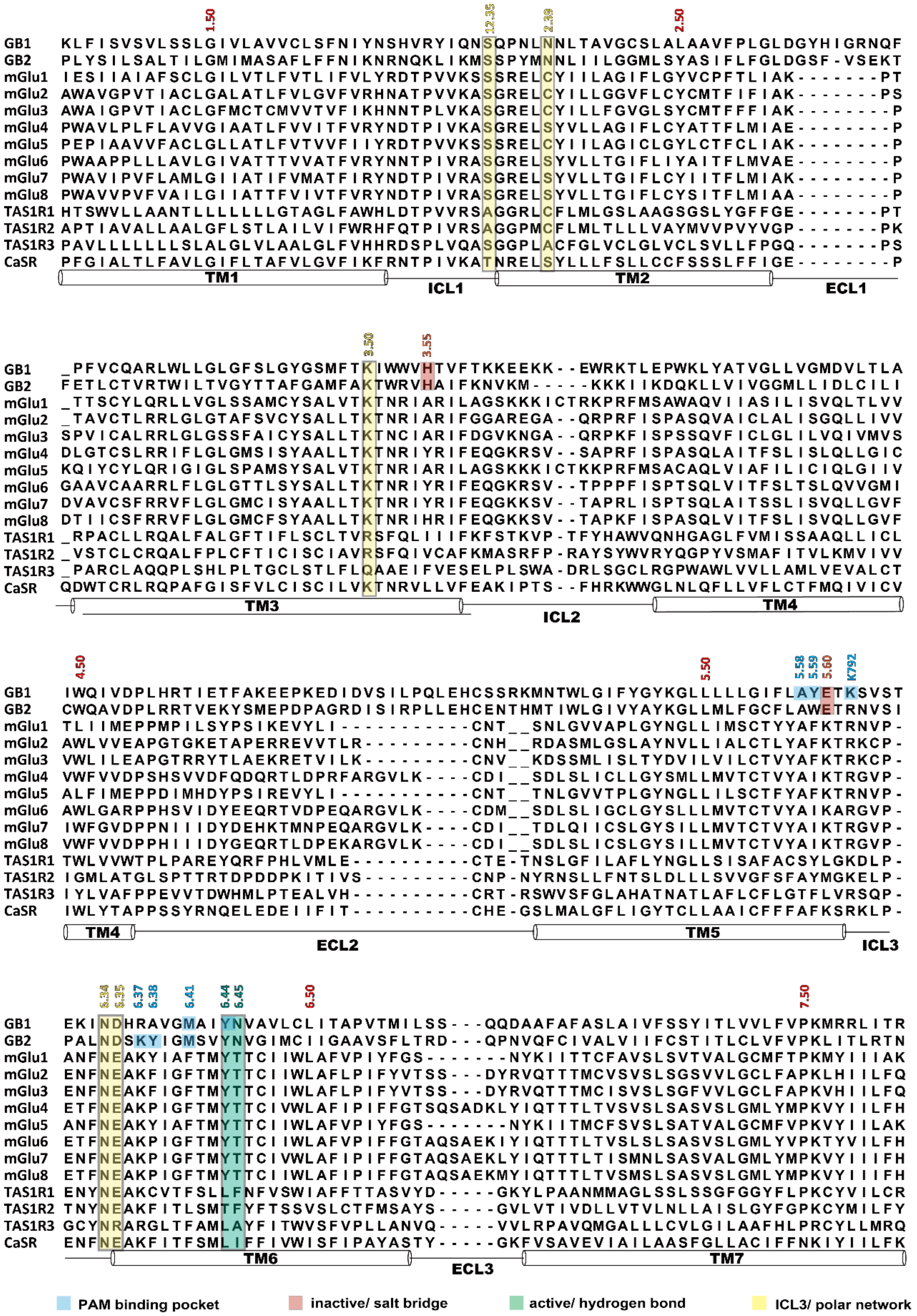
Supplementary information, Table S1



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GB1     KLFISVSVLSSLGIVLAVVCLSFNIYNSHVRYIQNSQPNLNNLTAVGCSLALAAVFPLGLDGYHIGRNQF
GB2     PLYSILSALTILGMIMASAFLFFNIKNRNQKLIKMSSPYMNNLIILGGMLSYASIFLFGLDGSF-VSEKT
mGlu1   IESIIAIAFSCLGILVTLFVTLIFVLYRDTPVVKSSSRELCYIILAGIFLGYVCPFTLIAK-------PT
mGlu2   AWAVGPVTIACLGALATLFVLGVFVRHNATPVVKASGRELCYILLGGVFLCYCMTFIFIAK-------PS
mGlu3   AWAIGPVTIACLGFMCTCMVVTVFIKHNNTPLVKASGRELCYILLFGVGLSYCMTFFFIAK--------P
mGlu4   PWAVLPLFLAVVGIAATLFVVITFVRYNDTPIVKASGRELSYVLLAGIFLCYATTFLMIAE--------P
mGlu5   PEPIAAVVFACLGLLATLFVTVVFIIYRDTPVVKSSSRELCYIILAGICLGYLCTFCLIAK--------P
mGlu6   PWAAPPLLLAVLGIVATTTVVATFVRYNNTPIVRASGRELSYVLLTGIFLIYAITFLMVAE--------P
mGlu7   PWAVIPVFLAMLGIIATIFVMATFIRYNDTPIVRASGRELSYVLLTGIFLCYIITFLMIAK--------P
mGlu8   PWAVVPVFVAILGIIATTFVIVTFVRYNDTPIVRASGRELSYVLLTGIFLCYSITFLMIAA--------P
TAS1R1  HTSWVLLAANTLLLLLLLGTAGLFAWHLDTPVVRSAGGRLCFLMLGSLAAGSGSLYGFFGE-------PT
TAS1R2  APTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAGGPMCFLMLTLLLVAYMVVPVYVGP-------PK
TAS1R3  PAVLLLLLLLSLALGLVLAALGLFVHHRDSPLVQASGGPLACFGLVCLGLVCLSVLLFPGQ-------PS
