.1     Gd5621       DmGluR21     NP_00103673.1     Glutamate receptor	Drosophila melanogaster		
DmGluR2     AAA28575.1     Glutamate receptor subunit kainate subtype       DmGluR3     AAC00192.1     Glutamate receptor DGlu/BIIB       DmGluR4     AAJ3933.1     GH2591p       DmGluR5     AAM46167.1     AF381249_1 NMDA receptor 2       DmGluR6     AAM49854.1     HL08030p       DmGluR7     AM69083.1     RE0730p       DmGluR8     NP_703940.1     NMDA receptor 1       DmGluR4     AAV38092.1     AT31673p       DmGluR10     NP_727328.1     Ionotropic receptor 8a       DmGluR11     AAV3690.1     RE13419p       DmGluR12     AAV36912.1     RE07945p       DmGluR14     NP_649176.1     Ionotropic receptor 76b       DmGluR14     NP_649176.1     Ionotropic receptor 76b       DmGluR15     NP_572751.1     Ionotropic receptor 7c       DmGluR16     NP_00137996.2     Ir75b       DmGluR2     NP_00137995.1     Ionotropic receptor 7c       DmGluR2     NP_001037935.1     CG5621       DmGluR2     NP_001037935.1     CG5621       DmGluR3     AA6250.1.1     Glutamate receptor <tr< td=""><td>DmGluR1</td><td>AAA28574.1</td><td>Glutamate receptor subunit</td></tr<>	DmGluR1	AAA28574.1	Glutamate receptor subunit
DmGluR3     AAC00192.1     Glutamate receptor DGluRIIB       DmGluR4     AAL3934.1     GH25591p       DmGluR5     AAM4967.1     AF381249_1 NMDA receptor 2       DmGluR6     AAM4985.1     HL08030p       DmGluR7     AAM5983.1     REC6730p       DmGluR8     NP_730840.1     NIDA receptor 1       DmGluR8     NP_72732.1     Ionotopic receptor 8a       DmGluR10     NP_727328.1     Ionotopic receptor 7a       DmGluR1     AAV36909.1     RE13413p       DmGluR1     AAV3690.1     RE24732p       DmGluR13     AAX51647.1     RE24732p       DmGluR14     NP_69776.1     Ionotopic receptor 7b       DmGluR15     NP_57275.1     Ionotopic receptor 7c       DmGluR14     NP_60113766.2     Ir75b       DmGluR16     NP_00113766.2     Ir75b       DmGluR20     NP_00113766.2     Ir75b       DmGluR21     NP_00103637.1     CG5621       DmGluR3     AA62505.1     Glutamate receptor       DrGluR3     AA62505.1     Glutamate receptor       DrGluR4     XP_693260.4	DmGluR2	AAA28575.1	Glutamate receptor subunit kainate subtype
DmGluR4     AAl3834.1     GH25591p       DmGluR5     AAM46167.1     AF381242_1 NMDA receptor 2       DmGluR6     AAM48954.1     HL08030p       DmGluR7     AAM50963.1     RE06730p       DmGluR8     NP_730840.1     NMDA receptor 1       DmGluR9     AN71127.1     A731673p       DmGluR1     AAV39809.1     RE13415p       DmGluR1     AAV39809.1     RE13415p       DmGluR1     AAV39809.1     RE24732p       DmGluR1     AAV36902.1     RE24732p       DmGluR14     NP_64976.1     Ionotropic receptor 76b       DmGluR15     NP_572785.1     Ionotropic receptor 72       DmGluR16     NP_572411.1     Ionotropic receptor 72       DmGluR18     NP_00139769.2     I726       DmGluR20     NP_00139786.2     I726       DmGluR21     NP_00139736.1     GG6821       DmGluR2     NP_00139736.1     GG6821       DmGluR3     AA6250.1     Glutamate receptor       DrGluR4     XP_69970.4     PREDICTED: Glutamate receptor       DrGluR4     AP69976.4     PREDI	DmGluR3	AAC00192.1	Glutamate receptor DGluRIIB
