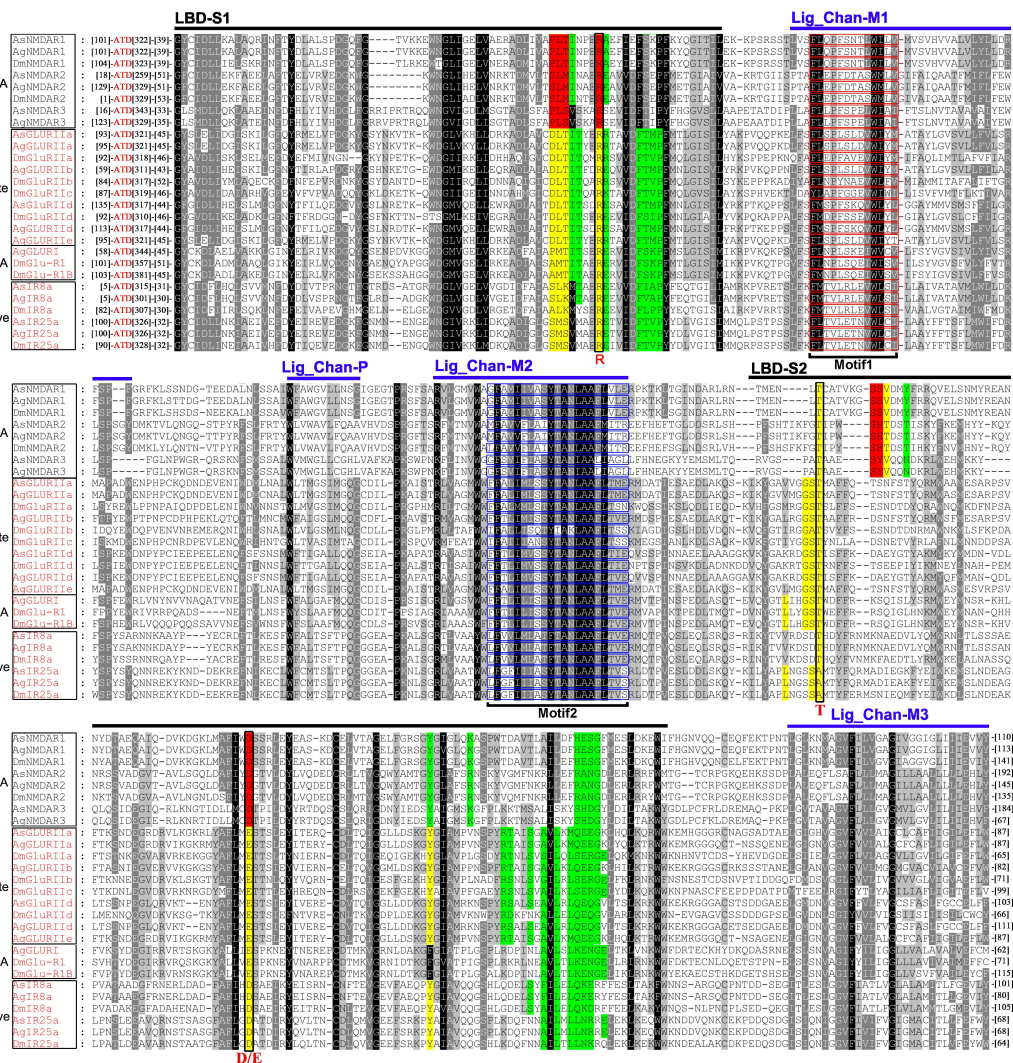


a



b

Lig. Chan-M1

AsIR75k : [268]-LAAVVSFTFVDSWGYRD---PKTGRYNVIGELTOSDLADGGTALFFTQRIHIIDYLSMTTPSRVKTFRAAK---LSFTDNVFLDSDQVTCG--SFTLLSGVLLAVVLRTGEQR-----TGFPQA
AgIR75k : [287]-LAAVVSFTFVDSWGYRD---RETDRNVLIGELTOSDLADGGTALFFTQRIHIIDYLSMTTPSRVKTFRAAK---LSFTDNVFLDSDQVTCG--SFTLLSGVLLAVVLRTGEQR---IGSNPFAA
AsIR75d : [269]-LAPFLNNVYDAGGYK---HNGTPTLMLGKQFNHVSVDGCMGCLNRTPELEVMDPMLVILVRSSI--PQRP--LSIVSNIFLPSVSGVMSG--AMAMAYWIAVGLRFPFYG-----AE
AgIR75d : [276]-LAPFLNNVQLDRVGYK---QNGTFSGVMGKFNRSIDPSCGLTLMRTPELEVADFMVITLLIKSSI--PQRP--LSIVANIFLPSVSGVMSG--FALMAVYMTIAIROLTYS-----GE
DmIR75a : [253]-LHCKMKKFIISDSWSKSD---VVGSGAGWQDTADTATPSLATEGRKYLISAIETGFFRSVCFRTNHN--AGLRGDVFLPSVSGVMSG--GGVLSIGVLLMTIFYMECK---MQKRWRLDY
DmIR75d : [303]-LHMSYNTYVTQYVGNWRQ---FNGSFDGLMGRFQRYELDQAQLATFMRLRDLALMDVFAETVYVRAGIFPROBP---LSAVANIFAMFENDMYSI--MLLILITTVVVDLLETFSPH-----H
AsIR31a : [256]-HPTFLIKYRPTRGWAGRL---P-SGYRLGLGVWRLETTMAATGLIMRLSPCLPDSIHSYWAFFETGFKITPDIGSKSEGNQF--PSVSGVMSG--VSLIAAVVVKYLARFSER-----P
AgIR31a : [144]-HPTFLIKYRPTRGWAGRL---R-SGYRLGLGVWRLETTMAATGLIMRLSPCLPDSIHSYWAFFETGFKITPDIGSKSEGNQF--PSVSGVMSG--LSTASGVLLGYLAREAD-----N
DmIR31a : [253]-PFLHVNPNRNSRGWAGRL---GNTTFLRLGLGVWRNADLAASGAFNRIRKFAFDFTTHQSKKPEFAEYAYTSDLDTHGKSGNF--PSVSGVMSG--LTLGAFSIWVLEFELIDYKEHLNKGQSVICI
AsIR76b : [135]-FNFVYEIVMPEQNIQVSSNDMEG---SVLQLANGSADAVAFITPLADARQHITRYSTGLDEGEWIMVVRME--SAS-GSGLDLPSVSGVMSG--IS-ILAVGPTIYGLLLLRRLTKDKEQVLYT
AgIR76b : [150]-FNFVYEIVMPEQNIQVSSNDMEG---SVLQLTNGTADAVSFITPLADARQHITRYSTGLDEGEWIMVVRME--SAS-GSGLDLPSVSGVMSG--IS-ILAVGPTIYGLLLLRRLTKDKEQIYIT
AsIR21a : [357]-QVDFPDIVS-PKRP---QMSGD---AVDDEKRKQCGVLGAGFVFNHRLNATLMBXSVHSDDCAAPFLMSSA--LPR-YRAITLPSVSGVMSG--PYLIALFPAFSDKMTLRHLGWNSEIEM
