

AgGluCl-a1	MASGHFFWAIIFYFACLCSASLANNAKVN----FRE-----	31
AgGluCl-a2	MASGHFFWAIIFYFACLCSASLANNAKVN----FRE-----	31
AgGluCl-b	MASGHFFWAIIFYFACLCSASLANNAKVN----FRE-----	31
AgGluCl-c	MASGHFFWAIIFYFACLCSASLANNAKVN----FRE-----	31
DmGluCl	MGSGHYFWAILYFASLCSASLANNAKVN----FRE-----	31
CeGluCl α	MAT--WIVGKLI IASLILGIQAQQARTKSQDI FEDDNDNGTTTLESRLRLTSPHIPIEQ	58
	*	
AgGluCl-a1	---KEKKILDQILGAGKYDARIRPSGNGTDG-PAIVRINLNFVRSIMTISDIKMEYSVQL	87
AgGluCl-a2	---KEKKILDQILGAGKYDARIRPSGNGTDG-PAIVRINLNFVRSIMTISDIKMEYSVQL	87
AgGluCl-b	---KEKKILDQILGAGKYDARIRPSGNGTDG-PAVVRVNI FVRSISKIDDDVMEYSVQL	87
AgGluCl-c	---KEKKILDQILGAGKYDARIRPSGNGTDDKATQVFVNMFLRSISKIDDDYKMEYSVQL	88
DmGluCl	---KEKKVLDQILGAGKYDARIRPSGNGTDG-PAIVRINLNFVRSIMTISDIKMEYSVQL	87
CeGluCl α	PQTSDSKILAHLFTSG-YDFRVRPP---TDNGGPVVSVNMLLRTISKIDVVNMEYSVQL	114
	* * *	
AgGluCl-a1	TFREQWLDERLKFDDIG-GRLYLTLTEANRVWMPDLFFSNEKEGHFHNI IMPNVYIRIF	146
AgGluCl-a2	TFREQWLDERLKFDDIG-GRLYLTLTEANRVWMPDLFFSNEKEGHFHNI IMPNVYIRIF	146
AgGluCl-b	TFREQWLDERLKFDDIG-GRLYLTLTEANRVWMPDLFFSNEKEGHFHNI IMPNVYIRIF	146
AgGluCl-c	TFREQWLDERLKFDDIG-GRLYLTLTEANRVWMPDLFFSNEKEGHFHNI IMPNVYIRIF	147
DmGluCl	TFREQWTDERLKFDDIQ-GRLYLTLTEANRVWMPDLFFSNEKEGHFHNI IMPNVYIRIF	146
CeGluCl α	TLRESWIDKRLSYGVKGDGQDPFVILTVGHQIWMPDTFFPNKQAYKHTIDKPNVLRIRIH	174
	* ** *	
AgGluCl-a1	PYGSVLYSIRVSLTLACPMNLKLYPLDRQVCSLRMASYGWTTADLVFLWKEGDPVQVVKV	206
AgGluCl-a2	PYGSVLYSIRVSPPTLACPTNLKLYPLDRQVCSLRMASYGWTTADLVFLWKEGDPVQVVKV	206
AgGluCl-b	PYGSVLYSIRVSLTLACPMNLKLYPLDRQVCSLRMASYGWTTADLVFLWKEGDPVQVVKV	206
AgGluCl-c	PYGSVLYSIRVSLTLACPMNLKLYPLDRQVCSLRMASYGWTTADLVFLWKEGDPVQVVKV	207
DmGluCl	PNGSVLYSIRISLTLACPMNLKLYPLDRQVCSLRMASYGWTTNDLVFLWKEGDPVQVVKV	206
CeGluCl α	NDGTVLYSVRISLVLSCPMYLQYYPMDVQCCSIDLASAYATTKDIEYLWKEHSPLQLKVG	234
	* * #	
AgGluCl-a1	LH--LPRFTELEKFLTDYCNSKNTTGEYSCLKVDLLFKREFSYLIQIYIPCCMLVIVSWV	264
AgGluCl-a2	LH--LPRFTELEKFLTDYCNSKNTTGEYSCLKVDLLFKREFSYLIQIYIPCCMLVIVSWV	264
AgGluCl-b	LH--LPRFTELEKFLTDYCNSKNTTGEYSCLKVDLLFKREFSYLIQIYIPCCMLVIVSWV	264