DmGluR5     AAM46167.1     AF381249_1 NMDA receptor 2       DmGluR6     AAM4984.1     HL08030p       DmGluR7     AAM60983.1     RE6730p       DmGluR8     NP_30940.1     MNDA receptor 1       DmGluR9     AAN1127.1     AT31673p       DmGluR10     NP_727328.1     Iontorpic receptor 8a       DmGluR12     AAV38902.1     RE17345p       DmGluR13     AAX5147.1     RE24732p       DmGluR13     AX5147.1     RE24732p       DmGluR14     NP_549176.1     Ionotropic receptor 76b       DmGluR15     NP_572795.1     Ionotropic receptor 76       DmGluR16     NP_57241.1     Ionotropic receptor 75d       DmGluR17     ACU43550.1     IP3516p       DmGluR18     NP_00137966.2     I75b       DmGluR20     NP_00136735.1     CG5621       DmGluR21     NP_00136735.1     Cds521       DmGluR3     AAI62450.1     Glutamate receptor       DrGluR3     AAI62505.1     Glutamate receptor       DrGluR3     AAI62505.1     Glutamate receptor       DrGluR4     XP_694772.3	DmGluR4	AAL39343.1	GH25591p
DmGluR6     AAM49854.1     HL08030p       DmGluR7     AAM50863.1     RE06730p       DmGluR8     NP.730840.1     NMDA receptor 1       DmGluR9     AAN11127.1     AT31673p       DmGluR10     NP_727328.1     Ionotropic receptor 8a       DmGluR11     AAV38009.1     RE13419p       DmGluR12     AAV38012.1     RE07945p       DmGluR14     NP_640176.1     Ionotropic receptor 76b       DmGluR15     NP_572795.1     Ionotropic receptor 7c       DmGluR16     NP_0713766.2     I755       DmGluR17     ACU43550.1     IP13516p       DmGluR18     NP_00113766.2     I755       DmGluR21     NP_001036735.1     CG5521       DmGluR21     NP_001036735.1     CG5521       DmGluR2     AAI62459.1     Glutamate receptor       DrGluR3     AP_699070.4     PREDICTED: Glutamate receptor       DrGluR4     XP_699070.4     PREDICTED: Glutamate-like       DrGluR4     XP_698260.1     Glutamate receptor       DrGluR4     XP_698260.1     Glutamate receptor       DrGluR5 <td< td=""><td>DmGluR5</td><td>AAM46167.1</td><td>AF381249_1 NMDA receptor 2</td></td<>	DmGluR5	AAM46167.1	AF381249_1 NMDA receptor 2
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DmGluR9     AAI     AT1127.1     AT31673p       DmGluR10     NP_727328.1     Ionotropic receptor 8a       DmGluR11     AAV3690.1     RE13419p       DmGluR12     AAV36912.1     RE13419p       DmGluR13     AAX51647.1     RE24732p       DmGluR14     NP_64976.1     Ionotropic receptor 76b       DmGluR15     NP_572795.1     Ionotropic receptor 7c       DmGluR14     NP_697295.1     Ionotropic receptor 7c       DmGluR15     NP_572411.1     Ionotropic receptor 7c       DmGluR14     NP_001137969.1     Ionotropic receptor 75d       DmGluR18     NP_00103795.1     CG5621       DmGluR20     NP_00103673.1     CG5621       DmGluR21     NP_00103673.1     CG5621       DmGluR2     AA62459.1     Glutamate receptor       DrGluR2     AA62459.1     Glutamate receptor       DrGluR3     AA62620.1     Glutamate receptor       DrGluR4     XP_69970.4     PREDICTED: Glutamate-like       DrGluR3     AA62620.1     Glutamate receptor       DrGluR4     XP_699070.4     PREDICTED: Glutamate-like	DmGluR8	NP 730940.1	NMDA receptor 1
