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On the ligand binding profile and desensitization of plant ionotropic glutamate receptor (iGluR)-like channels functioning in MAMP-triggered Ca2+ influx

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Supplemental Figure 1. Transmembrane and CaMBD predictions for individual Arabidopsis iGluRs.

Transmembrane (TM) domain prediction:

http://aramemnon.botanik.uni-koeln.de. Data shown are the results of TmHMM_v2 (Hidden Markov Model prediction of TM), which are representative for the majority of the prediction tools.

Calmodulin binding domain prediction:

http://calcium.uhnres.utoronto.ca/ctdb/ctdb/home.html

Color coding of the predicted TM domains:

IQTPILLSFLLVLLFFISNCF: predicted TM domain at the extreme N-terminus of the N-terminal extracellular domain

KSLWLASGAFFVLTGIVVWLV: TM1, predicted TM domain that overlaps with the published first TM domain of iGluRs.

SWGQQLSMMLWFGFSTIVF: TM2, predicted TM domain that represents and overlaps with the iGluR ion pore domain.

RFLVIVWVFVVLILTSSYSAN: TM3, predicted TM domain that overlaps with published second TM domain of iGluRs.

RGLFIIAGAAHVLVLALHLFH: TM4, predicted TM domain that overlaps with published third TM domain of iGluRs.

ELWFLTAASFLYIGIMSYTA: No TM1 predicted in GLR2.6 using TmHMM_v2; instead TmConsens used to assign most N-terminal TM domain and start point CaMBD predictions

Coding of CaMBD predictions:

GLR1.1 (last 268 AA): GLR family member plus (in brackets) amino acids (AA) taken for CaMBD prediction

TSTKTISRMQLNHQ: Amino acids included in CaMDB prediction

AHREKLQKMSS: Predicted CaMBD. Red values have a score of 9, orange values have scores from 6 to 8.

GLR1.1 (last 268 AA)

MEILFSISILALLFSGVVAAPSDDDVFEEVRVGLVVDLSSIQGKILETSFNLALSDFYGINNGYRTRVSVLVRDSQGDPIIALAAA
TDLLKNAKAEAIVGAQSLQEAKLLATISEKAKVPVISTFLPNTLSLKKYDNFIQWTHDTTSEAKGITSLIQDFSCKSVVVIYEDA
DDWSESLQILVENFQDKGIYIARSASFAVSSSGENHMMNQLRKLKVSRASVFVVHMSEILVSRLFQCVEKLGLMEEAFAWI

LTARTMNYLEHFAITRSMQGVIGFKSYIPVSEEVKNFTSRLRKRMGDDTETEHSSVIIGLRAHDIACILANAVEKFSVSGKVEA
SSNVSADLLDTIRHSRFKGLSGDIQISDNKFISETFEIVNIGREKQRRIGLWSGGSFSQRRQIVWPGRSRKIPRHRVLAEKGEK
KVLRVLVTAGNKVPHLVSVRPDPETGVNTVSGFCVEVFKTCIAPFNYELEFIPYRGNNDNLAYLLSTQRDKYDAAVGDITITS
NRSLYVDFTLPYTDIGIGILTVKKKSQGMWTFFDPFEKSLWLASGAFFVLTGIVVWLVERSVNPEFQGSWGQQLSMMLWF
GFSTIVFAHREKLQKMSSRFLVIVWVFVVLILTSSYSANLTSTKTISRMQLNHQMVFGGSTTSMTAKLGSINAVEAYAQLLR
DGTLNHVINEIPYLSILIGNYPNDFVMTDRVTNTNGFGFMFQKGSDLVPKVSREIAKLRSLGMLKDMEKKWFQKLDSLNVH
SNTEEVASTNDDDEASKRFTFRELRGLFIIAGAAHVLVLALHLFHTRQEVSRLCTKLQSFYK

GLR1.2 (last 308 AA)

MVRICIQTPILLSFLLVLLFFISNCFASSQNNDDDKRIRVRVGLVLDLGSVEGKIVRSSVSMALSDFYDNHNDYKTRLSLLVRDS
HGEPLLALDSVVDLLQTEGVQAIIGGNSLLEAKLLAELGEKARVPVISLNSPMSLSLSKYTHLIQATHNSASEVKGITAFLHGFD
WNSVALVLEDHDDWRESMHFMVDHFHENNVHVQSKVAFSVTSSEDSLMDRLRELKDLGTTVFVVHLSEVIATRLFPCAE
KLGMMGEGFAWILTSRSMSSFHDQFIDDLTKEAMEGVVGFKSYIPMSKELHNFTLRWRKTLPVEEVTGSEITRLSISGVWA
HDVAWSLASAAEVTRMPTVTSTLLEAIKESRFKGLSGNFQLDDMKLLSDKFEIVNMIGSGERRVGFWNSNGSFSNRRQLSS
THDNLETIIWPGGSAQSPKGRSLRESGRKKLRVLVTSSNRFPRLMKVETDPITHEITIVEGFCIEVFQASIAPFNYEVEYIRWLN
GTNYTKLAYALHSQKDKYDAAVGDITITSDRSMYVDFTLPYTEMGLGIVAAKERSMWVFFQPLTPNLWITSAAFFVLTGIIV
WLIERAENKEFQGSWPQQIGVVIWFGFSTLVYAHREKLQHNLSRFVVTVWVFAVLILVTSYTATLTSMMTVQQIRFNANE
DYVGHLSGSLIANAALTNSSLRAMRLLGLNTSEDYAQALMNKSVSYIVSELPYLKILLGENPGHFLMVKTQSTTNGFGFMFQ
KGSELAPNVSREIAKLRTSERLNEMERRWFDKQLPYTTDDTSNPITLYRFRGLFMITGVSFAFALAVLLILWLRERWEILVNSV
NIYFSQRLRHFRILFTRTIHPSPLGLDNPIGENAVQMAQRNRR

