

Figure S1.

<i>Schgr</i> -CCAPR-1	1	-----M
<i>Schgr</i> -CCAPR-2	1	-----M
<i>Schgr</i> -CCAPR-3	1	-----MGA-----M
<i>Rhopr</i> -CCAPR	1	-----M
<i>Drome</i> -CCAPR	1	MLHLRLFDSSLYYTLASASESSGLASSTSTERSFNQTQGAGGVAAGGESLTPTDVAAVNLM
<i>Trica</i> -CCAPR-1	1	-----M
<i>Trica</i> -CCAPR-2	1	-----M
<i>Schgr</i> -CCAPR-1	2	DDING-----TNASDAAPVINSFY
<i>Schgr</i> -CCAPR-2	2	DASAGGNATAS-----SLLPGDGADN-----LTADAAAANDTQEVINSFY
<i>Schgr</i> -CCAPR-3	5	EEPPPAAVTSPDSEAALTSPAPSPAVVTTTAVPDWSTTDFSGLLYTAATSGEDINSFY
<i>Rhopr</i> -CCAPR	2	DWVIRDNYSNP-----AANITNTTDEINSFY
<i>Drome</i> -CCAPR	61	TYFTPAISHVMLAPTTIATTTASATMVQIQTTAAPSHDLETGGNSTSSDPGEFDNINSFY
<i>Trica</i> -CCAPR-1	2	SYIEDAN-----ETDSNNTSLDAFY
<i>Trica</i> -CCAPR-2	2	SGAPIPDVGQS-----WLKSNSLAGFEVNS-----SEQLTTPPT-DINSFY
<i>Schgr</i> -CCAPR-1	21	FYETEQFAVLWSLFTLIVVGNAAVLVTLLAGKRRKSRMNFFIVQLALADLSVGLISVLTD
<i>Schgr</i> -CCAPR-2	42	FYETEQFTVLWILFASIVLGNAAVLVALLVNKARKSRMNFFIMHLALADLSVGLISVLTD
<i>Schgr</i> -CCAPR-3	65	FYQTEQFTVLWILFALIVLGNASVLIALLYINKNRKSRMNFFIMQLALADLTVGLINVLTD
<i>Rhopr</i> -CCAPR	28	FYQTEQFTVLWILFAAIVLGNASVLIALLFNKSSKSRMNFFIMHLAFADLSVGLISVLTD
<i>Drome</i> -CCAPR	121	FYETEQFAVLWILFTVIVLGNASVLFVFMFINKNRKSARMNYFIKQLALADLCVGLINVLTD
<i>Trica</i> -CCAPR-1	22	FETEQFTLLWVLFVIVVAGNVGVLYTLLFGRSRKSRMNIFYITHLALADLSVGLINVLTD
<i>Trica</i> -CCAPR-2	44	FYKTEQFTVLWVLFMIVLGNASVLLVSKSRKSRMNFFICQLATADLAVGLISVSTD
<i>Schgr</i> -CCAPR-1	81	IWRMTVAWNAGNAACKLIRFLQAVVTSSTYVLVALSIDRYDAITHPMNFGSGSWRRARL
<i>Schgr</i> -CCAPR-2	102	IWRMTVSWNAGNAACKLIRFLQVVVTSSTYVLVALSIDRYDAITHPMNFGSGSWRRARL
<i>Schgr</i> -CCAPR-3	125	ITRITLVWYAGNVACKIVRFLQAVVTSSTYVLVALSIDRYDAITHPMNFGSGSWRRARA
<i>Rhopr</i> -CCAPR	88	IWRITVWKAGNVCKVRFVQAVVTSSTYVLVALSIDRLDAITRPMNFGSGSWRRARL
<i>Drome</i> -CCAPR	181	IWRITVWRAGNLACKAIRFSQVCVTSSTYVLVAMSIDRYDAITHPMNFSKSWKRARH
<i>Trica</i> -CCAPR-1	82	IWRITVVAWYAGNVACKIVRFLQVVVTSSTYVLVALSIDRYDAIRHPMKFSGSWKRARY
<i>Trica</i> -CCAPR-2	104	IWRITVAWYAGNVLCIIRFLQAVVTSSTYVLVALSIDRYDAITHPMNFGSGSWKRARV
<i>Schgr</i> -CCAPR-1	141	LVAAWLLSAVFSVPVIAVLYHERPVEGRLLQCWIDFPQAWQWQLYMTLVALTFLFALPAVIL
<i>Schgr</i> -CCAPR-2	162	LVLSAWLLSFLFSVPILIFYEEKTIQGHQPQCWIDFQERWQWRLYMTLVTTTLFVLPAII
<i>Schgr</i> -CCAPR-3	185	LVVTAWGLSFLFSIPSMIFFEEQPIQGHACQWIDFPHNWQWQVYMTLVAVALFIVPTVIL
<i>Rhopr</i> -CCAPR	148	LVGFSWALSFAFFSSPILILYKERLIQGSFQCWIELGSTLKWQIYMSLVAVSLFLVPAVIL
<i>Drome</i> -CCAPR	241	LVAGAWLLSALFSLPILVLYEEKLIQGHQPQCWIELGSPIAWQVYMSLVSATLFAIPALII
<i>Trica</i> -CCAPR-1	142	LIIAAWFFSALYSLPILIFYEEKIVKGLQCWIEFHQPQWKQVYMTLVSLSLFIIPASII
<i>Trica</i> -CCAPR-2	164	LVLAWLLSILFSLPTVFLFEKKQVQSMQPQCWIDLQT-WQWKVYITLVALLVLFVFPALII
<i>Schgr</i> -CCAPR-1	201	SACYTVIVSTIWSKGRHMAPPPPYTDARTGSCRPHQLLHQHSHSRLSSGKSRDDEADGRR
<i>Schgr</i> -CCAPR-2	222	TACYTVIVLTIWSKSKVLTPPSRLK-----NGDHRSG-----DDHDSRR
<i>Schgr</i> -CCAPR-3	245	SACYAVIVFTIWSKSKLIAPACGRPG-----GNSRAGSGVSRGPAPSFSDDQDCRR
<i>Rhopr</i> -CCAPR	208	TACYTVIVYTIWTKSIHISRDSQQST-----PLKNGGDKGDDNDIRR
<i>Drome</i> -CCAPR	301	SACYATIVKTIWAKGSIFVPTER-----AGFGAAPARR
<i>Trica</i> -CCAPR-1	202	ATCYAIIITIWSKN-----A-----KGFIKNTKAVNGSDNSRR
<i>Trica</i> -CCAPR-2	223	SACYAVIVRTIWSKSKLLIPVGHIP-----RQCDDHRDRPPRHFEHHDTRR
<i>Schgr</i> -CCAPR-1	261	ASSRGIIPKAKIKTVKMTFVIVFVFCWSPYIVFDLLQVYGOVPRQTQANIIVASFIQSL
<i>Schgr</i> -CCAPR-2	261	ASSRGIIPKAKIKTVKMTFVIVFVFCWSPYIVFDLLQVYDHVPTTQTNIIVASFIQSL
<i>Schgr</i> -CCAPR-3	296	ASSRGIIPRAKIKTVKMTFVIVFVFCWSPYIVFDLLQVFGHVPRQTQTMVALATFIQSL
<i>Rhopr</i> -CCAPR	250	ASSRGIIPRAKIKTVKMTFVIVFVFCWSPYIVFDLLQVFGYVPRQTQNIIVATFIQSL
<i>Drome</i> -CCAPR	334	ASSRGIIPRAKIKTVKMTLTIVFVFIICWSPYIIFDLLQVFGQIPHSTQNIIVATFIQSL
<i>Trica</i> -CCAPR-1	236	ASSRGIIPRAKIKTVKMTFVIVFVFCWSPYIIFDLLQVFGQIPGTQNIIVATFIQSL
<i>Trica</i> -CCAPR-2	271	ASSRGIIPRAKIKTVKMTLVIVFVFCWSPYIVFDLLQVYGHIPKQTQNIIVATFIQSL