AgIR21a : [355]-LDFYDILIP-PORT---ELGPGD---AVDEKRKQCGVLGAGFVFNHRLNATLMBXSVHSDDCAAPFLMSSA--LPR-YRAITLPSVSGVMSG--LVLIALFPAFSDKMTLRHLGWNSEIEM
DmIR21a : [323]-LDFDIDITETPTSRN--TRGVVD---TDFQLEIETVDMGSIYITQSLMDSAMSVGHSDDCAAPFLASKA--LPR-YRAITLPSVSGVMSG--LVYLGIETPFTFDRITLSHLMGWQZVEM
AsIR93a : [455]-LDFYITLITISQF---IKGISSDIPQEFNTIINNKLIIAAIGSTVNEHCKKFSVYTIPTISQTSFISRRER--LSR-VLLFSLPSVSGVMSG--AAAVAMGPTICANKLSP--YVEVHNKPTDTG
AgIR93a : [485]-LDFYITMVISQPAEING-LKTISSDIPQEFSTIWNKKIILAAVGAFTVNEHCKKFSVTFDPTISQTSFISRRER--LSR-VLLFSLPSVSGVMSG--AAAVAMGPTICANKLSP--YVEVHNKPTDTG
AsIR93a : [473]-LDFYITLHEASAKWEEDLVGSMTRFIRPYVEMVQGNQFTAAVAATVEDDQKPFNYITQISVQKYSFTRKDE--VSR-IYLFTEPRVETVTCG--GILITLAPTIVAINLAP-LKEMR-----IVG
AsIR41a : [264]-LHCSLEISDEAG---QIFDNKTGDTGIAVERRAVGVGALISWYHSEFRISLSLRKFSIKSTGVTCAPKELP--LSS-WMTPLPSVSGVMSG--GSPFLAIVDFVLSFVTHKPTPSSGSRVDIC
AgIR41a : [248]-LHCSLEISDEAG---QIFDNKTGDTGIAVERRAVGVGALISWYHSEFRISLSLRKFSIKSTGVTCAPKELP--LSS-WMTPLPSVSGVMSG--GSPFLAIVDFVLSFVTHKPTPSSGSRVDIC
AsIR41a : [264]-LHCSLEISDEAG---QIFDNKTGDTGIAVERRAVGVGALISWYHSEFRISLSLRKFSIKSTGVTCAPKELP--LSS-WMTPLPSVSGVMSG--GSPFLAIVDFVLSFVTHKPTPSSGSRVDIC
AsIR41a : [264]-LHCSLEISDEAG---QIFDNKTGDTGIAVERRAVGVGALISWYHSEFRISLSLRKFSIKSTGVTCAPKELP--LSS-WMTPLPSVSGVMSG--GSPFLAIVDFVLSFVTHKPTPSSGSRVDIC
AgIR40a : [291]-LHMFQYVEPPEKIQIALGSEONASFSAGAGMORREVEPLGDVAUTWHRKKAVERFFFTLADSAABTHARRK--LNE-ALALHPSVSGVMSG--ITLITLISGPTIYIISTFYPRNSAQTVHARNA
AsIR40a : [291]-LHMFQYVEPPEKIQIALGSEONASFSAGAGMORREVEPLGDVAUTWHRKKAVERFFFTLADSAABTHARRK--LNE-ALALHPSVSGVMSG--ITLITLISGPTIYIISTFYPRNSAQTVHARNA
AsIR40a : [291]-LHMFQYVEPPEKIQIALGSEONASFSAGAGMORREVEPLGDVAUTWHRKKAVERFFFTLADSAABTHARRK--LNE-ALALHPSVSGVMSG--ITLITLISGPTIYIISTFYPRNSAQTVHARNA
AsIR40a : [291]-LHMFQYVEPPEKIQIALGSEONASFSAGAGMORREVEPLGDVAUTWHRKKAVERFFFTLADSAABTHARRK--LNE-ALALHPSVSGVMSG--ITLITLISGPTIYIISTFYPRNSAQTVHARNA