DmGluR10     NP_727328.1     Ionotropic receptor 8a       DmGluR11     AAV3690.1     RE13419p       DmGluR12     AAV3691.1     RE07945p       DmGluR13     AAX51647.1     RE24732p       DmGluR14     NP_649176.1     Ionotropic receptor 76b       DmGluR15     NP_572951.1     Ionotropic receptor 7c       DmGluR16     NP_572411.1     Ionotropic receptor 7c       DmGluR17     ACU43550.1     IP13516p       DmGluR18     NP_001137966.2     Ir75b       DmGluR20     NP_001097043.1     Ionotropic receptor 75d       DmGluR21     NP_001097043.1     CG5621       DmGluR22     NP_00108735.1     CG5621       DmGluR21     NP_001036373.1     clumsy       DrGluR2     AAl62459.1     Glutamate receptor       DrGluR3     AAl62459.1     Glutamate receptor       DrGluR4     XP_699070.4     PREDICTED: Glutamate-like       DrGluR4     XP_69970.4     PREDICTED: Glutamate-like       DrGluR4     XP_69970.4     PREDICTED: Glutamate receptor       DrGluR4     XP_699070.4     PREDICTED: Glutamate receptor <td>DmGluR9</td> <td> AAN71127.1</td> <td>AT31673p</td>	DmGluR9	 AAN71127.1	AT31673p
DmGluR11     AV36909.1     RE1319p       DmGluR12     AV36902.1     RE07945p       DmGluR13     AX31647.1     RE24732p       DmGluR14     NP_649176.1     Ionotropic receptor 7b       DmGluR15     NP_572795.1     Ionotropic receptor 7c       DmGluR16     NP_572795.1     Ionotropic receptor 7c       DmGluR17     ACU43550.1     IP13516p       DmGluR18     NP_001137969.2     Ir75b       DmGluR20     NP_001097043.1     Ionotropic receptor 7cd       DmGluR21     NP_001036373.1     CG6521       DmGluR22     NP_001036373.1     clumsy       Danio rerio     Unitamate receptor       DrGluR2     AM62505.1     Glutamate receptor       DrGluR3     AM62505.1     Glutamate receptor       DrGluR4     XP_69320.4     PREDICTED: Glutamate-like       DrGluR3     AM62620.1     Glutamate receptor       DrGluR4     XP_69320.4     PREDICTED: Glutamate-like       DrGluR5     AAI62620.1     Glutamate-like       DrGluR4     XP_69040.3     PREDICTED: Glutamate-like       DrGluR4	DmGluR10	NP 727328.1	Ionotropic receptor 8a
DmGluR12     AAV36912.1     RE0794\$       DmGluR13     AAX51647.1     RE24732p       DmGluR14     NP_649176.1     Ionotropic receptor 76b       DmGluR15     NP_572786.1     Ionotropic receptor 71a       DmGluR16     NP_572786.1     Ionotropic receptor 7c       DmGluR17     ACU43550.1     IP13516p       DmGluR18     NP_001137969.1     Ionotropic receptor 75d       DmGluR19     NP_00103795.1     Ionotropic receptor 71a       DmGluR20     NP_00103673.1     CG5621       DmGluR21     NP_00103673.1     CG5621       DmGluR22     NP_00103673.1     CG5621       DmGluR22     NP_00103673.1     cdurmsy       DrGluR2     AAI6250.1     Glutamate receptor       DrGluR2     AAI6250.1     Glutamate receptor       DrGluR3     AAI6250.1     Glutamate receptor       DrGluR4     XP_69376.4     PREDICTED: Glutamate-like       DrGluR4     XP_694772.3     PREDICTED: Glutamate-like       DrGluR4     XP_694772.3     PREDICTED: Similar to N-methyl-D-aspartate receptor channel subunit epsiton 1       DrGluR4     XP	DmGluR11	_ AAV36909.1	RE13419p