GLR1.3 (last 304 AA)

MERFCIQTQTLLSFLLVLLLFISRSFASTKNDDVDGGKRVQIRVGLVLDLGSLKGKIVKNSVSMALSYFYAIHNDYKTRVSVSLR
NSHGEPLLALASAVDLLKTEGVEAIIGGNSLLEAKLLGELGEKARVPMISLDSPFSLSLSKYTHLIQATHDSTSEAKGITSFINVF
DWNSVALVYEDHDDWRESMQLLVEHFHENGVRVQSKVGFTVSSSEDFVMGRLQQLKDLGTTVFVVHLSEVIATHLFPCA
RRLGLMGDGFVWILTAKTMNSFHENIDDFTKQAMEGVVGFKSYIPMSIELQNFTLRWRKSLPVEEAELTRLSISGIWAHDI
AFALARAAEVIRMPNVTSTLLEEITKTRFNGLSGDFQLNDKKLLSNKFEIINMIGSSERRVGFLNSNGSFSNRRHLSSTHNKLE
TIIWPGGSAQSPKGTSLIDSDRKKLRVLVTSSNRFPRLMKVETDPVTNELIVEGFCIEVFRASISPFNYEVEYIPWLNGSNYDN
LAYALHSQKDKYDAAVGDITITSNRSTYVDFTLPFTEMGLGIVAVKERSMWVFFQPLTPDLWITSAFFFVLTGVIVWLIERAE
NKEFQGSWPQQIGVVLWFGFSTLVYAHREKLKHNLSRFVVTVWVFAVLILTASYTATLTSMMTVQQIRFNSNEDYVGHLS
GSLIANVALTSSSLRAMRSLGLNSAADYAQALLNKTVSFVVDELPYLKVVLGENPTHFFMVKTQSTTNGFGFMFQKGFELV
PNVSREISKLRTSEKLNEMEKRWFDNQLPYTTDDTSNPITLYRFRGLFIIIGVSFAFALAVLVILCLRDKWEILVDNLDLSQRLR
HFRIHFVRSIHTSPLDDPIGETAVQMAQQNRQ

GLR1.4 (last 294 AA)

MENCMIRNTGYFLTIFFLAFISFAVTCSGTNQKDNVDRLPVVYEDVRIGLVVDMGSMEGKLVTTSISMALSDFYHVNNGYR
TRVSVLSRDSHGDPLQALAAAMDLLQTEQVEALVGGQSLLEAKNLAELGEKTKVPVISSFQVPSSLSLAKYNYFIQATHDTSS
EAKGIAALFSNFDWRTAVLIYEDDDDWRESIQPLVGHFQQNAIHIEYKAEFSVSSNEECIMKQLRKFKASGIRIFVAHISERIA
NRLFPCARRLGMMEEGYAWILTARSMNNFQDTNYLAKEEMEGVIGFKSYIPLTEELHNFTLRWKRSLRLEEVVTRMSVCSI
WAHDIAWSLARAAEVAKLPGLSVYDLLEAIPESAKHKGLSGDIKFIDKKFISDKFEIVNMIGRGERSVGLWNSGSFISNRRRR
LSSTKALETIIWPGGSTRIPKIRSLKEKRHGKKKKLRVLVPAGNITPQILEVKTDFKTGVTAATGYCIDVFETSILPFNYEVEYIPW
PGAINYKNYNDLVYTLYSQKDKYDAAVGDITITDNRSLYVDFTLPFTDMGLAVVTAKDKSMWIIFKPLTLSLWLTIASFFILTG

AIVWLIERHDNADFQGSCFQQIGTLLCFGFSTLVFAHRERLQHNMSRFVVIVWIFAVLILTSNYTATLTSVMTVQQIRGLKS
NENIGFFSASIAANVVNDNPTFQGPRYKGLKTADDFTNALRNGTISFIVDEVPYVKLFVAKHPSEFVIVETESVTNGFGFAFQ
KGSPLVQKVSREIEKLRRTEKLKAIENWWFQRQTTSATSEDTFHPLTVYTFRGLFMITGVSFAFALIVYLIPWNREQRQVVLK
HFHRYVSHRFAREIRPSPTTPNRQNENSVI

GLR2.1 (last 328 AA)

MKRENNLVLSLLFFVIVFLMQVGEAQNRITNVNVGIVNDIGTAYSNMTLLCINMSLSDFYSSHPETQTRLVTTVVDSKNDV
VTAAAAALDLITNKEVKAILGPWTSMQAQFMIEMGQKSQVPIVTYSATSPSLASIRSQYFFRATYDDSSQVHAIKEIIKLFGW
REVAPVYVDDTFGEGIMPRLTDVLQEINVRIPYRTVISPNATDDEISVELLRMMTLPTRVFVVHLVELLASRFFAKATEIGLM
KQGYVWILTNTITDVLSIMNETEIETMQGVLGVKTYVPRSKELENFRSRWTKRFPISDLNVYGLWAYDATTALALAIEEAGTS
NLTFVKMDAKRNVSELQGLGVSQYGPKLLQTLSRVRFQGLAGDFQFINGELQPSVFEIVNVNGQGGRTIGFWMKEYGLFK
NVDQKPASKTTFSSWQDRLRPIIWPGDTTSVPKGWEIPTNGKRLQIGVPVNNTFQQFVKATRDPITNSTIFSGFSIDYFEAVI
QAIPYDISYDFIPFQDGGYDALVYQVYLGKYDAVVADTTISSNRSMYVDFSLPYTPSGVGLVVPVKDSVRRSSTIFLMPLTLAL
WLISLLSFFIIGLVVWVLEHRVNPDFDGPGQYQLSTIFWFSFSIMVFAPRERVLSFWARVVVIIWYFLVLVLTQSYTASLASLL
TTQHLHPTVTNINSLLAKGESVGYQSSFILGRLRDSGFSEASLVSYGSPEHCDALLSKGQAEGGVSAVLMEVPYVRIFLGQYC
NKYKMVQTPFKVDGLGFVFPIGSPLVADISRAILKVEESNKANQLENAWFKPIDESCPDPLTNPDPNPSVSFRQLGFDSFWV
LFLVAAIVCTMALLKFVYQFLKENPNQRNLRVLWEKFNEPDQKSYIKDVTKCQCSSGQGMPKNGQEGANAVNNGN

