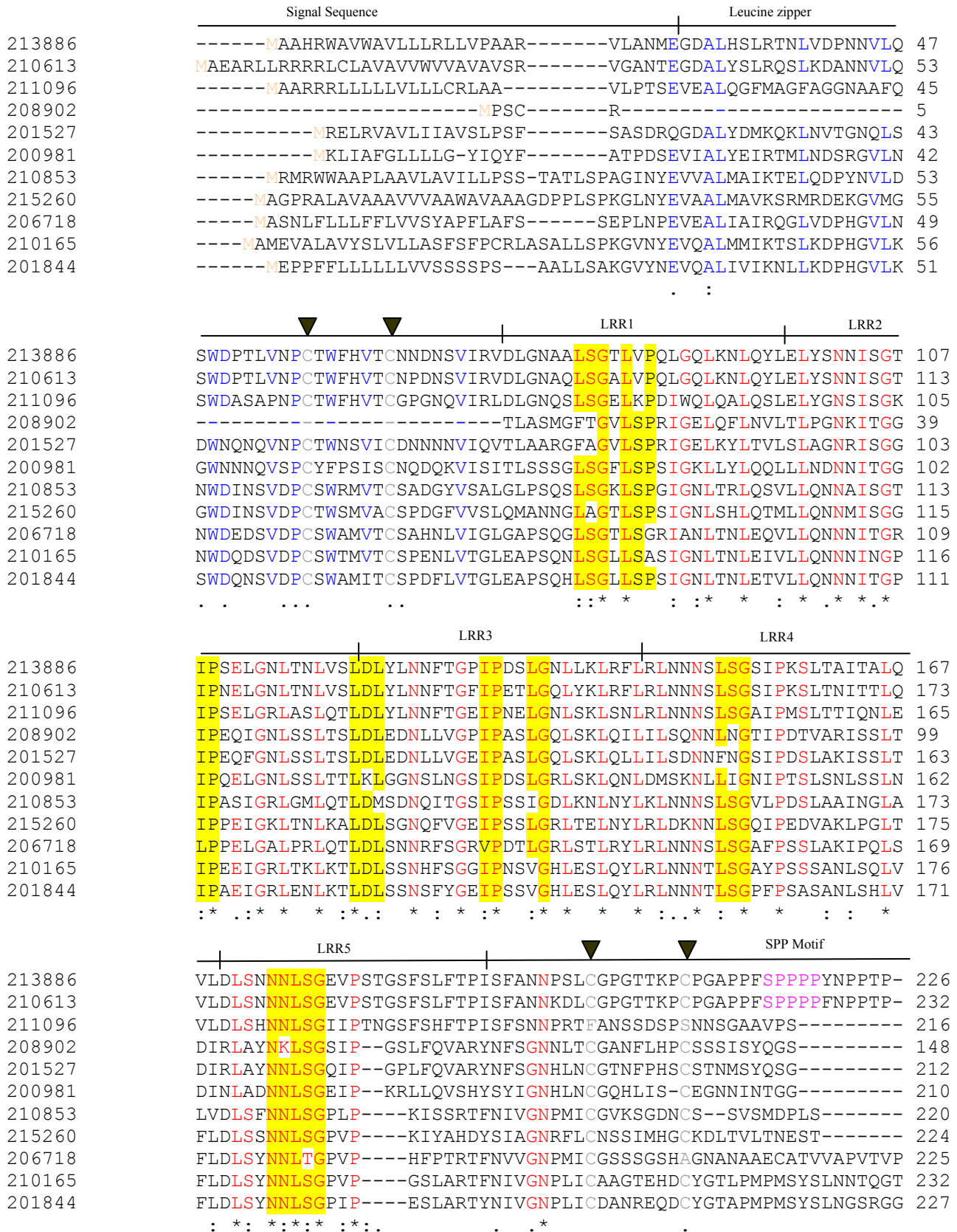


Supplementary Figure 1



Transmembrane Domain

213886 ---VQSPGSSSSTGAIAG---GVAAGAALLFAI-----PAIGFAWYRRR-KPQ 267
 210613 ---TVSQGDSK-TGAIAG---GVAAAAALLFAV-----PAIGFAWRRR-KPE 272
 211096 -----GRSSASSIGTIAG---GAAAGAAMLFAA-----PIVLFAWWRR-KPH 255
 208902 -----SHGSKVGIVLG---TVVGAIGLIIIG-----AVFIVCNGRRKSHLR 186
 201527 -----SHSSKIGIVLG---TVGGVIGLLIVA-----ALFLFCKGRKSHLW 250
 200981 -----SNNSKLVVA---SIGGALTLVII-----VLFLLLWQRMR-HRP 246
 210853 -----YPPDDLKTQPQQ---GIARSHRIAIICGVTVGSVAFATIIIVSMLLWRRHRRNQ 270
 215260 -----ISSPSKKTNSHH---QLALAISLSIIC-----ATVFLVLFVICWLKYCRW 265
 206718 FPLDSTPSSSSRAAAA AVGRSKGGGGAARLP IGVGTS LGASALVLLAVSCFLWRRRRRHR 285
 210165 LMP--AKSKSHKVAIAFG---STIGCISFLIPVMG-----LLFWWRHRRNH 273
 201844 ALPPAARDRGHKFAVAFG---STAGCMGLLLLAAG-----FLFWWRHRRNR 270

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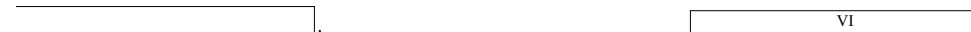
213886 EHF-----FDVPAEEDPEVHLGQLKRFSLR**ELQVATDTFSNKNILGRGGF** 312
 210613 EHF-----FDVPAEEDPEVHLGQLKRFSLR**ELQVATDNFSNKNILGRGGF** 317
 211096 DQF-----FDLLEETPEVHLGQLRRFTLR**ELQVATDNFSQTNLLGRGGF** 300
 208902 EVF-----VDVSGEDDRRIAFGQLKRFAWR**ELQLATDSFSEKNVLGQGGF** 231
 201527 EVF-----VDVAGEDDRRIAFGQLKRFAWR**ELQIATDNFSERNVLGQGGF** 295
 200981 EIY-----VDVPGQHDHNFEGQIKRFSLR**ELQIATNNFSEQNVLGKGGF** 291