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DescriptionDescriptionDmGluR14NP_649176.1Ionotropic receptor 76bDmGluR15NP_572795.1Ionotropic receptor 7cDmGluR16NP_572411.1Ionotropic receptor 7cDmGluR17ACU43550.1IP13516pDmGluR18NP_001137969.1Ionotropic receptor 75dDmGluR19NP_001137966.2Ir75bDmGluR20NP_001097043.1Ionotropic receptor 21aDmGluR21NP_001036735.1CG5621DmGluR22NP_00103673.1clumsyDanio rerioDescriptionDrGluR2AAI62459.1Glutamate receptorDrGluR3AAI62505.1Glutamate receptorDrGluR4XP_699070.4PREDICTED: Glutamate receptorDrGluR3AAI62505.1Glutamate receptorDrGluR4XP_693260.4PREDICTED: Glutamate-likeDrGluR5AAI6260.1Glutamate receptorDrGluR6XP_69377.3PREDICTED: Glutamate-likeDrGluR6XP_69375.2PREDICTED: Glutamate-likeDrGluR7AAL1322.1AF361751_1 AMPA receptor subunit 2bDrGluR8XP_691754.2PREDICTED: Glutamate receptor f-blikeDrGluR9XP_690040.3PREDICTED: Glutamate receptor f-blikeDrGluR11XP_686883.3PREDICTED: Glutamate receptor f-blikeDrGluR14XP_002664030.1PREDICTED: Glutamate receptorDrGluR13XP_68375.4PREDICTED: Glutamate receptorDrGluR14XP_002664030.1PREDICTED: Glutamate receptorDrGluR14XP_002664030.1PREDICTED: Glutamate recept	DmGluR13	AAX51647.1	RE24732p
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DrGluR5AAl62620.1Glutamate receptorDrGluR6XP_694772.3PREDICTED: Glutamate-likeDrGluR7AAL13229.1AF361751_1 AMPA receptor subunit 2bDrGluR8XP_691754.2PREDICTED: similar to N-methyl-D-aspartate receptor channel subunit epsilon 1DrGluR9XP_690040.3PREDICTED: Glutamate receptor 5-likeDrGluR10XP_685683.3PREDICTED: Glutamate receptor delta-1 subunit-likeDrGluR11XP_684512.3PREDICTED: Glutamate receptorDrGluR12CAM14407.1Glutamate receptorDrGluR13XP_683795.4PREDICTED: Glutamate receptorDrGluR14XP_002664030.1PREDICTED: MMDA receptor NR2C subunit-likeDrGluR15XP_002661775.1PREDICTED: Glutamate-likeDrGluR16XP_002661175.1PREDICTED: MMDA receptor NR2C subunit-likeDrGluR16XP_002661175.1PREDICTED: NMDA receptor NR2C subunit-likeDrGluR16NP_001074079.1Vomeronasal 2	DrGluR4	XP_693260.4	PREDICTED: Glutamate-like
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DrGluR8XP_691754.2PREDICTED: similar to N-methyl-D-aspartate receptor channel subunit epsilon 1DrGluR9XP_690040.3PREDICTED: Glutamate receptor 5-likeDrGluR10XP_685683.3PREDICTED: Glutamate receptor delta-1 subunit-likeDrGluR11XP_684512.3PREDICTED: Glutamate receptorDrGluR12CAM14407.1Glutamate receptorDrGluR13XP_683795.4PREDICTED: Glutamate receptorDrGluR14XP_002664030.1PREDICTED: NMDA receptor NR2C subunit-likeDrGluR15XP_002663775.1PREDICTED: Glutamate-likeDrGluR16XP_002661175.1PREDICTED: NMDA receptor NR2C subunit-likeDrGluR17NP_001074079.1Vomeronasal 2	DrGluR7	AAL13229.1	AF361751_1 AMPA receptor subunit 2b
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DrGluR10XP_685683.3PREDICTED: Glutamate receptor delta-1 subunit-likeDrGluR11XP_684512.3PREDICTED: Glutamate receptorDrGluR12CAM14407.1Glutamate receptorDrGluR13XP_683795.4PREDICTED: Glutamate receptorDrGluR14XP_002664030.1PREDICTED: Glutamate receptor NR2C subunit-likeDrGluR15XP_002663775.1PREDICTED: Glutamate-likeDrGluR16XP_002661175.1PREDICTED: NMDA receptor NR2C subunit-likeDrGluR17NP_001074079.1Vomeronasal 2	DrGluR9	XP_690040.3	PREDICTED: Glutamate receptor 5-like