Lig. Chan-P **Lig. Chan-M2** **R** **Motif1**

AsIR75k : R--LSADLLNVGGTTCQGS-FIEPKTPPSCLILLCHVWIRVWASANVACVCGEST-KIQTDLDDLASRLKTGAEDTVNRYFYQHETEPVRKALYERKRNKD---GTENFPLAEGVEAIRQGHYAF
AgIR75k : VTGLSDTLLNVGGTTCQGS-FIEPQTAPSCILLCHVWIRVWASANVACVCGEST-KIQTDLDDLASRLKTGAEDTVNRYFYFHETEPSPRKALYERKRNKD---GTENFPLAEGVELLRQGHYAF
AsIR75d : RYVIESLITLIGIMCGGY-ELVPHNCTCLMLSPFCLVWIRVWASANVACVCGEST-KIQTDLDDLASRLKTGAEDTVNRYFYFHETEPSPRKALYERKRNKD---GTENFPLAEGVELLRQGHYAF
AgIR75d : RGAIESIVYIGTMCQGG-DIVPQFNCTCLMLSPFCLVWIRVWASANVACVCGEST-KIQTDLDDLASRLKTGAEDTVNRYFYFHETEPSPRKALYERKRNKD---GTENFPLAEGVELLRQGHYAF
DmIR75a : LPSLLSTFLISFGAICQSS-SLIPRSAGGLIYALFHSISLVWYHSVSSISSEVKSKITMRQLAESLTVGLIEPLPHKSYLINSRLPEIHLFKKKES-QTONPELPLPAEQGLVRNDPQYNI
DmIR75d : DMSYMDTLNVFGWAGMCGGF-YVEVNRNSAIIIVETTKQVWIRVWASANVACVCGEST-KIQTDLDDLASRLKTGAEDTVNRYFYFHETEPSPRKALYERKRNKD---GTENFPLAEGVELLRQGHYAF
AsIR31a : SRATVAYLVDDVSCVAGQGV-PVSRSLVPAVALIIVLIVWIRVWASANVACVCGEST-KIQTDLDDLASRLKTGAEDTVNRYFYFHETEPSPRKALYERKRNKD---GTENFPLAEGVELLRQGHYAF
AgIR31a : TRATMAYVLDDVACVAGQGV-PVSRSLVPAVALIIVLIVWIRVWASANVACVCGEST-KIQTDLDDLASRLKTGAEDTVNRYFYFHETEPSPRKALYERKRNKD---GTENFPLAEGVELLRQGHYAF
DmIR31a : KTFCTERLITQFGACG-DRNVGDRPFTMLTFLSADVWIRVWASANVACVCGEST-KIQTDLDDLASRLKTGAEDTVNRYFYFHETEPSPRKALYERKRNKD---GTENFPLAEGVELLRQGHYAF
AsIR76b : LPHCVWFVYVGLMKQCG---NSTLTFASWVWIRVWASANVACVCGEST-KIQTDLDDLASRLKTGAEDTVNRYFYFHETEPSPRKALYERKRNKD---GTENFPLAEGVELLRQGHYAF
AgIR76b : LPHCVWFVYVGLMKQCG---NSTLTFASWVWIRVWASANVACVCGEST-KIQTDLDDLASRLKTGAEDTVNRYFYFHETEPSPRKALYERKRNKD---GTENFPLAEGVELLRQGHYAF
AsIR21a : FWFVEGTFTNSLTQFQNS--WNTTKKASTMLIGIYVWIRVWASANVACVCGEST-KIQTDLDDLASRLKTGAEDTVNRYFYFHETEPSPRKALYERKRNKD---GTENFPLAEGVELLRQGHYAF
AgIR21a : FWFVEGTFTNSLTQFQNS--WNTTKKASTMLIGIYVWIRVWASANVACVCGEST-KIQTDLDDLASRLKTGAEDTVNRYFYFHETEPSPRKALYERKRNKD---GTENFPLAEGVELLRQGHYAF