GLR2.2 (last 341 AA)

MKNSKLFFRFLFLFFFFCLESSRGQDNGKTQVNIGVVSDVGTSYPDVAMLCINMSLADFYSSRPQFQTRLVVNVGDSKNDV
VGAATAAIDLIKNKQVKAILGPWTSMQAHFLIEIGQKSRVPVVSYSATSPSLTSLRSPYFFRATYEDSSQVHAIKAIIKLFGWR
EVVPVYIDNTFGEGIMPRLTDSLQDINVRIPYRSVIPLNATDQDISVELLKMMNMPTRVFIVHMSSSLASTVFIKAKELGLMK
PGYVWILTNGVMDGLRSINETGIEAMEGVLGIKTYIPKSKDLETFRSRWKRRFPQMELNVYGLWAYDATTALAMAIEDAGI
NNMTFSNVDTGKNVSELDGLGLSQFGPKLLQTVSTVQFKGLAGDFHFVSGQLQPSVFEIVNMIGTGERSIGFWTEGNGLV
KKLDQEPRSIGTLSTWPDHLKHIIWPGEAVSVPKGWEIPTNGKKLRIGVPKRIGFTDLVKVTRDPITNSTVVKGFCIDFFEAVI
QAMPYDVSYEFFPFEKPNGEPAGNHNDLVHQVYLGQFDAVVGDTTILANRSSFVDFTLPFMKSGVGLIVPLKDEVKRDKFS
FLKPLSIELWLTTLVFFFLVGISVWTLEHRVNSDFRGPANYQASTIFWFAFSTMVFAPRERVLSFGARSLVVTWYFVLLVLTQ
SYTASLASLLTSQQLNPTITSMSSLLHRGETVGYQRTSFILGKLNETGFPQSSLVPFDTAEECDELLKKGPKNGGVAAAFLGTP
YVRLFLGQYCNTYKMVEEPFNVDGFGFVFPIGSPLVADVSRAILKVAESPKAVELEHAWFKKKEQSCPDPVTNPDSNPTVT
AIQLGVGSFWFLFLVVFVVCVLALGKFTFCFLWKTKGKDLWKEFLKRDTDSYINDIEKCLCSQEMPENSNKATNQTNYGME
LRVRNIVQVNQTDPDCL

GLR2.3 (last 316 AA)

MRTEKLFFCILLVFFFCLEFNRGQNNGKTLVDVGVVTDVDTSHSKVVMLCINMSISDFYSSNPQFETRLVVNVGDSKSDVV
GAAIAALDLIKNKQVKAILGPWTSMQAHFLIEIGQKSRVPIVSYSATSPILTSLRSPYFLRATYEDSFQVQPIKAIIKLFGWREVV
PVYIDNTFGEGIMPRLTDALQDINVRIPYRSVIAINATDHEISVELLKMMNMPTRVFLVHMYYDLASRFFIKAKELGLMEPGY
VWILTNGVIDDLSLINETAVEAMEGVLGIKTYIPKSPDLEKFRSRWRSLFPRVELSVYGLWAYDATTALAVAIEEAGTNNMTF
SKVVDTGRNVSELEALGLSQFGPKLLQTLLTVQFRGLAGEFRFFRGQLQPSVFEIVNIINTGEKSIGFWKEGNGLVKKLDQQA
SSISALSTWKDHLKHIVWPGEADSVPKGWQIPTKGKKLRIGVPKRTGYTDLVKVTRDPITNSTVVTGFCIDFFEAVIRELPYD
VSYEFIPFEKPDGKTAGNYNDLVYQVYLGRYDAVVGDTTILVNRSSYVDFTFPFIKSGVGLIVEMTDPVKRDYILFMKPLSWK
LWLTSFISFFLVGCTVWVLEYKRNPDFSGPPRFQASTICWFAFSTMVFAPRERVFSFWARALVIAWYFLVLVLTQSYTASLAS
LLTSQKLNPTITSMSSLLEKGETVGYQRTSFILGKLKERGFPQSSLVPFDTAEECDELLSKGPKKGGVSGAFLEIPYLRLFLGQFC

NTYKMVEEPFNVDGFGFVFPIGSPLVADVSRAILKVAESPKAMELERAWFKKKEQSCPDPITNPDPNPSFTSRQLDIDSFLFLFVGVLLVCVMALGNFTYCFLAKDQVSYLDKVEMSPCSSSQQMPVKRKTQLNMSQVHDQDSL

GLR2.4 (last 317 AA)