CaSR    PFGIALTLFAVLGIFLTAFVLGVFIKFRNTPIVKATNRELSYLLLFSLLCCFSSSLFFIGE--------P

GB1     _PFVCQARLWLLGLGFSLGYGSMFTKIWWVHTVFTKKEEKK--EWRKTLEPWKLYATVGLLVGMDVLTLA
GB2     FETLCTVRTWILTVGYTTAFGAMFAKTWRVHAIFKNVKM-----KKKIIKDQKLLVIVGGMLLIDLCILI
mGlu1   _TTSCYLQRLLVGLSSAMCYSALVTKTNRIARILAGSKKKICTRKPRFMSAWAQVIIASILISVQLTLVV
mGlu2   _TAVCTLRRLGLGTAFSVCYSALLTKTNRIARIFGGAREGA--QRPRFISPASQVAICLALISGQLLIVV
mGlu3   SPVICALRRLGLGSSFAICYSALLTKTNCIARIFDGVKNGA--QRPKFISPSSQVFICLGLILVQIVMVS
mGlu4   DLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEQGKRSV--SAPRFISPASQLAITFSLISLQLLGIC
mGlu5   KQIYCYLQRIGIGLSPAMSYSALVTKTNRIARILAGSKKKICTKKPRFMSACAQLVIAFILICIQLGIIV
mGlu6   GAAVCAARRLFLGLGTTLSYSALLTKTNRIYRIFEQGKRSV--TPPPFISPTSQLVITFSLTSLQVVGMI
mGlu7   DVAVCSFRRVFLGLGMCISYAALLTKTNRIYRIFEQGKKSV--TAPRLISPTSQLAITSSLISVQLLGVF
mGlu8   DTIICSFRRVFLGLGMCFSYAALLTKTNRIHRIFEQGKKSV--TAPKFISPASQLVITFSLISVQLLGVF
TAS1R1  _RPACLLRQALFALGFTIFLSCLTVRSFQLIIIFKFSTKVP-TFYHAWVQNHGAGLFVMISSAAQLLICL
TAS1R2  _VSTCLCRQALFPLCFTICISCIAVRSFQIVCAFKMASRFP-RAYSYWVRYQGPYVSMAFITVLKMVIVV
TAS1R3  _PARCLAQQPLSHLPLTGCLSTLFLQAAEIFVESELPLSWA-DRLSGCLRGPWAWLVVLLAMLVEVALCT
CaSR    QDWTCRLRQPAFGISFVLCISCILVKTNRVLLVFEAKIPTS--FHRKWWGLNLQFLLVFLCTFMQIVICV