DmIR21a : FWFVEGTFTNSLTQFQNS--WNTTKKASTMLIGIYVWIRVWASANVACVCGEST-KIQTDLDDLASRLKTGAEDTVNRYFYFHETEPSPRKALYERKRNKD---GTENFPLAEGVELLRQGHYAF
AsIR93a : LGKVNCFWYIYGALLCG--LILYADSGTIIITGTWVWIRVWASANVACVCGEST-KIQTDLDDLASRLKTGAEDTVNRYFYFHETEPSPRKALYERKRNKD---GTENFPLAEGVELLRQGHYAF
AgIR93a : LGKVNCFWYIYGALLCG--LILYADSGTIIITGTWVWIRVWASANVACVCGEST-KIQTDLDDLASRLKTGAEDTVNRYFYFHETEPSPRKALYERKRNKD---GTENFPLAEGVELLRQGHYAF
DmIR93a : LSTVKSFCWYIYGALLCGG-MPLTADSGLVGVFWVWIRVWASANVACVCGEST-KIQTDLDDLASRLKTGAEDTVNRYFYFHETEPSPRKALYERKRNKD---GTENFPLAEGVELLRQGHYAF
AsIR41a : ESMVAIMSIFILQAVLMR---INKNPVSGMILIGTFTLVGMLGNATSGSSGVWVWERY-EKSIDTVQELADRN--LRWGSTDWAFISIQATOPTIVKLNNF--LTAPEKVLHR--NATERMNA--YSI
AgIR41a : ESMVAIMSIFILQAVLMR---INKNPVSGMILIGTFTLVGMLGNATSGSSGVWVWERY-EKSIDTVQELADRN--LRWGSTDWAFISIQATOPTIVKLNNF--LTAPEKVLHR--NATERMNA--YSI
DmIR41a : ESMVAIMSIFILQAVLMR---INKNPVSGMILIGTFTLVGMLGNATSGSSGVWVWERY-EKSIDTVQELADRN--LRWGSTDWAFISIQATOPTIVKLNNF--LTAPEKVLHR--NATERMNA--YSI
AgIR41a : ESMVAIMSIFILQAVLMR---INKNPVSGMILIGTFTLVGMLGNATSGSSGVWVWERY-EKSIDTVQELADRN--LRWGSTDWAFISIQATOPTIVKLNNF--LTAPEKVLHR--NATERMNA--YSI
DmIR41a : ESMVAIMSIFILQAVLMR---INKNPVSGMILIGTFTLVGMLGNATSGSSGVWVWERY-EKSIDTVQELADRN--LRWGSTDWAFISIQATOPTIVKLNNF--LTAPEKVLHR--NATERMNA--YSI
AgIR40a : WNPTRSRLL---RPAFYNLIRVWIRVWASANVACVCGEST-KIQTDLDDLASRLKTGAEDTVNRYFYFHETEPSPRKALYERKRNKD---GTENFPLAEGVELLRQGHYAF
AsIR40a : WNPTRSRLL---RPAFYNLIRVWIRVWASANVACVCGEST-KIQTDLDDLASRLKTGAEDTVNRYFYFHETEPSPRKALYERKRNKD---GTENFPLAEGVELLRQGHYAF
AsIR40a : WNPTRSRLL---RPAFYNLIRVWIRVWASANVACVCGEST-KIQTDLDDLASRLKTGAEDTVNRYFYFHETEPSPRKALYERKRNKD---GTENFPLAEGVELLRQGHYAF
AsIR40a : WNPTRSRLL---RPAFYNLIRVWIRVWASANVACVCGEST-KIQTDLDDLASRLKTGAEDTVNRYFYFHETEPSPRKALYERKRNKD---GTENFPLAEGVELLRQGHYAF