MSSKYFQDVYIPRYLTKTKNKRKMKRHLNDVVLVFLVFIFGVKLGKGQNTTIQVINVGVVTDVGTTASNLSLLAINMSLSDFYSSRPESRTRLLLNFADSRDDVVGAAAAALDLIKNKEVKAILGPRTTMQASFVIEVGQKSQVPIISFSATSPFLDSGRSPYFFRSTYDDSSQVQAISEIIKVFGWREVVPVYENNAFGEGIMPGLTDALQAINIRIPYRTVISPNATDDEISVDLLKLMTKPTRVFVVHMNRFLASRVFSKARETGLMKQGYAWILTNGVIDHLVLMNGTDIEAMQGVIGIRTHFPISEELQTFRSRLAKAFPVSELNIYGLRAYDATTALAMAVEEAGTTNLTFSKMDGRNISDLEALSVSEYGPKLIRSLSQIQFKGLSGDYHFVDGQLHASVFEIVNVIDGGGILVGFWTQDKGLVKDLSPSSGTTRTFSSWKNHLNPILWPGITLTVPKGWEIPTNGKELQIGVPVGTFPQFVKVTTDPLTHETIVTGFCIDFFEAVIQAMPYDVSHRFIPFGDDDGKTNDTTILANRSSYVDFTLPYTTSGVGMVVPLKDNVARSSLIFFKPLTPGLWGMTLGSFFVVGFVVWILEHRVNSEFTGPPQYQISTMFWFAFSIMVFAPRERVMSFTARVVVITCLSSLLTTQQLNPTETSIKNVLAKGGPVAYQRDSFVLGKLRESGFPESRLVPFTSPEKCEELLNKGPSKGGVSAAFMEVPYVRVFLGQYCKKYKMVEVPFDVDGFGFVFPIGSPLVADVSRAILKVAESNKATQLETAWFKNIDKTCPDPMNNPDPNPTVSFRKLSLDSFLLLFVAAATVCTLALLKFVICFLIQNRIILNDEFYRGKRMKEMWLKFMESDGESYISRVRSTCPQVLIQPREEDIDPING

GLR2.5 (last 317 AA)

MASRQGLSSTSETPNKLLLVLPLQKREVVAIIGPGTSMQAPFLINLGNQSKVPIISFSATSPLLDSLRSPYFIRATHDDSSQVQAISAIIESFRWREVVPIYVDNEFGEGILPNLVDAFQEINVRIRYRSAISLHYSDDQIKKELYKLMTMPTRVFIVHMLPDLGSRLFSIAKEIDMLSKGYVWIVTNGIADLMSIMGESSLVNMHGVLGVKTYFAKSKELLHLEARWQKRFGGEELNNFACWAYDAATALAMSVEEIRHVNMSFNTTKEDTSRDDIGTDLDELGVALSGPKLLDALSTVSFKGVAGRFQLKNGKLEATTFKIINIEESGERTVGFWKSKVGLVKSLRVDKVSHSSRRLRPIIWPGDTIFVPKGWEFPTNAKKLRIAVPKKDGFNNFVEVTKDENTNVPTVTGFCIDVFNTVMSQMPYAVSYEYIPFDTPDGKPRGSYDEMVYNVFLGEFDGAVGDTTILANRSHYVDFALPYSETGIVFLVPVKDGKEKGEWVFLKPLTKELWLVTAASFLYIGIMVWIFEYQADEEFREQMIIDKISSVFYFSFSTLFFAHRRPSESFFTRVLVVVWCFVLLILTQSYTATLTSMLTVQELRPTVRHMDDLRKSGVNIGYQTGSFTFERLKQMRFDESRLKTYNSPEEMRELFLHKSSNGGIDAAFDEVAYIKLFMAKYCSEYSIIEPTFKADGFGFAFPLGSPLVSDISRQILNITEGDAMKAIENKWFLGEKHCLDSTTSDSPIQLDHHSFEALFLIVFVVSVILLLLMLASRGYQERQHNASPNLPNDQANAAQEEVNEEGNVGDHIVEVDTALAKVSIVKPKL

GLR2.6 (last 317 AA)

MSLFNHLLSRALPLWLLFFINFLVLLGKSQQEVLQVQVGIVLDTNATLAALSLRAINMSLSEFYNTHNGFKTRIVLNIRDSKRTVVGAAASALYLIKKREVVAIIGPGNSMQAPFLINLGNQSQVPIISFSASSPVLDSLRSPYFIRATHDDSSQVHAISAIIESFRWREVVPIYADNEFGEGILPYLVDAFQEINVRIRYRSAISVHSTDDLVKKELYKLMTMPTRVFIVHMLPDLGSRLFSIAKEIGMMTKGYVWIVTNGIADQMSVMGESSLENMHGVLGVKTYFSRSKELMYLETRWRKRFGGEELNNFECWGYDTATALAMSIEEISSNVNMSFSQTKRNTSRDDTGTDLDDLSFALSGPKLLQALATVSFKGVAGRFQLKNGKLEATTFKIVNIEESGERTVGFWKSKVGLVKSLRVNQTGIKISHSSHRLRPIIWPGDTIFVPKGWEFPTNAKKLRIAVPKKDGFNNFVEVTKDANTNAPTITGFCIDVFDTAMRQMPYAVPYEYIPFETPDGKPRGSYDEMVYHVFLGEFDGAVGDTTILANRSTYVDFALPYSETGIVVVVPVKDEREKGKWVFLKPLTRELWFLTAASFLYIGIMSYTATLTSMLTVQELRPTVRHMDDLRNSGVNIGYQTGSFTFERLKQMGYKESRLKTYDTPQEMHELFLKKSSNGGIDAAFDEVAYVKLFMAKYCSKYTIIEPTFKADGFGFAFPLGSPLVPDLSRQILNITEGETMKAIENKWLLGEKHCLDSTTSDSPIRLDHHSFEALFTIVFVVSMLLLLAMLVCRRYRQESKSGEINANNSPTDGNMRAPPNQPTDDNMRAPTSPPIDDQVLEPPGPALNEADDQDQLLNDEVNVGDRNEVDIIVEVDPTLVHRRNLITSKTIPTRRAALFSRIKSA

GLR2.7 (last 371 AA)