 210853 QIF-----FDVNDQYDPEVCLGHLKRYAFK**ELRAATNNFN**SKNILGEGGY 315
 215260 RLP-----FASADQ-DLEIELGHLKHFSF**HELQSATDNFN**SKNILGQGGF 309
 206718 CLLSGPSSVLGILEKGRDVEDGGGGEVMARLGNVRQFGLR**ELHAATDGF**SARNILGKGGF 345
 210165 QIL-----FDVD-----GK----- 282
 201844 QIL-----FDVDEQQIENVNLGNVKRFSFR**ELQAATEG**FSGKNILGKGGF 315

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213886 **GKVYKGR**L--ADGSLVAVKRLKEERTPGGELQ**FQTEVEMISMAVHRNLLRLRGFC**MTPT- 369
 210613 **GKVYKGR**L--ADGSLVAVKRLKEERTPGGELQ**FQTEVEMISMAVHRNLLRLRGFC**MTPT- 374
 211096 **GKVYKGR**L--LDGSLIAIKRLNEDRIGTGERQ**FLMEVEIISMAVHQNLLRLQGYC**MTPT- 357
 208902 **GKVYKGA**L--PDGTKIAVKRLTDYESPGGEAA**FLREVELISVAVHRNLLRLIGFCT**TQT- 288
 201527 **GKVYKGV**L--PDGTKIAVKRLTDYESPGGEAA**FLREVELISVAVHRNLLKLIGFCT**TQT- 352
 200981 **GKVYKGV**LSGPHGRKVAVKR**LFVEKPEG**IAFLREVELIS**IAVHKNILRLIGFCT**TTK- 350
 210853 **GIVYKGF**LR--DGAIVAVKRLKDYNAGG**EVQFQTEVEV**ISLAVHRNLLRLIGFCTTEN- 372
 215260 **GVVYKGL**R--NGALVAVKRLKDPDITG-**EVQFQTEVELIGLAVHRNLLRLYGFC**MTSK- 365
 206718 **GDVYRGR**LS--DGTVVAVKRLKDP-TASGEA**QFRTEVEMISLAVHRHLLRLVGFC**AAASG 402
 210165 -----**QKAKLLSIMPQC**SSNLG---AYWH---AMVFI**VTHWLLQSN**----- 318
 201844 **GNVYRQ**L--PDGTLMAVKRLKDGNAAG**EAQFQTEVEMISLALHRNLLRLYGLL**HDRHR 373