Motif2 **T** **Lig. Chan-M3**

AsIR75k : NVLGVCKYKISETFQEE--EKCGLQELEYK---VIDPYAOKNNSREFRITLFLKLEFGIQRENTLLYTKKPRCTG-----GSS-FIPISIVDVWPAIMTLGWGYELTVCILAE-[19]
AgIR75k : NVLGVCKYKISETFQEE--EKCGLQELEYK---VIDPYAOKNNSREFRITLFLKLEFGIQREHTLLYTKKPRCTG-----GSS-FIPISIVDVWPAIMTLGWGYELTVCILAE-[18]
AsIR75d : EELNNAAYKIKETFAPE--EVCKLHELEAK---LPPFGIPTVKGSKYRELIRQRLMORREVGILIKRFNIWIHQKPCQEN-----PTAGYTSGLVEMVRYLMLFLAVGFLAAILVLGIE-[27]
AgIR75d : EELNNAAYKIKETFAPE--EVCKLHELEAK---LPPFGIPTVKGSKYRELIRQRLMORREVGILIKRFNIWIHQKPCQEN-----LNAGFSSGLVEMVRYLMLFLAVGFLAAILVLGIE-[24]
DmIR75a : VEFSSQYAVERYPTAQ---EICOLNLEPRFQPLPYTHIRNATKELRLRLIRLETFVGRKRSYVWMLKUYA---QNFVITIGVEMVAPILLMLTCAQVLLVLE-[15]
DmIR75d : QVQLAGQVYSVDTFSEF---EKCGLEMEFQPLFMIAIPTRNFFPKELIRQLRQWOREVSYNREERKWIIPQKPKCEG-----GVGGVYSGLTECYALGFLGCGAAVSVFLIE-[21]
AsIR31a : HCELTVEVPALANOPTAN--EICELRMVEGVYKYDIRVMAFVLPKHSWYAEAFKIT-----SAT-VYSGLTECYALGFLGCGAAVSVFLIE-[19]
AgIR31a : HCELTVEVPALANOPTAN--EICELRMVEGVYKYDIRVMAFVLPKHSWYAEAFKIT-----SAT-VYSGLTECYALGFLGCGAAVSVFLIE-[19]
DmIR31a : HCELVDAEPISCEYFDAN--EICDLREVSGHM--EVEILNWLHNQSYTEIFKTAMCNAQKGFVERILRRRQIKKPAQCS-----LYT-VYPSLSGVLPGFVILLICKSNKFS-----[114]
AsIR76b : RIEFALDHMYADILVR---RKINPINEIRHCPATATPTPLRNARFVPTTEWNRLDDELLMVEGGLIKYKHLHD---RLPKAEICPNLGGTERQDORLDVMTYFVMTVEFTSVIVFASE-[137]
AgIR76b : RIEFALDHMYADILVR---RKINPINEIRHCPATATPTPLRNARFVPTTEWNRLDDELLMVEGGLIKYKHLHD---RLPKAEICPNLGGTERQDORLDVMTYFVMTVEFTSVIVFASE-[137]
AsIR21a : GSKLELEFLIKSNLSHQF--ENKRYGLHVSRECFALYGVSVFPFNSVHRDFINNAILYMOAGLIGKLNLDVWTWTKDKGRKEASVGERSTAFSEERG--TLADTEGEMFLMLFGYVALGVLSIE-[229]
AgIR21a : GSKLELEFLIKSNLSHQF--ENKRYGLHVSRECFALYGVSVFPFNSVHRDFINNAILYMOAGLIGKLNLDVWTWTKDKGRKEASVGERSTAFSEERG--TLADTEGEMFLMLFGYVALGVLSIE-[229]
AsIR93a : DAEINRLMLKRQELQT---DRCDALSTDBFLDEQIALVMPDPSYLELNMDEIKRMQGFSTQRWVAQYLPAKDKCS---GAGRVMDNHT-----NSSDMAGSWMILLGFSGCMGTIVGE-[21]
AgIR93a : DAEINRLMLKRQELQT---DRCDALSTDBFLDEQIALVMPDPSYLELNMDEIKRMQGFSTQRWVAQYLPAKDKCS---GAGRVMDNHT-----NSSDMAGSWMILLGFSGCMGTIVGE-[21]
DmIR93a : DAEINRLMLKRQELQT---DRCDALSTDBFLDEQIALVMPDPSYLELNMDEIKRMQGFSTQRWVAQYLPAKDKCS---GAGRVMDNHT-----NSSDMAGSWMILLGFSGCMGTIVGE-[21]
AsIR93a : DAEINRLMLKRQELQT---DRCDALSTDBFLDEQIALVMPDPSYLELNMDEIKRMQGFSTQRWVAQYLPAKDKCS---GAGRVMDNHT-----NSSDMAGSWMILLGFSGCMGTIVGE-[21]
AsIR41a : ERLPYGHVAYGSEYITD---VSNFNEIMEDIYENCVAMATKTWPLMNELDLTLITPQSGIQRWFENKVVSKFADNK---VQHAISTHFGNPGPIAPQSILGALFLLAFGLGLGVCFAC-[15]
AgIR41a : ERLPYGHVAYGSEYITD---VSNFNEIMEDIYENCVAMATKTWPLMNELDLTLITPQSGIQRWFENKVVSKFADNK---VQHAISTHFGNPGPIAPQSILGALFLLAFGLGLGVCFAC-[15]
DmIR41a : ERLPYGHVAYGSEYITD---VSNFNEIMEDIYENCVAMATKTWPLMNELDLTLITPQSGIQRWFENKVVSKFADNK---VQHAISTHFGNPGPIAPQSILGALFLLAFGLGLGVCFAC-[15]
AgIR40a : WILRELENRNREGYQLL--VERQSAPHAALVNSTGVLRQLRLYLR---GRSNDSPFLGVSGEGRVLQADPKYAVFGGRETLFYNTKRYGRFQLSEKLYTRYSAAVAVGICGFLDSINDVIMHFE-[116]
AsIR40a : WILRELENRNREGYQLL--VERQSAPHAALVNSTGVLRQLRLYLR---GRSNDSPFLGVSGEGRVLQADPKYAVFGGRETLFYNTKRYGRFQLSEKLYTRYSAAVAVGICGFLDSINDVIMHFE-[112]

D/E

class of iGURs:	representative Antenna IR subfamily		
Domains:	Lig. Chan (M1, P, M2, M3):		
ligand binding sites:	arginine: R	Threonine: T	aspartate / glutamate: D or E
Motifs:	Motif1 (part of transmembrane region M1): A.A. Motif2 (part of transmembrane region M2): A.A.		