MKVMNPRKTNNTFMYYFVLFVCGFVLMEGCLGQNQTTEIKVGVVLDLHTSFSKLCLTSINISLSDFYKYHSDYTTRLAIHIRDSMEDVVQASSAALDLIKNEQVSAIIGPRTSMQAEFMIRLADKSQVPTITFSATCPLLTSINSPYFVRATLDDSSQVKAIAAIVKSFGWRNVVAIYVDNEFGEGILPLLTDALQDVQAFVVNRCLIPQEANDDQILKELYKLMTMQTRVFVVHMPPTLGFRFFQKAREIGMMEEGYVWLLTDGVMNLLKSNERGSSLENMQGVLGVRSHIPKSKKLKNFRLRWEKMFPKKGNDEEMNIFALRAYDSITALAMAVEKTNIKSLRYDHPIASGNNKTNLGTLGVSRYGPSLLKALSNVRFNGLAGEFELINGQLESSVFDVINIIGSEERIIGLWRPSNGIVNAKSKNTTSVLGERLGPVIWPGKSKDVPKGWQIPTNGKMLRVGIPVKKGFLEFVDAKIDPISNAMTPTGYCIEIFEAVLKKLPYSVIPKYIAFLSPDENYDEMVYQVYTGAYDAVVGDVTIVANRSLYVDFTLPYTESGVSMMVPLKDNKNTWVFLRPWSLDLWVTTACFFVFIGFIVWILEHRVNTDFRGPPHHQIGTSFWFAFSTMNFAHREKVVSNLARFVVLVWCFVVLVLIQSYTANLTSFFTVKLLQPTVTNWKDLIKFNKNIGYQRGTFVRELLKSQGFDESQLKPFGSAVECDELFSNGTITASFDEVAYIKVILSQNSSKYTMVEPSFKTAGFGFVFPKKSPLTDDVSRAILNVTQGEEMQHIENKWFKKPNNCPDLNTSLSSNHLSLSSFWGLFLIAGIASFLALLIFVANFLYEHKHTLFDDSENSFRGKLKFLVRNFDEKDIKSHMFKENAVHNVSSPITQGSSSPLTDQSTPLPRSPEQYRELELRRVSSISSGELFTTQSEQVEDEESAIIQCEGE

GLR2.8 (last 371 AA)

MNPKKNNNTFLSYFVCLFLLLEVGLGQNQISEIKVGVVLDLNTTFSKICLTSINLALSDFYKDHPNYRTRLALHVRDSMKDTVQASAAALDLIQNEQVSAIIGPIDSMQAKFMIKLANKTQVPTISFSATSPLLTSIKSDYFVRGTIDDSYQVKAIAAIFESFGWRSVVAIYVDNELGEGIMPYLFDALQDVQVDRSVIPSEANDDQILKELYKLMTRQTRVFVVHMASRLASRIFEKATEIGMMEEGYVWLMTNGMTHMMRHIHHGRSLNTIDGVLGVRSHVPKSKGLEDFRLRWKRNFKKENPWLRDDLSIFGLWAYDSTTALAMAVEKTNISSFPYNNASGSSNNMTDLGTLHVSRYGPSLLEALSEIRFNGLAGRFNLIDRQLESPKFEIINFVGNEERIVGFWTPSNGLVNVNSNKTTSFTGERFGPLIWPGKSTIVPKGWEIPTNGKKIKVGVPVKKGFFNFVEVITDPITNITTPKGYAIDIFEAALKKLPYSVIPQYYRFESPDDDYDDLVYKVDNGTLDAVVGDVTITAYRSLYADFTLPYTESGVSMMVPVRDNENKNTWVFLKPWGLDLWVTTACFFVLIGFVVWLFEHRVNTDFRGPPHHQIGTSFWFSFSTMVFAHREKVVSNLARFVVVVWCFVVLVLTQSYTANLTSFLTVQRFQPAAINVKDLIKNGDYVGYQHGAFVKDFLIKEGFNVSKLKPFGSSEECHALLSNGSISAAFDEVAYLRAILSQYCSKYAIVEPTFKTAGFGFAFPRNSPLTGDVSKAILNVTQGDEMQHIENKWFMKQNDCPDPKTALSSNRLSLRSFWGLFLIAGIASFLALLIFVFLFLYENRHTLCDDSEDSIWRKLTSLFRNFDEKDIKSHTFKSSAVHHVSSPMTQYIPSPSTLQIAPRPHSPSQDRAFELRRVSFTPNEERLTTQTIHFEDEESDIECVVEQ

GLR2.9 (last 375 AA)

MKTNNTFLSYFVCGFLLMGVGLGQNQTSEIKVGVVLDLNTTFSKICLTSIKMAVSDFYADHPNYLTRLTLHVRDSMEDTVQASAAALDLIKTEQVSAIIGPINSMQADFMIKLANKTQVPTITFSATSPLLTSIKSPYFVRATIDDSSQVRAIASIFKFFRWRRVVAIYVDNEFGEGFMPFLFDALQDVEVKRSVIPPEAIDDEIQKELRKLMERQARVFVVHMESSLALRVFQIARDIGMMEEGYVWLMTNGMTHMMRHINNGRSLNTIEGVLGVRSHVPKSKELGDFRLRWKRTFEKENPSMRDDLNVFALWAYDSITALAKAVEKANTKSLWYDNGSTLSKNRTDLGNVGVSLYGPSLQKAFSEVRFNGLAGEFKLIDGQLQSPKFEIINFVGNEERIIGFWTPRDGLMDATSSNKKTLGPVIWPGKSKIVPKGWEIPGKKLRVGVPMKKGFFDFVKVTINPITNKKTPTGYAIEIFEAALKELPYLVIPEYVSFESPNNYNNLVYQVYDKTWDAVVGDITITANRSLYADFTLPFTESGVSMMVPVRDNENKDTWVFLEPWSLELWVTTGCFFVFIGFVVWLFEHRVNTDFRGPPQYQIGTSLWFSFSTMVFAHRENVVSNLARFVVVVWCFVVLVLTQSYTASLTSFLTVQSLQPTVTNVNDLIKNRDCVGYQGGAFVKDILLGLGFHEDQLKPFDSAKDADDLLSKGKSKGIAAAFDEVAYLKAILSQSCSKYVMVEPTFKTGGFGFAFPKNSPLTGEFSRAILNLTQNNVTQQIEDRWFPKKNDCPDPMTALSSNRLNLSSFLGLFLIAGTAISFSLLVFVALFLYEHRHTLGDDSEDSLWRKLKFLFKIFDEKDMNSHTFKNSAIHNISSPMTHKTPSPSTVQITPWPQSPSQNREFELRRVSFSPSEERFTTQPIIHHEDGESDIECRVEQ