DrGluR11XP_684512.3PREDICTED: Glutamate receptorDrGluR12CAM14407.1Glutamate receptorDrGluR13XP_683795.4PREDICTED: Glutamate receptorDrGluR14XP_002664030.1PREDICTED: NMDA receptor NR2C subunit-likeDrGluR15XP_002663775.1PREDICTED: Glutamate-likeDrGluR16XP_002661175.1PREDICTED: NMDA receptor NR2C subunit-likeDrGluR17NP_001074079.1Vomeronasal 2	DrGluR10	XP_685683.3	PREDICTED: Glutamate receptor delta-1 subunit-like
DrGluR12CAM14407.1Glutamate receptorDrGluR13XP_683795.4PREDICTED: Glutamate receptorDrGluR14XP_002664030.1PREDICTED: NMDA receptor NR2C subunit-likeDrGluR15XP_002663775.1PREDICTED: Glutamate-likeDrGluR16XP_002661175.1PREDICTED: NMDA receptor NR2C subunit-likeDrGluR17NP_001074079.1Vomeronasal 2	DrGluR11	XP_684512.3	PREDICTED: Glutamate receptor
DrGluR13     XP_683795.4     PREDICTED: Glutamate receptor       DrGluR14     XP_002664030.1     PREDICTED: NMDA receptor NR2C subunit-like       DrGluR15     XP_002663775.1     PREDICTED: Glutamate-like       DrGluR16     XP_002661175.1     PREDICTED: NMDA receptor NR2C subunit-like       DrGluR17     NP_001074079.1     Vomeronasal 2	DrGluR12	CAM14407.1	Glutamate receptor
DrGluR14     XP_002664030.1     PREDICTED: NMDA receptor NR2C subunit-like       DrGluR15     XP_002663775.1     PREDICTED: Glutamate-like       DrGluR16     XP_002661175.1     PREDICTED: NMDA receptor NR2C subunit-like       DrGluR17     NP_001074079.1     Vomeronasal 2	DrGluR13	XP_683795.4	PREDICTED: Glutamate receptor
DrGluR15 XP_002663775.1 PREDICTED: Glutamate-like   DrGluR16 XP_002661175.1 PREDICTED: NMDA receptor NR2C subunit-like   DrGluR17 NP_001074079.1 Vomeronasal 2	DrGluR14	XP_002664030.1	PREDICTED: NMDA receptor NR2C subunit-like
DrGluR16 XP_002661175.1 PREDICTED: NMDA receptor NR2C subunit-like   DrGluR17 NP_001074079.1 Vomeronasal 2	DrGluR15		PREDICTED: Glutamate-like
DrGluR17 NP_001074079.1 Vomeronasal 2	DrGluR16	XP_002661175.1	PREDICTED: NMDA receptor NR2C subunit-like
	DrGluR17		Vomeronasal 2

DrGluR18	NP_001121809.1	Glutamate [NMDA] receptor subunit epsilon-2		
DrGluR19	NP_001137603.1	Glutamate receptor		
DrGluR20	NP_001138274.1	si:ch211-251b21.1		
DrGluR21	XP_001924038.2	PREDICTED: Glutamate receptor		
DrGluR22	XP_001923977.1	PREDICTED: Kainate receptor beta subunit-like		
DrGluR23	XP_001921725.1	PREDICTED: Glutamate-like		
DrGluR24	NP_938174.1	Glutamate receptor		
DrGluR25	XP_001921158.1	PREDICTED: N-methyl-D-aspartate receptor subunit 2D		
DrGluR26	NP_991293.1	Glutamate receptor		
DrGluR27	XP 001339222.3	PREDICTED: Glutamate receptor		
DrGluR28	 XP_001333587.2	PREDICTED: Glutamate receptor delta-1 subunit-like		
Nematostella vectensis				
NvGluR1	XP_001622303.1	Hypothetical protein NEMVEDRAFT_v1g141731		
NvGluR2	XP_001641049.1	Predicted protein		
NvGluR3	XP_001626463.1	Predicted protein		
NvGluR4	XP_001627645.1	Predicted protein		
NvGluR5	XP_001629139.1	Predicted protein		
NvGluR6	XP_001629614.1	Predicted protein		
NvGluR7	XP_001633354.1	Predicted protein		
NvGluR8	XP_001639888.1	Predicted protein		
NvGluR9	XP_001636905.1	Predicted protein		