C

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AsIR7t      : [251]-MNFSTIVYQLPEGNVKGWIFRSPENSTGLVGLVLR-REVDVFGESCIGISLSRYQHLRLGTTSTRYGQILLALPK-RPYTSFERLQEDSLSQSMWCIVCYAICVTAQAIFNVRQAPG
AgIR7t      : [263]-FNFTPEYRISNGSTRWGFAR--AVNSTGLMGWQIR-GEVDFGLGSGISLSRVQHLRPGIASRFGQIALALPK-RPDSSEVERLHKPESTOTMHCIVLGLAGISTIAWALFGIGWRLV
AsIR7u      : [232]-FNFTPEYRISNGSTRWGFAR--ATNSTGMMGQIR-GEVDFGLGSGISLSRVQHLRPGIASRFGQIALALPK-RPDSSEVERLHKPESTOTMHCIVLGLAGISTIAWALFGIGWRLV
AgIR7u      : [258]-FNFTPEYRISNGSTRWGFAR--AANSTGMMGQIR-NEVAFGFGCLGMYNEVRRNYLTKMGAPSFLLTQITVAEPD-KPYTSLEKLEQEDSLSQSMWCIVCYAIGYGLLTIVLFDKSLVKVP
AsIR7w      : [251]-LNFTFRYVRPTDGVKWLILY--PGNSTGLVGLQIR-REVDFGFGSLGFSHSRHTFLKWTSPSHVTQMIIGTPPK-RPYTSLEKLEQEDSLSQSMWCIVCYAIGYGLLTIVLFDKSLVKVP
AgIR7w      : [268]-LNFTFRYVRPTDGVKWLILY--AANSTGLVGLQIR-RGADFGFGSLGFSLSNRHTYLRMGVNNHMTQMIIGTPPK-RPYTSLEKLEQEDSLSQSMWCIVCYAIGYGLLTIVLFDKSLVKVP
AsIR7h.1    : [254]-LNFTFRYVRPTDGVKWLILY--AANSTGLVGLQIR-RGADFGFGSLGFSLSNRHTYLRMGVNNHMTQMIIGTPPK-RPYTSLEKLEQEDSLSQSMWCIVCYAIGYGLLTIVLFDKSLVKVP
AgIR7h.1    : [280]-LNFRVAIVQPADGRTWGRYIP-NGTANGALGULN-GTVHMTVGGYFPYPALLAATTQTHYYTAELIVAVEELATLSPLEQDKREROPATITVAVELAIG-----ALG
DmIR7a      : [261]-FDFTRLLEPEPCNKCLSPDKDKDCSGCFDQVILSNS---SILIGAMSGSHQHRSHFSTSSYHQSSIVFLHMS-SQFGAVACDAVEFTIVLMDAVVSSLLLVLLVLMWNRN---LVC
DmIR7b      : [477]-LNFRVGLVYWMKKEVLATFDESGRIFDELFGHADFSLGGFHKPKSAGSEIPIS---QSTYFMSHILTLNLQSAISAYEKSTFPPPLPLRAAGLVLLIACLLMLLVR---WRH
DmIR7c      : [255]-MNFTEIKLVQKDKNRGELLF--DGNFTGLLQVVD-VGNLTVGVCFMYSKARSDMLFSTSTSFVIVVDSG-GSISPMGCHIRHREKVLKSCGLLSLIFGFVLLICLLKITALNLV
DmIR7d      : [250]-MNFTEIKLVQKDKNRGELLF--DGNFTGLLQVVD-VGNLTVGVCFMYSKARSDMLFSTSTSFVIVVDSG-GSISPMGCHIRHREKVLKSCGLLSLIFGFVLLICLLKITALNLV
AsIR136     : [219]-QSTFVEYKYTEHPQ--MDWSNNTSIDFATYRFLQR-GFTDR-ESALYFPNO-----FRWCDAVEKQ-YQRIIHEQVHNSDEVDLHHLISG-----
AgIR136     : [233]-QSTFAFFNYSTKPGPIFVFWDDRTDFATYRFLYK-GAVQYPPSSLLFPDR-----QSSCAVEKRW-FNRVLQEQVHNSDEVDLHHLISG-----
AsIR137     : [233]-QRTSYEYATVPVHKVFEPWYDRTIDFATYRISRGTTKLLPESALYFPNO-----YRWCDAVEKRY-KYRIIHEQVHNSDEVDLHHLISG-----
AgIR137     : [234]-QHTVADYRYTAQPIELFEPWHSSTEIDFATYRFL--TEQAYKALFLFPNO-----NLWCDAVEKT-YNRILHQCIMHNSDEVDLHHLISG-----
AsIR138     : [206]-QRTSYEYATVPVHKVFEPWYDRTIDFATYRISRGTTKLLPESALYFPNO-----YRWCDAVEKRY-KYRIIHEQVHNSDEVDLHHLISG-----
AgIR138     : [235]-QRTVAQFKHTADPIKQKFSWYDVEFDMATYRQPD--GGALYFPAFLYFPNO-----FRWCDAVEKT-YDRVLDQVHNSDEVDLHHLISG-----
AgIR140.1   : [226]-RNASFEISSLY-----DASVDYGVNMGVPPPTTD--KTVALGST-----FVSMVFRS-KPKPIIAVLHNSDEVDYTHHGLFLIFLLALVLSLFG---KVL
AsIR140.1   : [260]-RNASFEVVKAA-----VSVNTDYGVMHMGVPLIGTH--HIRALGST-----FMVALFRS-KPKKSVISVLHNSDEVDYTHHGLFLIFLLALVLSLFG---HTL
AsIR140.2   : [230]-RNASFEVNTINDIRISVEIDYGAHSGSPSTTD--SIRALGST-----FVALVFRS-KPKKSVISVLHNSDEVDYTHHGLFLIFLLALVLSLFG---HSL
AgIR140.2   : [175]-RNAYELQSLIN-----STLLDYGVVHIGIPLIGTGD--KTVALGST-----FVSMVFRS-KPKPIIAVLHNSDEVDYTHHGLFLIFLLALVLSLFG---KVL
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Motif1