GLR3.1 (last 335 AA)

MSFPTFSFHFSKVSLCFLLKQLLLYGFFFSMNWVLLSFIIVLGGGLLLSEGASSSRPPVIKVGAIFGLNTMYGETANIAFKAAEE
DVNSDPSFLGGSKLRILMNDAKRSGFLSIMGALQFMETDVVAIIGPQTSIMAHVLSHLANELTVPMLSFTALDPTLSPLQFP
FFVQTAPSDLFLMRAIAEMITYYGWSDVVALYNDDDNSRNGVTALGDELEERRCKISYKAVLPLDVVITSPVEIIEELIKIRGM
ESRVIVVNTFPNTGKMIFKFEAERLGMMEKGYVWIATTWLSSVLDSNLPLDTKLVNGVLTLRLHTPDSRKKRDFAARWKN
KLSNNKTIGLNVYGLYAYDTVWIIARAVKTLLEAGGNLSFSNDAKLGSLKGEALNLSALSRFDQGSQLLDYIVHTKMSGLTGP
VQFHPDRSMLQPSYDIINLVDDRVHQIGYWSNYSGLSIVPPESFYSKPPNRSSSNQHLNSVTWPGGTSVTPRGWIFRNNG
RRLRIGVPDRASFKDFVSRVNGSSNKVQGYCIDVFEAAVKLLSYPVPHEFIFFGDGLTNPNYNELVNKVTTGVDFDAVVGDI
AIVTKRTRIVDFTQPYIESGLVVVAPVTRLNENPWAFLRPFTLPMWAVTASFFVIVGAAIWILEHRINDEFRGPPRRQIITILW
FTFSTMFFSHRETTVSTLGRMVLLIWLFVVLIITSSYTASLTSILTVQQLNSPIKGVDTLISSTGRIGFQVGSFAENYMTDELNIA
SSRLVPLASPEEYANALQNGTVAAIVDERPYIDLFLSDYCKFAIRGQEFTRCGWGFAFPRDSPLAVDMSTAILGLSETGELQKI
HDRWLSKSNCSSPHGSQSGDSEQLNVHSFWGMFLVVGIACLVALFIHFFKIIRDFCKDTPEVVVEEAIPSPKSSRLTKLQTFL
AFVDEKEEETKRRLKRKRNNDHSMNANSIISRTASRRPI

GLR3.2 (last 324 AA)

MFWVLVLLSFIVLIGDGMISEGAGLRPRYVDVGAIFSLGTLQGEVTNIAMKAAEEDVNSDPSFLGGSKLRITTYDAKRNGFLT
IMGALQFMETDAVAIIGPQTSIMAHVLSHLANELSVPMLSFTALDPSLSALQFPFFVQTAPSDLFLMRAIAEMISYYGWSEV
IALYNDDDNSRNGITALGDELEGRRCKISYKAVLPLDVVITSPREIINELVKIQGMESRVIIVNTFPKTGKKIFEEAQKLGMMEK
GYVWIATTWLTSLLDSVNPLPAKTAESLRGVLTLRIHTPNSKKKKDFVARWNKLSNGTVGLNVYGLYAYDTVWIIARAVKRL
LDSRANISFSSDPKLTSMKGGGSLNLGALSIFDQGSQFLDYIVNTNMTGVTGQIQFLPDRSMIQPSYDIINVVDDGFRQIGY
WSNHSGLSIIPPESLYKKLSNRSSSNQHLNNVTWPGGTSETPRGWVFPNNGRRLRIGVPDRASFKEFVSRLDGSNKVQGYA
IDVFEAAVKLISYPVPHEFVLFGDGLKNPNFNEFVNNVTIGVFDAVVGDIAIVTKRTRIVDFTQPYIESGLVVVAPVTKLNDTP
WAFLRPFTPPMWAVTAAFFLIVGSVIWILEHRINDEFRGPPRKQIVTILWFSFSTMFFSHRENTVSTLGRAVLLIWLFVVLIIT
SSYTASLTSILTVQQLNSPIRGVDTLISSSGRVGFQVGSYAENYMIDELNIARSRLVPLGSPKEYAAALQNGTVAAIVDERPYV
DLFLSEFCGFAIRGQEFTRSGWGFAFPRDSPLAIDMSTAILGLSETGQLQKIHDKWLSRSNCSNLNGSVSDEDSEQLKLRSF
WGLFLVCGISCFIALFIYFFKIVRDFFRHGKYDEEATVPSPESSRSKSLQTFLAYFDEKEDESKRRMKRKRNDDLSLKPSRPI

GLR3.3 (last 347 AA)

MKQLWTFFFLSFLCSGLFRRTHSEKPKVVKIGSIFSFDSVIGKVAKIAIDEAVKDVNSNPDILSGTKFSVSMQNSNCSGFMG
MVEALRFMEKDIVGIIGPQCSVVAHMISHMANELRVPLLSFAVTDPVMSPLQFPYFIRTTQSDLYQMDAIASIVDFYGWKE
VIAVFVDDDFGRNGVAALNDKLASRRLRITYKAGLHPDTAVNKNEIMNMLIKIMLLQPRIVVIHVYSELGFAVFKEAKYLGM
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GLDKFFKDGGNISFSNHSMLNTLGKSGNLNLEAMTVFDGGEALLKDILGTRMVGLTGQLQFTPDRSRTRPAYDIINVAGTG
VRQIGYWSNHSGLSTVLPELLYTKEKPNMSTSPKLKHVIWPGETFTKPRGWVFSNNGKELKIGVPLRVSYKEFVSQIRGTEN
MFKGFCIDVFTAAVNLLPYAVPVKFIPYGNGKENPSYTHMVEMITTGNFDGVVGDVAIVTNRTKIVDFTQPYAASGLVVVA
PFKKLNSGAWAFLRPFNRLMWAVTGCCFLFVGIVVWILEHRTNDEFRGPPKRQCVTILWFSFSTMFFAHRENTVSTLGRLV
LIIWLFVVLIINSSYTASLTSILTVQQLSSPIKGIESLRERDDPIGYQVGSFAESYLRNELNISESRLVPLGTPEAYAKALKDGPSKG
GVAAIVDERPYVELFLSSNCAYRIVGQEFTKSGWGFAFPRDSPLAIDLSTAILELAENGDLQRIHDKWLMKNACTLENAELES
DRLHLKSFWGLFLICGVACLLALFLYFVQIIRQLYKKPTDDAIARDQQQNHDSSSMRSTRLQRFLSLMDEKEESKHESKKRKI
DGSMNDTSGSTRSRGFDRERSFNSVNPLD