AgGluCl-c	LH--LPRFTELEKFLTDYCNSKNTTGEYSCLKVDLLFKREFSYLIQIYIPCCMLVIVSWV	265
DmGluCl	LH--LPRFTELEKFLTDYCNSKNTTGEYSCLKVDLLFRREFSYLIQIYIPCCMLVIVSWV	264
CeGluCl α	LSSSLPSFQLTNTSTTYCTSVTNTGIYSCLRRTIQLKREFSYLLQLYIPSCMLVIVSWV	294
	# #	
AgGluCl-a1	SFWLDQGAVPARVSLGVTLLTMTATQTSGINASLPPVSYTKAIDVWTGVCLTFVFGALLE	324
AgGluCl-a2	SFWLDQGAVPARVSLGVTLLTMTATQTSGINASLPPVSYTKAIDVWTGVCLTFVFGALLE	324
AgGluCl-b	SFWLDQGAVPARVSLGVTLLTMTATQTSGINASLPPVSYTKAIDVWTGVCLTFVFGALLE	324
AgGluCl-c	SFWLDQGAVPARVSLGVTLLTMTATQTSGINASLPPVSYTKAIDVWTGVCLTFVFGALLE	325
DmGluCl	SFWLDQGAVPARVSLGVTLLTMTATQTSGINASLPPVSYTKAIDVWTGVCLTFVFGALLE	324
CeGluCl α	SFWFDRTAIPARVTLGVTLLTMTAQAASAGINSQLPPVSYIKAIDVWIGACMTFIFCALLE	354
AgGluCl-a1	FALVNYASRS-----DMHRENMKKKRREMEQASLDAASDLLDTSNATFAMKPLVRHPGD	379
AgGluCl-a2	FALVNYASRS-----DMHRENMKKKRREMEQASLDAASDLLDTSNATFAMKPLVRHPGD	379
AgGluCl-b	FALVNYASRSADRAADMHRENMKKKRREMEQASLDAASDLLDTSNATFAMKPLVRHPGD	384
AgGluCl-c	FALVNYASRS-----DMHRENMKKKRREMEQASLDAASDLLDTSNATFAMKPLVRHPGD	380
DmGluCl	FALVNYASRSGSNKANMHKENMKKKRRDLEQASLDAASDLLDTSNATFAMKPLVRHPGD	384
CeGluCl α	FALVNHIANK-----QGVERKARTEREKAEIPLLQNLHNDVPTKVFNQEEKVRT---	403
AgGluCl-a1	PLALEKLRQCEVHMQAPKRPNCCRSWLSKFPTR-----QCSRSKRIDVISRITF	428
AgGluCl-a2	PLALEKLRQCEVHMQAPKRPNCCRSWLSKFPPTSPFKKVPCLGRGQCSRSKRIDVISRITF	439
AgGluCl-b	PLALEKLRQCEVHMQAPKRPNCCRSWLSKFPPTSPFKKVPCLGRGQCSRSKRIDVISRITF	444
AgGluCl-c	PLALEKLRQCEVHMQAPKRPNCCRSWLSKFPTR-----QCSRSKRIDVISRITF	429
DmGluCl	PLALEKLRQCEVHMQAPKRPNCCCKTWSKFPTR-----QCSRSKRIDVISRITF	433
CeGluCl α	-----VPLNRRQMNSFLNLETKT-----EWNDISKRVDLISRALF	439
AgGluCl-a1	PLVFALFNLVYWSTYLFREEEED	451
AgGluCl-a2	PLVFALFNLVYWSTYLFREEEED	462
AgGluCl-b	PLVFALFNLVYWSTYLFREEEED	467
AgGluCl-c	PLVFALFNLVYWSTYLFREEEED	452
DmGluCl	PLVFALFNLVYWSTYLFREEEED	456
CeGluCl α	PVLFFVFNILYWSRFGQQNVLF-	461

Fig. S1. ClustalW alignment of AgGluCl amino acid sequences with *D. melanogaster* GluCl (DmGluCl) and *C. elegans* GluCl (CeGluCl). Black bar denotes transmembrane domains. (*) glutamate binding residues; (#) critical residues for ivermectin binding.