NvGluR10	XP_001638696.1	Predicted protein		
Rattus norvegicus				
RnGluR1	C45219	N-methyl-D-aspartate receptor chain NMDAR2D-1		
RnGluR2	CAA46335.1	NMDA receptor subunit		
RnGluR3	CAA78937.1	Glutamate receptor subtype delta-2		
RnGluR4	NP 036707.3	Glutamate [NMDA] receptor subunit epsilon-3		
RnGluR5	NP_113696.1	Glutamate receptor		
RnGluR6	NP_113796.1	Glutamate receptor 1 precursor		
RnGluR7	NP_579842.2	Glutamate [NMDA] receptor subunit 3B precursor		
RnGluR8	P19491.2	Glutamate receptor 2		
RnGluR9	P19492.1	Glutamate receptor 3		
RnGluR10	P19493.1	Glutamate receptor 4		
RnGluR11	P22756.3	GRIK1 Glutamate receptor		
RnGluR12	P42260.2	GRIK2 Glutamate receptor		
RnGluR13	P42264.1	GRIK3 Glutamate receptor		
RnGluR14	Q00959.2	Glutamate [NMDA] receptor subunit epsilon-1		
RnGluR15	Q00960.1	Glutamate [NMDA] receptor subunit epsilon-2		
RnGluR16	Q01812.1	GRIK4 Glutamate receptor		
RnGluR17	S28857	Glutamate receptor delta-1 chain precursor		
RnGluR18	XP_002726571.1	PREDICTED: Glutamate receptor		
Strongylocentrotus purpuratus				
SpGluR1	XP_001188377.1	PREDICTED: Similar to AMPA receptor subunit GluR3B		
SpGluR2	XP_001197583.1	PREDICTED: Similar to AMPA receptor GluR3/C		
SpGluR3	XP_784968.2	PREDICTED: Similar to Glutamate receptor		
SpGluR4	XP_787239.2	PREDICTED: Similar to AMPA receptor GluR1/A		
SpGluR5	XP_789521.2	PREDICTED: Hypothetical protein		
SpGluR6	XP_792639.1	PREDICTED: Similar to glutamate receptor AMPA/kainate type		
SpGluR7	XP_794826.2	PREDICTED: Similar to AMPA GluR2		
SpGluR8	XP_796568.2	PREDICTED: Similar to AMPA receptor GluR2/B		

#### Trichoplax adherens TaGluR1 XP 002107780.1 Hypothetical protein TRIADDRAFT\_19383 TaGluR2 XP\_002108129.1 Hypothetical protein TRIADDRAFT\_18823 TaGluR3 XP\_002108130.1 Hypothetical protein TRIADDRAFT\_18262 TaGluR4 XP 002108131.1 Hypothetical protein TRIADDRAFT 18943 TaGluR5 XP\_002117385.1 Hypothetical protein TRIADDRAFT\_3218 TaGluR6 XP 002111317.1 Hypothetical protein TRIADDRAFT 55165 TaGluR7 XP\_002112358.1 Hypothetical protein TRIADDRAFT\_14565 TaGluR8 XP\_002112769.1 Hypothetical protein TRIADDRAFT\_25025 TaGluR9 XP\_002112772.1 Hypothetical protein TRIADDRAFT\_25027 TaGluR10 XP\_002116223.1 Hypothetical protein TRIADDRAFT\_30609 TaGluR11 XP 002116224.1 Hypothetical protein TRIADDRAFT 30612 Hypothetical protein TRIADDRAFT\_32461 TaGluR12 XP\_002117382.1 TaGluR13 XP\_002117383.1 Hypothetical protein TRIADDRAFT\_61396 PLANTS Arabidopsis thaliana AtGluR1 A84550 Probable ligand-gated ion channel protein AtGluR2 AAB61068.1 Similar to the ligand-gated ionic channels family AAB71458.1 AtGluR3 Similar to Arabidopsis putative ion-channel AtGluR4 NP\_199652.1 ATGLR1.3 Intracellular ligand-gated ion channel AtGluR5 AAC33237.1 Putative ligand-gated ion channel protein AtGluR6 AAC33239.1 Putative ligand-gated ion channel protein AtGluR7 AAD09173.1 Putative glutamate receptor AtGluR8 NP 199651.1 ATGLR1.2 Intracellular ligand-gated ion channel Ionotropic glutamate receptor ortholog GLR6 AF170494\_1 AtGluR9 AAD50976.1 AtGluR10 AAF02156.1 Unknown protein AC009853\_16 AtGluR11 AAF21042.1 Glr5 AF210701\_1 AtGluR12 AAK13248.1 Putative glutamate receptor