GLR3.4 (last 347 AA)

MGFLVMIREVSMAKAIRVVLLCVSVLWVVPKECACRSNFSRNSSSSSSSSLRPLRQRPSSVNVGALFTYDSFIGRAAKPAVKAAMDDVNADQSVLKGIKLNIIFQDSNCSGFIGTMGALQLMENKVVAAIGPQSSGIAHMISYVANELHVPLLSFGATDPTLSSLQFPYFLRTTQNDYFQMHAIADFLSYSGWRQVIAIFVDDECGRNGISVLGDVLAKKRSRISYKAAITPGADSSSIRDLLVSVNLMESRVFVVHVNPDSGLNVFSVAKSLGMMASGYVWIATDWLPTAMDSMEHVDSDTMDLLQGVVAFRHYTIESSVKRQFMARWKNLRPNDGFNSYAMYAYDSVWLVARALDVFFRENNNITFSNDPNLHKTNGSTIQLSALSVFNEGEKFMKIILGMNHTGVTGPIQFDSDRNRVNPAYEVLNLEGTAPRTVGYWSNHSGLSVVHPETLYSRPPNTSTANQRLKGIIYPGEVTKPPRGWVFPNNGKPLRIGVPNRVSYTDYVSKDKNPPGVRGYCIDVFEAAIELLPYPVPRTYILYGDGKRNPSYDNLVNEVVADNFDVAVGDITIVTNRTRYVDFTQPFIESGLVVVAPVKEAKSSPWSFLKPFTIEMWAVTGGFFLFVGAMVWILEHRFNQEFRGPPRRQLITIFWFSFSTMFFSHRENTVSSLGRFVLIIWLFVVLIINSSYTASLTSILTIRQLTSRIEGIDSLVTSNEPIGVQDGTFARNYLINELNILPSRIVPLKDEEQYLSALQRGPNAGGVAAIVDELPYIEVLLTNSNCKFRTVGQEFTRTGWGFAFQRDSPLAVDMSTAILQLSEEGELEKIHRKWLNYKHECSMQISNSEDSQLSLKSFWGLFLICGITCFMALTVFFWRVFWQYQRLLPESADEERAGEVSEPSRSGRGSRAPSFKELIKVVDKREAEIKEILKQKSSKKLKSTQSAAGTSQSQHGEIT

GLR3.5 (last 348 AA)

MGALQLMENKVVAAIGPQSSGIGHIISHVANELHVPFLSFAATDPTLSSLQYPYFLRTTQNDYFQMNAITDFVSYFRWREVVAIFVDDEYGRNGISVLGDALAKKRAKISYKAAFPPGADNSSISDLLASVNLMESRIFVVHVNPDSGLNIFSVAKSLGMMGSGYVWITTDWLLTALDSMEPLDPRALDLLQGVVAFRHYTPESDNKRQFKGRWKNLRFKESLKSDDGFNSYALYAYDSVWLVARALDVFFSQGNTVTFSNDPSLRNTNDSGIKLSKLHIFNEGERFLQVILEMNYTGLTGQIEFNSEKNRINPAYDILNIKSTGPLRVGYWSNHTGFSVAPPETLYSKPSNTSAKDQRLNEIIWPGEVIKPPRGWVFPENGKPLKIGVPNRVSYKNYASKDKNPLGVKGFCIDIFEAAIQLLPYPVPRTYILYGDGKKNPSYDNLISEVAANIFDVAVGDVTIITNRTKFVDFTQPFIESGLVVVAPVKGAKSSPWSFLKPFTIEMWAVTGALFLFVGAVIWILEHRFNEEFRGPPRRQIITVFWFSFSTMFFSHRENTVSTLGRFVLLVWLFVVLIINSSYTASLTSILTVQQLTSRIEGMDTLIASNEPIGVQDGTFAWKFLVNELNIAPSRIIPLKDEEEYLSALQRGPRGGGVAAIVDELPYIKALLSNSNCKFRTVGQEFTRTGWGFAFQRDSPLAVDMSTAILQLAEEGKLEKIRKKWLTYDHECTMQISDTENYQISVQSFWGLFLICGVVWFIALTLFCWKVFWQYQRLRPEESDEVQARSEEAGSSRGKSLRAVSFKDLIKVVDKREAEIKEMLKEKSSKKLKDGQSSAENSQSKDHETPQ

GLR3.6 (last 328 AA)