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AsIR7t      : RLPNSFYTHVLLVGGSCN---PLRLDSSRLFIGFGLNIVVIRTDHAGFERIQASDLSASDLNITFGEINKAGMNYMHKTTISLYEKDNFPQIDSRKRIIQDKATDWEQLMYALSQHLK
AgIR7t      : RLRRHPCYTHVLLVGGPCG---ALRMDSTRLFVSLVGNVVRVTHAAAFERIQASDLSASELDTLEQINRAGKTYIMHKTITLFFNDNPLVGRPRRIIRLHDNENWEELLYQLSQPGS
AsIR7u      : RFRNPNGYTHVLLVGGPTC---MLRQNSTRMFVIGFGLNIVVIRTDHAGFERIQASDLSASELDTLEQINRAGKTYIMHKTITLFFNDNPLVGRPRRIIRLHDNENWEELLYQLSQPGS
AgIR7u      : RFRNPAYNTHVLLVGGPSR---PVKQTSIRLFAQFGLNIVVIRTDHAGFERIQASDLSASELDTLEQINRAGKTYIMHKTITLFFNDNPLVGRPRRIIRLHDNENWEELLYQLSQPGS
AsIR7w      : YLPNPLYTHVLLVGGSCG---HFRLDSTRVIFIGFGLNIVVIRTDHAGFERIQASDLSASELDTLEQINRAGKTYIMHKTITLFFNDNPLVGRPRRIIRLHDNENWEELLYQLSQPGS
AgIR7w      : ALQHPLYTHVLLVGGAVG---WLRLDSTRVIFIGFGLNIVVIRTDHAGFERIQASDLSASELDTLEQINRAGKTYIMHKTITLFFNDNPLVGRPRRIIRLHDNENWEELLYQLSQPGS
AsIR7h.1    : YPRRIALDYTHVLLVGGSL--ILPRVARTRFMMLNLTHTVMDRECKKGLVETLTPPLN-DIHSIDALLDAGYREAMTETVYVKVHSESK---HRLVLEPADQGYLLQRTDLGE
AgIR7h.1    : R-RHRLHFRHTVLLVGGSLPGRVPRRTVARIALLLWVHAAAFERIQASDLSASELDTLEQINRAGKTYIMHKTITLFFNDNPLVGRPRRIIRLHDNENWEELLYQLSQPGS
DmIR7a      : DIASHALQHTTVMGNPLEARSLPRSSRLRLVYAGVLLVTVVIRTDHAGFERIQASDLSASELDTLEQINRAGKTYIMHKTITLFFNDNPLVGRPRRIIRLHDNENWEELLYQLSQPGS
DmIR7b      : LPRNPYYELVLLVGGNLEDRWVQRFPSRLVLLTWIFATYRISRGTTKLLPESALYFPNO-----YRWCDAVEKRY-KYRIIHEQVHNSDEVDLHHLISG-----
DmIR7c      : RNRLLPFMGWASLLGGIALY--NPORNFARYIVMMWILQHTVIRABMTQGVYIIGD-VEMRSPKSLSEVLADYERILPALRTIEKDSMPTN---FHAVLSLEESLYRREDD
DmIR7d      : ---LHWIIVG---SRWRMPSPIDAGWLVTFIRASVYASIVFNQNGVVKP-SPRTLDOALSGGFRITDHASVYMTLKIPIPSFOGKT---LISAGQVVDVFDALKAPK
AsIR136     : ---IVIFYTHYQIAVQVLLQRYPNVYAVINTPKIL-----HBYVYFALLTSSSLIGSOVFPYPTTIOEFVKTPTPLLVLRRLDISIQENKDFARK-MIFYENIEQYQHGQYALTO--L
AgIR136     : ---LAAFVYVYLLVLAHPLRQHRMDYDLVNTPHIRHIVLTVLHNSDEVDYTHHGLFLIFLLALVLSLFG---KVL
AsIR137     : ---TVVFFFTYETKLOKLFSSRYPSVYSVINTPTIMRMMLDSTLSBYVYFALLTSSSLIGSOVFPYPTTIOEFVKTPTPLLVLRRLDISIQENKDFARK-MIFYENIEQYQHGQYALTO--L
AgIR137     : ---IVICFLLYRLKHLTQRHHPNAPFIINTPHILHILVLLHNSDEVDYTHHGLFLIFLLALVLSLFG---KVL
AsIR138     : ---TVVFFFTYETKLOKLFSSRYPSVYSVINTPTIMRMMLDSTLSBYVYFALLTSSSLIGSOVFPYPTTIOEFVKTPTPLLVLRRLDISIQENKDFARK-MIFYENIEQYQHGQYALTO--L
AgIR138     : ---LAAFLLYRLKHLTQRHHPNAPFIINTPHILHILVLLHNSDEVDYTHHGLFLIFLLALVLSLFG---KVL
AgIR140.1   : NIAENALEIMCILLGGPTR---QYGGWFENQITNNYGLATVTVSSVQSLTHSYTYTYRYSPEINTMDEIRNCCIFPSGSSWAAFYDHTDGEYDDE--RD--NMCFLFASRDQKQITLLME
AsIR140.1   : HPIEVGIEIMCILLGGPSR---EYGGWFENQITTFQGLSTVTVSSVQSLTHSYTYTYRYSPEINTMDEIRNCCIFPSGSSWAAFYDHTDGEYDDE--RD--NMCFLFASRDQKQITLLME
AsIR140.2   : HLVEVGIEIMCILLGGPSR---KYGGWFENQITTFQGLSTVTVSSVQSLTHSYTYTYRYSPEINTMDEIRNCCIFPSGSSWAAFYDHTDGEYDDE--RD--NMCFLFASRDQKQITLLME
AgIR140.2   : NIENALEIMCILLGGPTR---QYGGWFENQITNNYGLATVTVSSVQSLTHSYTYTYRYSPEINTMDEIRNCCIFPSGSSWAAFYDHTDGEYDDE--RD--NMCFLFASRDQKQITLLME
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Motif2