GB1     IWQIVDPLHRTIETFAKEEPKEDIDVSILPQLEHCSSRKMNTWLGIFYGYKGLLLLLGIFLAYETKSVST
GB2     CWQAVDPLRRTVEKYSMEPDPAGRDISIRPLLEHCENTHMTIWLGIVYAYKGLLMLFGCFLAWETRNVSI
mGlu1   TLIIMEPPMPILSYPSIKEVYLI-----------CNT__SNLGVVAPLGYNGLLIMSCTYYAFKTRNVP-
mGlu2   AWLVVEAPGTGKETAPERREVVTLR---------CNH__RDASMLGSLAYNVLLIALCTLYAFKTRKCP-
mGlu3   VWLIILEAPGTRRYTLAEKRETVILK--------CNV__KDSSMLISLTYDVILVILCTVYAFKTRKCP-
mGlu4   VWFVVDPSHSVVDFQDQRTLDPRFARGVLK----CDI__SDLSLICLLGYSMLLMVTCTVYAIKTRGVP-
mGlu5   ALFIMEPPDIMHDYPSIREVYLI-----------CNT__TNLGVVTPLGYNGLLILSCTFYAFKTRNVP-
mGlu6   AWLGARPPHSVIDYEEQRTVDPEQARGVLK----CDM__SDLSLIGCLGYSLLLMVTCTVYAIKARGVP-
mGlu7   IWFGVDPPNIIIDYDEHKTMNPEQARGVLK----CDI__TDLQIICSLGYSILLMVTCTVYAIKTRGVP-
mGlu8   VWFVVDPPHIIIDYGEQRTLDPEKARGVLK----CDI__SDLSLICSLGYSILLMVTCTVYAIKTRGVP-
TAS1R1  TWLVVWTPLPAREYQRFPHLVMLE----------CTE-TNSLGFILAFLYNGLLSISAFACSYLGKDLP-
TAS1R2  IGMLATGLSPTTRTDPDDPKITIVS---------CNP-NYRNSLLFNTSLDLLLSVVGFSFAYMGKELP-
TAS1R3  IYLVAFPPEVVTDWHMLPTEALVH----------CRT-RSWVSFGLAHATNATLAFLCFLGTFLVRSQP-
CaSR    IWLYTAPPSSYRNQELEDEIIFIT----------CHE-GSLMALGFLIGYTCLLAAICFFFAFKSRKLP-

GB1     EKINDHRAVGMAIYNVAVLCLITAPVTMILSS---QQDAAFAFASLAIVFSSYITLVVLFVPKMRRLITR
GB2     PALNDSKYIGMSVYNVGIMCIIGAAVSFLTRD---QPNVQFCIVALVIIFCSTITLCLVFVPKLITLRTN
mGlu1   ANFNEAKYIAFTMYTTCIIWLAFVPIYFGS-------NYKIITTCFAVSLSVTVALGCMFTPKMYIIIAK
mGlu2   ENFNEAKFIGFTMYTTCIIWLAFLPIFYVTSS---DYRVQTTTMCVSVSLSGSVVLGCLFAPKLHIILFQ
mGlu3   ENFNEAKFIGFTMYTTCIIWLAFLPIFYVTSS---DYRVQTTTMCISVSLSGFVVLGCLFAPKVHIILFQ
mGlu4   ETFNEAKPIGFTMYTTCIVWLAFIPIFFGTSQSADKLYIQTTTLTVSVSLSASVSLGMLYMPKVYIILFH
mGlu5   ANFNEAKYIAFTMYTTCIIWLAFVPIYFGS-------NYKIITMCFSVSLSATVALGCMFVPKVYIILAK
mGlu6   ETFNEAKPIGFTMYTTCIIWLAFVPIFFGTAQSAEKIYIQTTTLTVSLSLSASVSLGMLYVPKTYVILFH
mGlu7   ENFNEAKPIGFTMYTTCIVWLAFIPIFFGTAQSAEKLYIQTTTLTISMNLSASVALGMLYMPKVYIIIFH
mGlu8   ETFNEAKPIGFTMYTTCIIWLAFIPIFFGTAQSAEKMYIQTTTLTVSMSLSASVSLGMLYMPKVYIIIFH
TAS1R1  ENYNEAKCVTFSLLFNFVSWIAFFTTASVYD-----GKYLPAANMMAGLSSLSSGFGGYFLPKCYVILCR
TAS1R2  TNYNEAKFITLSMTFYFTSSVSLCTFMSAYS-----GVLVTIVDLLVTVLNLLAISLGYFGPKCYMILFY
TAS1R3  GCYNRARGLTFAMLAYFITWVSFVPLLANVQ-----VVLRPAVQMGALLLCVLGILAAFHLPRCYLLMRQ
CaSR    ENFNEAKFITFSMLIFFIVWISFIPAYASTY-----GKFVSAVEVIAILAASFGLLACIFFNKIYIILFK
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🟦 PAM binding pocket
🟥 inactive/ salt bridge
🟩 active/ hydrogen bond
🟨 ICL3/ polar network

Table S1 Sequence alignment of TMs of class C GPCRs.

The sequence alignment of TMs of class C GPCRs was created using GPCRdb (http://www.gpcrdb.org) and Jalview software. Secondary structure elements are annotated underneath the sequences. Highlighted are residues involved in PAM binding pocket (blue), salt bridge in inactive TM interface, hydrogen bond in active TM interface (green) and polar network stabilizing ICL3 (yellow).