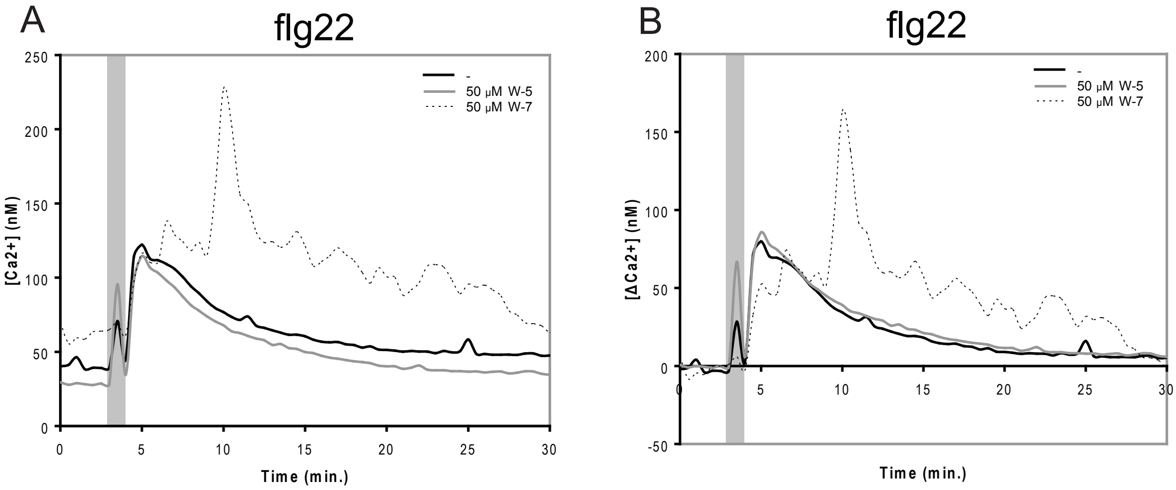
MKWFLLMLIICNAVPLQGLTKIVSARPQVVNIGSVFTFNSLIGKVIKVAMDAAVEDVNASPSILNTTTLRIIMHDTKYNGFMSIMEPLQFMESETVAIIGPQRSTTARVVAHVATELKIPILSFSATDPTMSPLQFPFFIRTSQNDLFQMAAIADIVQFYGWREVVAIYGDDDYGRNGVAALGDRLSEKRCRISYKAALPPAPTRENITDLLIKVALSESRIIVVHASFIWGLELFNVARNLGMMSTGYVWIATNWLSTIIDTDSPLPLDTINNIQGVITLRLHTPNSIMKQNFVQRWHNLTHVGLSTYALYAYDTVWLLAQAIDDFFKKGGNVSFSKNPIISELGGGNLHLDALKVFDGGKIFLESILQVDRIGLTGRMKFTSDRNLVNPAFDVLNVIGTGYTTIGYWFNHSGLSVMPADEMENTSFSGQKLHSVVWPGHSIKIPRGWVFSNNGRHLRIGVPNRYRFEEVVSVKSNGMITGFCVDVFIAAINLLPYAVPFELVAFGNGHDNPSNSELVRLITTGVYDAGVGDITIITERTKMADFTQPYVESGLVVVAPVRKLGSSAMAFLRPFTPQMWLIAAASFLIVGAVIWCLEHKHNDEFRGPPRRQVITTFWFSFSTLFFSHRETTTSNLGRIVLIIWLFVVLIINSSYTASLTSILTVHQLSSPIKGIETLQTNHDPIGYPQGSFVRDYLIHELNIHVSRLVPLRSPEEYDKALRDGPGKGGVAAVVDERAYIELFLSNRCEFGIVGQEFTKNGWGFAFPRNSPLAVDVSAAILQLSENGDMQRIRDKWLLRKACSLQGAEIEVDRLELKSFWGLFVVCGVACVLALAVYTVLMIRQFGQQCPEEAEGSIRRRSSPSARIHSFLSFVKEKEEDAKARSSRERQLEDISANGSSRCN

GLR3.7 (last 344 AA)

MGLGIDPSVAITALIVVILVVPMDCQRPQLVNIGAVFAFDSVIGRAAKVALEAAVSDVNNDKSFLKETELRLLMEDSACNVFRGSFGAFELLEKEVVAMIGPISSSVAHTISDIAKGLHFPLVSFAATDPTLSALQFPFFLRTTPNDAHQMSALVDLINFYGWKE

VISVYSDDELGRNGVSALDDELYKKRSRISYKVPLSVHSDEKFLTNALNKSKSIGPRVYILHFGPDPLLRIFDIAQKLQMMTHEYVWLATDWLSVTLDSLSDKGTLKRLEGVVGLRQHIPESVKMEHFTHKLQSNRSMNAYALHAYDTVWMIAHGIEELLNEGINITFSYSEKLLHARGTKLHLEKIKFFNSGELLLEKLLKVNFTGIAGQVQFGSGRNVIGCDYEIINVNKTDVHTVGFWSKNGGFSVVAPKTRHSQKKTSFVSDEKLGDITWPGGGREKPRGWVIADSADPLKIVVPRRVSFVEFVTEEKNSSHRIQGFCIDVFIEALKFVPYSVPYIFEPFGNGHSSPNYNHLIQMVTDGVYDAAVGDIAIVPSRSKLVDFSQPYASTGLVVVIPANDDNATWIFLRPFTSRLWCVVLVSFLVIAVVIWILEHRINEDFRGPPRRQLSTMLLFSFSTLFKRNQEDTISNLARLVMIVWLFLLMVLTASYTANLTSILTVQQLPSAITGIDSLRASEVPIGYQAGTFTLEYLTYSLGMARSRLVPLDSTEEYEKALKLGPTNWGGVAAIVDELPYIELFLAERTGFKIVGEPFMHRGWGFAFKRDSPLAIDMSTAILKLSETRKLQEIRKKWLCKTNCAGKSNWNPEPNQLHLKSFKGLYLVCIAITVSAFLVFVLRMIRQFVRYRRMERTSSMPRASWSASPTLRLRELVFDFVEFVDEKEEAIKRMFRRSDDSNNNPSHVGEVQADTEVPRN

Supplemental Figure 2



Supplemental Figure 1. Transmembrane and CaMBD predictions for individual Arabidopsis iGluRs.

Supplementary Figure 2. Individual seedling response curves upon treatment with the calmodulin antagonist W-7.