		TM-7
<i>Schgr</i> -CCAPR-1	321	APLNSAANPVVYCLFSRSASKAIRKVPFRWLRLSLCCPKAAA---AAASPGEEPAPVAAH
<i>Schgr</i> -CCAPR-2	321	APLNSAANPLIYCLFSTHICRSLRRMPPFSWLSCLR-----Q---QARSTTSTNTSSSTAD
<i>Schgr</i> -CCAPR-3	356	APLNSAANPVIYCVFSTQICRTLRLKLPLRLWLSVCFPRQAGR---DGRRIYDVTSTVTE
<i>Rhopr</i> -CCAPR	310	APLNSAANPVIYCLFSTHICRALSKLPPFSWICCCFA-N-----RGAESSSIID
<i>Drome</i> -CCAPR	394	APLNSAANPLIYCLFSSQVFRTLSRFPPFKWFTCCCKSYRNNSQQNRCHTVGRRLHNSCD
<i>Trica</i> -CCAPR-1	296	APLNSAANPLIYCLFSTHFCRTLGSLPPFKWLFKFKK-R--R---NRESTTNTQSSSLSE
<i>Trica</i> -CCAPR-2	331	APLNSAANPVIYCLFSTHICRNLR-----
<i>Schgr</i> -CCAPR-1	378	TSRRQPPPHWTTTRRQTHRRYIGEGLPFPVAVSI-----V
<i>Schgr</i> -CCAPR-2	373	TLTSSAPAPRHRAAGSLRQLNSVHFSSV-----L
<i>Schgr</i> -CCAPR-3	413	TLTQPSSRRRTSASVFRPHDATVSVRLLPASGRRFSNYGNSAASATSVATSAV
<i>Rhopr</i> -CCAPR	358	TVTST-----LRRATIRNQDN-----L
<i>Drome</i> -CCAPR	454	SMRTLTTSLTVSRRSTNKTNARVVICERPTKVVT-----VPAMSEV
<i>Trica</i> -CCAPR-1	350	FLTNTHKRKIENTSTTFNAHTVLI-----H
<i>Trica</i> -CCAPR-2		-----

Multiple sequence alignment of *Schgr*-CCAPRs with other insect CCAPRs. Identical residues between the aligned sequences are highlighted in black, and conservatively substituted residues in grey. Amino acid position is indicated at the left and dashes indicate gaps that are introduced to maximize similarities in the alignment. Putative transmembrane regions (TM1-5) of *Schgr*-CCAPR-1, -2 and -3 are indicated by dark grey bars and putative transmembrane regions (TM6-7) of *Schgr*-CCAPR-1 and -2 are indicated by light grey bars. Conserved residues that are predicted to form disulphide bridges in extracellular loop 1 and 2 are indicated (*). Rhodopsin-like DRY motif is boxed in a red dotted line. NXS/T consensus sequences for putative N-glycosylation sites are underlined in red. Abbreviations: CCAPR = crustacean cardioactive peptide receptor, *Schgr* = *Schistocerca gregaria*, *Rhopr* = *Rhodnius prolixus* (AGT02811.1), *Drome* = *Drosophila melanogaster* (AAO66429), *Trica* = *Tribolium castaneum* (1:ABN79651, 2:ABN79652)