like-protein AF159498\_1 AtGluR13 NP\_196682.1 ATGLR2.5 Intracellular ligand-gated ion channel AtGluR14 NP\_196679.1 ATGLR2.6 Intracellular ligand-gated ion channel AtGluR15 NP 194899.1 ATGLR2.4 Intracellular ligand-gated ion channel AtGluR16 NP\_180474.1 ATGLR2.9 Intracellular ligand-gated ion channel AtGluR17 AAR27949.1 GI R3 3 AtGluR18 NP\_180048.1 ATGLR2.2 Intracellular ligand-gated ion channel AtGluR19 NP\_180047.1 ATGLR2.3 Intracellular ligand-gated ion channel AtGluR20 CAB63012.1 Putative glutamate receptor Brachypodium distachyon BdGluR1 Bradi1g26030 BdGluR2 Bradi3g01620 BdGluR3 Bradi1g32800 BdGluR4 Bradi5g19560 BdGluR5 Bradi1g59600 BdGluR6 Bradi2g41790 BdGluR7 Bradi4g30850 BdGluR8 Bradi4g30860 BdGluR9 Bradi1g31350 BdGluR10 Bradi4g30880

BdGluR11

BdGluR12

Bradi4g30820

Bradi4g30840

BdGluR13	Bradi4g30810	
BdGluR14	Bradi3g53690	
BdGluR15	Bradi1g46910	
BdGluR16	Bradi3g51890	
Oryza sativa japonica	1	I
OsGluR1		116309819_emb_CAH668
OsGluR2	EAY87800.1	Hypothetical protein Osl_09220
OsGluR3	EAY99961.1	Hypothetical protein Osl_21965
OsGluR4	EAZ02098.1	Hypothetical protein Osl_24185
OsGluR5	EAZ02474.1	Hypothetical protein Osl_24580
OsGluR6	EEC80160.1	Hypothetical protein OsI_21975
OsGluR7	EAZ09182.1	Hypothetical protein OsI_31453
OsGluR8	EAZ09183.1	Hypothetical protein OsI_31454
OsGluR9	EAZ09184.1	Hypothetical protein Osl_31456
OsGluR10	EAZ09187.1	Hypothetical protein Osl_31459
OsGluR11	EAZ09194.1	Hypothetical protein Osl_31466
OsGluR12	EEC72350.1	Hypothetical protein Osl_05591
OsGluR13	EEC80154.1	Hypothetical protein Osl_21964
OsGluR14	EEC82165.1	Hypothetical protein Osl_26240
OsGluR15	EEC80159.1	Hypothetical protein Osl_21973
OsGluR18	EEC84618.1	Hypothetical protein Osl_31464
OsGluR19	EEC84617.1	Hypothetical protein Osl_31458
Physcomitrella patens	I	
PpGluR1	XP_001762626.1	Predicted protein
PpGluR2	XP_001779207.1	Predicted protein
BACTERIA	1	I
PGluR1	ZP_05036786.1	Bacterial extracellular solute-binding protein family 3 [Synechococcus sp. PCC
		7335]
PGluR2	ZP_05043015.1	Bacterial extracellular solute-binding protein family 3 [Alcanivorax sp. DG881]
PGluR3	NP_441171.1	Hypothetical protein slr1257 [Synechocystis sp. PCC 6803]
PGluR4	NP_894348.1	GIC family ligand gated channel [Prochlorococcus marinus str. MIT 9313]
PGluR5	NP_896860.1	GIC family ligand gated channel [Synechococcus sp. WH 8102]
PGluR6	ZP_05044674.1	Ionotropic glutamate receptor [Cyanobium sp. PCC 7001]
PGluR7	YP_001130102.1	Extracellular solute-binding protein [Prosthecochloris vibrioformis DSM 265]
PGluR8	YP_001224896.1	Hypothetical protein SynWH7803_1173 [Synechococcus sp. WH 7803]
PGluR9	YP_001227767.1	Hypothetical protein SynRCC307_1511 [Synechococcus sp. RCC307]
PGluR10	YP_001733604.1	Periplasmic substrate binding protein [Synechococcus sp. PCC 7002]
PGluR11	YP_001803825.1	Extracellular solute-binding protein [Cyanothece sp. ATCC 51142]
PGluR12	YP_001805997.1	Ligand gated channel [Cyanothece sp. ATCC 51142]
PGluR13	YP_001869676.1	Extracellular solute-binding protein [Nostoc punctiforme PCC 73102]
PGluR14	YP_001960498.1	lon transport 2 domain protein [Chlorobium phaeobacteroides BS1]