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213886 **ERLLVYPY**MANGSVASRLRERPPSE**PLDWRTRRRIALGSARGLSYLHDHCDPKI**IHRDV 429
 210613 **ERLLVYPY**MANGSVASRLRERQPN**DPLEWQTRTRIALGSARGLSYLHDHCDPKI**IHRDV 434
 211096 **ERLLVYPY**MENK**SLERLRECS**DSQ**PLDWPTRRKIALGSARGISYLHEGCDPKI**IHRDV 417
 208902 **ERLLVYPF**MQNL**SVAYRLREFK**PGEPIL**DWSARKRVAIGTARGLEYLHEHCNPKI**IHRDV 348
 201527 **ERLLVYPF**MQNL**SVAYRLRDFK**PGEPVL**NWPERKVAIGTARGLEYLHEHCNPKI**IHRDV 412
 200981 **ERLLVYPY**MENLSVASRLRDIKLNEPAL**DWPTRVRIALGAARGLEYLHEHCNPKI**IHRDV 410
 210853 **ERLLVYPY**MPNGSVAS**QLREL**VNGK**PALDWSRKR**IALGTARGLLYLHEQ**CDPKI**IHRDV 432
 215260 **ERLLVYPY**MPNGSVAD**RLRDYHHGKPSL**DWSK**RMIAVGA**ARGLLYLHEQ**CDPKI**IHRDV 425
 206718 **ERLLVYPY**MPNGSVASRLR----GK**PLDWQTRKRI**AVGTARGLLYLHEQ**CDPKI**IHRDV 458
 210165 -----TQ**RMST**----- 324
 201844 APPSLPLHVQRQ**RRLPPQSEAGVGVGDEEEDRGGGGEGPGV**PARAVRPQ**DHP**PRRQ**RQR** 433