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AsIR7t      : GVVTMPIDCKIKYTKQNGQGVVYAKSTGINVNTAFFPKTSLOESSSLRLRHSA-----ANFISQEFEDTRYWSNAKTDPEPSSLQWNOISGGFYHCGILHAAVLVFAFT-[221]
AgIR7t      : FVTVPLDPCIKYVQYQNGRLVYKGNHGTINNTAFFPKTSLOESSSLRLRHSA-----VQDARAFEDGRYWSNAKADPEPASLAWSHSGAFYHCGTMLHAAVLVFAFT-[221]
AsIR7u      : GVTVPLDPCIEYVYKNGHRLVYKGLHGINNMGLVYTKRSFPAEPNGICRFOAQD--MHSHKEQFRDNRVYTSVKSQPEPESLRWRCVCGCYVWALLIAVSLVAFG-[4]
AgIR7u      : GVTVPLDAIEYVYVNVQGRGLVYSSHTSINXNPGVLVPKASPLTEPESALICRYQAQ--VPLIREQFRDTRYWNNAKQHPEPISQWHSISGGCYVWACCLIAVSLVAFG-[36]
AsIR7w      : GVTVPLDGIAYYVYKRGKHGIVYKGTGFTYPIGMHPEKTPLOEPENTVHKLHAF--VIRYTEEFHNDNRVYWNDAKKEPPASLKNWQISGAFYHCGVVMMLMATVVFAG-[6]
AsIR7w      : GVMVSPDCAIAYYVYKRRGKNGVYVYKGTGFTYPIGMHPEKTPLOEPENTVHKLHAF--VIRYTEEFHNDNRVYWNDAKKEPPASLKNWQISGAFYHCGVVMMLMATVVFAG-[6]
AsIR7h.1    : LAIANPREEIALFNGRNRSINRYTSDEKLLTEHFCMYKRSPPVTAEDWYIRRLAT--VITRYTTSVDTQFLRPLTANSQAEVLSMRHIOGSMVLLAGLIVSAFT-[19]
AgIR7h.1    : LAFTSTREEIALFNGRNRSINRYTSDEKLLTEHFCMYKRSPPVTAEDWYIRRLAT--VITRYTTSVDTQFLRPLTANSQAEVLSMRHIOGSMVLLAGLIVSAFT-[19]
DmIR7a      : TTTSLIATMEYNNMHWS-TSRTHIKEHIFLQMVYILRRHSLKFAEDRKIKOLLAS--HIGYVREFDACQYRKPFEEDEYVTPIDPLDSFCGLMYSLIWLSAVAV-[13]
DmIR7b      : ARVAILTPEYFYFGFRKVMSSRLHVRERIYTOQLAFYVRRHSHLVGNLKOQHATH--FLEHTRQYVSADVEDKESVARRQNVLSMRELAALWILWANLGAUVV-[28]
DmIR7c      : GITVALLOPTVNGDFRSNKRHLTVLPDPLMTAPLTFYMRPHSYFKRRIDRLMMMS--FVARRKMVMDRIKRVSKRRNL-PKPLSIWRLSGIVCCAGLYLVALIV-[20]
DmIR7d      : GAFTSRAFLADHLVHRKHHRNLVLAEKIVDNMLCMYFPHGSFYAFWEINKLFNMRSF--FQHQHSQILAWDNLPTTDTDKRHSSTESVATGAESMSFVVAALNCLMGAL-[28]
AsIR136     : DMFMYTIGSITKYLKEMSYRHHYHIDEFFTITVTVMPFGKLNPRLKRFQMYNRLNEAGIWTVKKNLKLASGTQVVEYPPDDVD-ALFISLEHFPVPIASGYAYLITTFVELLER-[28]
AgIR136     : DMFMYTIGSITKYLKEMSYRHHYHIDEFFTITVTVMPFGKLNPRLKRFQMYNRLNEAGIWTVKKNLKLASGTQVVEYPPDDVD-ALFISLEHFPVPIASGYAYLITTFVELLER-[28]
AsIR137     : DNFPYTIALATKNLGKELTHRHHYHIDEPIRTAIGYSPEKSRPKLHREORYVSRLEAGIQWYIRKNIAIY-STSFHFYVDS-ASSLLYLNHFIPVIGAGYIYVLAIV-[16]
AgIR137     : DLFPYTIRATRLVKGKELSHHHYHIDEPIRTAIGYSPEKSRPKLHREORYVSRLEAGIQWYIRKNIAIY-STSFHFYVDS-ASSLLYLNHFIPVIGAGYIYVLAIV-[16]
AsIR138     : DNFPYTIALATKNLGKELTHRHHYHIDEPIRTAIGYSPEKSRPKLHREORYVSRLEAGIQWYIRKNIAIY-STSFHFYVDS-ASSLLYLNHFIPVIGAGYIYVLAIV-[16]
AgIR138     : DLFPYTIGDITQIMGKRLSHHHYHIDEPISTISICISPRKTSRPLVREQOXYVRLNEAGIWDQVSKMLKDGVRYSVAHGADKR-RSSIELFHFVPMVGGVLYTSALIT-[9]
AgIR140.1   : MRDIN-----PAAGQAYKRNLRADTVLFKYLYIYLNKRSIIRELFEPYGAFFRES--FDQHYRNKSIHTAIHSREMFV-VRSFNVADESIIYIYAGGVMSILMGV-[62]
AsIR140.1   : ARHHHNSHISKIPANAAQCHNLRADATFYQENLLYFYHKSIIRELFEPYGAFFRES--FDQHYRNKSIHTAIHSREMFV-VRSFNVADESIIYIYAGGVMSILMGV-[62]
AsIR140.2   : ARKQKHEMLGKAAEAQCHNLRADATFYHENLLYFNKAIKIRELFEPYGAFFRES--FDQHYRNKSIHTAIHSREMFV-VRSFNVADESIIYIYAGGVMSILMGV-[62]
AgIR140.2   : TRDID-----PAAGQAYKRNLRADTVLFKYLYIYLNKRSIIRELFEPYGAFFRES--FDQHYRNKSIHTAIHSREMFV-VRSFNVADESIIYIYAGGVMSILMGV-[62]
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class of iGluRs: representative Divergent IR subfamily

Motifs: Motif1 (part of transmembrane region):

A.A.

Motif2 (part of transmembrane region M2):

A.A.