PGluR15	YP_001997058.1	Extracellular solute-binding protein family 3 [Chloroherpeton thalassium ATCC
		35110]
PGluR16	YP_001997839.1	Extracellular solute-binding protein family 3 [Chlorobaculum parvum NCIB 8327]
PGluR17	ZP_05788417.1	Ionotropic glutamate receptor [Synechococcus sp. WH 8109]
PGluR18	YP_002954183.1	Bacterial extracellular solute-binding protein [Desulfovibrio magneticus RS-1]
PGluR19	YP_003267580.1	Extracellular solute-binding protein family 3 [Haliangium ochraceum DSM 14365]
PGluR20	YP_003585093.1	Ligand-gated ion channel family protein [Zunongwangia profunda SM-A87]
PGluR21	YP_321508.1	Ionotropic glutamate receptor [Anabaena variabilis ATCC 29413]

	PGluR22	YP_339120.1	Extracellular solute-binding protein [Pseudoalteromonas haloplanktis TAC125]
	PGluR23	YP_374461.1	Extracellular solute-binding protein [Chlorobium luteolum DSM 273]
	PGluR24	YP_376778.1	lonotropic glutamate receptor [Synechococcus sp. CC9902]
	PGluR25	YP_378562.1	Extracellular solute-binding protein [Chlorobium chlorochromatii CaD3]
	PGluR26	YP_723930.1	Extracellular solute-binding protein [Trichodesmium erythraeum IMS101]
	PGluR27	YP_730938.1	GIC family ligand gated channel [Synechococcus sp. CC9311]
	PGluR28	YP_861587.1	Ligand-gated ion channel family protein [Gramella forsetii KT0803]
	PGluR29	ZP_00517290.1	Extracellular solute-binding protein family 3:Bacterial extracellular solute-binding
			protein family 3 [Crocosphaera watsonii WH 8501]
	PGluR30	ZP_01042624.1	Extracellular solute-binding protein family 3 [Idiomarina baltica OS145]
	PGluR31	ZP_01080226.1	Possible ligand gated channel (GIC family protein) [Synechococcus sp. RS9917]
	PGluR32	ZP_01085070.1	Possible ligand gated channel (GIC family protein) [Synechococcus sp. WH
			5701]
	PGluR33	ZP_01124154.1	Possible ligand gated channel (GIC family) protein [Synechococcus sp. WH
			7805]
	PGluR34	ZP_01437479.1	Extracellular solute-binding protein family 3 [Fulvimarina pelagi HTCC2506]
	PGluR35	ZP_06369637.1	Extracellular solute-binding protein family 3 [Desulfovibrio sp. FW1012B]
	PGluR36	ZP_01628414.1	Possible ligand gated channel (GIC family) [Nodularia spumigena CCY9414]
	PGluR37	ZP_01691371.1	Extracellular solute-binding protein family 3 [Microscilla marina ATCC 23134]
	PGluR38	ZP_01720436.1	Hypothetical protein ALPR1_14489 [Algoriphagus sp. PR1]
	PGluR39	ZP_01731352.1	Possible ligand gated channel (GIC family) protein [Cyanothece sp. CCY0110]
	PGluR40	ZP_01893479.1	Extracellular solute-binding protein family 3 [Marinobacter algicola DG893]
	PGluR41	ZP_01909425.1	Extracellular solute-binding protein family 3 [Plesiocystis pacifica SIR-1]
	PGluR42	ZP_02003278.1	Bacterial extracellular solute-binding protein family 3 [Beggiatoa sp. PS]
	PGluR43	ZP_03130928.1	Extracellular solute-binding protein family 3 [Chthoniobacter flavus Ellin428]
	PGluR44	ZP_03157700.1	Ion transport 2 domain protein [Cyanothece sp. PCC 7822]
	PGluR45	ZP_05023856.1	Bacterial extracellular solute-binding protein family 3 [Microcoleus
			chthonoplastes PCC 7420]
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**Supplementary Table S3.** iGluR sequences included in the phylogenetic analysis.