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213886 KAANILLDEDFEAVVGFGLAKLMDYK DTHVTTAVRGTIGHIAPEYLS TGKSSSEKTDVFG 489
210613 KAANILLDEDFEAVVGFGLAKLMDYK DTHVTTAVRGTIGHIAPEYLS TGKSSSEKTDVFG 494
211096 KAANILLDEKLEAVVGFGLARIMDYK VSHVVTGVMGTLGHIPMEYLTAGRTSDKTDVFG 477
208902 KAANVLLDEDFEPVVGDFGLAKLVDVQKTSVTTQVRGTMGHIAPEYLS TGKSSERTDVF 408
201527 KAANVLLDEDFEPVVGDFGLAKLVDVQKTSVTTQVRGTMGHIAPEYLS TGKSSERTDVF 472
200981 KAANVLLDGNFEAVVGFGLAKMIDRERNTVTTGVRGTMGHIAPEYLSKTRPSVKTDIFG 470
210853 KASNVLLDEYFEAIVGDFGLAKLLDHRESHVTTAVRGTVGHIAPEYLS TGQSSEKTDVFG 492
215260 KAANILLDESFEAIVGDFGLAKLLDRQESHVTTAVRGTIGHIAPEYLS TGQSSEKTDVYG 485
206718 KAANVLLDECHEAVVGFGLAKLLDHGDSHVTTAVRGTVGHIAPEYLS TGQSSEKTDVFG 518
210165 -----
201844 AAGRGVRRRRRLRAGQAAGPPGVARHHGGAGHRRPHRAGVPVHGA VVGPDRRLRLRHPA 493
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213886 YGIMLLELITQRAFDLAR----LANDDDVMLLDWVKGLLKEKRLEMLVDPDLQSNY--- 542
210613 YGIMLLELITQRAFDLAR----LANDDDVMLLDWVKGLLKEKKVEMLVDPDLQSGF--- 547
211096 YGIMLFELISGKRGFDLVG----LANEENARVHDWVKKLEEDRLEVLIDPNLLEIYNGG 533
208902 YGIMLLELVTQRAIDFSR----LEEEDDVLLLDHVKKLQREGQLGAI VDRNLSSNYD-- 462
201527 YGIMLLELVTQRAIDFSR----LEEEDDVLLLDHVKKLQREGQLGSI VDRNLNQNYD-- 526
200981 YGVMLLEIVTGERAVFPEF----SEG DSEIMLNDQVKRLVQGGRLTDI VDHNLDTAYD-- 524
210853 FGVLLVELITGQKALDFGR----LANQ-KGGVLDWVKKLHQEKQLSMMVDKDLGSNYD-- 545
215260 FGILLLELITGPKTLSNGH----AQSQ-KGMILDWVREVKEENKLDKLVDRDLKYSFD-- 538
206718 FGILLLELVTQRALEVKGKS-GVIQH QKGVMLDWVRKVHQEKLHDL LVDQLGPHYD-- 575
210165 -----
201844 AGARHRPDGARVRQVVQPQGRHAGLGEEDAVGEEGGGAGGQGVRRRVRPGGGGGDGAGGS 553
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213886 ---IDVEVESLIQVALLCTQGSPTERPKMAEVVRMLEG-DGLAERWEEWQKIEVVRQEEV 598
210613 ---VEHEVESLIQVALLCTQGS PMDRPKMSEVVRMLEG-DGLAERWEEWQKVEVVRQEA 603
211096 EQGVREEMRLLVQIALLCTQESAPS RPRMSTVVTMLE--DGI AEHWDAWQRKTIVQASLQ 591
208902 ----GQEVEMMIQIALLCTQASPED RPSMSEVVRMLEG-EGLAERWEEWQQVEVTRRQDY 517
201527 ----DEEVEMMIQIALLCTQSSPED RPSMSEAVRMLEG-EGLAERWEEWQQVEVTRRQEY 581
200981 ----LQOLEKMIQIALLCTHVEPHLRPAMSEVVMLEGNVVP AEQWEEWQVAELARRHQH 580
210853 ----RVELEEMVQVALLCTQYYP SHRPRMSEVIRMLEG-DGLAEKWEASQNVDTPKSVSS 600
215260 ----FAELECSVDVILQCTQTNPIL RPKMSEVLNALEA-NVTLPE NGIDLNREVPPYGG 593
206718 ----RIEVAEMVQVALLCTQFQPSHRPRMSEVVRMLEG-DGLAEKWEANHRPAAMAAAA 630
210165 -----
201844 PLHPVPPRPPPHVRRRPHARGRRPRRPLGGLRPLHRRRRLPLPLP PHLRPGAARRRLR 613

213886 LGPHRNS--EWIVDSTDN-----LH AVELSGPR 624
210613 LAPRHN---DWIVDSTYN-----LRAME LSGPR 628
211096 GGQGV S---EARND SVAN-----LPPDT LSGPR 616
208902 ERMQQR--FDWGEDSIFN-----QEAI ELSAGR 543
201527 ERMQQR--FDWGEDSVYN-----QEAI ELSGGR 607
200981 EMNQQRRLFSFSEESLNI-----QEAIQLSSGR 608
210853 ELLPPKFMDFAADESSLG-----LEAME LSGPR 628
215260 CSFSVRHED-PHDS SFI-----IEPIELSGPR 620
206718 PHELG YDHRNDSNGSVFFNDFHDNDS SLSSEVRSIDMVEEMELSGPR 678
210165 -----
201844 RRLRPLLLRPHRRLLP RPGR-----ALRPQITPF-- 644
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